Total transcriptome, proteome, and allergome of Johnson grass pollen, which is important for allergic rhinitis in subtropical regions

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Background: Genomic data are lacking for many allergen sources. To circumvent this limitation, we implemented a strategy to reveal the repertoire of pollen allergens of a grass with clinical importance in subtropical regions, where an increasing proportion of the world's population resides.
Objective: We sought to identify and immunologically characterize the allergenic components of the Panicoideae Johnson grass pollen (JGP; *Sorghum halepense*).
Methods: The total pollen transcriptome, proteome, and allergome of JGP were documented. Serum IgE reactivities with pollen and purified allergens were assessed in 64 patients with grass pollen allergy from a subtropical region.
Results: Purified Sor h 1 and Sor h 13 were identified as clinically important allergen components of JGP with serum IgE reactivity in 49 (76%) and 28 (43.8%), respectively, of patients with grass pollen allergy. Within whole JGP, multiple cDNA transcripts and peptide spectra belonging to grass pollen allergen families 1, 2, 4, 7, 11, 12, 13, and 25 were identified. Pollen allergens restricted to subtropical grasses (groups 22-24) were also present within the JGP transcriptome and proteome. Mass spectrometry confirmed the IgE-reactive components of JGP included isoforms of Sor h 1, Sor h 2, Sor h 13, and Sor h 23.
Conclusion: Our integrated molecular approach revealed qualitative differences between the allergenic components of JGP and temperate grass pollens. Knowledge of these newly identified allergens has the potential to improve specific diagnosis and allergen immunotherapy treatment for patients with grass pollen allergy in subtropical regions and reduce the burden of allergic respiratory disease globally. (J Allergy Clin Immunol 2014;■■■:■■■-■■■.)

Key words: *Allergome, allergen components, allergic rhinitis, IgE, Johnson grass pollen, pollen allergy, proteome, transcriptome*

The incidences of allergic rhinitis (AR) and asthma have reached a plateau in developed nations, but the prevalence of allergic respiratory diseases shows greater variability in countries with emerging economies.[1] AR afflicts 500 million persons worldwide, adversely effecting patient health and quality of life.[2-5] The disease carries a substantial financial burden through lost productivity and increased health care costs.[6,7]

Grass pollen allergen sources vary according to climatic region, with subtropical grass pollens being more abundant in the subtropics.[8-10] Current demographic data indicate that the population of subtropical climates is increasing[11] and that tropical zones are widening polewards.[12] For example, the population in subtropical states of the United States is estimated at approximately 52.3 million, having increased by 18.3% between 2000 and 2010 (US Census Bureau for Florida, Louisiana, Mississippi, and Texas).[13] The contribution of subtropical grasses to allergic respiratory diseases, such as AR and asthma, is predicted to increase with global warming because of a competitive advantage for subtropical grass species over temperate grasses and a widening of their distribution.[14-16]

Airborne grass pollen levels affect hospital admissions for asthma.[17-19] However, most research has concentrated on the allergenicity of pollens from temperate grass species, such as timothy grass *(Phleum pratense)*.[20,21] Emerging evidence from subtropical regions indicates that subtropical pollen allergens show distinct immunologic reactivity from temperate grass pollens.[22-28] The allergenic molecules derived from the subtropical grass pollens characterized thus far differ considerably from homologous temperate grass pollen allergens in terms of amino acid sequence.[29,30] Johnson grass *(Sorghum halepense)*

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Abbreviations used
AR: Allergic rhinitis
2D: Two-dimensional
JGP: Johnson grass pollen
MS: Mass spectrometry
pI: Isoelectric point
SPT: Skin prick test

is a perennial weed of the Panicoideae subfamily of grasses that is distributed globally throughout the subtropics.[10,31,32] Although the 2 dominant pollen allergen components of Bahia grass *(Paspalum notatum)* have been determined[29,33] and allergen components of Bermuda grass *(Cynodon dactylon)* pollen have been extensively characterized, relatively little is known of Johnson grass pollen (JGP) allergens. We previously showed that 77% of patients with AR from a subtropical region of Queensland, Australia, were sensitized to JGP.[10] The sequence of the group 1 allergen of JGP, Sor h 1, has been described, and recombinant Sor h 1 reacted with a group 1–specific mAb.[34] However, allergic sensitivity of patients with grass pollen allergy to JGP has not been described. Here we investigate serum IgE reactivity of patients from a subtropical region with the dominant allergens purified from JGP based on the amount within the total pollen protein and observed IgE reactivity by using immunoblotting.

As with many clinically important allergen sources, the full genomic sequence of JGP is unknown. This can hamper implementation of in-depth molecular approaches to allergen discovery. We comprehensively analyze the proteome, transcriptome, and allergome of JGP using advanced molecular and bioinformatic techniques that do not rely on genomic data. This detailed approach provides a powerful and versatile data set of the clinically relevant allergen components within JGP and supports the future development of targeted immunodiagnosis and immunotherapies tailored to better meet the needs of patients with subtropical grass pollen allergy.

METHODS

Study participants

Participants were recruited consecutively from immunology or respiratory clinics at the Princess Alexandra Hospital, Brisbane, Australia, and regional parts of Queensland, Australia, with informed consent as approved by the Metro South Human Research Ethics Committee. Subjects were tested for allergic sensitivity to a panel of 10 common aeroallergen extracts, including Johnson, Bahia *(Paspalum notatum)*, Bermuda *(Cynodon dactylon)*, or Ryegrass *(Lolium perenne)* pollen extracts by using skin prick tests (SPTs; Hollister-Stier, Spokane, Wash), according to guidelines of the Australian Society for Clinical Immunology and Allergy.[10] The inclusion criteria for the group of patients with grass pollen allergy was a history of AR consistent with pollen allergy and an SPT response (>3 mm in diameter) to the pollen extract of at least 1 grass species (n = 64). Sera of 5 additional patients with AR from the temperate region of Melbourne were included in one assay. Nonatopic subjects with no history of allergic disease and no positive SPT response (n = 19) and subjects with histories of AR and asthma with SPT responses to allergens other than grass pollens, frequently house dust mite, cat dander, or *Alternaria* species, were included as control subjects (n = 23). Subjects less than 18 years of age and those receiving immunotherapy were excluded. Sera were obtained from participants by means of venipuncture.

One- and 2-dimensional gel electrophoresis and immunoblotting

JGP (Greer, Lenoir, NC) extracted in PBS was separated by means of 14% SDS-PAGE (10 μg per lane) and immunoblotted for mAb or serum IgE reactivity with the following modifications to published methods.[30] Immunoblots were incubated overnight with patient sera diluted 1:50 before incubation with rabbit anti-human IgE (Dako, Glostrup, Denmark) diluted 1:10,000 for 2 hours and subsequently goat anti-rabbit IgG–horseradish peroxidase conjugate (Promega, Madison, Wis) at 1:10,000 for 2 hours. IgE immunoblots were developed for 5 minutes by means of chemiluminescence (SuperSignal WestPico; Thermo Scientific, Rockford, Ill). Immunoblots probed with the mAbs 6C6[30] and AF6[35] were visualized by using standard 1,4-dichloronapthol development.[30]

JGP (50 μg per DryGel strip, pH 3-11; GE Healthcare, Uppsala, Sweden) was separated by charge and size by means of 2-dimensional (2D) gel electrophoresis and stained with Coomassie Brilliant Blue.[30] 2D gels of JGP were immunoblotted, as described above. 2D gels of JGP spiked with isoelectric focusing standard proteins were examined to determine the observed molecular weights and isoelectric focusing points of IgE reactive components.

Serum IgE reactivity with purified Sor h 1 and Sor h 13

The 2 dominant allergenic components of JGP were purified from an aqueous extract of JGP by means of ammonium sulfate precipitation, hydrophobic interaction, and size exclusion chromatography, as previously described.[33,36] Sera were tested for IgE reactivity with whole JGP extract (5 μg/mL) and purified allergens (1 μg/mL) by means of ELISA.[30]

Statistical analysis

Data were assessed for normality by using the Kolmogorov-Smirnov test. Differences between groups were assessed by using the Mann-Whitney *U* test for nonparametrically distributed data. Within-group differences were assessed by using the Wilcoxon signed-rank test for paired data. Correlations were determined with the Spearman rank test for paired data. *P* values of less than .05 were considered significant.

Transcriptome sequencing

Total RNA was extracted from pollen and treated with DNAse.[37] mRNA sequencing was performed with the Illumina RNA-seq pipeline by the Beijing Genomics Institute (Shenzhen, China). The total JGP transcriptome sequence assembly and analysis methods are detailed in the Methods section in this article's Online Repository at www.jacionline.org.

JGP allergens were deduced by means of comparison of translated JGP transcripts to the comprehensive allergen database Allergome.org (January 2014; www.allergome.org[38]) through BLASTP software.[39]

Mass spectrometry

Thirty micrograms of whole JGP extract was separated on SDS-PAGE into 8 × 1–mm bands. Liquid handler–assisted in-gel digest and shotgun proteomics analysis was performed by using an Agilent 6510 QTOF coupled with an HPLC-ChipCUBE.[40] Protein spots cut from Coomassie-stained 2D gels were processed similarly. The resulting mass spectrometry (MS)/MS spectra were searched against specified databases by using Spectrum Mill (Agilent B.04.00.127; Agilent, Technologies, Santa Clara, Calif). Cysteine carbamidomethylation and methionine oxidation were selected as fixed and variable modifications, respectively. Precursor and product mass tolerance were set to ±20 ppm and ±50 ppm, respectively. The peptide cutoff score was set to 9.

Proteome and allergome analysis

In the absence of knowledge of the Johnson grass genome, the mass spectra of tryptic digest peptide fragments observed in whole JGP and excised

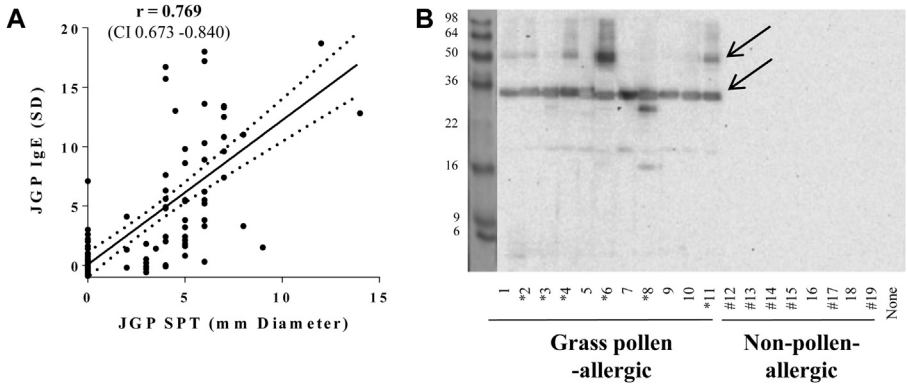


FIG 1. Allergic sensitivity to JGP allergens. **A,** Correlation between SPT response (millimeters in diameter) to commercial JGP extract and serum IgE to in-house JPG extract. IgE ELISA data are shown as the number of SDs above the mean of nonatopic donors shown in Fig 3. Spearman correlation and 95% CIs are shown. **B,** IgE immunoblots of JGP probed with sera from patients with grass pollen allergy with symptoms of AR and a positive SPT response to JGP *(1-11)* and control subjects without pollen allergy *(12-19)*, 2 of whom had house dust mite allergy (*15* and *18*), and 6 of whom were nonatopic. Molecular weights are shown in kilodaltons. *Arrows* mark major allergen components. *None*, No serum control. *Included in the serum pool from patients with JGP allergy in Fig 2. #Included in the serum pool from subjects without pollen allergy.

IgE-reactive spots were searched against all possible peptides predicted from all 6 reading frames of the transcriptome assembly (see the Methods section in this article's Online Repository).

The coverage of peptide spectra from the IgE-reactive spots were mapped against the predicted protein sequences from the relevant reading frame by using GENEIOUS (www.biomatters.com). Signal peptides were predicted with SignalP 4.1 (http://www.cbs.dtu.dk/services/SignalP/) and, if present, were excluded from calculations of isoelectric point (pI) and molecular mass. Where peptides were compared with multiple predicted proteins, alignments were performed with MUSCLE[41] in the GENEIOUS software environment. Measurement of molecular mass and the pI of predicted peptides from the JGP transcriptome was performed by using ExPASy proteomic tools (www.expasy.org).

The predicted peptide repertoire of JGP was used to identify putative allergen sequences by means of BLASTP 2.2.27 search of all allergen protein sequences in the Allergome.org database.[38] Matches were filtered for those expressed in the proteome, with a query length of more than 50 amino acids, percentage identity of 30% or greater (identities/[align length-gap length]), alignment of greater than 30% of the query length ([align length-gap length]/query length), and relevance to grass pollen (see the Methods section and Table E1 in this article's Online Repository at www.jacionline.org).[42,43]

Dendrograms of selected nonredundant grass pollen allergen sequences from Allergome.org and the predicted protein sequences from JGP were constructed by using ClustalW.[44]

RESULTS

Allergenic components of JGP for patients from a subtropical region

Serum IgE to JGP extract was highly correlated with JGP SPT response ($r = 0.769$, $P < .0001$; Fig 1, *A*) for the panel of 106 subjects, including 64 with grass pollen allergy, 23 with allergies other than grass pollen, and 19 nonatopic control subjects (Table I). Sera from all 11 randomly sampled patients with AR from Queensland with positive SPT responses to JGP showed IgE reactivity with a 30-kDa component of JGP, as determined by means of immunoblotting. This 30-kDa component is consistent in size with the known group 1 allergen Sor h 1 (Fig 1, *B*). Five of these 11 patients showed IgE reactivity with a component at 55 kDa. Patients with JGP allergy also showed IgE reactivity with other allergenic components at 28, 18, and 16 kDa (Fig 1, *B*). Eight randomly sampled participants without pollen allergy had no IgE with any JGP components.

TABLE I. Clinical characteristics and demographics of subjects

Parameter	Nonatopic	Grass pollen allergy	Other allergies
Subjects (no.)	19	64	23
Age (y), median (IQR)	33 (27.3-46.3)	36.5 (28.8-44.5)	37.5 (31.5-50.3)
Sex, female (%)	84	70.3	65.2
JGP SPT response, median (IQR)	0 (0-0)	5 (4-6)	0 (0-0)
AR (%)	0	89.1	68.2
Physician-diagnosed asthma (%)	15.8	45.3	68.2

IQR, Interquartile range.

IgE reactivity was detected with 18 of the 47 protein components of JGP separated by means of 2D gel electrophoresis (Fig 2, *A*) with serum pooled from patients with JGP allergy (Fig 2, *B*) but not from the donors without pollen allergy in Fig 1 (data not shown). Three proteins with neutral pI (6.3, 6.8, and 7.1) at 30 kDa reacted with patient IgE and with the 6C6 mAb to the group 1 allergen of Bermuda grass pollen (Cyn d 1),[30] confirming these to be isoforms of Sor h 1. An additional basic isoform of Sor h 1 present at a low amount (spot 3; Fig 2, *A*) showed reactivity with the 6C6 mAb (Fig 2, *C*) and weak IgE reactivity (Fig 2, *B*). Six spots with pIs from 5.7 to 7.6 at 54 to 55 kDa were IgE reactive with the JGP-allergic serum pool (Fig 2, *B*) and a group 13 allergen-specific mAbs[35] and were designated as Sor h 13 (Fig 2, *D*). Additional undetermined IgE-reactive spots at 28, 26, 18, and 16 kDa were observed.

Serum IgE reactivity with dominant allergenic components of JGP

Sor h 1 and Sor h 13 were each purified to a single protein band (Fig 3, *A*). Patients with grass pollen allergy had significantly higher serum IgE reactivity with Sor h 1 than the nonatopic and other allergy control groups (Fig 3, *B*). IgE reactivity with JGP and Sor h 1 was highly correlated ($r = 0.969$, $P < .0001$;

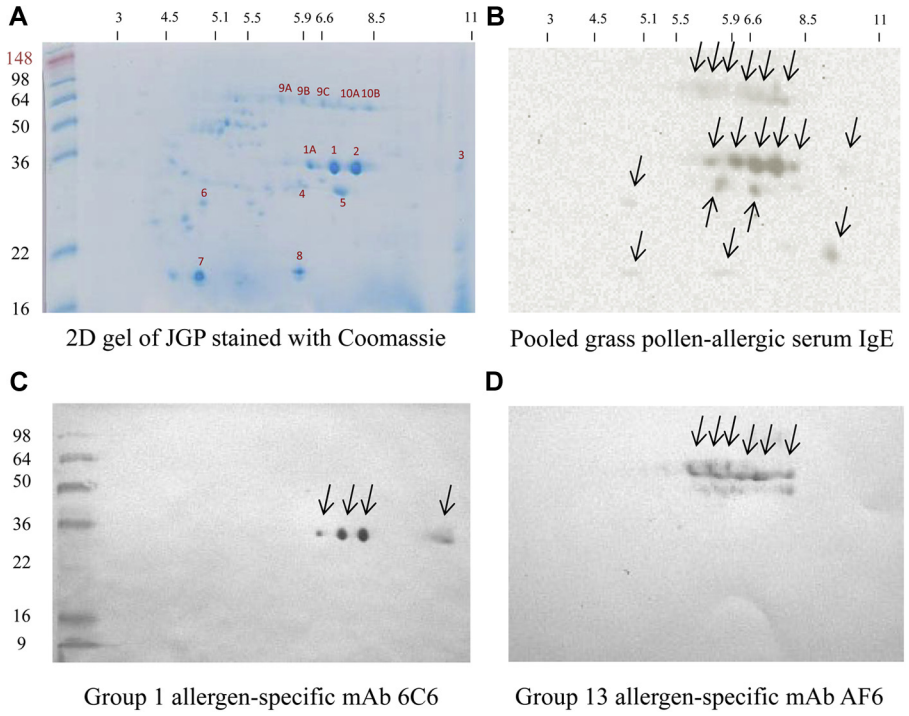


FIG 2. Identification of JGP allergenic components. **A,** 2D gel electrophoresis of JGP stained with Coomassie Blue. Numbers refer to spots excised for proteomics. 2D IgE immunoblots of JGP probed with a serum pool from patients with JGP allergy. **B,** Patients from Fig 1. *Arrows* mark IgE-reactive components. A replica immunoblot with a pool of sera from nonatopic subjects from Fig 1 showed no IgE reactivity (data not shown). **C** and **D,** Specific mAb. Sor h 1 and Sor h 13 isoforms are marked.

Fig 3, *D*). The frequency of IgE reactivity with purified Sor h 1 (49/64 [76%]) in sera from a patient with grass pollen allergy was higher than with JGP (Fig 3, *F*). JGP SPT response was highly correlated with IgE to Sor h 1 ($r = 0.790$, $P < .0001$; Fig 3, *G*).

Serum IgE with Sor h 13 was detected in 28 (43.8%) of the 64 donors with grass pollen allergy (Fig 3, *C* and *F*). IgE reactivity with Sor h 13 was significantly higher in the patients with grass pollen allergy than in the nonatopic and other allergy control groups (Fig 3, *C*). IgE reactivity with Sor h 13 and JGP was strongly correlated ($r = 0.769$, $P < .0001$; Fig 3, *E*), but the level of IgE reactivity with Sor h 13 in the group with grass pollen allergy was lower than with JGP (Fig 3, *C*). The JGP SPT response was highly correlated with IgE to Sor h 13 ($r = 0.451$, $P < .0001$; Fig 3, *H*).

Identification of potential allergens within JGP

The total JGP pollen transcriptome was sequenced and assembled into 17,356 distinct transcripts comprising gene products and isoforms thereof (Fig 4 and see the Results section in this article's Online Repository at www.jacionline.org). The JGP transcriptome had 76.4% identity with the closely related crop species *Sorghum bicolor*, 10.4% with *Zea mays*, and 8.6% with *Oryza sativa* (see Fig E2 in this article's Online Repository at www.jacionline.org).

Multiple transcripts matching known allergens of temperate grass pollens 1, 2, 4, 7, 11, 12, and 13 were observed in the JGP transcriptome (see Table E2 in this article's Online Repository at www.jacionline.org). Additionally, allergen groups specific to the subtropical grass pollens 22 and 23 were identified. Tandem MS of the tryptic digest of total JGP revealed 2522 spectra that matched sequences from a nonredundant plant database (see Tables E3 and E4 in this article's Online Repository at www.jacionline.org). However, a larger number of spectra (n = 5861) could be matched to protein sequences predicted from the total JGP transcriptome (Fig 4 and see Tables E5 and E6 in this article's Online Repository at www.jacionline.org). Within the proteome of whole JGP, multiple peptides matching grass pollen allergen groups 1, 2, 4, 10, 11, 12, 13, and 22, as well as other pollen allergen families (isoflavone reductase, heat shock protein 70, glucanase, chitinase, pectinesterase inhibitor, pathogenesis related protein 1A, and cyclophilin), were observed (see Tables E3 and E5).

The potential allergome (ie, the complete allergen repertoire) of JGP was deduced by comparison of the JGP transcriptome with the Allergome.org database. Particular JGP transcripts repeatedly matched multiple related Allergome.org sequences, revealing 41,946 matches (Fig 4). Sequence matches were filtered for their presence in the JGP proteome and relevance to grass pollens, yielding 1,110 matches to Allergome.org. There were 45 JGP transcripts relevant to 15 pollen allergen families identified (Table II[42,43,45] and see Table E7 in this article's Online Repository at www.jacionline.org). Notably, among the 1602 Allergome.org sequences with no match to JGP were 25 sequences for group 5 and 6 grass pollen allergens (Fig 4). Five low-identity (31% to 35%) matches with putative allergen transcripts for Aeg ta 5 (goatgrass; *Aegilops tauschii*) and 1 with Phl p 6 were discovered (Table II), but these transcripts more closely matched group 23 allergens (Table II and see Fig E6, *C*, in this article's Online Repository at www.jacionline.org).

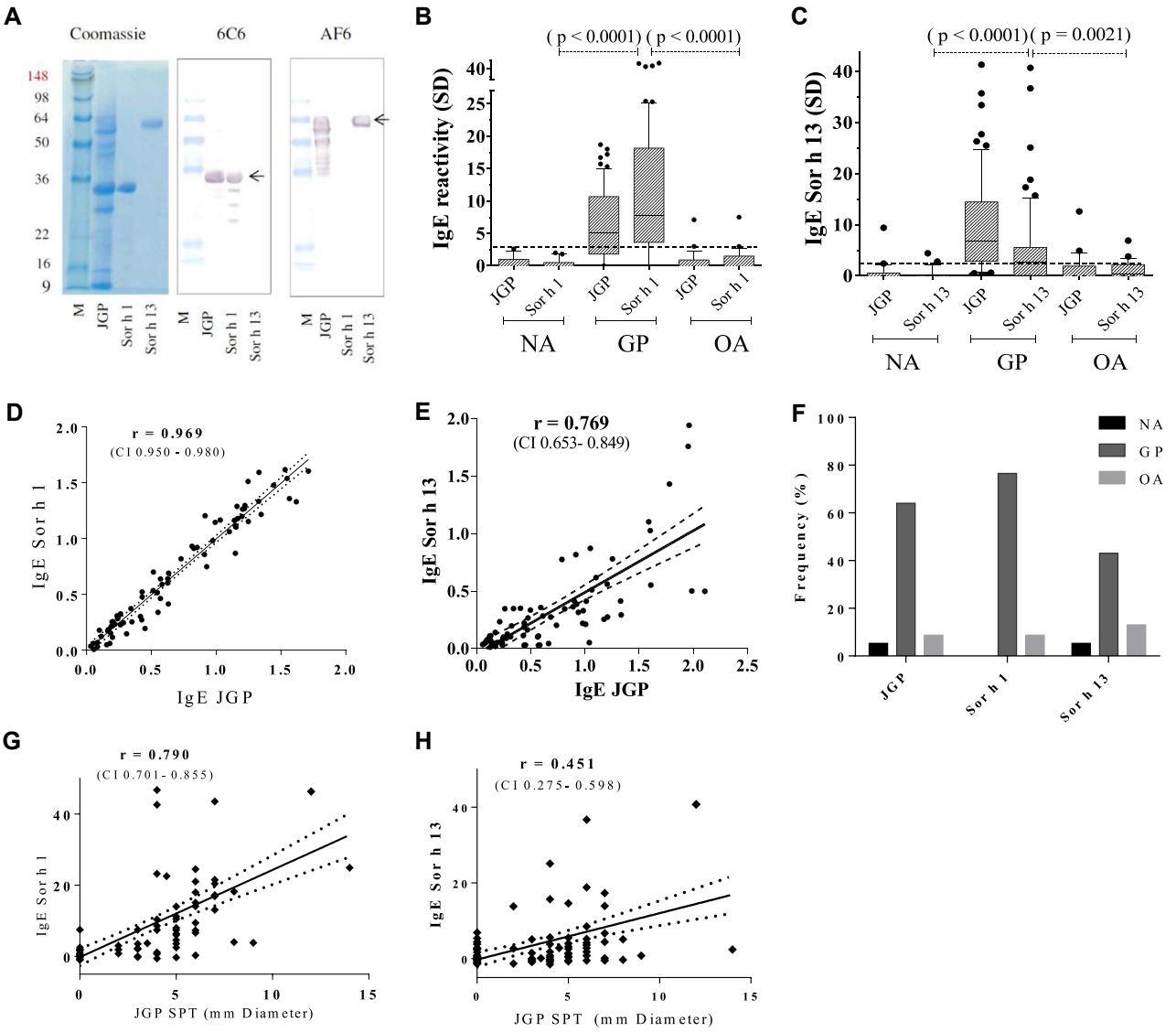


FIG 3. Serum IgE reactivity with Sor h 1 and Sor h 13. **A,** Purified JGP allergens stained with Coomassie blue and immunoblotted with mAb specific to group 1 and group 13 allergens (marked). **B** and **C,** IgE reactivity normalized to nonatopic *(NA)* donors. *Box,* Median and interquartile range; *whiskers,* 10th to 90th percentiles. The cutoff of 3 SDs above the mean of 23 nonatopic subjects is shown for JGP (OD = 0.410) and Sor h 1 (OD = 0.229) in Fig 3, *B,* and for JGP (OD = 0.371) and Sor h 13 (OD = 0.384) in Fig 3, *C. P* values were determined by using the Mann-Whitney *U* test. **D** and **E,** Spearman (with 95% CIs) correlation for IgE reactivity with JGP and Sor h 1 (Fig 3, *D*) and Sor h 13 (Fig 3, *E*). **F,** Frequency of IgE reactivity with JGP, Sor h 1, and Sor h 13. *GP,* Patients with grass pollen allergy; *OA,* subjects with allergies other than grass pollen.

Identification of IgE-reactive components of JGP

The 18 IgE-reactive components of JGP (Fig 2, *B*) matched 4 allergen families (Fig 4). The high percentage of coverage (44.8% to 78.2%) by peptide spectra detected by means of MS of excised IgE-reactive protein spots (Fig 2, *A*) and purified Sor h 13 allergen fractions A and B (see Fig E3 in this article's Online Repository at www.jacionline.org) provided good evidence that the identified sequences corresponded to the expressed protein (Table III and see Table E8 in this article's Online Repository at www.jacionline.org). The observed size and charge of IgE-reactive protein spots were similar to the peptide predicted from the encoding transcript (allowing for glycosylation) and allergen homologs, with the exception of Sor h 23, for which the observed size was larger than its closest matching allergen homolog, Cyn d 23 of Bermuda grass pollen (Table III and see Table E2), suggesting it markedly differs from Cyn d 23.

The predicted peptide of the transcript CL153.1 (Sor h 1.0101) showed 99% identity with the previously published Sor h 1 sequence,[34] validating the experimental strategy of combining transcriptomic and proteomic data in the absence of genomic data. A second group 1 allergen isoform designated Sor h 1.0201 was encoded by concatenation of 2 overlapping transcripts (see Fig E4 in this article's Online Repository at www.jacionline.org). These Sor h 1.0101 and Sor h 1.0201 isoforms are likely to be encoded by separate loci given that their

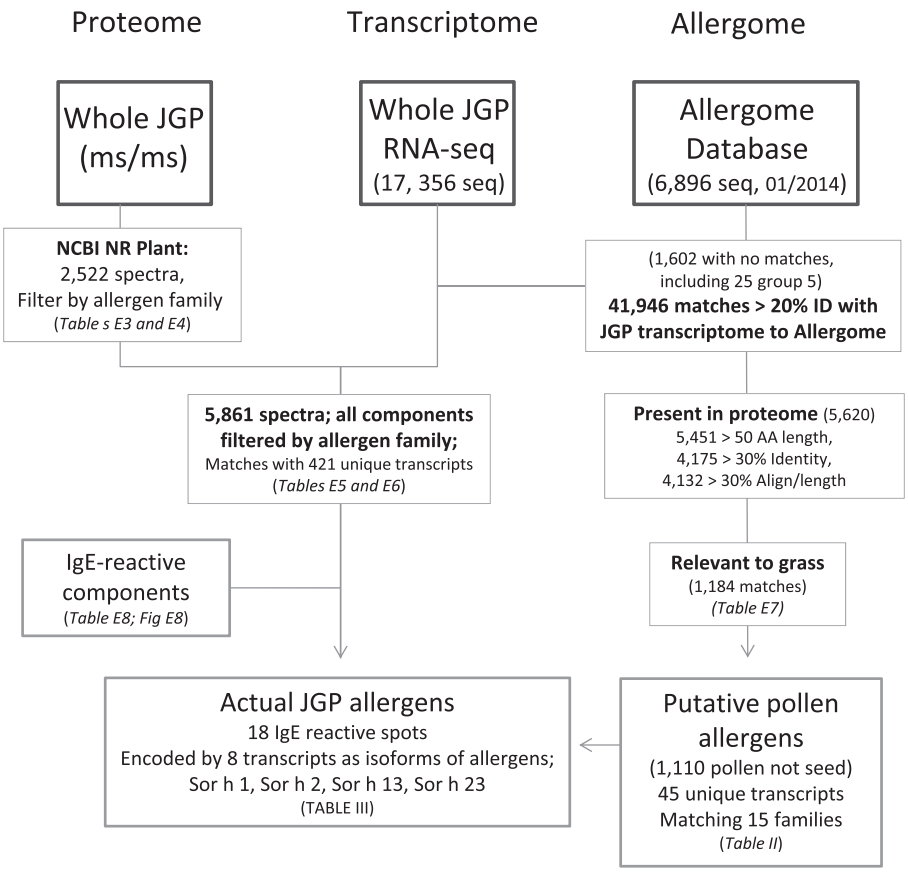


FIG 4. Analysis pipeline for the total JGP proteome, transcriptome, and allergome. Data file names of raw results and summaries for each step toward deducing the actual IgE-reactive allergen components and putative allergens of JGP are given. The number of entries in each data set are specified. *ms/ms*, Tandem mass spectrometry; *NCBI*, National Center for Biotechnology Information; *NR*, nonredundant plant database; *seq*, sequence.

charges (pI) differ (Table III) and their predicted peptide sequences share only 57% amino acid identity and 73% similarity, respectively (see Fig E5 in this article's Online Repository at www.jacionline.org). Moreover, these 2 isoforms aligned to separate branches of a dendrogram of group 1 grass pollen allergens (see Fig E6 in this article's Online Repository at www.jacionline.org).

Two IgE-reactive protein spots were identified as group 2 allergens (Sor h 2.01 and Sor h 2.02, Table III). A third IgE-reactive component matched the size and pI of the closely related mRNA transcript CL1122.2. Although there was insufficient protein in the 2D gel to examine its peptide spectra directly, the protein corresponding to this transcript was detected in the proteome of whole JGP (see Table E6). Although these 3 isoforms of Sor h 2 share between 48% and 63% identity with each other (see Table E9 in this article's Online Repository at www.jacionline.org), they clustered together in a dendrogram near Panicoideae homologs of group 2 allergens and were distinct from other types of β-expansin pollen allergens of groups 1 and 3 (see Fig E7 in this article's Online Repository at www.jacionline.org). Their identity with homologous subtropical grass pollen allergens was higher (50% to 75%) than with temperate allergens (Phl p 2/3, 24% to 31%, see Table E9).

Two polygalacturonase allergen components were designated isoforms Sor h 13.0101 and Sor h 13.0201, respectively (Table III). Mapping of the unique peptide spectra observed within purified Sor h 13 fractions A and B confirmed the presence of both transcripts (CL1737.1 and CL1737.2) in the JGP proteome (Table III and see Figs E8 and E9). The 3 predicted asparagine glycosylation sites in both sequences are suspected to account for the discrepancy in predicted and observed size (Table III and see Table E2). Although Sor h 13.0101(A) and Sor h 13.0201(B) showed high homology (86% to 88% amino acid identity) with group 13 allergens of subtropical grass pollens, their identity with Phl p 13 was markedly lower (38.3% to 68.8% identity; see Fig E6, *B*, and Table E10 in this article's Online Repository at www.jacionline.org).

The 2 IgE-reactive proteins of 28 kDa with pIs of 6.9 (spot 4) and 5.7 (spot 5), respectively, showed the closest sequence match to the allergen Cyn d 23 (Fig 2, *B*, and Table III). An allergen homolog of group 5 or 6 allergens was not detected in the IgE-reactive components of JGP. Whereas 4 of 5 sera of patients with AR from Melbourne, Australia,[30] and 8 of 13 patients with grass pollen allergy from Queensland showed IgE reactivity with Lol p 5 of *Lolium perenne* pollen by means of immunoblotting, none of these sera showed IgE reactivity with an equivalent band in *S halepense* pollen (see Fig E9 in this article's Online Repository at www.jacionline.org). An allergen homolog was not identified for IgE-reactive spot 6.

TABLE II. Putative allergen components of JGP: matches between JGP transcripts expressed in JGP proteome and grass pollen allergen sequences in the Allergome database

Allergen family	JGP transcripts	Protein family	Chloridoideae	Panicoideae	Ehrhartoideae	Pooideae
1	CL153.1, UG493, UG492, UG335, UG551	β-Expansin	41	49	49	130
2/3	CL1122.1, CL1122.2, CL1695.1	C-terminal β-expansin	4	66	160	98
4	UG808	Reticuline oxidase–like protein	1	1	0	17
5/6	UG397, UG1403, CL2015.1, CL962.1	Ribonuclease				6
7	CL1715.1, UG451, UG681, UG832	Polcalcin	22	22	7	28
11	CL1754.1, Cl2052.1, UG540, UG578, UG595	Glucuronosyltransferase	0	24	4	16
12	UG1043, UG308, UG342	Profilin-A	2	54	6	52
13	CL1737.1, CL1737.2, CL248, CK986.1, UG1334, UG332, UG552, CL110.1	Exopolygalacturonase	0	168	10	23
15	UG551, CL153.1, UG492, CL1122.1, CL1122.2, CL1695.1		6	0	0	0
22	CL70.1	Enolase 1	**1**	**1**	0	0
23	UG397, CL962.1, CL2015.1, CL2015.2, CL1403	Unknown	**5**	0	**6**	0
24	CL830.1	Pathogenesis-related protein 1A	**1**	0	0	0
25	CL1152.1, UG2745, UG5446, UG6038, UG6635, UG7876	Thioredoxin H-type	0	9	0	11
12pT	CL1444.1, CL200.1	β-Fructofuranosidase	0	0	0	4
	UG9701, UG11756	Chitinase		1		5
Total matches			83	395	242	390

Matches between peptides predicted by translation of JGP transcriptome in all 6 reading frames and allergen sequences in Allergome.org are shown. Matches were filtered for those JGP transcripts expressed in the proteome, with a query length of greater than 50 amino acids, percentage identity of 30% or greater (Identities/[Align length-gap length]), and alignment of greater than 30% of the query length ([Align length-gap length]/Query length). The number of matches with grass pollen allergens[42,43,45] (after exclusion of allergens restricted to seed or other tissue) within each subfamily and the corresponding JGP transcripts are given. Those matches specific to subtropical grasses are shown in boldface.

TABLE III. Characteristics of IgE-reactive molecular allergen components of JGP

Spot	Allergen designation (GenBank accession)*	JGP transcript	Predicted pI/MW (kDa)	Observed pI/MW (kDa)	No. of spectra	Peptide coverage (%)
1	Sor h 1.0101 (KF887425)	CL153.1	7.04/25.8‡	6.8/28	63	78.2
2	Sor h 1.0101	CL153.1	7.04/25.8‡	7.1/28	64	78.2
3	Sor h 1.0201 (KF887426)	UG 493/492	9.13/26.5‡	10.5/30	11	76.1
4	Sor h 23	CL2015.1	6.22/22.2	5.7/29	43	66.2
5	Sor h 23	CL2015.1	6.22/22.2	6.9/29	19	73
6	ND	UG388	5.06/19.0	5.0/25	17	56.8
7	Sor h 2.02 (KF887428)	CL1695	5.07/10.2	4.9/12	57	44.8
8	Sor h 2.01 (KF887427)	CL1122.1	6.19/10.4	5.9/12	571	67.4
8A	Sor h 2.03	CL1122.2	9.35/10.5	10/16		
9	Sor h 13.0101† (KF887429)	CL1737.1	6.59/41.6‡	5.7-6.6/55	568	56.3
10	Sor h 13.0201† (KF887430)	Cl1737.2	7.84/40.5‡	7.0-7.6/54	58	56.5

MW, Molecular weight; *ND*, not determined.
*Sequences matching recognized allergen components were submitted to GenBank.
†MS was performed on purified group 13 allergen bands (see Fig E3).
‡Asparagine glycosylation sites within sequence.

DISCUSSION

Knowledge of the unique repertoire of allergen components of subtropical grasses has the potential to improve the accuracy of immunodiagnosis and efficacy of allergen-specific immunotherapy for patients in warmer regions of the world, who are primarily sensitized to subtropical grass pollens. Our innovative approach of integrating proteomic and whole-transcriptome sequencing technologies in the absence of genomic data with serologic analysis has allowed a comprehensive picture of the diversity of JGP allergen components.

We demonstrated that Sor h 1 is a major and clinically significant allergen of JGP for patients with AR in a subtropical region. The sequence of a basic isoform of Sor h 1 that closely matched other major Panicoideae pollen allergens, Pas n 1[30] of Bahia grass and Sor b 1 of *S bicolor*,[25,46] was discovered. The higher frequency in patients with grass pollen allergy of serum IgE specific for Sor h 1 than JGP extract and the strong correlation between Sor h 1 IgE and JGP IgE suggest that Sor h 1 has potential to provide for more sensitive diagnosis of JGP allergy than JGP extract. The purification of Sor h 13, presence of IgE reactivity in 43.8% of patients with grass pollen allergy, and detection of 2 IgE-reactive isoforms expressed within the transcriptome and proteome confirm the presence of this allergen family in JGP. Although Sor h 13 was the second most IgE-reactive allergen of JGP, further investigation is required to determine whether this allergen would qualify as a major allergen for relevant patient populations exposed to JGP. Although it had been thought that group 2 allergens were not present in pollen of subtropical

grasses,[47,48] for the first time, we document multiple sequences encoding IgE-reactive isoforms of Sor h 2 in JGP.

Of note was the lack of evidence for grass pollen group 5 allergens within JGP, despite this comprehensive immunologic and molecular analysis. These findings are consistent with the reported absence of group 5 allergens in subtropical grass pollens.[30,47,49-51] However, low-identity matches with transcripts from a wild diploid progenitor species of wheat *(Aegilops tauschii)* that are listed in Allergome.org as group 5 allergens (Aeg ta 5), and transcripts encoding Sor h 23 were observed. Although Aeg ta 5 has not been confirmed as an allergen by the International Union of Immunological Societies and the homologies with Sor h 23 are low, this observation might suggest a protein superfamily relationship between group 23 allergens of subtropical grass pollens and group 5 (or 6) allergens of Pooideae grass pollens. The absence of a group 5 allergen has implications for standardization of JGP and other subtropical grass pollen extracts for diagnosis and immunotherapy because group 5 allergens are currently the benchmark for allergen content in grass pollen extracts.[52] Further studies are required to quantify the frequency of IgE reactivity to Sor h 2 and Sor h 23.

Several IgE-reactive isoforms of Sor h 1, Sor h 2, Sor h 13, and Sor h 23 were observed. Multiple transcripts encoded β-expansins and polygalacturonases within the transcriptome and proteome of JGP, but only a few of these showed IgE reactivity. Post-translational modifications, alternative splicing of mRNA, and paralogous loci are likely to contribute to isoform diversity within these allergen families. Differences in expression levels and primary sequences of protein isoforms might affect allergenicity and epitope recognition by T and B cells.[23,26,27] Further studies are required to compare the structure and immunologic recognition of proteins within a given family with and without detectible IgE reactivity. Such studies could inform properties of the allergenic components that confer IgE reactivity to certain proteins and not other members of the same biochemical family.

JGP contained molecules identified as allergens in other sources, including berbine bridge oxidase, polcalcins, extensins, profilins, and enolase, with which IgE reactivity was not observed. That IgE reactivity was not detected with these components might be due to the level of protein expression within mature pollen or sensitivity of the IgE immunoblot. It is also possible that the sample size of the study population was too small to reveal IgE reactivity with minor allergens. In patients primarily exposed to temperate grass pollens, most of these proteins (eg, Phl p 7, [polcalcin] and Phl p 12 [profilin]) are minor allergens.[53-56] Similarly, polcalcin was not identified as an allergen in proteomic studies of Bermuda grass or ryegrass *(L perenne)* pollen.[45,57] The importance of these proteins as potential JGP allergens, particularly those with homology to allergens described in other subtropical grass pollens (Cyn d 22 [enolase] and Cyn d 4 [reticuline oxidase][57]) needs to be determined in larger patient populations from other subtropical regions where JGP is an important pollen allergen source, such as the southern United States, Australia, South Africa, and India. Additionally, comparative evaluation of sera from patients in temperate regions without exposure to JGP (eg, Europe and parts of North America) for IgE reactivity with these subtropical grass pollen allergens could deepen our understanding of the specificity of allergen recognition at a molecular level.

Although several transcriptomic or proteomic studies describe repertoires of putative allergens of important grasses/cereals,[35,45,57-60] our study makes several methodological advances. First, we used a strategy that allowed us to discern putative allergens within the pollen proteome based on the pollen transcriptome without the costly and technically demanding acquisition of a whole genome sequence. Second, our systematic molecular and bioinformatics approach revealed the full potential repertoire of allergenic components of JGP based on the Allergome.org database. Within the proteome and transcriptome of the analyzed mature JGP pollen sample, the relevant developmental stage of pollen to which persons are exposed, we were able to detect more than 17,000 transcripts and identify a wide range of putative allergen components from 15 protein families. However, the expressed pollen allergen repertoire might well be affected by varying environmental conditions[61] or stages of pollen maturation and could be expanded with further analysis. Knowledge of the broader putative allergome of JGP enables future analysis of the "immunome" of JGP, as recently reported for timothy grass pollen.[62] However, currently, the allergome of JGP should include those components for which IgE reactivity was demonstrated in clinically relevant patients, namely Sor h 1, Sor h 13, Sor h 2, and Sor h 23.

The newly identified molecular allergenic components of JGP identified here will have global utility to customize the diagnosis and treatment of subtropical grass pollen allergy. There is evidence for subfamily-specific IgE[10,25,28,30] and T-cell epitope[26,27] recognition of subtropical grass pollen allergens. Thus adequate representation of the allergen components of subtropical grass pollens is likely to increase the efficacy of allergen-specific immunotherapy over treatment with extracts of temperate grass pollens for patients primarily allergic to subtropical grass pollens.

Knowledge of the total JGP transcriptome, proteome, and allergome provides the basis for standardizing diagnosis and targeted specific immunotherapy for patients who are primarily sensitized to subtropical grass pollens. Our combined molecular and bioinformatics approach is amenable for discovery of unknown allergenic components of diverse sources for which the genome has not been determined.

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Clinical implications: Allergy to subtropical grass pollen is a global problem likely to increase with climate and demographic change. Identification of major allergen components within clinically relevant subtropical grass pollens will facilitate improved diagnosis and targeted immunotherapy outcomes.

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Supplementary material

Supplementary methods

Quality of JGP transcriptome sequencing.

The quality of RNA extracted from JGP was visualised by agarose gel electrophoresis and confirmed using an Agilent 2100 Bioanalyzer (Santa Clara, CA, USA). The RNA Integrity Number value was 8.7. The concentration of RNA was measured using a NanoDrop 8000 Multi-Sample Micro-Volume UV-Vis Spectrophotometer (Thermo Fisher Scientific, WilmingtonDE, USA). Sequencing of the JGP transcriptome [*Sorghum halepense* (L.) Pers, 2n = 2x = 40], yielded a total of 44, 686, 994 raw and 39, 503, 924 clean reads with a Q20 quality score of 96.54% (**FIG E1**). Transcriptome assembly identified 56, 319 contigs and 22, 223 unigenes (**FIG E1**).

Transcriptome assembly

De novo transcriptome assembly was carried out with the short reads assembly program - Trinity.[E1] Once assembled, a BLASTX [E2] alignment (*e*-value < 0.00001) between Unigenes and protein databases NCBI-nr [E3], Swiss-Prot [E4], KEGG [E5] and COG [E6] was performed. The transcripts with the best alignment scores were used to inform Unigene sequence direction and functional annotation. Conflicting database results were resolved using the priority order of nr (non-reductant genbank sequences), Swiss-Prot, KEGG, COG and manual data curation when deciding sequence direction of Unigenes. When a Unigene could not be aligned to any of the above databases, ESTScan was utilised to determine the expressed region. [E7]

Comparison of JGP predicted peptides to Allergome.org sequences

A set of predicted peptide sequences were constructed from the total JGP messenger RNA transcriptome assembly that was translated in all six frames by sequentially running the total JGP transcriptome library through the Sequence Manipulation Suite (SMS; http://www.bioinformatics.org/sms2/translate.html). A concatenated file containing all six

frames of possible peptides was then compared to grass pollen allergen protein sequences in Allergome.org detected by BLASTP 2.2.27+ with a Blossom 62 amino acid substitution matrix and gap opening penalty of 11 and gap extension penalty of 1. [E8] A list of the grass species names from Allergome.org sequences is found in **Supplementary TABLE E1**.

Comparison of JGP predicted peptides to observed peptide spectra

Spectrum Mill MS Proteomics Workbench (Agilent) was used to compare observed peptide spectra against the peptide sequences of the NCBI non-redundant plant database and the predicted peptide sequences deduced from the total JGP transcriptome library translated into all 6 possible reading frames.

Phylogenetic analysis of allergen groups

Dendrograms of selected Allergome.org sequences and the predicted protein sequences from the JGP transcriptome were constructed using ClustalW within GENEIOUS (www.biomatters.com). Redundant Allergome.org entries with identical sequences were removed. Multiple non-redundant entries with the same name within Allergome.org were augmented with a number at the end of their sequence name to delineate between sequences.

Supplementary Results and Discussion

Purified Sor h 13 fractions A and B

Two fractions of Sor h 13 were derived during the purification from JGP extract (**FIG. E3**). Sor h 13 A was eluted earlier from the hydrophobic interaction chromatography and had a higher apparent molecular weight of 55kDa than Sor h 13 B that was observed at 54 kDa. Sor h 13A was further purified by size exclusion chromatography and used for the ELISA determination of IgE reactivity in serum of patients with grass pollen allergy. As it was possible that Sor h 13B was a variant of Sor h 13 A arising from separate genes, alternative splicing of mRNA, post-translation modification or truncation due to proteolysis, we subjected Sor h 13 samples A fraction 1 and B fraction 3 to mass spectrometry.

Identification of allergens within the proteome and transcriptome of JGP

β-expansin related allergens

The β-expansin proteins comprise the group 1 pollen allergen family, yet share sequence similarity with members of the group 2, 3 and 15 allergens as well. The β-expansin protein family are cell wall loosening enzymes found in the cell walls of most plant tissues. [E9] Sor h 1 is a β- expansin, with a sequence identity with Phl p 1 (P43213.1), of 73%. Further, all cDNA transcripts for Sor h 1 displayed a predicted signal peptide, as well as a putative N-glycosylation site at position 10 characteristic of β-expansins. Typical β-expansin domains, rare lipoprotein A (Rlp-A-)-like double-psi beta barrel motif were predicted.

Within the JGP transcriptome, 51 different cDNA transcripts matching Sor h 1 transcripts were identified, with representatives matching several different sub-families of expansins (B11, A32, A26, B9, B1, B4, B7). Of the 51 cDNA transcripts, 5 were recognized as isomers of each other and the IgE reactive proteins were closely related to the B11 and B9 sub-family of expansins in maize. Both isomers had highly abundant transcripts which were present in the proteome. In fact, MS data revealed that only 9 cDNA transcripts encoding expansins were actively translated into protein and the transcript abundance ranged from 33,574 to 2351 reads per kilobase /million (RPKM) [E10] (**Table E2** and **II**).

A pair of sequences (UG493 and UG492) encoded polypeptides with high similarity to group 1 allergens. UG493 matched the amino (99% identity over amino acids 1-159) and UG492 matched the carboxyl terminus (98% identity over amino acids 158-266) of a *S. bicolor* sequence (XP_002467539) with an 8 nucleotide overlap, suggesting these sequences are encoded by the one transcript (UG 493/492) (**Suppl. FIG E4**).

Sor h 2 are clearly related to the C-terminal domain of Sor h 1 but still separate out into their own clade, consistent with literature on Phl p 2 and 3 and Lol p 2 and 3. [E11, E12] Within the Sor h 2 allergens, 71 cDNA transcripts were observed, 9 of which were translated into

protein. The expansin, cellulose-binding-like domain (IPR007117) was found with a close sequence match to Phl p 2. CL1122.1 (Sor h 2.01) and CL1695 (Sor h 2.02) had a mature peptide length of 96 amino acids (with 23 residue signal peptides) and 96 amino acids (with 25 residue signal peptide) respectively. Sequence identity between Sor h 2.01 and Sor h 2.02 was 63% (**Suppl Table E9**). The transcript CL1122.2 encodes a peptide predicted to have basic pI of 9.35 (**TABLE E2**), more consistent with group 3 allergens [E13] , but all three of these Sor h sequences clustered together, and not with group 3 allergens (**Suppl Fig E7**).

Reticuline oxidases

Related to the FAD/FMN-containing dehydrogenases with berbine bridge domain, 8 cDNA transcripts were identified in JGP and only one was detected in the proteome. Demonstrating 66% amino acid identity with Phl p 4, the identified transcript (UG808) matched closely with reticuline oxidase from *Zea mays.* UG808 had a gene length of 1913 base pairs and predicted protein length of 527 amino acids including a 22 residue signal peptide. Both the FAD/FMN-containing dehydrogenase and FAD-binding domain were observed. Relative transcript abundance was 1200 RKPM, indicating that this transcript was relatively low in frequency.

Sor h 7 – Polcalcins

Previously, the presence of a polcalcin allergen in JGP has been suggested [E14], but it has not been confirmed. Transcripts matching polcalcin allergens were abundant in number of unique cDNA transcripts and transcript frequency. However, transcripts of JGP that were expressed in the proteome matched polcalcins of maize with 30.5% - 47.5% amino acid identity (**Suppl. Table E7**) and 68 cDNA transcripts were observed in the JGP transcriptome. Interestingly, 18 cDNA transcripts were identified as belonging to 7 different loci, an example being transcript CL216 which had 4 isomers present.

The characteristic EF-hand domain of polcalcin transcripts were observed and the gene ontology (GO) identified amongst several different databases showed that these transcripts

encoded polcalcins with Ca2+- binding capacity. Transcript abundance ranged from 80390 to 1 RPKM amongst the cDNA transcripts of which only 6 were shown to be translated into protein.

Isoflavone reductase homolog

Three cDNA transcripts from JGP were shown to match the minor Birch pollen allergen Bet v 6 with transcript CL2295 having a sequence identity 100% identity with a *S. bicolor* (Sb03g008760) protein related to an isoflavone reductase homolog. Similarly, JGP GO annotation matched that of an isoflavone reductase, a class of proteins believed to be involved in plant defence. Contig CL2295 was shown to be expressed in the proteome, the relative transcript abundance was quite low at 763.

Extensins

There were 15 unique cDNA transcripts identified which had a close match to either the major pollen allergen Lol p 11 or Phl p 11. UG540 had a sequence match of 37.3% and 31.6% identity with Phl p 11 and Lol p 11. There was a protein motif in keeping with the trypsin inhibitor-like family. Unlike Phl p 11, allergens associated with Lol p 11 do not have trypsin-inhibitory capability, but are closer in function to proteins called extensins, which are important constituents of primary cell walls and maintain their integrity. For example, transcript CL1754 has its GO biological process listed as glucuronoxylan biosynthetic process highlighting the link to the extensin family of proteins. Transcript abundance varied widely, with the highest expression for CL1754 at 499143, and lowest of 2 for UG15400. There were 5 cDNA transcripts translated into protein with the best match belonging to UG540, which had an RPKM of 2479 and 100% identity with the *S. bicolor* gene Sb09g007260. Mature peptide length for UG540 was 125 AA with a signal peptide of 19 AA (**Tables E2**).

Sor h 12 – Profilins

Closely related to the known pollen allergen Phl p 12, 16 cDNA transcripts were identified, with close matches to different profilins such as prf A, prf 1 and prf 2. UG308 had the highest sequence identity at 73% with *S. bicolor* gene Sb03g034110. Transcript abundance ranged from 26487 to as low as 3, with 4 cDNA transcripts being detected in the proteome. UG308 had the highest RPKM at 26487 and was also expressed in the proteome. Profilins are believed to regulate the dynamics of the pollen actin cytoskeleton in germinating pollen, and each of the cDNA transcripts had GO linking them to actin binding and actin cytoskeleton organisation. Three profilin sequences have been described as putative allergens of maize pollen. [E15]

Sor h 13 – polygalacturonase

Polygalacturonase allergens are located in the internal cell wall and cytoplasm of mature pollen grains and have previously been shown to accumulate in mature barley pollen. [E16, E17] Polygalacturonase arise from a large gene family. [E18] These enzymes may serve to supply wall precursors for pollen tube growth, as well as assist the penetration of the pollen tube into the stigma and style tissues via degradation of their cell walls. [E19, E20] There were 17 cDNA transcripts matching polygalacturonase genes. Similarly, peptides of Sor h 13 within the proteome of JGP matched 8 unique cDNA transcripts. These cDNA transcripts matched closely to the exopolygalacturonase proteins from *Zea mays*. Most transcripts had the glycosyl hydrolase family-28 domain commonly found in polygalacturonases. Of the 17 cDNA transcripts, CL248.1 had the highest RPKM value of 272,584, while UG17192 had the lowest at 1. Like Sor h 7, Sor h 13 was observed to have several isoforms, with CL986 transcript 1 being observed in the proteome, while transcript 2 was absent. The other isoforms present belonged to CL1737, with both contigs being expressed in the proteome. The two Sor h 13 isoforms were most divergent within the signal peptide and N terminal 150 amino acids (**Suppl. Fig E8**). That these transcripts only differ in the first 150 AA suggests

there could be alternative splicing of mRNA. It is tempting to speculate that these transcripts arise by alternative splicing of mRNA transcribed from a single gene but each of the best matches identified for each of the Sor h 13 isoforms were with different *S. bicolor* sequences (**Suppl. TABLE E10**). CL1737.1 and CL1737.2 also differed in degree of similarity with Pas n 13 of Bahia grass pollen (73% and 79%) [37] and Phl p 13 (38.3% and 68.8%). Both Sor h 13 isoforms show three predicted glycosylation sites.

Sor h 22 – Enolase

Within the JGP transcriptome, 5 cDNA transcripts closely matched the enolase allergen of Bermuda grass pollen Cyn d 22. Peptides matching cDNA CL70 transcripts 1 and 2 were identified in the transcriptome (RPKM ranging up to 729) and proteome.

Sor h 23 – Cyn d 23-like protein

There were 36 cDNA transcripts identified matching the uncharacterised pollen allergen Cyn d 23, 3 of which were isomers of each other. Relatively abundant, 7 of the transcripts including CL2015.1 were detected in the proteome, and the highest had an mRNA expression RPKM of 211351. A second transcript CL2015.2 was also detected in the transcriptomic data, however, it only had low expression (RPKM count 54). The 67.6% pair-wise identity between the two sequences suggested the second transcript may belong to another genetic loci. The degree of sequence difference is consistent with the lack of observed IgE reactivity and may indicate that the second contig encoded a protein of limited allergenic importance. The observed peptide spectra of IgE-reactive spots 4 and 5 only matched CL2015.1.

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Supplementary TABLE E1. Grass species with allergens listed in Allergome.org and IUIS

Number	**Allergen source**	**species**	**Common Name**	**Subfamily**
1	Aeg ta	*Aegilops tauschii*	Goat grass	Pooideae
2	Agr ca	*Agrostis capillaris*	Colonial Bent	Pooideae
3	Agr g	*Agrostis gigantea*	Black Bent	Pooideae
4	Alo p	*Alopecurus_pratensis*	Meadow Foxtail	Pooideae
5[a]	Ant o	*Anthoxanthum odoratum*	Sweet Vernal	Pooideae
6	Arr e	*Arrhenatherum elatius*	Tall Oat-Grass	Pooideae
7	Ave s	*Avena sativa*	Common Oat	Pooideae
8	Bou g	*Bouteloua gracilis*	Blue Grama	Chloridoideae
9	Bra di	*Brachypodium distachyon*	Purple False Brome	Pooideae
10	Bra sy	*Brachypodium sylvaticum*	False Brome	Pooideae
11	Bro a	*Bromus arvensis*	Field Brome	Pooideae
12	Bro i	*Bromus inermis*	Smooth Brome	Pooideae
13	Cyn cr	*Cynodon cristatus*	Dogstail	Chloridoideae
14[a]	Cyn d	*Cynodon dactylon*	Bermuda	Chloridoideae
15[a]	Dac g	*Dactylis glomerata*	Orchard	Pooideae
16	Dis s	*Distichlis spicata*	Salt Grass	Chloridoideae
17	Fes e	*Festuca elatior*	Reed Fescue	Pooideae
18[a]	Fes p	*Festuca pratensis*	Meadow Fescue	Pooideae
19	Fes r	*Festuca rubra*	Red Fescue	Pooideae
20[a]	Hol l	*Holcus lanatus*	Velvet	Pooideae
21[a]	Hor v	*Hordeum vulgare*	Barley	Pooideae
22[a]	Lol p	*Lolium perenne*	Ryegrass	Pooideae
23	Lol m	*Lolium multiforum*	Annual ryegrass	Pooideae
24[a]	Ory s	*Orzya sativa*	Rice	Ehrhartoideae
25[a]	Pas n	*Paspalum notatum*	Bahia	Panicoideae
26[a]	Pha a	*Phalaris aquatica*	Canary	Pooideae
27[a]	Phl p	*Phleum pratense*	Timothy	Pooideae
28	Phr a	*Phragmites australis*	Common Reed	Arundinoideae
29[a]	Poa p	*Poa pratensis*	Kentucky Blue	Pooideae
30	Sec c	*Secale cereale*	Rye	Pooideae
31	Sor b	*Sorghum bicolor*	Sorghum	Panicoideae
32[a]	Sor h	*Sorghum halepense*	Johnson	Panicoideae
33[a]	Tri a	*Triticum aestivum*	Wheat	Pooideae
34	Tri ur	*Trictium urartu*	Wild wheat	Pooideae
35	Tri p	*Trisetum paniceum*	Wild Oat	Pooideae
36[a]	Zea m	*Zea mays*	Corn	Panicoideae

[a] Sources for which allergen have been included in International Union of Immunological Societies Allergen Nomenclature list of verified allergens.[42]

Supplementary Table E2 Putative grass pollen allergen encoding transcripts identified within the whole Johnson grass pollen transcriptome

Group	Number of transcipts	Putative allergen candidates	Predicted pI/ MW (kDa)	N-Glycosylation	SP/ mature peptide	Annotation/ comments
1	51	CL153.1	7.04 / 25.8	Asn10	27/ 239	β-Expansin
		CL153.2	7.04 / 25.8	Asn10	27/239	
		UG 493/492	9.13/ 26.5	Asn10	24/ 137	
2	71	CL1122.1	6.19 / 10.4	none	23/ 96	Expansin C-terminal fragment
		CL1122.2	9.35 / 10.5	none	23/98	
		CL1695.1	5.07 / 10.2	none	25/ 96	
4	8	UG 808	9.35 / 55.5	Asn335	22/ 504	reticuline oxidase, berberine-bridge
7	67	UG 451 UG 293	4.22/8.9	none	0/ 96	EF hand-like calcium binding protein
11	14	UG 540	5.09 / 13.6	Asn30	19/125	extensin family
12	15	UG 308	4.91 / 14.3	none	-/ 131	Profilin
13	17	CL1737.1	6.59 / 41.6	Asn80, 235 and 376	23/ 399	Polygalacturonase
		CL1737.2	7.84 / 40.5	Asn69, 224, 365	22/ 388	
22	5	CL70.1	4.94/ 48.1	Asn19, 146 and 335	-/ 446	Enolase
23	36	CL2015.1	6.22 / 22.2	none	17/ 211	Unknown protein with 39% identical to Cyn d 23 : gb AAP80170.1

Supplementary Table E3. Detection of peptides in the whole JGP proteome matching potential allergen sequences in the non-redundant plant database[a]

Protein Family	Grass pollen allergen Group	Peptides in Proteome	Number of unique spectra
β-expansins	1	71	8
Expansin-Group 2, C terminal of expansin	2	14	3
Berbine bridge family, reticuline oxidases, FAD/FMN-containing dehydrogenase	4	28	6
Cytochrome C	10	22	7
Extensin	11	30	9
Profilin	12	62	6
Polygalacturonase	13	102	20
Enolase	22	64	14
Isoflavone reductase[b] (e.g. Bet v 6)		3	3
Cyclophilin[b] (e.g. Bet v 7)		17	7
Heat shock protein 70[b]		6	4
Glucanase[b]		15	7

[a] non-redundant plant database within NCBI searched on 12 July 2012 (proteomic data available Suppl. Table E4)

[b] Matches with members of the 29 allergen families within which pollen allergens have been identified[43]. Proteins for which only one peptide spectra was detected were excluded.

Table E4 Mass spectra data for JGP proteome analysed against the NR NCBI plant database

number	filename	parent_charge	score	percent_scored_peak_intensity	totalIntensity	sequence	modifications		parent_m_over_z	matched_parent_mass	delta_parent_mass	delta_parent_mass_ppm	species	accession_number	entry_name
1363	JGP_1_8.10196.10205.3	3	13.06	79.9	5.58E+04	(R)HIEILGYLLYVAK(V)	511.3069	1531.888	0.0179	11.7	Zea mays	162464249	14 kDa zinc-binding protein		
2321	JGP_1_7.6050.6055.2	2	10.46	65.9	2.46E+05	(K)TVDVEELTVEER(N)	709.8578	1418.701	0.0074	5.2	Nicotiana tabacum	44917151	14-3-3 e-1 protein		
1417	JGP_1_3.6554.6554.3	3	12.92	64.2	1.32E+05	(K)AAQDIAVAELAPTHPIR(L)	591.6612	1772.965	0.0037	2.1	Solanum tuberosum	3777447	14-3-3 protein		
1722	JGP_1_8.7176.7176.3	3	12.05	60.4	2.29E+05	(K)AAQDIAVAELAPTHPIR(L)	591.6613	1772.965	0.004	2.2	Solanum tuberosum	3777447	14-3-3 protein		
1262	JGP_1_7.4222.4336.2	2	13.39	85.8	1.68E+06	(R)YLAEFK(S)	385.7099	770.408	0.0042	5.5	Arabidopsis thaliana	30698124	14-3-3-like protein GF14 kappa		
1521	JGP_1_7.5715.5718.2	2	12.57	74	1.01E+06	(R)NLLSVAYK(N)	454.2684	907.525	0.0048	5.3	Arabidopsis thaliana	30698124	14-3-3-like protein GF14 kappa		
1579	JGP_1_8.5714.5747.2	2	12.43	69.6	1.31E+05	(R)NLLSVAYK(N)	454.2643	907.525	-0.0034	-3.8	Arabidopsis thaliana	30698124	14-3-3-like protein GF14 kappa		
1623	JGP_1_2.5133.5144.2	2	12.29	71.8	1.01E+05	(R)NLLSVAYK(N)	454.266	907.525	0	0	Arabidopsis thaliana	30698124	14-3-3-like protein GF14 kappa		
1991	JGP_1_7.0912.0917.2	2	11.26	83	1.36E+05	(K)LAEQAER(Y)	408.7153	816.421	0.0023	2.8	Arabidopsis thaliana	30698124	14-3-3-like protein GF14 kappa		
2356	JGP_1_1.5358.5436.2	2	10.39	62.2	2.78E+05	(R)NLLSVAYK(N)	454.266	907.525	0	0	Arabidopsis thaliana	30698124	14-3-3-like protein GF14 kappa		
2400	JGP_1_7.2236.2239.2	2	10.31	76.7	5.94E+05	(R)IVSSIEQK(E)	452.2616	903.515	0.0014	1.5	Arabidopsis thaliana	30698124	14-3-3-like protein GF14 kappa		
322	JGP_1_4.7660.7781.2	2	17.97	80.1	5.11E+06	(R)LDQLQILLK(G)	542.3464	1083.677	0.0083	7.7	Zea mays	195628730	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"		
531	JGP_1_1.7442.7531.2	2	16.6	81.4	3.27E+05	(R)LDQLQILLK(G)	542.3432	1083.677	0.0019	1.8	Zea mays	195628730	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"		
839	JGP_1_5.7760.7863.2	2	15.01	78.2	2.87E+05	(R)LDQLQILLK(G)	542.3376	1083.677	-0.0093	-8.6	Zea mays	195628730	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"		
943	JGP_1_4.7479.7589.2	2	14.6	81.6	2.55E+05	(R)LDQLQILLK(G)	542.3419	1083.677	-0.0007	-0.6	Zea mays	195628730	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"		
1005	JGP_1_2.6983.7052.2	2	14.32	76.2	2.01E+05	(R)LDQLQILLK(G)	542.3438	1083.677	0.0031	2.9	Zea mays	195628730	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"		
1419	JGP_1_6.8237.8245.2	2	12.92	68.6	8.51E+04	(R)LDQLQILLK(G)	542.3343	1083.677	-0.0159	-14.7	Zea mays	195628730	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"		
1502	JGP_1_5.7833.7833.2	2	12.63	61.8	1.97E+05	(R)LDQLQILLK(G)	542.3376	1083.677	-0.0093	-8.6	Zea mays	195628730	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"		
1806	JGP_1_4.7484.7484.2	2	11.8	72.1	1.85E+05	(R)LDQLQILLK(G)	542.3419	1083.677	-0.0007	-0.6	Zea mays	195628730	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"		
1596	JGP_1_1.7167.7170.3	3	12.38	75.7	9.16E+04	(R)IDHILGFFR(I)	373.2118	1117.615	0.0056	5	Arabidopsis thaliana	42569818	4-alpha-glucanotransferase		
77	JGP_1_3.7715.7820.4	4	21.09	85.2	3.54E+05	(K)SEHAFYLDWAVHSFR(I)	466.9787	1864.877	0.0164	8.8	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
113	JGP_1_3.5293.5376.3	3	20.34	90.1	2.07E+06	(K)YGAGIGPGVYDIHSPR(I)	553.618	1658.829	0.0109	6.6	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
353	JGP_1_3.6204.6281.2	2	17.76	88.5	1.57E+06	(K)YLFAGVVDGR(N)	548.7944	1096.579	0.003	2.7	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
657	JGP_1_4.5523.5529.3	3	15.95	76	3.00E+05	(K)YGAGIGPGVYDIHSPR(I)	553.6177	1658.829	0.01	6	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
810	JGP_1_3.6556.6561.2	2	15.13	73	6.42E+05	(K)SWLAFAAQK(V)	511.2785	1021.547	0.0032	3.1	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
817	JGP_1_3.9441.9513.2	2	15.09	75.2	1.81E+06	(K)GmLTGPVTILNWSFVR(N) m:Oxidized methionine	903.9859	1790.962	16.0023	4.1	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
874	JGP_1_4.6509.6514.2	2	14.89	84.1	3.03E+05	(K)YLFAGVVDGR(N)	548.7953	1096.579	0.0048	4.3	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
913	JGP_1_3.8033.8039.2	2	14.73	77.7	3.24E+05	(K)FALESFWDGK(S)	600.2933	1199.573	0.0062	5.1	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
962	JGP_1_3.6366.6371.2	2	14.49	82.1	1.42E+06	(K)YLFAGVVDGR(N)	548.7949	1096.579	0.004	3.6	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
1138	JGP_1_3.7831.7968.2	2	13.8	68.1	7.30E+05	(K)FALESFWDGK(S)	600.2937	1199.573	0.007	5.8	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
1411	JGP_1_4.9765.9769.2	2	12.94	64.7	1.14E+05	(K)GmLTGPVTILNWSFVR(N) m:Oxidized methionine	903.9827	1790.962	15.9959	0.6	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
1427	JGP_1_5.6700.6705.2	2	12.89	72.5	1.07E+05	(K)YLFAGVVDGR(N)	548.7953	1096.579	0.0048	4.3	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
1654	JGP_1_1.6315.6329.2	2	12.22	68.5	7.31E+04	(K)YLFAGVVDGR(N)	548.7913	1096.579	-0.0032	-3	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
1656	JGP_1_3.7775.7775.3	3	12.22	61.4	1.78E+05	(K)SEHAFYLDWAVHSFR(I)	622.3045	1864.877	0.0224	12	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
1668	JGP_1_6.7046.7050.2	2	12.2	70.6	3.16E+05	(K)YLFAGVVDGR(N)	548.7952	1096.579	0.0046	4.2	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
2104	JGP_1_2.5963.5984.2	2	10.99	68	1.70E+05	(K)YLFAGVVDGR(N)	548.7944	1096.579	0.003	2.7	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
2285	JGP_1_3.4013.4111.2	2	10.55	71	1.50E+06	(K)VVEVNALAK(A)	471.7862	942.562	0.0033	3.5	Arabidopsis thaliana	15238686	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase		
697	JGP_1_5.6605.6605.2	2	15.71	73.2	1.78E+05	(K)GLLYLGmGVSGGEEGAR(N) m:Oxidized methionine	841.4205	1665.826	16.0072	7.3	Arabidopsis thaliana	15238151	6-phosphogluconate dehydrogenase		
1167	JGP_1_5.5689.5689.2	2	13.67	76.8	2.17E+05	(K)VAAQVPDSGPCVTYIGK(G) C:Carbamidomethylation	881.4482	1761.884	0.0051	2.9	Glycine max	351722265	6-phosphogluconate dehydrogenase		
1291	JGP_1_7.8416.8451.2	2	13.32	78	1.11E+05	(K)LAEPPYLEAVDWSK(W)	809.4218	1617.816	0.0204	12.6	Zea mays	226496323	6-phosphogluconolactonase		
267	JGP_1_7.7659.7738.2	2	18.38	91	6.27E+05	(K)LAFDGFLSK(V)	499.2727	997.535	0.0028	2.8	Arabidopsis thaliana	15238523	6-phosphogluconolactonase 4		
395	JGP_1_7.7506.7584.2	2	17.44	92.2	4.61E+05	(K)LAFDGFLSK(V)	499.2727	997.535	0.0028	2.8	Arabidopsis thaliana	15238523	6-phosphogluconolactonase 4		
1114	JGP_1_5.2611.2769.2	2	13.89	82.6	3.49E+06	(K)VPIPDK(N)	334.704	668.398	0.003	4.4	Arabidopsis thaliana	15238526	6-phosphogluconolactonase 5		

2453	JGP_1_4.6234.6347.2	2	10.18	83.6	1.73E+06	(R)LLPDLPK(I)		398.2535	795.497	0.0023	2.8	Arabidopsis thaliana	15232458	ABC transporter-like protein		
779	JGP_1_3.8966.8974.3	3	15.27	81.1	1.23E+05	(R)VLLQDFTGVPAVVDLACmR(D)	C:Carbamidomethylation m:Oxidized methionine	707.3716	2104.093	16.0073	5.8	Arabidopsis thaliana	599625	aconitase		
1148	JGP_1_2.8473.8533.3	3	13.73	75.1	3.13E+05	(R)VLLQDFTGVPAVVDLACmR(D)	C:Carbamidomethylation m:Oxidized methionine	707.3711	2104.093	16.0058	5.1	Arabidopsis thaliana	599625	aconitase		
1401	JGP_1_2.5291.5366.2	2	12.96	85.3	4.57E+05	(R)ILLESAIR(N)		457.7884	914.567	0.0026	2.8	Arabidopsis thaliana	599625	aconitase		
1848	JGP_1_2.7838.7848.2	2	11.68	70.6	9.67E+03	(R)SNLVGmGIIPLCFK(A)	C:Carbamidomethylation m:Oxidized methionine	782.916	1548.828	15.9971	1.4	Arabidopsis thaliana	599625	aconitase		
2516	JGP_1_4.5810.5823.2	2	10.02	73	1.10E+05	(R)ILLESAIR(N)		457.7871	914.567	0	0	Arabidopsis thaliana	599625	aconitase		
102	JGP_1_2.8752.8827.3	3	20.57	90.5	2.95E+05	(K)INPLVPVDLVIDHSVQVDVAR(S)			766.7684	2298.282	0.009	3.9	Arabidopsis thaliana	15233349	aconitate hydratase 1	
540	JGP_1_3.9264.9275.3	3	16.55	83.3	9.49E+04	(K)INPLVPVDLVIDHSVQVDVAR(S)			766.7677	2298.282	0.0069	3	Arabidopsis thaliana	15233349	aconitate hydratase 1	
704	JGP_1_6.10246.10251.3	3	15.68	81.8	1.04E+05	(K)INPLVPVDLVIDHSVQVDVAR(S)			766.7671	2298.282	0.0051	2.2	Arabidopsis thaliana	15233349	aconitate hydratase 1	
1525	JGP_1_1.9316.9316.3	3	12.55	70.4	9.57E+04	(K)INPLVPVDLVIDHSVQVDVAR(S)			766.766	2298.282	0.0018	0.8	Arabidopsis thaliana	15233349	aconitate hydratase 1	
2269	JGP_1_2.4424.4434.2	2	10.61	69.8	8.78E+04	(K)IIDWEK(T)		402.2226	803.43	0.0081	10.1	Arabidopsis thaliana	30678219	aconitate hydratase 2		
48	JGP_1_1.8230.8299.4	4	21.98	96.8	1.14E+06	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)			788.6702	3151.642	0.0167	5.3	Arabidopsis thaliana	11276980	actin (ACT3)	
940	JGP_1_2.7732.7754.4	4	14.62	81.4	2.10E+04	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)			788.6706	3151.642	0.0183	5.8	Arabidopsis thaliana	11276980	actin (ACT3)	
1302	JGP_1_5.2631.2634.2	2	13.28	70.5	2.67E+05	(K)AGFAGDDAPR(A)		488.7323	976.448	0.009	9.3	Arabidopsis thaliana	11276980	actin (ACT3)		
1385	JGP_1_4.1994.2004.2	2	12.99	76.9	1.03E+05	(K)VVAPPER(K)		384.225	767.441	0.0017	2.2	Arabidopsis thaliana	11276980	actin (ACT3)		
1404	JGP_1_5.1865.1865.2	2	12.96	78.9	7.69E+04	(K)DAYVGDEAQSK(R)		591.77	1182.527	0.0054	4.6	Arabidopsis thaliana	11276980	actin (ACT3)		
1496	JGP_1_2.1994.2062.2	2	12.64	79.7	1.79E+05	(K)VVAPPER(K)		384.2239	767.441	-0.0005	-0.6	Arabidopsis thaliana	11276980	actin (ACT3)		
1543	JGP_1_3.2057.2063.2	2	12.5	80.6	1.10E+05	(K)VVAPPER(K)		384.2238	767.441	-0.0007	-0.9	Arabidopsis thaliana	11276980	actin (ACT3)		
1646	JGP_1_1.1840.1918.2	2	12.23	71.8	1.78E+05	(K)DAYVGDEAQSK(R)		591.7691	1182.527	0.0036	3	Arabidopsis thaliana	11276980	actin (ACT3)		
1726	JGP_1_3.8201.8201.4	4	12.03	68.9	1.22E+05	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)			788.6708	3151.642	0.0191	6.1	Arabidopsis thaliana	11276980	actin (ACT3)	
1880	JGP_1_1.2511.2594.2	2	11.58	70.1	5.94E+05	(K)AGFAGDDAPR(A)		488.7291	976.448	0.0026	2.7	Arabidopsis thaliana	11276980	actin (ACT3)		
2050	JGP_1_6.9102.9102.4	4	11.12	64.6	1.52E+05	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)			788.6714	3151.642	0.0215	6.8	Arabidopsis thaliana	11276980	actin (ACT3)	
2211	JGP_1_6.2752.2760.2	2	10.73	61.4	3.35E+05	(K)AGFAGDDAPR(A)		488.7339	976.448	0.0122	12.5	Arabidopsis thaliana	11276980	actin (ACT3)		
2222	JGP_1_5.1930.1936.2	2	10.71	68.2	1.65E+05	(K)VVAPPER(K)		384.2237	767.441	-0.0009	-1.2	Arabidopsis thaliana	11276980	actin (ACT3)		
2257	JGP_1_1.1960.2033.2	2	10.63	75.4	5.53E+05	(K)VVAPPER(K)		384.2244	767.441	0.0005	0.7	Arabidopsis thaliana	11276980	actin (ACT3)		
2340	JGP_1_6.2055.2143.2	2	10.42	67.6	2.40E+05	(K)VVAPPER(K)		384.2237	767.441	-0.0009	-1.2	Arabidopsis thaliana	11276980	actin (ACT3)		
269	JGP_1_2.3324.3337.3	3	18.35	75.7	1.57E+05	(K)AEYDESGPSIVHR(K)		487.2364	1459.681	0.0134	9.2	Arabidopsis thaliana	18409908	actin 3		
896	JGP_1_1.3431.3441.3	3	14.79	70.4	3.93E+05	(K)AEYDESGPSIVHR(K)		487.2355	1459.681	0.0107	7.4	Arabidopsis thaliana	18409908	actin 3		
1219	JGP_1_8.1971.2079.2	2	13.53	83.7	3.49E+06	(K)MIYASSK(D)		400.2068	799.402	0.0045	5.6	Arabidopsis thaliana	30697300	actin depolymerizing factor 4		
212	JGP_1_1.4420.4491.2	2	18.97	86.8	5.05E+05	(K)INENVQQVVVDR(L)		706.8792	1412.749	0.0019	1.3	Zea mays	226493187	actin-depolymerizing factor		
251	JGP_1_1.8566.8634.2	2	18.54	88	5.00E+05	(K)IFFISWAPDTSR(V)		720.3716	1439.732	0.0041	2.9	Zea mays	226503551	actin-depolymerizing factor		
385	JGP_1_8.9350.9419.2	2	17.52	85.4	9.57E+05	(K)IFFISWAPDTSR(V)		720.3721	1439.732	0.0051	3.6	Zea mays	226503551	actin-depolymerizing factor		
469	JGP_1_3.4539.4606.2	2	17.04	80.2	2.56E+05	(K)INENVQQVVVDR(L)		706.8804	1412.749	0.0043	3	Zea mays	226493187	actin-depolymerizing factor		
482	JGP_1_4.4643.4648.2	2	16.9	77.3	2.70E+05	(K)INENVQQVVVDR(L)		706.8815	1412.749	0.0065	4.6	Zea mays	226493187	actin-depolymerizing factor		
532	JGP_1_6.9418.9492.2	2	16.6	86.3	2.04E+05	(K)IFFISWAPDTSR(V)		720.3721	1439.732	0.0051	3.6	Zea mays	226503551	actin-depolymerizing factor		
624	JGP_1_7.9314.9393.2	2	16.15	81.4	1.78E+05	(K)IFFISWAPDTSR(V)		720.3746	1439.732	0.0101	7	Zea mays	226503551	actin-depolymerizing factor		
707	JGP_1_2.8058.8132.2	2	15.67	83.1	3.05E+05	(K)IFFISWAPDTSR(V)		720.3723	1439.732	0.0055	3.9	Zea mays	226503551	actin-depolymerizing factor		
718	JGP_1_8.9332.9346.2	2	15.62	65.6	6.80E+04	(R)YAVFDFDFVTDENCQK(S)	C:Carbamidomethylation	999.4452	1997.859	0.0246	12.3	Zea mays	226493187	actin-depolymerizing factor		
753	JGP_1_5.9019.9085.2	2	15.4	75.3	1.32E+05	(K)IFFISWAPDTSR(V)		720.3716	1439.732	0.0041	2.9	Zea mays	226503551	actin-depolymerizing factor		
930	JGP_1_1.8699.8705.2	2	14.65	73.8	2.74E+05	(K)IFFISWAPDTSR(V)		720.3717	1439.732	0.0043	3	Zea mays	226503551	actin-depolymerizing factor		
1024	JGP_1_7.4973.4979.2	2	14.23	71.1	2.32E+05	(K)INENVQQVVVDR(L)		706.8795	1412.749	0.0025	1.8	Zea mays	226493187	actin-depolymerizing factor		
1097	JGP_1_8.4884.4884.2	2	13.97	73.7	1.13E+06	(K)INENVQQVVVDR(L)		706.8812	1412.749	0.0059	4.2	Zea mays	226493187	actin-depolymerizing factor		
1173	JGP_1_3.8515.8590.2	2	13.65	72.5	3.08E+05	(K)IFFISWAPDTSR(V)		720.3726	1439.732	0.0061	4.3	Zea mays	226503551	actin-depolymerizing factor		
1215	JGP_1_2.4307.4307.2	2	13.54	68.4	2.96E+05	(K)INENVQQVVVDR(L)		706.8781	1412.749	-0.0003	-0.2	Zea mays	226493187	actin-depolymerizing factor		
1220	JGP_1_8.4888.4888.2	2	13.53	70.3	1.13E+06	(K)INENVQQVVVDR(L)		706.8812	1412.749	0.0059	4.2	Zea mays	226493187	actin-depolymerizing factor		
1259	JGP_1_4.8751.8816.2	2	13.4	74.4	2.09E+05	(K)IFFISWAPDTSR(V)		720.3718	1439.732	0.0045	3.2	Zea mays	226503551	actin-depolymerizing factor		
1460	JGP_1_2.4238.4241.2	2	12.78	74.3	2.77E+05	(K)INENVQQVVVDR(L)		706.8781	1412.749	-0.0003	-0.2	Zea mays	226493187	actin-depolymerizing factor		
1517	JGP_1_6.5009.5009.2	2	12.59	72	3.04E+05	(K)INENVQQVVVDR(L)		706.8783	1412.749	0.0001	0.1	Zea mays	226493187	actin-depolymerizing factor		

1642	JGP_1_5.4817.4817.2	2	12.24	65.7	2.18E+05	(K)INENVQQVVVDR(L)		706.8777	1412.749	-0.0011	-0.8	Zea mays	226493187	actin-depolymerizing factor			
1779	JGP_1_1.4436.4440.3	3	11.88	73.9	1.16E+05	(K)INENVQQVVVDR(L)		471.5904	1412.749	0.0074	5.3	Zea mays	226493187	actin-depolymerizing factor			
1900	JGP_1_6.5020.5020.2	2	11.53	63.3	3.20E+05	(K)INENVQQVVVDR(L)		706.8783	1412.749	0.0001	0.1	Zea mays	226493187	actin-depolymerizing factor			
1245	JGP_1_1.7315.7325.3	3	13.44	74.5	1.25E+05	(R)ELDGIQCEIQATDPSEmSLDIVR(S)	C:Carbamidomethylation	m:Oxidized methionine	879.0822	2619.228	16.0044	3.6	Zea mays	164414398	actin-depolymerizing factor 1		
1421	JGP_1_2.6854.6854.3	3	12.91	67.4	1.58E+05	(R)ELDGIQCEIQATDPSEmSLDIVR(S)	C:Carbamidomethylation	m:Oxidized methionine	879.0837	2619.228	16.0089	5.3	Zea mays	164414398	actin-depolymerizing factor 1		
28	JGP_1_8.8361.8441.2	2	22.66	93.6	3.51E+05	(R)YAIYDLDFTTVENCQK(S)	C:Carbamidomethylation		990.4597	1979.906	0.0066	3.3	Zea mays	162462304	actin-depolymerizing factor 2		
158	JGP_1_8.6776.6780.2	2	19.52	83.7	2.93E+05	(R)LGEPNQGYGDFTDSLPADECR(Y)	C:Carbamidomethylation		1171.0088	2341.004	0.0066	2.8	Zea mays	162462304	actin-depolymerizing factor 2		
349	JGP_1_2.8418.8483.2	2	17.77	89.1	3.38E+05	(K)IFFFSWSPDTAR(T)		737.3643	1473.716	0.0052	3.5	Zea mays	162462304	actin-depolymerizing factor 2			
364	JGP_1_8.9682.9755.2	2	17.64	88.5	1.11E+06	(K)IFFFSWSPDTAR(T)		737.3661	1473.716	0.0088	6	Zea mays	162462304	actin-depolymerizing factor 2			
407	JGP_1_8.9814.9820.2	2	17.4	90.5	9.39E+05	(K)IFFFSWSPDTAR(T)		737.3665	1473.716	0.0096	6.5	Zea mays	162462304	actin-depolymerizing factor 2			
412	JGP_1_3.8891.8953.2	2	17.36	90.4	3.05E+05	(K)IFFFSWSPDTAR(T)		737.3649	1473.716	0.0064	4.3	Zea mays	162462304	actin-depolymerizing factor 2			
434	JGP_1_8.6781.6784.3	3	17.27	87.7	2.65E+05	(R)LGEPNQGYGDFTDSLPADECR(Y)	C:Carbamidomethylation		781.0107	2341.004	0.0138	5.9	Zea mays	162462304	actin-depolymerizing factor 2		
670	JGP_1_7.9695.9763.2	2	15.89	83.6	1.54E+04	(K)IFFFSWSPDTAR(T)		737.3644	1473.716	0.0054	3.7	Zea mays	162462304	actin-depolymerizing factor 2			
683	JGP_1_4.9149.9214.2	2	15.81	86.6	2.26E+05	(K)IFFFSWSPDTAR(T)		737.3659	1473.716	0.0084	5.7	Zea mays	162462304	actin-depolymerizing factor 2			
843	JGP_1_1.2645.2650.3	3	14.99	66.9	4.72E+05	(R)IDDKDmEIKVDR(L)	m:Oxidized methionine		498.25	1476.736	15.9992	2.9	Zea mays	162462304	actin-depolymerizing factor 2		
979	JGP_1_1.7552.7552.2	2	14.45	72.5	6.63E+04	(R)YAIYDLDFTTVENCQK(S)	C:Carbamidomethylation		990.4642	1979.906	0.0156	7.9	Zea mays	162462304	actin-depolymerizing factor 2		
1054	JGP_1_1.8930.9034.2	2	14.12	83.2	5.75E+05	(K)IFFFSWSPDTAR(T)		737.3659	1473.716	0.0084	5.7	Zea mays	162462304	actin-depolymerizing factor 2			
1142	JGP_1_2.8543.8550.2	2	13.78	79	1.71E+05	(K)IFFFSWSPDTAR(T)		737.3642	1473.716	0.005	3.4	Zea mays	162462304	actin-depolymerizing factor 2			
1178	JGP_1_6.9843.9910.2	2	13.64	81.2	7.36E+04	(K)IFFFSWSPDTAR(T)		737.3694	1473.716	0.0154	10.4	Zea mays	162462304	actin-depolymerizing factor 2			
1431	JGP_1_1.8941.9049.3	3	12.87	65.2	1.52E+05	(K)IFFFSWSPDTAR(T)		491.9143	1473.716	0.0122	8.3	Zea mays	162462304	actin-depolymerizing factor 2			
1475	JGP_1_1.2624.2714.4	4	12.72	71.6	1.33E+06	(R)IDDKDmEIKVDR(L)	m:Oxidized methionine		373.9402	1476.736	16.0027	5.2	Zea mays	162462304	actin-depolymerizing factor 2		
1508	JGP_1_1.9091.9094.2	2	12.61	69.1	1.75E+05	(K)IFFFSWSPDTAR(T)		737.3648	1473.716	0.0062	4.2	Zea mays	162462304	actin-depolymerizing factor 2			
1730	JGP_1_1.1658.1749.3	3	12.01	71	7.14E+05	(R)IDDKDmEIK(V)	m:Oxidized methionine		374.8524	1106.54	16.0028	7.1	Zea mays	162462304	actin-depolymerizing factor 2		
2362	JGP_1_5.9457.9533.2	2	10.39	76.4	1.70E+05	(K)IFFFSWSPDTAR(T)		737.3672	1473.716	0.011	7.5	Zea mays	162462304	actin-depolymerizing factor 2			
2473	JGP_1_2.8458.8464.3	3	10.13	64.3	4.92E+04	(K)IFFFSWSPDTAR(T)		491.914	1473.716	0.0113	7.7	Zea mays	162462304	actin-depolymerizing factor 2			
2500	JGP_1_3.9014.9020.2	2	10.07	65.5	1.45E+05	(K)IFFFSWSPDTAR(T)		737.365	1473.716	0.0066	4.5	Zea mays	162462304	actin-depolymerizing factor 2			
2256	JGP_1_8.5013.5017.2	2	10.64	82.9	8.27E+05	(R)FITFK(M)	328.1961		655.381	0.0035	5.4	Zea mays	162459533	actin-depolymerizing factor 3			
149	JGP_1_1.7011.7091.2	2	19.6	94	5.91E+05	(K)SYELPDGQVITIGAER(F)			874.4477	1747.886	0.002	1.2	Solanum tuberosum	81076210	actin-like		
471	JGP_1_2.6609.6613.2	2	17.01	91	1.83E+05	(K)SYELPDGQVITIGAER(F)			874.4484	1747.886	0.0034	2	Solanum tuberosum	81076210	actin-like		
660	JGP_1_3.7023.7029.2	2	15.94	84.9	1.19E+05	(K)SYELPDGQVITIGAER(F)			874.4508	1747.886	0.0082	4.7	Solanum tuberosum	81076210	actin-like		
1041	JGP_1_6.7868.7887.2	2	14.16	82.6	1.72E+05	(K)SYELPDGQVITIGAER(F)			874.4488	1747.886	0.0042	2.4	Solanum tuberosum	81076210	actin-like		
144	JGP_1_6.8712.8792.2	2	19.66	90.2	4.03E+05	(K)VLPYADYIFGNETEAK(I)			915.457	1829.896	0.0111	6.1	Zea mays	4582787	adenosine kinase		
254	JGP_1_2.7583.7653.2	2	18.5	89.9	2.16E+05	(K)TFPVILLPK(E)			514.3327	1027.655	0.0031	3	Oryza sativa	21698922	adenosine kinase		
287	JGP_1_1.7977.7980.2	2	18.22	90.7	1.54E+05	(K)VLPYADYIFGNETEAK(I)			915.4544	1829.896	0.0059	3.2	Zea mays	4582787	adenosine kinase		
310	JGP_1_6.11627.11695.3	3	18.03	89.2	1.58E+05	(K)VFLmNLSAPFICEFFR(D)	C:Carbamidomethylation	m:Oxidized methionine	669.6737	1990.992	16.0148	9.9	Zea mays	4582787	adenosine kinase		
327	JGP_1_6.8811.8885.2	2	17.96	90.7	6.31E+05	(K)TFPVILLPK(E)			514.3332	1027.655	0.0041	4	Oryza sativa	21698922	adenosine kinase		
380	JGP_1_2.7454.7454.2	2	17.54	87.6	1.31E+05	(K)VLPYADYIFGNETEAK(I)			915.4559	1829.896	0.0089	4.9	Zea mays	4582787	adenosine kinase		
384	JGP_1_6.11626.11696.2	2	17.52	85	2.24E+05	(K)VFLmNLSAPFICEFFR(D)	C:Carbamidomethylation	m:Oxidized methionine	1003.9999	1990.992	16.0008	2.9	Zea mays	4582787	adenosine kinase		
411	JGP_1_6.6919.6925.2	2	17.38	84.7	4.68E+05	(R)IAVITQGADPVVVAEDGK(V)			891.4886	1781.964	0.0056	3.1	Zea mays	4582787	adenosine kinase		
453	JGP_1_6.8952.8958.2	2	17.13	92.2	3.04E+05	(K)TFPVILLPK(E)			514.3333	1027.655	0.0043	4.2	Oryza sativa	21698922	adenosine kinase		
637	JGP_1_3.8009.8070.2	2	16.07	82.7	1.24E+05	(K)TFPVILLPK(E)			514.3328	1027.655	0.0033	3.2	Oryza sativa	21698922	adenosine kinase		
661	JGP_1_6.5012.5018.2	2	15.94	87.1	1.23E+06	(K)ISQLPLASGK(Q)			507.3052	1013.599	0.0042	4.1	Oryza sativa	21698922	adenosine kinase		
941	JGP_1_1.8096.8164.2	2	14.6	81.5	2.83E+05	(K)TFPVILLPK(E)			514.3328	1027.655	0.0033	3.2	Oryza sativa	21698922	adenosine kinase		
1238	JGP_1_1.7995.8012.3	3	13.46	78.4	1.50E+05	(K)VLPYADYIFGNETEAK(I)			610.6411	1829.896	0.0131	7.2	Zea mays	4582787	adenosine kinase		
1242	JGP_1_1.4479.4486.2	2	13.45	76.1	1.44E+05	(K)ISQLPLASGK(Q)			507.3009	1013.599	-0.0044	-4.4	Oryza sativa	21698922	adenosine kinase		
1305	JGP_1_4.8281.8285.2	2	13.26	77.4	5.95E+04	(K)TFPVILLPK(E)			514.3339	1027.655	0.0055	5.3	Oryza sativa	21698922	adenosine kinase		
1412	JGP_1_5.8480.8483.2	2	12.94	75.1	5.78E+04	(K)TFPVILLPK(E)			514.3311	1027.655	-0.0001	-0.1	Oryza sativa	21698922	adenosine kinase		
1710	JGP_1_6.8743.8747.3	3	12.09	67.3	2.30E+05	(K)VLPYADYIFGNETEAK(I)			610.6402	1829.896	0.0104	5.7	Zea mays	4582787	adenosine kinase		
2007	JGP_1_6.6935.6940.3	3	11.22	65.1	3.12E+05	(R)IAVITQGADPVVVAEDGK(V)			594.6554	1781.964	-0.0127	-7.1	Zea mays	4582787	adenosine kinase		
2015	JGP_1_2.4308.4312.2	2	11.19	78.6	1.87E+05	(K)ISQLPLASGK(Q)			507.3034	1013.599	0.0006	0.5	Oryza sativa	21698922	adenosine kinase		
2236	JGP_1_2.5832.5839.3	3	10.68	68.7	1.15E+05	(R)IAVITQGADPVVVAEDGK(V)			594.6614	1781.964	0.0053	3	Zea mays	4582787	adenosine kinase		

964	JGP_1_6.6696.6699.2	2	14.49	75.7	4.13E+05	(R)SLIANLSAANCYK(V)	C:Carbamidomethylation	712.8648	1424.72	0.0021	1.5	Arabidopsis thaliana	15232763	adenosine kinase 1
223	JGP_1_6.5083.5100.2	2	18.91	89.6	3.76E+05	(K)SNVEYIAGGATQNSIR(V)		840.4239	1679.835	0.0058	3.4	Nicotiana tabacum	51949800	adenosine kinase isoform 1S
1321	JGP_1_6.4663.4669.2	2	13.2	70.7	6.37E+05	(K)HLPmYDELASK(N)	m:Oxidized methionine	660.3203	1303.635	15.9982	2.5	Nicotiana tabacum	51949796	adenosine kinase isoform 1T
642	JGP_1_5.4618.4624.2	2	16.03	83.7	3.26E+05	(K)IPDPESTDNAEFK(I)		731.8431	1462.67	0.0093	6.4	Zea mays	226491362	adenosylhomocysteinase
1524	JGP_1_5.6374.6387.4	4	12.56	67.1	1.49E+05	(K)SQADYISVPIEGPYKPAHYR(Y)			573.5443	2291.146	0.0099	4.3	Zea mays	226491362	adenosylhomocysteinase
1741	JGP_1_4.6616.6626.2	2	11.99	82.6	1.64E+05	(K)IVLTIIR(D)		414.2897	827.571	0.0008	1	Zea mays	226491362	adenosylhomocysteinase
1821	JGP_1_1.6445.6534.2	2	11.74	87.7	2.90E+05	(K)IVLTIIR(D)		414.2908	827.571	0.003	3.7	Zea mays	226491362	adenosylhomocysteinase
1965	JGP_1_5.6739.6829.2	2	11.34	83.8	4.78E+05	(K)IVLTIIR(D)		414.2905	827.571	0.0024	2.9	Zea mays	226491362	adenosylhomocysteinase
2038	JGP_1_4.4505.4505.2	2	11.14	67.6	1.43E+05	(K)IPDPESTDNAEFK(I)		731.843	1462.67	0.0091	6.2	Zea mays	226491362	adenosylhomocysteinase
30	JGP_1_5.6600.6600.3	3	22.64	77.7	1.75E+05	(R)WCSCNIFSTQDHAAAAIAR(D)	C:Carbamidomethylation	727.0041	2178.981	0.017	7.8	Arabidopsis thaliana	15229522	adenosylhomocysteinase 2
1264	JGP_1_5.8835.8839.3	3	13.38	79.9	4.02E+04	(R)LYQmQETGALLFPAINVNDSVTK(S)	m:Oxidized methionine	856.7787	2552.307	16.015	7.8	Arabidopsis thaliana	15229522	adenosylhomocysteinase 2
691	JGP_1_8.9922.9930.3	3	15.75	73.4	1.76E+05	(K)LGEIVTTIPTIGFNVETVEYK(N)		775.0897	2323.243	0.0114	4.9	Arabidopsis thaliana	15226521	ADP-ribosylation factor 1
733	JGP_1_8.8315.8327.2	2	15.52	74.8	2.13E+05	(K)NISFTVWDVGGQDK(I)		783.387	1565.759	0.0073	4.6	Arabidopsis thaliana	15226521	ADP-ribosylation factor 1
1846	JGP_1_8.6735.6809.2	2	11.7	79.3	2.10E+05	(R)ILMVGLDAAGK(T)		544.3131	1087.618	0.0009	0.9	Arabidopsis thaliana	15226521	ADP-ribosylation factor 1
1887	JGP_1_1.8966.8995.3	3	11.56	65.9	1.03E+05	(K)LGEIVTTIPTIGFNVETVEYK(N)			775.0928	2323.243	0.0207	8.9	Arabidopsis thaliana	15226521	ADP-ribosylation factor 1
1589	JGP_1_1.5362.5466.2	2	12.4	77.5	2.97E+05	(K)IIGVDINPDK(C)		542.3092	1083.604	0.0067	6.2	Zea mays	195626420	alcohol dehydrogenase 1
1016	JGP_1_1.9051.9110.3	3	14.27	77.2	1.67E+05	(K)GSTVAIFGLGAVGLAAAEGAR(I)			630.0186	1888.029	0.0126	6.7	Triticum aestivum	119388723	alcohol dehydrogenase ADH1A
584	JGP_1_2.2899.2982.2	2	16.28	80.9	5.19E+05	(R)TFVHEK(V)		380.7045	760.399	0.0029	3.8	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
608	JGP_1_7.2855.2950.2	2	16.18	85.1	7.49E+06	(R)TFVHEK(V)		380.705	760.399	0.0039	5.1	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
918	JGP_1_7.2685.2780.2	2	14.7	80.4	8.09E+06	(R)TFVHEK(V)		380.7053	760.399	0.0045	5.9	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
950	JGP_1_3.2992.3086.2	2	14.55	78.7	4.58E+05	(R)TFVHEK(V)		380.705	760.399	0.0039	5.1	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
1266	JGP_1_6.3153.3253.2	2	13.38	77.5	1.06E+06	(R)TFVHEK(V)		380.7054	760.399	0.0047	6.2	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
1307	JGP_1_1.2906.2998.2	2	13.25	73.5	2.61E+06	(R)TFVHEK(V)		380.7043	760.399	0.0025	3.3	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
1598	JGP_1_5.2991.3088.2	2	12.37	69.6	5.71E+05	(R)TFVHEK(V)		380.7057	760.399	0.0053	7	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
1744	JGP_1_4.2991.3086.2	2	11.98	65.2	5.57E+05	(R)TFVHEK(V)		380.705	760.399	0.0039	5.1	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
1827	JGP_1_1.3079.3084.2	2	11.73	75.1	1.14E+06	(R)TFVHEK(V)		380.7044	760.399	0.0027	3.6	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
1833	JGP_1_7.3035.3135.2	2	11.73	69.7	1.95E+06	(R)TFVHEK(V)		380.7051	760.399	0.0041	5.4	Arabidopsis thaliana	15228319	aldehyde dehydrogenase 2B4
813	JGP_1_6.6751.6753.2	2	15.12	83.7	1.56E+05	(K)LGDLLAVAR(V)		464.2848	927.562	0.0001	0.1	Zea mays	162457728	"aldo-keto reductase family 1, member B1"
2138	JGP_1_6.7282.7321.2	2	10.9	62.9	1.14E+05	(K)EPIIISIAEK(L)		556.8306	1112.656	-0.0022	-2	Zea mays	162457728	"aldo-keto reductase family 1, member B1"
731	JGP_1_3.6339.6344.3	3	15.53	81.8	1.80E+05	(R)FFGHVEILPDGSR(K)		491.925	1473.748	0.012	8.1	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
796	JGP_1_1.6715.6794.3	3	15.19	69.8	4.34E+05	(R)ALTNAVGNLGITGAYAEAVKK(F)			687.7187	2061.134	0.0077	3.7	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
972	JGP_1_2.5996.6002.3	3	14.47	81.4	2.01E+05	(R)FFGHVEILPDGSR(K)		491.9238	1473.748	0.0084	5.7	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
997	JGP_1_1.7235.7235.2	2	14.34	71.7	2.45E+05	(R)ALTNAVGNLGITGAYAEAVK(K)			967.0244	1933.039	0.0026	1.3	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
1179	JGP_1_2.7975.8064.2	2	13.63	80.4	1.43E+05	(R)QLLNILGAVYR(Y)		630.378	1259.747	0.0017	1.3	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
1263	JGP_1_3.7172.7176.3	3	13.38	67.4	2.89E+05	(K)VAVQLNDTHPTLAIPELmR(L)	m:Oxidized methionine	712.053	2118.138	16.0069	5.6	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
1435	JGP_1_1.6333.6338.3	3	12.86	75.6	7.35E+05	(R)FFGHVEILPDGSR(K)		491.9238	1473.748	0.0084	5.7	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
1444	JGP_1_1.8485.8554.2	2	12.84	75.6	4.83E+05	(R)QLLNILGAVYR(Y)		630.3789	1259.747	0.0035	2.8	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
1691	JGP_1_1.3061.3071.2	2	12.14	64	3.37E+05	(K)mSILNTAGSGK(F)	m:Oxidized methionine	547.7799	1078.556	15.9964	1.4	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
2162	JGP_1_2.6789.6789.3	3	10.84	64.1	1.87E+05	(R)ALTNAVGNLGITGAYAEAVK(K)			645.0177	1933.039	-0.0004	-0.2	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
2171	JGP_1_1.7202.7285.3	3	10.81	64.5	1.35E+06	(K)VAVQLNDTHPTLAIPELmR(L)	m:Oxidized methionine	712.0519	2118.138	16.0036	4.1	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
2422	JGP_1_2.7992.7992.2	2	10.24	69.5	1.17E+05	(R)QLLNILGAVYR(Y)		630.378	1259.747	0.0017	1.3	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
2467	JGP_1_1.9406.9462.4	4	10.15	75.5	2.45E+05	(K)VVFIPNYNVSVAEVLIPGSELSQHISTAGmEASGTSNmK(F)	m:Oxidized methionine		1028.0114	4077.031	31.993	0.8	Oryza sativa	12025466	"alpha 1,4-glucan phosphorylase H isozyme"
686	JGP_1_6.7084.7173.2	2	15.8	79	6.00E+05	(K)LGTIDPYFVK(L)		576.8204	1152.63	0.0036	3.1	Zea mays	162463414	"alpha-1,4-glucan-protein synthase [UDP-forming]"
1890	JGP_1_1.2851.2868.2	2	11.55	70.2	4.67E+05	(K)AFATYTNAK(R)		493.7514	986.494	0.0014	1.4	Arabidopsis thaliana	15232704	alpha-glucan phosphorylase isozyme H
1963	JGP_1_2.2863.2863.2	2	11.34	63.5	2.48E+03	(K)AFATYTNAK(R)		493.7501	986.494	-0.0012	-1.3	Arabidopsis thaliana	15232704	alpha-glucan phosphorylase isozyme H
2037	JGP_1_1.4312.4395.3	3	11.14	77.7	1.82E+05	(R)HDVVFPVR(F)		323.5161	968.531	0.0025	2.6	Arabidopsis thaliana	15232704	alpha-glucan phosphorylase isozyme H
2064	JGP_1_1.2209.2294.2	2	11.08	80.6	3.84E+05	(R)TIAQYAK(E)		397.7244	794.441	0.0008	1.1	Arabidopsis thaliana	15232704	alpha-glucan phosphorylase isozyme H
2335	JGP_1_2.4174.4186.3	3	10.42	67	6.69E+04	(R)HDVVFPVR(F)		323.5152	968.531	-0.0002	-0.2	Arabidopsis thaliana	15232704	alpha-glucan phosphorylase isozyme H
2496	JGP_1_1.2546.2590.2	2	10.07	64.1	3.19E+05	(R)LWEAK(A)	323.6863	646.356	0.0094	14.6	Arabidopsis thaliana	15232704	alpha-glucan phosphorylase isozyme H	

1369	JGP_1_4.10017.10017.3	3	13.03	76	2.55E+04	(R)AmHNVGLAGLTFWSPNINIFR(D)	m:Oxidized methionine	792.0815	2358.218	16.0124	7.4	Hordeum vulgare	18025340	alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I
2047	JGP_1_4.6119.6119.2	2	11.12	64.9	4.16E+04	(R)LGFFDGDPR(Q)		512.2541	1023.489	0.0115	11.2	Hordeum vulgare	18025340	alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I
2286	JGP_1_3.2691.2691.2	2	10.54	62.3	8.53E+04	(R)LTLAEK(V)		337.7069	674.408	-0.0018	-2.7	Hordeum vulgare	18025340	alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I
1987	JGP_1_6.1437.1575.2	2	11.27	61.7	1.08E+05	(R)LIYHGK(Y)		365.7121	730.425	-0.0077	-10.6	Zea mays	226508406	alpha-L-fucosidase 2 precursor
1810	JGP_1_6.7902.7986.2	2	11.79	76.1	4.96E+05	(K)ISGVYDDAKDVAR(K)		704.8614	1408.707	0.0088	6.3	Arabidopsis thaliana	15229641	aluminum-activated malate transporter 9
1885	JGP_1_5.7510.7514.2	2	11.57	75.8	1.41E+05	(K)ISGVYDDAKDVAR(K)		704.8622	1408.707	0.0104	7.4	Arabidopsis thaliana	15229641	aluminum-activated malate transporter 9
1214	JGP_1_6.7428.7512.3	3	13.55	84.3	2.30E+05	(K)LIISILAHR(N)		345.8957	1035.667	0.0052	5	Arabidopsis thaliana	15238320	annexin D2
2405	JGP_1_7.6959.6971.3	3	10.29	80.2	1.68E+05	(K)LIISILAHR(N)		345.8974	1035.667	0.0103	10	Arabidopsis thaliana	15238320	annexin D2
178	JGP_1_7.7156.7164.3	3	19.36	82.8	1.51E+05	(R)SLEEDVAAHVTGDFR(K)		549.2683	1645.782	0.0087	5.3	Zea mays	162459661	annexin2
978	JGP_1_7.2265.2270.3	3	14.46	63.9	5.35E+05	(R)ALGDEIHGK(F)		313.8364	939.489	0.0052	5.6	Zea mays	162459661	annexin2
1592	JGP_1_7.8073.8080.2	2	12.4	81.9	3.83E+05	(K)LLVPLVSAYR(Y)		565.8532	1130.693	0.0059	5.2	Zea mays	162459661	annexin2
1766	JGP_1_6.8306.8310.2	2	11.93	71.7	1.35E+05	(K)LLVPLVSAYR(Y)		565.8497	1130.693	-0.0011	-1	Zea mays	162459661	annexin2
123	JGP_1_6.6494.6500.2	2	20.18	86	5.89E+05	(R)VALGPSGDLSLTSR(I)		686.8778	1372.743	0.0053	3.8	Zea mays	226495363	apospory-associated protein C
488	JGP_1_6.8647.8650.3	3	16.87	83.2	2.64E+05	(K)AFVDLILKPSEEDLK(I)		572.9882	1716.942	0.0082	4.8	Zea mays	226495363	apospory-associated protein C
778	JGP_1_1.5795.5808.2	2	15.27	77.1	2.32E+05	(R)VALGPSGDLSLTSR(I)		686.8726	1372.743	-0.0051	-3.7	Zea mays	226495363	apospory-associated protein C
2464	JGP_1_8.1958.2063.2	2	10.16	78.5	2.61E+06	(R)ALIAEK(N)		322.7037	644.398	0.0024	3.7	Solanum tuberosum	24636598	ascorbate peroxidase
793	JGP_1_7.6314.6436.2	2	15.21	82.1	8.80E+05	(K)EGLLQLPSDK(A)		550.3054	1099.599	0.0042	3.8	Glycine max	351723275	"ascorbate peroxidase 1, cytosolic"
2209	JGP_1_8.6519.6523.2	2	10.74	72.6	4.17E+05	(K)EGLLQLPSDK(A)		550.3023	1099.599	-0.002	-1.9	Glycine max	351723275	"ascorbate peroxidase 1, cytosolic"
341	JGP_1_7.3241.3250.2	2	17.86	87.7	3.65E+05	(R)LPDATQGSDHLR(Q)		655.3299	1309.65	0.003	2.3	Zea mays	162457709	ascorbate peroxidase2
399	JGP_1_8.3115.3232.3	3	17.42	73.2	2.57E+06	(R)LPDATQGSDHLR(Q)		437.224	1309.65	0.0079	6.1	Zea mays	162457709	ascorbate peroxidase2
535	JGP_1_7.6995.7074.3	3	16.58	83.7	8.20E+05	(K)ALLSDPSFRPLVDK(Y)		519.962	1557.863	0.0079	5.1	Zea mays	162457709	ascorbate peroxidase2
720	JGP_1_8.7202.7292.3	3	15.61	83.7	5.70E+05	(K)ALLSDPSFRPLVDK(Y)		519.962	1557.863	0.0079	5.1	Zea mays	162457709	ascorbate peroxidase2
923	JGP_1_7.7145.7150.3	3	14.68	82.7	6.47E+05	(K)ALLSDPSFRPLVDK(Y)		519.9626	1557.863	0.0097	6.2	Zea mays	162457709	ascorbate peroxidase2
1122	JGP_1_8.7256.7256.2	2	13.87	72.9	1.16E+05	(K)ALLSDPSFRPLVDK(Y)		779.4333	1557.863	-0.0042	-2.7	Zea mays	162457709	ascorbate peroxidase2
1472	JGP_1_8.2399.2405.2	2	12.74	72.1	1.09E+06	(K)TGGPFGTmK(N)	m:Oxidized methionine	456.2226	895.434	16.0037	9.6	Zea mays	162457709	ascorbate peroxidase2
1934	JGP_1_8.2216.2315.2	2	11.44	64.4	1.65E+06	(K)TGGPFGTmK(N)	m:Oxidized methionine	456.2215	895.434	16.0015	7.2	Zea mays	162457709	ascorbate peroxidase2
1582	JGP_1_6.7580.7586.2	2	12.42	80.5	2.68E+05	(R)ISLAGLSLAK(C)		486.8091	972.609	0.0021	2.2	Arabidopsis thaliana	15236129	aspartate aminotransferase
2466	JGP_1_8.8124.8199.3	3	10.16	65.5	1.29E+07	(K)LLSQLSALLSDIGLNIK(E)		600.033	1798.068	0.016	8.9	Zea mays	226504772	ATP binding protein
264	JGP_1_1.6562.6572.3	3	18.44	78.4	1.43E+05	(R)VGLTGLTVAEHFR(D)		467.2666	1399.769	0.016	11.4	Zea mays	162462751	"ATP synthase subunit beta, mitochondrial precursor"
864	JGP_1_1.5783.5790.2	2	14.91	81.2	1.41E+05	(R)VLNTGSPITVPVGR(A)		705.4063	1409.811	-0.0058	-4.1	Zea mays	162462751	"ATP synthase subunit beta, mitochondrial precursor"
1234	JGP_1_2.6168.6188.3	3	13.47	62.5	6.79E+04	(R)VGLTGLTVAEHFR(D)		467.2645	1399.769	0.0097	6.9	Zea mays	162462751	"ATP synthase subunit beta, mitochondrial precursor"
536	JGP_1_1.5835.5850.2	2	16.57	83.2	7.67E+03	(R)VVDALGVPIDGK(G)		591.8416	1182.673	0.0031	2.6	Triticum aestivum	81176509	atp1
1615	JGP_1_5.5358.5446.2	2	12.32	81.4	3.32E+06	(K)IFIYSK(E)		385.728	770.445	0.004	5.2	Arabidopsis thaliana	15219635	auxin response factor 14
1679	JGP_1_6.5580.5747.2	2	12.18	78.3	1.03E+06	(K)IFIYSK(E)		385.727	770.445	0.002	2.6	Arabidopsis thaliana	15219635	auxin response factor 14
2517	JGP_1_6.5753.5753.2	2	10.02	73.2	5.70E+05	(K)IFIYSK(E)		385.727	770.445	0.002	2.6	Arabidopsis thaliana	15219635	auxin response factor 14
252	JGP_1_6.2750.2759.2	2	18.54	91	2.61E+05	(R)GQETPGEDPAVSAR(Y)		707.3355	1413.661	0.0033	2.3	Zea mays	195614824	auxin-induced beta-glucosidase
279	JGP_1_5.2580.2584.2	2	18.29	90.7	2.20E+05	(R)GQETPGEDPAVSAR(Y)		707.337	1413.661	0.0063	4.4	Zea mays	195614824	auxin-induced beta-glucosidase
408	JGP_1_4.2523.2657.2	2	17.39	91	7.02E+05	(R)GQETPGEDPAVSAR(Y)		707.337	1413.661	0.0063	4.4	Zea mays	195614824	auxin-induced beta-glucosidase
1186	JGP_1_7.2725.2725.2	2	13.61	70.9	1.17E+04	(R)GQETPGEDPAVSAR(Y)		707.3358	1413.661	0.0039	2.7	Zea mays	195614824	auxin-induced beta-glucosidase
1554	JGP_1_4.2541.2554.3	3	12.47	72.9	1.46E+05	(R)GQETPGEDPAVSAR(Y)		471.8938	1413.661	0.0064	4.5	Zea mays	195614824	auxin-induced beta-glucosidase
1785	JGP_1_7.4020.4020.2	2	11.86	81	6.12E+05	(R)IGFYQR(Y)		392.2119	783.415	0.0017	2.2	Arabidopsis thaliana	15451096	basic chitinase
83	JGP_1_7.4502.4597.3	3	21.04	92.5	8.93E+06	(K)AFGSLAKPGLNDK(I)		439.9137	1317.716	0.0104	7.9	Zea mays	14193761	beta-expansin 1
604	JGP_1_7.1882.1989.2	2	16.19	62.9	1.85E+07	(K)GCGSCYEVR(C)	C:Carbamidomethylation	544.2218	1087.43	0.0068	6.2	Zea mays	14193761	beta-expansin 1
613	JGP_1_4.2018.2141.2	2	16.16	62.9	8.74E+05	(K)GCGSCYEVR(C)	C:Carbamidomethylation	544.2198	1087.43	0.0028	2.6	Zea mays	14193761	beta-expansin 1
649	JGP_1_7.4682.4832.3	3	15.98	80.4	5.18E+06	(K)AFGSLAKPGLNDK(I)		439.9138	1317.716	0.0107	8.1	Zea mays	14193761	beta-expansin 1
673	JGP_1_3.2079.2152.2	2	15.87	63.2	1.26E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	544.2208	1087.43	0.0048	4.4	Zea mays	14193761	beta-expansin 1
730	JGP_1_2.2016.2086.2	2	15.54	61.2	1.05E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	544.2198	1087.43	0.0028	2.6	Zea mays	14193761	beta-expansin 1
870	JGP_1_1.2006.2079.2	2	14.9	60.7	1.20E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	544.2194	1087.43	0.002	1.8	Zea mays	14193761	beta-expansin 1
931	JGP_1_3.4362.4477.3	3	14.65	67.7	5.47E+05	(K)AFGSLAKPGLNDK(I)		439.9128	1317.716	0.0077	5.9	Zea mays	14193761	beta-expansin 1
1157	JGP_1_6.2089.2177.2	2	13.71	60.7	1.98E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	544.2208	1087.43	0.0048	4.4	Zea mays	14193761	beta-expansin 1
1172	JGP_1_7.4258.4361.2	2	13.66	93.9	1.90E+07	(K)GPFSIR(L)		338.6951	676.378	0.0052	7.7	Zea mays	14193761	beta-expansin 1
1295	JGP_1_7.4452.4457.2	2	13.31	90.5	1.30E+07	(K)GPFSIR(L)		338.6952	676.378	0.0054	8	Zea mays	14193761	beta-expansin 1
1322	JGP_1_8.4530.4539.2	2	13.2	66.9	3.60E+05	(K)AFGSLAKPGLNDK(I)		659.3639	1317.716	0.0044	3.3	Zea mays	14193761	beta-expansin 1
1348	JGP_1_7.0729.0735.2	2	13.11	83	1.32E+05	(R)LTSESGK(K)		361.1909	721.373	0.0019	2.6	Zea mays	14193761	beta-expansin 1
1569	JGP_1_7.4514.4607.2	2	12.44	70.4	3.49E+06	(K)AFGSLAKPGLNDK(I)		659.3658	1317.716	0.0082	6.2	Zea mays	14193761	beta-expansin 1
1905	JGP_1_6.4578.4672.2	2	11.52	77.3	2.63E+06	(K)GPFSIR(L)		338.6943	676.378	0.0036	5.4	Zea mays	14193761	beta-expansin 1
1995	JGP_1_8.4499.4620.3	3	11.25	61.3	1.23E+06	(K)AFGSLAKPGLNDK(I)		439.9127	1317.716	0.0074	5.6	Zea mays	14193761	beta-expansin 1
2377	JGP_1_4.4277.4368.2	2	10.35	65	1.33E+06	(K)GPFSIR(L)		338.6942	676.378	0.0034	5.1	Zea mays	14193761	beta-expansin 1
2502	JGP_1_5.4197.4285.2	2	10.06	65	1.59E+06	(K)GPFSIR(L)		338.6939	676.378	0.0028	4.2	Zea mays	14193761	beta-expansin 1

1584	JGP_1_7.8854.8949.2	2	12.42	84	7.06E+05	(K)NVNLPPFSAMTSCGNQPLFK(D)	C:Carbamidomethylation	1111.5611	2222.073	0.0417	18.7	Zea mays	226493239	beta-expansin 1a precursor
1896	JGP_1_2.7614.7708.2	2	11.54	80.8	4.47E+05	(K)NVNLPPFSAMTSCGNEPLFK(D)	C:Carbamidomethylation	1112.0531	2223.057	0.0416	18.7	Zea mays	162458364	beta-expansin 7 precursor
2062	JGP_1_4.8392.8485.2	2	11.09	67.8	2.83E+05	(K)NVNLPPFSAMTSCGNEPLFK(D)	C:Carbamidomethylation	1112.0525	2223.057	0.0404	18.2	Zea mays	162458364	beta-expansin 7 precursor
1091	JGP_1_7.5547.5648.2	2	13.98	79.7	1.59E+07	(R)HSWGAIWR(M)		506.7632	1012.511	0.008	7.9	Triticum aestivum	51242715	beta-expansin TaEXPB4
1455	JGP_1_6.5850.5943.2	2	12.8	75.4	1.45E+06	(R)HSWGAIWR(M)		506.7615	1012.511	0.0046	4.5	Triticum aestivum	51242715	beta-expansin TaEXPB4
1825	JGP_1_7.5354.5462.2	2	11.74	77	2.10E+07	(R)HSWGAIWR(M)		506.7605	1012.511	0.0026	2.5	Triticum aestivum	51242715	beta-expansin TaEXPB4
1853	JGP_1_2.5089.5161.3	3	11.67	69.4	7.43E+05	(R)HSWGAIWR(M)		338.1765	1012.511	0.0038	3.7	Triticum aestivum	51242715	beta-expansin TaEXPB4
2107	JGP_1_4.5487.5492.2	2	10.99	68.8	6.72E+05	(R)HSWGAIWR(M)		506.7577	1012.511	-0.003	-3	Triticum aestivum	51242715	beta-expansin TaEXPB4
2153	JGP_1_4.5582.5587.3	3	10.86	82.8	7.00E+05	(R)HSWGAIWR(M)		338.1771	1012.511	0.0056	5.5	Triticum aestivum	51242715	beta-expansin TaEXPB4
2212	JGP_1_6.5843.5939.3	3	10.73	79.5	1.61E+06	(R)HSWGAIWR(M)		338.1769	1012.511	0.005	4.9	Triticum aestivum	51242715	beta-expansin TaEXPB4
2376	JGP_1_7.5548.5649.3	3	10.36	84.5	9.69E+06	(R)HSWGAIWR(M)		338.1781	1012.511	0.0086	8.5	Triticum aestivum	51242715	beta-expansin TaEXPB4
2521	JGP_1_7.5367.5467.3	3	10.01	83.5	1.50E+07	(R)HSWGAIWR(M)		338.1779	1012.511	0.008	7.9	Triticum aestivum	51242715	beta-expansin TaEXPB4
115	JGP_1_3.6242.6332.2	2	20.32	90.3	1.30E+06	(K)YFVGSVLSGGGSVPAEK(A)		827.4306	1653.848	0.0057	3.4	Zea mays	162464328	beta-glucanase precursor
343	JGP_1_4.6493.6506.2	2	17.84	82.5	4.39E+05	(K)YFVGSVLSGGGSVPAEK(A)		827.4321	1653.848	0.0087	5.2	Zea mays	162464328	beta-glucanase precursor
382	JGP_1_3.2046.2121.2	2	17.53	76.8	9.96E+05	(K)IGQmSQIER(A)	m:Oxidized methionine	539.2738	1061.541	15.9995	4.3	Zea mays	162464328	beta-glucanase precursor
699	JGP_1_3.3666.3766.2	2	15.7	84.7	7.29E+05	(K)SVDQLPmNYGDK(R)	m:Oxidized methionine	691.8197	1366.631	16.0014	4.7	Zea mays	162464328	beta-glucanase precursor
709	JGP_1_4.1989.2071.2	2	15.66	76.1	4.25E+05	(K)IGQmSQIER(A)	m:Oxidized methionine	539.273	1061.541	15.9979	2.8	Zea mays	162464328	beta-glucanase precursor
891	JGP_1_3.7113.7119.3	3	14.82	75.8	1.90E+05	(R)ATGIPYTFAPCVAVCR(D)	C:Carbamidomethylation	594.9638	1782.867	0.0103	5.8	Zea mays	162464328	beta-glucanase precursor
954	JGP_1_3.7102.7189.2	2	14.54	83.2	3.78E+05	(R)ATGIPYTFAPCVAVCR(D)	C:Carbamidomethylation	891.9387	1782.867	0.0036	2	Zea mays	162464328	beta-glucanase precursor
998	JGP_1_3.2689.2781.2	2	14.34	79.8	9.11E+05	(K)ASASVWQK(M)		438.7336	876.457	0.0025	2.9	Zea mays	162464328	beta-glucanase precursor
1181	JGP_1_4.5664.5674.4	4	13.62	67.4	3.52E+05	(K)ILVAGSHAHDLGSQCGGWTIK(W)	C:Carbamidomethylation	552.5345	2207.103	0.0136	6.1	Zea mays	162464328	beta-glucanase precursor
1402	JGP_1_3.1552.1631.2	2	12.96	83.2	7.99E+05	(K)HFVGDGGTTR(G)		523.7555	1046.501	0.0023	2.2	Zea mays	162464328	beta-glucanase precursor
1418	JGP_1_4.2713.2716.2	2	12.92	73.4	3.42E+05	(K)ASASVWQK(M)		438.7334	876.457	0.0021	2.4	Zea mays	162464328	beta-glucanase precursor
1448	JGP_1_4.7380.7395.2	2	12.82	82.5	1.74E+05	(R)ATGIPYTFAPCVAVCR(D)	C:Carbamidomethylation	891.9381	1782.867	0.0024	1.3	Zea mays	162464328	beta-glucanase precursor
1856	JGP_1_3.3343.3358.2	2	11.66	72.4	5.35E+04	(K)IGQMSQIER(A)		531.2735	1061.541	-0.0011	-1	Zea mays	162464328	beta-glucanase precursor
1948	JGP_1_4.1492.1567.2	2	11.4	78.8	3.19E+05	(K)HFVGDGGTTR(G)		523.7555	1046.501	0.0023	2.2	Zea mays	162464328	beta-glucanase precursor
2444	JGP_1_5.1463.1471.2	2	10.2	71.1	1.00E+05	(K)HFVGDGGTTR(G)		523.7567	1046.501	0.0047	4.5	Zea mays	162464328	beta-glucanase precursor
201	JGP_1_5.5437.5443.3	3	19.09	86.4	4.18E+05	(K)YGQDATNVGDEGGFAPNIQENK(E)			775.3599	2324.043	0.0226	9.7	Arabidopsis thaliana	15227987	bifunctional enolase 2/transcriptional activator
505	JGP_1_5.5123.5123.3	3	16.76	83.5	1.60E+05	(K)KYGQDATNVGDEGGFAPNIQENK(E)			818.0607	2452.137	0.03	12.2	Arabidopsis thaliana	15227987	bifunctional enolase 2/transcriptional activator
713	JGP_1_5.5458.5458.2	2	15.65	84.1	2.31E+05	(K)YGQDATNVGDEGGFAPNIQENK(E)			1162.5283	2324.043	0.0068	2.9	Arabidopsis thaliana	15227987	bifunctional enolase 2/transcriptional activator
1170	JGP_1_5.5114.5193.2	2	13.66	78.7	2.05E+05	(K)TYDLNFK(E)		450.7299	900.446	0.0064	7.1	Arabidopsis thaliana	15227987	bifunctional enolase 2/transcriptional activator
1267	JGP_1_2.5228.5228.2	2	13.37	87.8	4.38E+05	(K)EGLELLK(T)		401.2408	801.472	0.0027	3.3	Arabidopsis thaliana	15227987	bifunctional enolase 2/transcriptional activator
1893	JGP_1_2.4778.4783.3	3	11.55	70.4	3.76E+04	(K)YGQDATNVGDEGGFAPNIQENK(E)			775.3578	2324.043	0.0163	7	Arabidopsis thaliana	15227987	bifunctional enolase 2/transcriptional activator
2336	JGP_1_5.0780.0786.2	2	10.42	71.5	8.02E+03	(K)TGAPCR(S)	C:Carbamidomethylation	331.1625	661.309	0.0091	13.8	Arabidopsis thaliana	15227987	bifunctional enolase 2/transcriptional activator
2426	JGP_1_8.4129.4228.2	2	10.24	79.4	1.07E+06	(R)TFSAGVLK(K)		411.7411	822.472	0.0029	3.6	Arabidopsis thaliana	15235728	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein
1865	JGP_1_7.3119.3216.2	2	11.63	87.8	1.26E+06	(R)IISSIEQK(E)		459.27	917.53	0.0025	2.7	Oryza sativa	303859	brain specific protein
644	JGP_1_8.6904.6909.3	3	16.02	80.2	1.17E+05	(K)EAFSLFDKDGDGCITTK(E)	C:Carbamidomethylation	635.3084	1903.874	0.0364	19.1	Arabidopsis thaliana	15225840	calmodulin 5
1100	JGP_1_1.6169.6203.3	3	13.95	78.6	6.72E+04	(R)VFDKDQNGFISAAELR(H)		603.9776	1809.913	0.0053	2.9	Arabidopsis thaliana	15225840	calmodulin 5
421	JGP_1_5.1935.2018.2	2	17.33	89.4	9.42E+05	(K)AAFDAAEK(K)		411.7047	822.399	0.0029	3.5	Triticum aestivum	56606827	calreticulin-like protein
830	JGP_1_3.5547.5626.2	2	15.04	88.5	5.84E+05	(K)EAVNVSLENLK(T)		608.3347	1215.658	0.0042	3.4	Zea mays	162459147	carbonic anhydrase
1121	JGP_1_6.6211.6219.2	2	13.87	78.3	3.43E+05	(K)EAVNVSLENLK(T)		608.3334	1215.658	0.0016	1.3	Zea mays	162459147	carbonic anhydrase
1300	JGP_1_2.5208.5286.2	2	13.28	76.1	7.39E+05	(K)EAVNVSLENLK(T)		608.3349	1215.658	0.0046	3.8	Zea mays	162459147	carbonic anhydrase
1367	JGP_1_6.4638.4643.2	2	13.04	81.3	2.36E+05	(K)TYPFVK(E)		377.7097	754.413	-0.0013	-1.7	Oryza sativa	3345477	carbonic anhydrase
1552	JGP_1_2.5123.5196.3	3	12.47	88.5	3.51E+05	(K)KPELFEPLK(A)		367.552	1100.635	0.0064	5.8	Oryza sativa	3345477	carbonic anhydrase
1567	JGP_1_1.4144.4225.2	2	12.44	81.7	4.06E+05	(K)TYPFVK(E)		377.7115	754.413	0.0023	3.1	Oryza sativa	3345477	carbonic anhydrase
1700	JGP_1_7.4432.4439.2	2	12.13	82.3	2.88E+05	(K)TYPFVK(E)		377.7115	754.413	0.0023	3.1	Oryza sativa	3345477	carbonic anhydrase
1869	JGP_1_1.5489.5581.2	2	11.61	83.1	1.14E+06	(K)EAVNVSLENLK(T)		608.3332	1215.658	0.0012	1	Zea mays	162459147	carbonic anhydrase
1936	JGP_1_8.4404.4407.2	2	11.43	77.9	4.01E+05	(K)TYPFVK(E)		377.7119	754.413	0.0031	4.1	Oryza sativa	3345477	carbonic anhydrase

1942	JGP_1_5.4383.4393.2	2	11.41	74.1	1.79E+05	(K)TYPFVK(E)		377.7116	754.413	0.0025	3.3	Oryza sativa	3345477	carbonic anhydrase
2004	JGP_1_2.3962.4047.2	2	11.22	76.1	3.01E+05	(K)TYPFVK(E)		377.7117	754.413	0.0027	3.6	Oryza sativa	3345477	carbonic anhydrase
2012	JGP_1_3.4234.4317.2	2	11.2	73.9	2.63E+05	(K)TYPFVK(E)		377.7116	754.413	0.0025	3.3	Oryza sativa	3345477	carbonic anhydrase
2096	JGP_1_4.5753.5758.2	2	11.01	66.3	3.41E+05	(K)EAVNVSLENLK(T)		608.3293	1215.658	-0.0066	-5.4	Zea mays	162459147	carbonic anhydrase
2174	JGP_1_4.4310.4312.2	2	10.8	67.2	1.44E+05	(K)TYPFVK(E)		377.7126	754.413	0.0045	6	Oryza sativa	3345477	carbonic anhydrase
2246	JGP_1_2.3848.3937.2	2	10.65	69.3	6.10E+05	(R)NIASmVPPYDK(I)	m:Oxidized methionine	625.8084	1234.614	15.9959	0.8	Zea mays	162459147	carbonic anhydrase
2465	JGP_1_8.6151.6155.2	2	10.16	74	2.91E+05	(K)EAVNVSLENLK(T)		608.3344	1215.658	0.0036	2.9	Zea mays	162459147	carbonic anhydrase
2519	JGP_1_3.5432.5512.3	3	10.01	79.8	2.24E+05	(K)KPELFEPLK(A)		367.5522	1100.635	0.007	6.4	Oryza sativa	3345477	carbonic anhydrase
2163	JGP_1_8.3166.3287.2	2	10.84	81.5	2.86E+06	(K)GPLTIR(V)		328.7123	656.409	0.0083	12.7	Arabidopsis thaliana	15226241	CBL-interacting serine/threonine-protein kinase 13
1171	JGP_1_5.9759.9850.2	2	13.66	82.6	1.30E+05	(K)LYEVVPPILTELGK(V)		785.9596	1570.909	0.0029	1.8	Oryza sativa	11066954	citrate synthase
1441	JGP_1_6.5860.5865.3	3	12.85	84.3	1.86E+05	(R)ALGLPLERPK(S)		365.2301	1093.673	0.0029	2.7	Nicotiana tabacum	1556429	citrate synthase
1606	JGP_1_5.5604.5609.3	3	12.35	82.8	2.57E+05	(R)ALGLPLERPK(S)		365.2305	1093.673	0.0041	3.8	Nicotiana tabacum	1556429	citrate synthase
1647	JGP_1_1.5267.5273.3	3	12.23	78	1.30E+05	(R)ALGLPLERPK(S)		365.2301	1093.673	0.0029	2.7	Nicotiana tabacum	1556429	citrate synthase
1655	JGP_1_1.9221.9290.2	2	12.22	83.3	1.50E+05	(K)LYEVVPPILTELGK(V)		785.9595	1570.909	0.0027	1.7	Oryza sativa	11066954	citrate synthase
1916	JGP_1_5.2165.2168.2	2	11.47	76.5	1.94E+05	(K)EQVDALSK(E)		445.2358	889.462	0.0018	2	Oryza sativa	11066954	citrate synthase
1966	JGP_1_5.9790.9810.3	3	11.34	64.8	7.75E+04	(K)LYEVVPPILTELGK(V)		524.3084	1570.909	0.0016	1	Oryza sativa	11066954	citrate synthase
2180	JGP_1_2.8729.8732.2	2	10.79	76.9	8.98E+04	(K)LYEVVPPILTELGK(V)		785.9592	1570.909	0.0021	1.3	Oryza sativa	11066954	citrate synthase
2251	JGP_1_2.5059.5063.3	3	10.64	74.3	7.33E+04	(R)ALGLPLERPK(S)		365.231	1093.673	0.0056	5.2	Nicotiana tabacum	1556429	citrate synthase
582	JGP_1_6.6351.6450.2	2	16.29	84.6	8.49E+05	(R)CPGVVSCADIVAMAAR(D)	C:Carbamidomethylation	838.9109	1676.792	0.0228	13.6	Arabidopsis thaliana	17530547	class III peroxidase ATP32
958	JGP_1_7.6190.6198.2	2	14.51	74.7	4.33E+05	(R)CPGVVSCADIVAMAAR(D)	C:Carbamidomethylation	838.91	1676.792	0.021	12.5	Arabidopsis thaliana	17530547	class III peroxidase ATP32
937	JGP_1_4.5970.5985.2	2	14.63	79.5	1.60E+05	(K)EVPTSFGFDTACK(V)	C:Carbamidomethylation	729.8365	1458.657	0.0088	6	Arabidopsis thaliana	3377841	contains similarity to
phosphofructokinases (Pfam	" PFK.hmm, score"	36.60)												
1260	JGP_1_3.2837.2921.2	2	13.39	94.5	4.72E+06	(K)ILYAR(H)	318.199	635.388	0.0032	5	Arabidopsis thaliana	18411857	COP9 signalosome complex subunit 1	
1881	JGP_1_4.2824.2916.2	2	11.58	92.3	8.07E+06	(K)ILYAR(H)	318.1994	635.388	0.004	6.3	Arabidopsis thaliana	18411857	COP9 signalosome complex subunit 1	
2206	JGP_1_2.2761.2841.2	2	10.74	85.5	6.11E+05	(K)ILYAR(H)	318.1983	635.388	0.0018	2.8	Arabidopsis thaliana	18411857	COP9 signalosome complex subunit 1	
2343	JGP_1_1.2793.2888.2	2	10.41	81.9	1.37E+06	(K)ILYAR(H)	318.1983	635.388	0.0018	2.8	Arabidopsis thaliana	18411857	COP9 signalosome complex subunit 1	
405	JGP_1_8.4283.4283.2	2	17.4	79.1	3.07E+05	(R)AVVVHADPDDLGK(G)		668.351	1335.69	0.0044	3.3	Arabidopsis thaliana	15238738	copper/zinc superoxide dismutase 3
514	JGP_1_8.4216.4322.3	3	16.72	83.3	2.42E+06	(R)AVVVHADPDDLGK(G)		445.9044	1335.69	0.0083	6.2	Arabidopsis thaliana	15238738	copper/zinc superoxide dismutase 3
2030	JGP_1_7.4253.4253.3	3	11.16	73.4	3.51E+05	(R)AVVVHADPDDLGK(G)		445.9042	1335.69	0.0077	5.8	Arabidopsis thaliana	15238738	copper/zinc superoxide dismutase 3
632	JGP_1_8.6924.6924.3	3	16.09	74.4	1.08E+05	(R)AFVVHELEDDLGK(G)		491.2542	1471.743	0.0053	3.6	Triticum aestivum	1572627	Cu/Zn superoxide dismutase
20	JGP_1_8.7002.7005.2	2	22.92	94.2	2.80E+05	(K)VYFDIEIDGKPAGR(V)		790.4121	1579.812	0.0054	3.4	Triticum aestivum	82547208	cyclophilin
59	JGP_1_8.9471.9547.2	2	21.56	92.8	3.62E+05	(R)IIPSFMIQGGDFTLGDGR(G)			962.4883	1923.963	0.006	3.1	Triticum aestivum	82547214	cyclophilin
64	JGP_1_8.8966.9049.2	2	21.38	88.7	4.62E+05	(R)IIPSFmIQGGDFTLGDGR(G)	m:Oxidized methionine	970.4843	1923.963	15.998	1.6	Triticum aestivum	82547214	cyclophilin
65	JGP_1_8.7566.7570.2	2	21.36	91	7.58E+05	(R)VIPDFMCQGGDFTR(G)	C:Carbamidomethylation	821.8765	1642.735	0.0105	6.4	Triticum aestivum	14334173	cyclophilin
257	JGP_1_8.10676.10690.3	3	18.48	77	1.47E+05	(R)DTNGSQFFITTVTTSWLDGK(H)			740.0326	2218.066	0.017	7.7	Triticum aestivum	82547216	cyclophilin
321	JGP_1_8.9477.9545.3	3	17.98	89.9	4.89E+05	(R)IIPSFMIQGGDFTLGDGR(G)			641.9969	1923.963	0.0128	6.7	Triticum aestivum	82547214	cyclophilin
377	JGP_1_8.6425.6508.2	2	17.57	77.3	1.05E+06	(R)VIPDFmCQGGDFTR(G)	C:Carbamidomethylation	m:Oxidized methionine	829.8745	1642.735	16.0065	7	Triticum aestivum	14334173	cyclophilin
428	JGP_1_3.5768.5789.2	2	17.28	75.6	1.11E+05	(R)VIPDFmCQGGDFTR(G)	C:Carbamidomethylation	m:Oxidized methionine	829.8757	1642.735	16.0089	8.4	Triticum aestivum	14334173	cyclophilin
465	JGP_1_1.5759.5762.2	2	17.06	76.7	4.79E+04	(R)VIPDFmCQGGDFTR(G)	C:Carbamidomethylation	m:Oxidized methionine	829.8787	1642.735	16.0149	12	Triticum aestivum	14334173	cyclophilin
499	JGP_1_7.7606.7629.2	2	16.82	87	5.48E+03	(R)VIPDFMCQGGDFTR(G)	C:Carbamidomethylation	821.878	1642.735	0.0135	8.2	Triticum aestivum	14334173	cyclophilin
696	JGP_1_8.7592.7602.3	3	15.72	77.9	8.59E+04	(R)VIPDFMCQGGDFTR(G)	C:Carbamidomethylation	548.2565	1642.735	0.0197	12	Triticum aestivum	14334173	cyclophilin
743	JGP_1_8.8984.9059.3	3	15.46	80.2	4.23E+05	(R)IIPSFmIQGGDFTLGDGR(G)	m:Oxidized methionine	647.327	1923.963	16.0031	4.2	Triticum aestivum	82547214	cyclophilin
754	JGP_1_8.5851.5854.2	2	15.4	81.4	6.11E+05	(R)VLSGMDVVYK(V)		555.7976	1110.586	0.0016	1.4	Triticum aestivum	82547214	cyclophilin
1278	JGP_1_2.5444.5454.2	2	13.35	75.6	2.19E+04	(R)VIPDFmCQGGDFTR(G)	C:Carbamidomethylation	m:Oxidized methionine	829.8791	1642.735	16.0157	12.5	Triticum aestivum	14334173	cyclophilin
1781	JGP_1_8.10671.10671.2	2	11.87	66.5	1.36E+05	(R)DTNGSQFFITTVTTSWLDGK(H)			1109.5394	2218.066	0.0053	2.4	Triticum aestivum	82547216	cyclophilin
2440	JGP_1_8.4213.4217.2	2	10.21	65	1.07E+06	(R)VLSGmDVVYK(V)	m:Oxidized methionine		563.7962	1110.586	15.9988	3.4	Triticum aestivum	82547214	cyclophilin
1533	JGP_1_7.4264.4276.2	2	12.53	69.2	5.23E+05	(R)VVEGMDVVK(A)		488.2647	975.518	0.0042	4.3	Oryza sativa	600769	cyclophilin 2
724	JGP_1_8.8302.8311.2	2	15.59	78.2	1.59E+05	(K)VYFDISIGNPVGK(N)		704.8795	1408.747	0.0046	3.3	Triticum aestivum	37788308	cyclophilin-like protein
230	JGP_1_8.7251.7385.3	3	18.79	78.3	1.44E+05	(R)WVIQNGGLTTEANYPYQAR(R)			727.6994	2181.072	0.0113	5.2	Zea mays	226509942	cysteine protease precursor

1068	JGP_1_8.7261.7370.2	2	14.07	60.4	1.44E+05	(R)WVIQNGGLTTEANYPYQAR(R)		1091.0467	2181.072	0.0138	6.3	Zea mays	226509942 cysteine protease precursor
887	JGP_1_8.6501.6505.3	3	14.85	61.3	1.52E+05	(K)VWEKPWENFK(E)	454.9047	1362.684	0.0154	11.3	Zea mays	1498133	cysteine proteinase inhibitor
454	JGP_1_7.6370.6370.2	2	17.13	80.5	1.74E+05	(K)LVSLSEQELVDCDTK(K) C:Carbamidomethylation	868.4297	1735.842	0.0103	5.9	Glycine max	351726339	cysteine proteinase precursor
636	JGP_1_8.7269.7354.2	2	16.08	83.8	1.49E+06	(R)TDLIAYLK(E)	468.7762	936.54	0.0051	5.4	Zea mays	195619230	cytochrome c
975	JGP_1_8.7434.7442.2	2	14.47	77.4	2.02E+04	(R)TDLIAYLK(E)	468.776	936.54	0.0047	5	Zea mays	195619230	cytochrome c
1043	JGP_1_8.7716.7737.2	2	14.16	80.9	6.89E+04	(R)TDLIAYLK(E)	468.7767	936.54	0.0061	6.5	Zea mays	195619230	cytochrome c
1339	JGP_1_8.6510.6593.3	3	13.16	84.5	9.19E+05	(K)ERTDLIAYLK(E)	407.901	1221.684	0.0047	3.8	Zea mays	195619230	cytochrome c
2354	JGP_1_8.6614.6619.2	2	10.4	80.1	4.21E+05	(K)ERTDLIAYLK(E)	611.3471	1221.684	0.0032	2.6	Zea mays	195619230	cytochrome c
1141	JGP_1_8.1939.1949.2	2	13.79	73.9	4.55E+05	(R)FPTTNQTR(H)	482.7473	964.485	0.0027	2.8	Arabidopsis thaliana	15219886	cytochrome C oxidase 6B
774	JGP_1_8.1520.1688.2	2	15.3	91.2	1.11E+07	(K)YIPGTK(M)	339.6965	678.382	0.0036	5.3	Arabidopsis thaliana	15234910	cytochrome c-2
1079	JGP_1_8.7211.7295.2	2	14.01	74.5	1.09E+06	(R)ADLIAYLK(E)	453.7702	906.529	0.0036	4	Arabidopsis thaliana	15234910	cytochrome c-2
1712	JGP_1_7.7054.7141.2	2	12.09	63.4	1.13E+05	(R)ADLIAYLK(E)	453.7691	906.529	0.0014	1.6	Arabidopsis thaliana	15234910	cytochrome c-2
2273	JGP_1_8.6504.6520.2	2	10.6	76	1.08E+05	(K)MVFPGLK(K)	396.2293	791.448	0.0029	3.7	Arabidopsis thaliana	15234910	cytochrome c-2
2447	JGP_1_8.3706.3787.2	2	10.2	72	3.51E+06	(R)LLEVDNR(V)	429.7398	858.468	0.0044	5.1	Triticum aestivum	14321	cytochrome-c oxidase
70	JGP_1_6.8947.9027.2	2	21.2	88.4	9.71E+04	(K)TVIWNGPmGVFEFEK(F) m:Oxidized methionine	885.4341	1753.862	15.9991	2.4	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
82	JGP_1_6.7862.7940.3	3	21.04	94.8	5.19E+06	(K)LASVADLYVNDAFGTAHR(A)		640.6639	1919.961	0.0161	8.4	Zea mays	28172915 cytosolic 3-phosphoglycerate kinase
87	JGP_1_6.9483.9557.3	3	20.89	94.2	2.72E+05	(K)GVSLLLPTDIVVADK(F)	513.9735	1539.899	0.0067	4.4	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
140	JGP_1_6.8642.8765.3	3	19.83	95.5	1.39E+06	(K)IVPATAIPDDWmGLDVGPDATK(T) m:Oxidized methionine	766.7213	2282.137	16.012	7.5	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
150	JGP_1_6.8525.8610.3	3	19.6	82	1.43E+06	(K)SLVEEDKLELATSLIEK(A)	639.6906	1917.043	0.0146	7.6	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
168	JGP_1_6.1422.1507.2	2	19.42	94.7	3.03E+06	(K)FAADAESK(I)	419.7024	838.394	0.0034	4.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
228	JGP_1_5.9105.9120.3	3	18.81	90.4	1.03E+05	(K)GVSLLLPTDIVVADK(F)	513.9728	1539.899	0.0046	3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
248	JGP_1_6.9511.9558.2	2	18.58	94.2	2.46E+05	(K)IVPATAIPDDWMGLDVGPDATK(T)		1141.5749	2282.137	0.0052	2.3	Zea mays	28172915 cytosolic 3-phosphoglycerate kinase
280	JGP_1_6.8265.8345.2	2	18.28	94.5	5.25E+06	(K)IGVIESLLAK(V)	521.833	1042.651	0.0081	7.7	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
323	JGP_1_6.9488.9560.3	3	17.97	89.2	4.92E+05	(K)IVPATAIPDDWMGLDVGPDATK(T)		761.3892	2282.137	0.0157	6.9	Zea mays	28172915 cytosolic 3-phosphoglycerate kinase
367	JGP_1_5.7468.7548.3	3	17.62	86.9	1.05E+06	(K)LASVADLYVNDAFGTAHR(A)		640.6628	1919.961	0.0128	6.7	Zea mays	28172915 cytosolic 3-phosphoglycerate kinase
371	JGP_1_5.8050.8155.3	3	17.59	83.6	4.13E+05	(K)SLVEEDKLELATSLIEK(A)	639.6881	1917.043	0.0071	3.7	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
433	JGP_1_6.7164.7180.3	3	17.27	80.5	4.27E+05	(K)LASVADLYVNDAFGTAHR(A)		640.6623	1919.961	0.0113	5.9	Zea mays	28172915 cytosolic 3-phosphoglycerate kinase
447	JGP_1_6.10132.10208.3	3	17.19	83.5	2.27E+04	(K)VDILILGGGmIYTFYK(A) m:Oxidized methionine	606.9985	1802.976	16.0048	5.5	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
461	JGP_1_6.8367.8447.3	3	17.08	84.1	1.62E+06	(K)SLVEEDKLELATSLIEK(A)	639.6894	1917.043	0.011	5.7	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
559	JGP_1_5.1304.1378.2	2	16.44	86.1	8.80E+05	(K)FAADAESK(I)	419.702	838.394	0.0026	3.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
561	JGP_1_6.7427.7511.3	3	16.42	79.7	5.90E+05	(K)KLASVADLYVNDAFGTAHR(A)		683.3612	2048.056	0.0131	6.4	Zea mays	28172915 cytosolic 3-phosphoglycerate kinase
592	JGP_1_5.7849.7997.2	2	16.23	85.3	1.79E+06	(K)IGVIESLLAK(V)	521.8312	1042.651	0.0045	4.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
627	JGP_1_6.8691.8766.2	2	16.11	89.4	6.32E+05	(K)IVPATAIPDDWmGLDVGPDATK(T) m:Oxidized methionine	1149.5741	2282.137	16.0036	3.8	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
666	JGP_1_6.10106.10175.2	2	15.9	79.3	1.94E+05	(K)VDILILGGGmIYTFYK(A) m:Oxidized methionine	909.9955	1802.976	16.0076	7	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
721	JGP_1_7.8078.8084.2	2	15.6	89	4.49E+05	(K)IGVIESLLAK(V)	521.8327	1042.651	0.0075	7.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
748	JGP_1_5.8319.8400.3	3	15.43	85.2	6.42E+05	(K)IVPATAIPDDWmGLDVGPDATK(T) m:Oxidized methionine	766.7216	2282.137	16.0129	7.8	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
948	JGP_1_8.8056.8150.2	2	14.56	79.3	1.06E+05	(K)IGVIESLLAK(V)	521.8288	1042.651	-0.0003	-0.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1019	JGP_1_5.2869.2973.2	2	14.25	80.4	1.70E+06	(K)LAELTTTK(G)	438.7563	876.504	0.0016	1.9	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1062	JGP_1_2.7107.7184.2	2	14.1	81.3	1.74E+05	(K)IGVIESLLAK(V)	521.8307	1042.651	0.0035	3.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1131	JGP_1_6.7455.7540.3	3	13.84	81.9	1.57E+06	(K)YLKPAVAGFLMQK(E)	489.2823	1465.824	0.0088	6	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1169	JGP_1_6.6810.6894.2	2	13.67	67.7	8.40E+05	(K)YLKPAVAGFLmQK(E) m:Oxidized methionine	741.4154	1465.824	16	3.4	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1177	JGP_1_1.7566.7644.2	2	13.64	80.1	3.57E+05	(K)IGVIESLLAK(V)	521.8304	1042.651	0.0029	2.7	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1213	JGP_1_6.2713.2819.2	2	13.55	77.8	2.08E+06	(K)KLAELTTTK(G)	502.8045	1004.599	0.0031	3.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1256	JGP_1_4.7767.7786.2	2	13.41	79.9	9.20E+04	(K)IGVIESLLAK(V)	521.8299	1042.651	0.0019	1.8	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1309	JGP_1_6.8503.8503.2	2	13.24	70.1	2.73E+05	(K)SLVEEDKLELATSLIEK(A)	959.0275	1917.043	0.0051	2.6	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1325	JGP_1_5.9050.9118.2	2	13.19	87.5	1.63E+06	(K)GVSLLLPTDIVVADK(F)	770.4572	1539.899	0.0079	5.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1371	JGP_1_6.9991.10065.3	3	13.03	83.7	2.36E+05	(K)GVSLLLPTDIVVADKFAADAESK(I)		787.102	2359.276	0.0159	6.8	Zea mays	28172915 cytosolic 3-phosphoglycerate kinase
1383	JGP_1_6.7918.7922.4	4	13	74.3	2.19E+05	(K)LASVADLYVNDAFGTAHR(A)		480.7487	1919.961	0.012	6.2	Zea mays	28172915 cytosolic 3-phosphoglycerate kinase

1388	JGP_1_6.6781.6868.3	3	12.99	68.3	5.07E+06	(K)YLKPAVAGFLmQK(E)	m:Oxidized methionine	494.6141	1465.824	16.0042	6.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1405	JGP_1_5.8324.8338.2	2	12.96	76.3	2.11E+05	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine	1149.5721	2282.137	15.9996	2	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1414	JGP_1_6.1265.1347.2	2	12.93	70.7	6.96E+04	(K)FAADAESK(I)		419.7023	838.394	0.0032	3.8	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1440	JGP_1_6.3015.3123.2	2	12.85	74.8	4.55E+06	(K)LAELTTTK(G)		438.7577	876.504	0.0044	5.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1459	JGP_1_6.9417.9485.2	2	12.79	85.5	2.92E+06	(K)GVSLLLPTDIVVADK(F)		770.4542	1539.899	0.0019	1.2	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1541	JGP_1_5.7085.7085.3	3	12.51	65.9	1.73E+04	(K)KLASVADLYVNDAFGTAHR(A)		683.3577	2048.056	0.0026	1.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1862	JGP_1_6.14482.14586.3	3	11.64	64.7	1.15E+04	(K)SLVEEDKLELATSLIEK(A)		639.6877	1917.043	0.0059	3.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1875	JGP_1_3.7531.7534.2	2	11.59	73.7	1.06E+05	(K)IGVIESLLAK(V)		521.8307	1042.651	0.0035	3.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1911	JGP_1_5.2600.2604.2	2	11.5	60.1	6.40E+05	(K)KLAELTTTK(G)		502.8042	1004.599	0.0025	2.5	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1915	JGP_1_6.14525.14598.3	3	11.49	72.5	1.15E+04	(K)SLVEEDKLELATSLIEK(A)		639.6877	1917.043	0.0059	3.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
1939	JGP_1_7.2480.2480.2	2	11.42	67.1	1.47E+05	(K)KLAELTTTK(G)		502.8028	1004.599	-0.0003	-0.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
2006	JGP_1_6.1394.1513.2	2	11.22	66.9	2.69E+06	(K)AQGYSVGK(S)		405.2129	809.415	0.0033	4.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
2126	JGP_1_7.7096.7101.3	3	10.93	61.6	1.25E+05	(K)YLKPAVAGFLMQK(E)		489.2748	1465.824	-0.0137	-9.4	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
2177	JGP_1_6.9550.9627.2	2	10.8	75	3.56E+06	(K)GVSLLLPTDIVVADK(F)		770.4581	1539.899	0.0097	6.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
2227	JGP_1_5.1339.1418.2	2	10.7	72.6	8.19E+05	(K)AQGYSVGK(S)		405.2121	809.415	0.0017	2.1	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
2240	JGP_1_5.7074.7147.3	3	10.67	64	3.04E+05	(K)YLKPAVAGFLMQK(E)		489.2825	1465.824	0.0094	6.4	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
2299	JGP_1_6.8693.8698.3	3	10.51	60.1	2.53E+05	(K)SLVEEDKLELATSLIEK(A)		639.6881	1917.043	0.0071	3.7	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
2363	JGP_1_6.7893.7903.2	2	10.39	67.6	3.25E+05	(K)LASVADLYVNDAFGTAHR(A)			960.4885	1919.961	0.0087	4.5	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
2399	JGP_1_5.9189.9194.2	2	10.31	71.2	2.10E+04	(K)GVSLLLPTDIVVADK(F)		770.4573	1539.899	0.0081	5.3	Zea mays	28172915	cytosolic 3-phosphoglycerate kinase
554	JGP_1_7.6165.6165.3	3	16.47	84.1	1.07E+05	(K)LVEIPFKPAR(V)		390.5752	1169.704	0.0069	5.9	Nicotiana tabacum		11066033	cytosolic aconitase
587	JGP_1_2.5449.5522.3	3	16.27	80.7	5.22E+05	(K)LVEIPFKPAR(V)		390.5761	1169.704	0.0096	8.2	Nicotiana tabacum		11066033	cytosolic aconitase
474	JGP_1_7.6756.6759.3	3	16.97	84.4	3.16E+05	(K)QmGLSDKDIVALSGGHTLGR(C)	m:Oxidized methionine	691.0157	2055.065	15.9674	-13.3	Nicotiana tabacum	1389654	cytosolic ascorbate peroxidase
84	JGP_1_6.2850.2855.2	2	21.02	89	1.44E+05	(K)AQASALEAHAAPNCK(V)	C:Carbamidomethylation	769.8736	1538.738	0.0019	1.2	Triticum aestivum		37928995	cytosolic malate dehydrogenase
375	JGP_1_8.9107.9186.3	3	17.58	84.3	3.80E+05	(K)LVDLANKPDWLFEINPEGK(V)			733.3911	2198.149	0.0096	4.3	Zea mays	226531648	dehydroascorbate reductase
829	JGP_1_7.9058.9130.3	3	15.06	77.1	3.66E+05	(K)LVDLANKPDWLFEINPEGK(V)			733.3912	2198.149	0.0099	4.5	Zea mays	226531648	dehydroascorbate reductase
1836	JGP_1_7.5654.5660.2	2	11.72	79.3	3.27E+05	(R)VLLTIEEK(H)		472.7875	944.566	0.0014	1.5	Zea mays	226531648	dehydroascorbate reductase
1491	JGP_1_7.3532.3575.2	2	12.66	81.7	4.19E+05	(K)LNVVVK(R)		336.2262	671.445	0.0001	0.1	Zea mays	162461292	delta-COP
2324	JGP_1_7.6108.6114.2	2	10.45	76	2.03E+05	(K)VTGILPLK(E)		420.7803	840.555	-0.002	-2.4	Zea mays	162461292	delta-COP
1143	JGP_1_3.5711.5796.2	2	13.78	92.5	1.88E+06	(K)ILSVFR(L)		367.7329	734.456	0.0026	3.5	Arabidopsis thaliana	145358264	dicer-like protein 4
1158	JGP_1_6.6345.6360.2	2	13.71	89.7	2.41E+05	(K)ILSVFR(L)		367.7328	734.456	0.0024	3.3	Arabidopsis thaliana	145358264	dicer-like protein 4
1808	JGP_1_4.5915.5918.2	2	11.79	83.6	1.67E+05	(K)ILSVFR(L)		367.7322	734.456	0.0012	1.6	Arabidopsis thaliana	145358264	dicer-like protein 4
2452	JGP_1_3.5868.5873.2	2	10.18	81.9	8.98E+05	(K)ILSVFR(L)		367.7333	734.456	0.0034	4.6	Arabidopsis thaliana	145358264	dicer-like protein 4
2514	JGP_1_2.5422.5497.2	2	10.03	80.1	1.81E+05	(K)ILSVFR(L)		367.7324	734.456	0.0016	2.2	Arabidopsis thaliana	145358264	dicer-like protein 4
2339	JGP_1_6.1435.1517.2	2	10.42	68.5	1.72E+06	(R)AVmDAIK(L)	m:Oxidized methionine	382.2058	747.407	15.9974	3.2	Arabidopsis thaliana	12322541	"disease resistance gene, putative"
2474	JGP_1_6.2918.3032.2	2	10.13	71.6	2.60E+06	(K)NVLLDK(S)		351.2148	701.419	0.0031	4.4	Arabidopsis thaliana	9758472	disease resistance protein kinase Pto-like protein
2446	JGP_1_7.5497.5597.2	2	10.2	72.8	1.97E+06	(K)LIGEMGLHTK(I)		549.8089	1098.598	0.0129	11.8	Arabidopsis thaliana	79323389	DNA repair protein RAD51-like 2
2306	JGP_1_1.8492.8551.2	2	10.49	65.2	1.22E+05	(K)LSISNIPTGSSR(F)		616.3474	1231.664	0.0234	19	Arabidopsis thaliana	15233100	early-responsive to dehydration stress-related protein
1585	JGP_1_2.4539.4539.2	2	12.41	74.8	1.19E+05	(K)IGGIGTVPVGR(V)		513.3082	1025.61	-0.0011	-1.1	Oryza sativa		2662343	EF-1 alpha
2438	JGP_1_1.4717.4726.2	2	10.21	69.8	3.45E+05	(K)IGGIGTVPVGR(V)		513.3094	1025.61	0.0013	1.3	Oryza sativa		2662343	EF-1 alpha
1063	JGP_1_1.10441.10441.3	3	14.09	74.1	6.73E+04	(R)LLEPVYLVEIQAPENALGGIYGVLNQK(R)			980.8661	2940.608	-0.0243	-8.3	Triticum aestivum	32400836	elongation factor
2353	JGP_1_8.6268.6354.2	2	10.4	79.2	8.59E+06	(R)SIAELLR(E)		401.2476	801.483	0.005	6.3	Arabidopsis thaliana	42565086	endonuclease/exonuclease/phosphatase domain-containing protein
2518	JGP_1_8.6091.6183.2	2	10.02	76	8.17E+06	(R)SIAELLR(E)		401.2478	801.483	0.0054	6.8	Arabidopsis thaliana	42565086	endonuclease/exonuclease/phosphatase domain-containing protein
692	JGP_1_2.5813.5894.3	3	15.73	74.5	2.49E+05	(K)IPLYKHIANIAGNK(K)		517.963	1551.901	-0.0261	-16.8	Glycine max	351724891	enolase
823	JGP_1_5.9769.9833.3	3	15.07	78.7	2.61E+05	(R)SGETEDTFIADLSVGLATGQIK(T)			751.3869	2252.129	0.0169	7.5	Glycine max	351724891	enolase
1470	JGP_1_5.10725.10739.3	3	12.74	66.7	5.32E+04	(R)SGETEDNFIADLAVGLASGQIK(T)			745.7107	2235.114	0.0036	1.6	Zea mays	226499996	enolase
19	JGP_1_5.5536.5637.2	2	22.94	96.1	9.12E+05	(R)IEEELGDAAVYAGAK(F)		768.3858	1535.759	0.0055	3.6	Zea mays	162458207	enolase 1
68	JGP_1_5.5982.6068.3	3	21.2	92.3	1.92E+06	(K)KIPLYQHIANLAGNK(T)		560.6615	1679.959	0.0108	6.4	Zea mays	162458207	enolase 1
108	JGP_1_4.5355.5440.2	2	20.46	85.9	4.45E+05	(R)IEEELGDAAVYAGAK(F)		768.3878	1535.759	0.0095	6.2	Zea mays	162458207	enolase 1
121	JGP_1_2.5842.5911.2	2	20.2	94.3	5.69E+05	(K)VNQIGSVTESIEAVR(M)		801.4316	1601.849	0.0066	4.1	Zea mays	162458207	enolase 1
147	JGP_1_1.6195.6267.2	2	19.62	93.1	7.88E+05	(K)VNQIGSVTESIEAVR(M)		801.4302	1601.849	0.0038	2.4	Zea mays	162458207	enolase 1
148	JGP_1_5.7798.7873.2	2	19.62	90.4	6.39E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	951.9743	1870.944	31.9972	3.9	Zea mays	162458207	enolase 1
153	JGP_1_4.5885.5967.3	3	19.56	86.7	8.23E+05	(K)KIPLYQHIANLAGNK(T)		560.6604	1679.959	0.0075	4.5	Zea mays	162458207	enolase 1
164	JGP_1_1.5684.5773.3	3	19.45	85.6	7.16E+05	(K)KIPLYQHIANLAGNK(T)		560.6602	1679.959	0.0069	4.1	Zea mays	162458207	enolase 1
206	JGP_1_5.7960.8082.2	2	19.05	77.3	1.88E+06	(R)GAVPSGASTGIYEALELR(D)			895.9706	1790.928	0.0056	3.1	Zea mays	162458207	enolase 1

270	JGP_1_2.5401.5484.3	3	18.35	82.8	3.35E+05	(K)KIPLYQHIANLAGNK(T)	560.6602	1679.959	0.0069	4.1	Zea mays	162458207	enolase 1	
300	JGP_1_6.9335.9342.3	3	18.1	78.8	8.61E+04	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		842.1166	2524.362	-0.0265	-10.5	Zea mays	162458207	enolase 1
308	JGP_1_2.7887.7952.3	3	18.03	82.2	4.92E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		842.1185	2524.362	-0.0208	-8.2	Zea mays	162458207	enolase 1
329	JGP_1_5.6506.6513.3	3	17.95	77.7	5.10E+05	(K)IPLYQHIANLAGNK(T)	517.962	1551.864	0.0073	4.7	Zea mays	162458207	enolase 1	
378	JGP_1_3.8339.8408.3	3	17.55	81.9	3.37E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		842.1194	2524.362	-0.0181	-7.2	Zea mays	162458207	enolase 1
396	JGP_1_3.6188.6263.2	2	17.43	88.8	3.89E+05	(K)VNQIGSVTESIEAVR(M)	801.4313	1601.849	0.006	3.7	Zea mays	162458207	enolase 1	
424	JGP_1_4.5090.5094.3	3	17.31	77.6	2.04E+05	(K)ISGDSLKDLYK(S)	413.5612	1238.663	0.0064	5.1	Zea mays	162458207	enolase 1	
477	JGP_1_5.9020.9144.3	3	16.93	77.5	1.61E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		842.1191	2524.362	-0.019	-7.5	Zea mays	162458207	enolase 1
508	JGP_1_4.2741.2747.2	2	16.74	69.7	1.59E+05	(R)AGWGVmASHR(S)	m:Oxidized methionine	544.2634	1071.515	16.0043	8.6	Zea mays	162458207	enolase 1
515	JGP_1_5.6584.6677.2	2	16.71	84.3	2.51E+06	(K)VNQIGSVTESIEAVR(M)	801.4332	1601.849	0.0098	6.1	Zea mays	162458207	enolase 1	
545	JGP_1_4.7607.7681.2	2	16.52	74.7	3.63E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	951.9737	1870.944	31.996	3.2	Zea mays	162458207	enolase 1
571	JGP_1_4.6413.6498.2	2	16.37	87	9.83E+05	(K)VNQIGSVTESIEAVR(M)	801.4328	1601.849	0.009	5.6	Zea mays	162458207	enolase 1	
586	JGP_1_4.6430.6433.3	3	16.28	78.4	7.32E+05	(K)VNQIGSVTESIEAVR(M)	534.6252	1601.849	0.0117	7.3	Zea mays	162458207	enolase 1	
634	JGP_1_5.4604.4696.2	2	16.08	76.4	2.92E+06	(K)TCNALLLK(V)	C:Carbamidomethylation	466.7672	932.523	0.0038	4	Zea mays	162458207	enolase 1
639	JGP_1_1.8409.8474.3	3	16.05	74.7	7.57E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		842.1184	2524.362	-0.0211	-8.3	Zea mays	162458207	enolase 1
785	JGP_1_4.8607.8674.3	3	15.25	81.3	4.15E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		842.118	2524.362	-0.0223	-8.8	Zea mays	162458207	enolase 1
790	JGP_1_2.6942.7007.2	2	15.22	77.6	2.33E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	951.9736	1870.944	31.9958	3.1	Zea mays	162458207	enolase 1
859	JGP_1_5.8903.8908.2	2	14.93	70.3	1.48E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		1262.6673	2524.362	-0.0344	-13.6	Zea mays	162458207	enolase 1
866	JGP_1_2.4934.4942.2	2	14.91	81.1	3.54E+05	(R)IEEELGDAAVYAGAK(F)	768.3859	1535.759	0.0057	3.7	Zea mays	162458207	enolase 1	
879	JGP_1_2.4234.4306.2	2	14.88	71.6	4.28E+05	(K)TCNALLLK(V)	C:Carbamidomethylation	466.7629	932.523	-0.0048	-5.2	Zea mays	162458207	enolase 1
951	JGP_1_5.8887.8957.3	3	14.55	62.7	6.81E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		842.1181	2524.362	-0.022	-8.7	Zea mays	162458207	enolase 1
1007	JGP_1_1.8434.8439.2	2	14.31	71.1	1.48E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		1262.6704	2524.362	-0.0282	-11.2	Zea mays	162458207	enolase 1
1029	JGP_1_5.4397.4408.3	3	14.2	71.4	3.01E+05	(K)MGVEVYHNLK(S)	397.21	1189.603	0.012	10.1	Zea mays	162458207	enolase 1	
1075	JGP_1_1.7397.7402.2	2	14.02	65.4	2.16E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	951.9726	1870.944	31.9938	2.1	Zea mays	162458207	enolase 1
1088	JGP_1_1.7464.7464.2	2	13.99	70.4	2.65E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	951.9726	1870.944	31.9938	2.1	Zea mays	162458207	enolase 1
1112	JGP_1_1.4852.4903.3	3	13.89	71.9	2.64E+04	(K)ISGDSLKDLYK(S)	413.5601	1238.663	0.0031	2.5	Zea mays	162458207	enolase 1	
1151	JGP_1_1.6162.6239.3	3	13.72	65.9	2.58E+05	(K)IPLYQHIANLAGNK(T)	517.9628	1551.864	0.0097	6.2	Zea mays	162458207	enolase 1	
1216	JGP_1_5.3444.3448.2	2	13.54	60.8	5.00E+05	(K)mGVEVYHNLK(S)	m:Oxidized methionine	603.3049	1189.603	15.9991	3.5	Zea mays	162458207	enolase 1
1253	JGP_1_5.7799.7872.3	3	13.42	84.3	6.43E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	634.9862	1870.944	31.9999	5.3	Zea mays	162458207	enolase 1
1277	JGP_1_8.4633.4645.2	2	13.36	63.9	1.83E+05	(K)TCNALLLK(V)	C:Carbamidomethylation	466.7678	932.523	0.005	5.3	Zea mays	162458207	enolase 1
1292	JGP_1_1.5146.5151.2	2	13.31	68	3.91E+05	(R)IEEELGDAAVYAGAK(F)	768.3839	1535.759	0.0017	1.1	Zea mays	162458207	enolase 1	
1301	JGP_1_3.5719.5802.3	3	13.28	60.8	3.61E+05	(K)KIPLYQHIANLAGNK(T)	560.6599	1679.959	0.006	3.6	Zea mays	162458207	enolase 1	
1426	JGP_1_5.1705.1878.2	2	12.89	87.7	2.55E+06	(K)ISGDSLK(D)	360.2048	719.393	0.0089	12.4	Zea mays	162458207	enolase 1	
1503	JGP_1_5.7962.8092.3	3	12.63	64.7	5.72E+05	(R)GAVPSGASTGIYEALELR(D)		597.6498	1790.928	0.0065	3.7	Zea mays	162458207	enolase 1
1505	JGP_1_1.6277.6284.3	3	12.62	66.1	6.44E+05	(K)VNQIGSVTESIEAVR(M)	534.6234	1601.849	0.0063	3.9	Zea mays	162458207	enolase 1	
1519	JGP_1_5.6589.6592.3	3	12.57	67.4	1.18E+06	(K)VNQIGSVTESIEAVR(M)	534.625	1601.849	0.0111	6.9	Zea mays	162458207	enolase 1	
1523	JGP_1_4.4594.4677.2	2	12.56	62.2	9.91E+05	(K)TCNALLLK(V)	C:Carbamidomethylation	466.7673	932.523	0.004	4.2	Zea mays	162458207	enolase 1
1558	JGP_1_1.4421.4490.2	2	12.46	65.8	5.17E+05	(K)TCNALLLK(V)	C:Carbamidomethylation	466.7663	932.523	0.002	2.1	Zea mays	162458207	enolase 1
1732	JGP_1_3.7374.7374.2	2	12.01	61.6	1.69E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	951.9746	1870.944	31.9978	4.2	Zea mays	162458207	enolase 1
1773	JGP_1_2.5916.5921.3	3	11.9	66.9	4.75E+05	(K)VNQIGSVTESIEAVR(M)	534.6239	1601.849	0.0078	4.9	Zea mays	162458207	enolase 1	
1774	JGP_1_2.7907.7907.2	2	11.9	67.3	1.03E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		1262.6679	2524.362	-0.0332	-13.1	Zea mays	162458207	enolase 1
1789	JGP_1_6.6990.6994.2	2	11.85	75.4	3.46E+05	(K)VNQIGSVTESIEAVR(M)	801.432	1601.849	0.0074	4.6	Zea mays	162458207	enolase 1	
1882	JGP_1_5.5978.6072.4	4	11.58	71.1	1.46E+06	(K)KIPLYQHIANLAGNK(T)	420.7481	1679.959	0.0114	6.8	Zea mays	162458207	enolase 1	
1930	JGP_1_3.6199.6207.3	3	11.44	65.8	3.36E+05	(K)VNQIGSVTESIEAVR(M)	534.6225	1601.849	0.0036	2.3	Zea mays	162458207	enolase 1	
2049	JGP_1_6.4924.5013.2	2	11.12	68.2	4.87E+05	(K)TCNALLLK(V)	C:Carbamidomethylation	466.7661	932.523	0.0016	1.7	Zea mays	162458207	enolase 1
2259	JGP_1_2.6934.7001.3	3	10.63	77.3	3.06E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	634.9871	1870.944	32.0026	6.7	Zea mays	162458207	enolase 1
2275	JGP_1_5.9505.9505.2	2	10.58	62.2	1.72E+04	(K)LAMQEFMILPTGASSFK(E)	935.9787	1870.944	0.006	3.2	Zea mays	162458207	enolase 1	
2310	JGP_1_3.5224.5224.2	2	10.48	60.4	1.95E+05	(R)IEEELGDAAVYAGAK(F)	768.3877	1535.759	0.0093	6.1	Zea mays	162458207	enolase 1	
2359	JGP_1_3.7379.7379.2	2	10.39	66.1	1.70E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	951.9746	1870.944	31.9978	4.2	Zea mays	162458207	enolase 1
2424	JGP_1_3.8375.8375.2	2	10.24	60.2	1.02E+05	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)		1262.6684	2524.362	-0.0322	-12.7	Zea mays	162458207	enolase 1
2501	JGP_1_5.6043.6043.2	2	10.07	65.6	2.20E+05	(K)KIPLYQHIANLAGNK(T)	840.4848	1679.959	0.0032	1.9	Zea mays	162458207	enolase 1	
2513	JGP_1_3.7358.7368.3	3	10.04	69.3	2.19E+05	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	634.9883	1870.944	32.0062	8.6	Zea mays	162458207	enolase 1
1537	JGP_1_1.5128.5131.3	3	12.51	65.2	2.31E+05	(R)ILASGVHVVVGTPGR(V)	487.9557	1461.854	-0.0011	-0.7	Zea mays	162460883	eukaryotic initiation factor 4A	
1906	JGP_1_4.4915.4993.2	2	11.51	82.5	5.82E+05	(R)IAIWTK(N)	366.228	731.445	0.0037	5	Zea mays	162458915	eukaryotic translation initiation factor 4E-1	
238	JGP_1_2.5712.5792.2	2	18.65	81.8	3.03E+05	(R)LPTDETLVAQIK(E)	664.3786	1327.747	0.0032	2.4	Zea mays	162458009	eukaryotic translation initiation factor 5A	
272	JGP_1_3.6068.6071.2	2	18.33	85.7	1.81E+05	(R)LPTDETLVAQIK(E)	664.3771	1327.747	0.0002	0.1	Zea mays	162458009	eukaryotic translation initiation factor 5A	
479	JGP_1_2.2203.2274.2	2	16.92	87	2.28E+05	(K)TYPQQAGTVR(K)	560.7919	1120.574	0.002	1.8	Zea mays	162458009	eukaryotic translation initiation factor 5A	
542	JGP_1_3.2257.2263.2	2	16.53	83.2	2.46E+05	(K)TYPQQAGTVR(K)	560.7921	1120.574	0.0024	2.1	Zea mays	162458009	eukaryotic translation initiation factor 5A	
717	JGP_1_1.6044.6123.2	2	15.62	76.6	3.70E+05	(R)LPTDETLVAQIK(E)	664.3774	1327.747	0.0008	0.6	Zea mays	162458009	eukaryotic translation initiation factor 5A	
719	JGP_1_6.2369.2373.2	2	15.61	87.4	3.67E+05	(K)TYPQQAGTVR(K)	560.7913	1120.574	0.0008	0.7	Zea mays	162458009	eukaryotic translation initiation factor 5A	
2078	JGP_1_1.2189.2273.2	2	11.05	72.5	2.93E+05	(K)TYPQQAGTVR(K)	560.7909	1120.574	0	0	Zea mays	162458009	eukaryotic translation initiation factor 5A	
89	JGP_1_7.7538.7618.2	2	20.81	86.9	7.03E+06	(K)GSNPNYLAVLVK(F)	637.8643	1274.71	0.011	8.6	Triticum aestivum	44894804	expansin EXPB5	
93	JGP_1_7.7390.7468.2	2	20.78	88.1	1.23E+07	(K)GSNPNYLAVLVK(F)	637.864	1274.71	0.0104	8.2	Triticum aestivum	44894804	expansin EXPB5	
142	JGP_1_1.6976.7125.2	2	19.73	85.6	5.81E+06	(K)GSNPNYLAVLVK(F)	637.8615	1274.71	0.0054	4.2	Triticum aestivum	44894804	expansin EXPB5	
172	JGP_1_3.7092.7207.2	2	19.39	83.9	2.23E+06	(K)GSNPNYLAVLVK(F)	637.8619	1274.71	0.0062	4.9	Triticum aestivum	44894804	expansin EXPB5	
194	JGP_1_3.6943.7021.2	2	19.15	84.3	3.82E+06	(K)GSNPNYLAVLVK(F)	637.8617	1274.71	0.0058	4.6	Triticum aestivum	44894804	expansin EXPB5	
209	JGP_1_4.7328.7461.2	2	19.03	78.2	1.15E+06	(K)GSNPNYLAVLVK(F)	637.8607	1274.71	0.0038	3	Triticum aestivum	44894804	expansin EXPB5	
219	JGP_1_6.7896.7996.2	2	18.92	83.4	2.07E+06	(K)GSNPNYLAVLVK(F)	637.8621	1274.71	0.0066	5.2	Triticum aestivum	44894804	expansin EXPB5	
258	JGP_1_2.6564.6641.2	2	18.47	80.9	3.83E+06	(K)GSNPNYLAVLVK(F)	637.8616	1274.71	0.0056	4.4	Triticum aestivum	44894804	expansin EXPB5	
263	JGP_1_2.6706.6821.2	2	18.45	82.4	2.42E+06	(K)GSNPNYLAVLVK(F)	637.8619	1274.71	0.0062	4.9	Triticum aestivum	44894804	expansin EXPB5	
336	JGP_1_5.7370.7447.2	2	17.89	79.1	1.59E+06	(K)GSNPNYLAVLVK(F)	637.8605	1274.71	0.0034	2.7	Triticum aestivum	44894804	expansin EXPB5	
511	JGP_1_4.7180.7259.2	2	16.73	75.9	1.86E+06	(K)GSNPNYLAVLVK(F)	637.861	1274.71	0.0044	3.5	Triticum aestivum	44894804	expansin EXPB5	

628	JGP_1_1.7130.7196.2	2	16.1	73.7	4.08E+06	(K)GSNPNYLAVLVK(F)		637.8617	1274.71	0.0058	4.6	Triticum aestivum	44894804	expansin EXPB5	
716	JGP_1_2.6597.6671.3	3	15.63	74.8	4.20E+05	(K)GSNPNYLAVLVK(F)		425.5777	1274.71	0.0082	6.5	Triticum aestivum	44894804	expansin EXPB5	
768	JGP_1_6.7737.7820.2	2	15.34	68.5	3.15E+06	(K)GSNPNYLAVLVK(F)		637.8619	1274.71	0.0062	4.9	Triticum aestivum	44894804	expansin EXPB5	
1078	JGP_1_3.6979.7056.3	3	14.01	80.5	3.88E+05	(K)GSNPNYLAVLVK(F)		425.5769	1274.71	0.0058	4.6	Triticum aestivum	44894804	expansin EXPB5	
1160	JGP_1_1.7006.7089.3	3	13.7	75.8	6.00E+05	(K)GSNPNYLAVLVK(F)		425.5771	1274.71	0.0064	5	Triticum aestivum	44894804	expansin EXPB5	
1193	JGP_1_4.7236.7238.3	3	13.59	69.2	1.63E+05	(K)GSNPNYLAVLVK(F)		425.5771	1274.71	0.0064	5	Triticum aestivum	44894804	expansin EXPB5	
1675	JGP_1_5.7422.7428.3	3	12.19	66.2	1.33E+05	(K)GSNPNYLAVLVK(F)		425.5769	1274.71	0.0058	4.6	Triticum aestivum	44894804	expansin EXPB5	
1888	JGP_1_5.7555.7559.2	2	11.56	61.8	1.89E+05	(K)GSNPNYLAVLVK(F)		637.8609	1274.71	0.0042	3.3	Triticum aestivum	44894804	expansin EXPB5	
2372	JGP_1_7.7408.7489.3	3	10.37	61.9	9.04E+05	(K)GSNPNYLAVLVK(F)		425.5778	1274.71	0.0085	6.7	Triticum aestivum	44894804	expansin EXPB5	
431	JGP_1_1.6590.6673.3	3	17.27	78.1	4.85E+05	(R)LSLLHEFDVSNNR(F)		515.2699	1543.786	0.0088	5.7	Zea mays	600118	extensin-like protein	
702	JGP_1_1.9309.9371.2	2	15.68	81.8	3.77E+04	(R)FVGVFPYVCLEmVSLK(Y)	C:Carbamidomethylation	m:Oxidized methionine	952.492	1887.975	16.002	3.7	Zea mays	600118	extensin-like protein
740	JGP_1_1.7457.7460.2	2	15.46	78.6	1.77E+05	(K)TLDEIIFLNNK(L)		660.3631	1319.72	-0.0016	-1.2	Zea mays	600118	extensin-like protein	
1077	JGP_1_1.5838.5842.4	4	14.01	74.6	5.31E+05	(K)ALVNLDDRDNCLGALRPAQK(T)		C:Carbamidomethylation	560.5497	2239.161	0.0158	7.1	Zea mays	600118	extensin-like protein
2368	JGP_1_8.10625.10702.2	2	10.38	63.3	1.21E+05	(R)GFIFGPPIALAIGAK(F)		736.4381	1471.867	0.0018	1.2	Arabidopsis thaliana	9802535	F17L21.24	
989	JGP_1_4.5384.5468.2	2	14.4	90.7	6.42E+05	(K)SIVILK(L)		336.7375	672.465	0.0023	3.4	Arabidopsis thaliana	6049880	F5I10.18 gene product	
1553	JGP_1_3.5249.5336.2	2	12.47	85.7	2.04E+06	(K)SIVILK(L)		336.738	672.465	0.0033	4.9	Arabidopsis thaliana	6049880	F5I10.18 gene product	
942	JGP_1_3.2399.2404.2	2	14.6	76.5	1.79E+05	(R)TPFPHR(A)		377.704	754.399	0.0012	1.6	Arabidopsis thaliana	15221492	FAD-binding and BBE domain-containing protein	
1559	JGP_1_5.2238.2245.2	2	12.46	76.9	3.71E+05	(R)TPFPHR(A)		377.7041	754.399	0.0014	1.9	Arabidopsis thaliana	15221492	FAD-binding and BBE domain-containing protein	
2032	JGP_1_4.2363.2367.2	2	11.15	65.3	2.47E+05	(R)TPFPHR(A)		377.7036	754.399	0.0004	0.6	Arabidopsis thaliana	15221492	FAD-binding and BBE domain-containing protein	
2333	JGP_1_8.2720.2725.2	2	10.43	61.2	5.90E+05	(R)QAYVNYR(D)		457.2319	913.453	0.0039	4.2	Arabidopsis thaliana	15241476	FAD-binding and BBE domain-containing protein	
1406	JGP_1_6.0950.0953.2	2	12.96	71.3	1.22E+05	(K)AAKEAEMEK(T)		503.7492	1006.487	0.0038	3.7	Arabidopsis thaliana	15240854	formin-like protein 19	
391	JGP_1_6.3849.3860.2	2	17.47	84.6	5.03E+05	(R)FANACGAITTTK(K)	C:Carbamidomethylation	627.8134	1254.615	0.0048	3.8	Arabidopsis thaliana	15221365	fructokinase	
441	JGP_1_6.5293.5299.2	2	17.23	89	6.49E+05	(K)APGGAPANVAIAVSR(L)		675.8814	1350.749	0.0067	5	Arabidopsis thaliana	15221365	fructokinase	
688	JGP_1_6.7507.7595.2	2	15.79	90.2	1.64E+06	(R)TALAFVTLK(K)		482.2993	963.587	0.004	4.1	Arabidopsis thaliana	15234986	fructokinase	
705	JGP_1_6.8726.8805.3	3	15.68	78.5	7.36E+05	(K)FGDDEFGHmLVNILK(K)	m:Oxidized methionine	584.2905	1734.852	16.005	5.7	Arabidopsis thaliana	15234986	fructokinase	
988	JGP_1_6.6830.6921.2	2	14.41	83.3	4.55E+05	(K)EAGALLSYDPNLR(L)		709.8705	1418.727	0.0063	4.4	Nicotiana tabacum	23978579	fructokinase	
1090	JGP_1_1.6796.6880.2	2	13.98	87.3	3.15E+05	(R)TALAFVTLK(K)		482.2982	963.587	0.0018	1.8	Arabidopsis thaliana	15234986	fructokinase	
1140	JGP_1_6.4799.4804.2	2	13.79	82.6	1.89E+06	(R)LGGSSAFIGK(V)		468.7626	936.515	0.003	3.2	Arabidopsis thaliana	15242193	fructokinase	
1243	JGP_1_2.6399.6468.2	2	13.45	80.6	1.20E+05	(R)TALAFVTLK(K)		482.2977	963.587	0.0008	0.8	Arabidopsis thaliana	15234986	fructokinase	
1407	JGP_1_6.10073.10150.3	3	12.96	62.6	3.58E+05	(K)FGDDEFGHMLVNILK(K)		578.9588	1734.852	0.0099	5.7	Arabidopsis thaliana	15234986	fructokinase	
1577	JGP_1_7.7189.7283.2	2	12.43	84.1	3.27E+05	(R)TALAFVTLK(K)		482.2976	963.587	0.0006	0.6	Arabidopsis thaliana	15234986	fructokinase	
1705	JGP_1_1.6953.6958.2	2	12.11	84.3	8.22E+04	(R)TALAFVTLR(G)		496.3007	991.593	0.0006	0.6	Arabidopsis thaliana	15242193	fructokinase	
1707	JGP_1_6.7658.7745.2	2	12.1	84.4	8.01E+05	(R)TALAFVTLR(G)		496.3025	991.593	0.0042	4.3	Arabidopsis thaliana	15242193	fructokinase	
1816	JGP_1_7.4559.4652.2	2	11.76	74.6	7.80E+05	(R)LGGSSAFIGK(V)		468.7616	936.515	0.001	1.1	Arabidopsis thaliana	15242193	fructokinase	
2184	JGP_1_6.7673.7673.2	2	10.78	68.5	1.74E+04	(R)TALAFVTLK(K)		482.2995	963.587	0.0044	4.5	Arabidopsis thaliana	15234986	fructokinase	
694	JGP_1_6.7438.7523.2	2	15.73	86.2	6.86E+05	(K)LLLVTLGDQGCK(Y)	C:Carbamidomethylation	658.8687	1316.724	0.0059	4.5	Zea mays	162460362	fructokinase-1	
832	JGP_1_6.1625.1634.2	2	15.03	83.5	1.54E+05	(K)DPSSLQDEK(K)		509.7399	1018.469	0.0038	3.7	Zea mays	162460362	fructokinase-1	
1103	JGP_1_6.9096.9173.2	2	13.95	85.4	2.77E+05	(R)TQILSIWDQADIVK(V)		815.4496	1629.885	0.0073	4.5	Zea mays	162460362	fructokinase-1	
2029	JGP_1_6.10808.10812.3	3	11.16	62.3	9.50E+04	(K)GAIPSLPTEAEVLQLIEK(A)			636.6961	1908.069	0.0049	2.6	Zea mays	162460362	fructokinase-1
2271	JGP_1_6.7518.7518.3	3	10.6	64.4	9.99E+04	(K)LLLVTLGDQGCK(Y)	C:Carbamidomethylation	439.5819	1316.724	0.0069	5.2	Zea mays	162460362	fructokinase-1	
2316	JGP_1_6.10800.10867.2	2	10.47	77.5	1.78E+05	(K)GAIPSLPTEAEVLQLIEK(A)			954.539	1908.069	0.0019	1	Zea mays	162460362	fructokinase-1
2475	JGP_1_6.5458.5465.3	3	10.13	66.6	2.91E+05	(R)DFHGAVPSFK(V)		368.8556	1104.547	0.005	4.5	Zea mays	162460362	fructokinase-1	
69	JGP_1_6.7403.7490.2	2	21.2	93.6	1.26E+06	(R)LPLWPSPDAAR(E)		611.8357	1222.658	0.0062	5.1	Zea mays	162460525	fructokinase-2	
167	JGP_1_6.5095.5192.2	2	19.44	92.9	1.94E+06	(K)APGGAPANVACAIAK(L)	C:Carbamidomethylation	684.3619	1367.71	0.0065	4.8	Zea mays	162460525	fructokinase-2	
204	JGP_1_7.7080.7163.2	2	19.09	90.2	3.84E+05	(R)LPLWPSPDAAR(E)		611.8337	1222.658	0.0022	1.8	Zea mays	162460525	fructokinase-2	
638	JGP_1_6.7567.7567.2	2	16.06	83.7	6.29E+05	(R)LPLWPSPDAAR(E)		611.8357	1222.658	0.0062	5.1	Zea mays	162460525	fructokinase-2	
861	JGP_1_6.3597.3602.2	2	14.93	76.2	4.46E+05	(K)DDSIFHNEEK(L)		617.2767	1233.538	0.0079	6.4	Zea mays	162460525	fructokinase-2	
905	JGP_1_6.8246.8325.2	2	14.77	76.2	5.79E+05	(R)EGILSIWK(E)		473.2764	945.54	0.0051	5.4	Zea mays	162460525	fructokinase-2	
1382	JGP_1_1.6730.6740.2	2	13	73.7	1.83E+05	(R)LPLWPSPDAAR(E)		611.8314	1222.658	-0.0024	-1.9	Zea mays	162460525	fructokinase-2	
1398	JGP_1_6.3514.3625.2	2	12.97	77.9	8.90E+05	(K)FSNACGAICTTK(K)	C:Carbamidomethylation	665.3026	1329.593	0.0053	4	Zea mays	162460525	fructokinase-2	
1570	JGP_1_7.5028.5033.2	2	12.44	72.9	7.76E+05	(K)APGGAPANVACAIAK(L)	C:Carbamidomethylation	684.3594	1367.71	0.0015	1.1	Zea mays	162460525	fructokinase-2	
1708	JGP_1_6.3472.3479.2	2	12.09	73.2	1.29E+06	(K)EADFIK(V)		361.6911	722.372	0.003	4.1	Zea mays	162460525	fructokinase-2	

1805	JGP_1_6.9362.9430.2	2	11.81	83.1	5.85E+05	(K)GAIPALPTXATAQDLIAK(A)		882.5199	1764.027	0.006	3.4	Zea mays	195639126	fructokinase-2
1912	JGP_1_7.3471.3478.3	3	11.5	65.5	4.17E+05	(K)DDSIFHNEEK(L)	411.8543	1233.538	0.0101	8.2	Zea mays	162460525	fructokinase-2	
2043	JGP_1_7.8040.8045.2	2	11.13	65.7	2.07E+05	(R)EGILSIWK(E)	473.2764	945.54	0.0051	5.4	Zea mays	162460525	fructokinase-2	
2194	JGP_1_2.8000.8008.2	2	10.76	77.1	8.11E+04	(K)GAIPALPTXATAQDLIAK(A)		882.5146	1764.027	-0.0046	-2.6	Zea mays	195639126	fructokinase-2
2433	JGP_1_7.3460.3460.2	2	10.23	67.1	3.47E+05	(K)FSNACGAICTTK(K)	C:Carbamidomethylation	665.3025	1329.593	0.0051	3.9	Zea mays	162460525	fructokinase-2
2494	JGP_1_7.3215.3351.2	2	10.08	63.1	5.47E+05	(K)EADFIK(V)	361.69	722.372	0.0008	1.1	Zea mays	162460525	fructokinase-2	
2431	JGP_1_6.6801.6806.2	2	10.23	77.3	1.89E+05	(-)SLSFSFGR(A)	450.7343	900.457	0.0039	4.4	Arabidopsis thaliana	62319651	fructose bisphosphate aldolase - like protein	
307	JGP_1_6.9736.9817.3	3	18.04	91.4	1.60E+04	(R)TVPAAVPAVVFLSGGQSEEEATLNLNAmNK(L)		m:Oxidized methionine	1025.1925	3057.556	16.0068	3.9	Zea mays	226492743 fructose-bisphosphate aldolase cytoplasmic isozyme
1035	JGP_1_6.10173.10180.3	3	14.18	72.6	1.88E+04	(R)YAAIAQDNGLVPIVEPEILLDGDHGIER(T)		1006.5229	3017.558	-0.0037	-1.2	Triticum aestivum	300681519	"fructose-bisphosphate aldolase, chloroplast precursor, expressed"
125	JGP_1_6.5069.5168.2	2	20.15	88.3	2.64E+06	(K)GILAADESTGTIGK(R)	666.8572	1332.7	0.0066	4.9	Arabidopsis thaliana	15236768	"fructose-bisphosphate aldolase, class I"	
833	JGP_1_6.2318.2322.2	2	15.03	87.2	3.88E+05	(R)TLEVAEK(V)	395.2225	789.435	0.0025	3.1	Arabidopsis thaliana	15226185	"fructose-bisphosphate aldolase, class I"	
1702	JGP_1_3.4651.4658.2	2	12.12	70.8	5.17E+04	(K)GILAADESTGTIGK(R)	666.8537	1332.7	-0.0004	-0.3	Arabidopsis thaliana	15236768	"fructose-bisphosphate aldolase, class I"	
1909	JGP_1_1.4534.4609.2	2	11.5	76.9	2.14E+05	(K)GILAADESTGTIGK(R)	666.8521	1332.7	-0.0036	-2.7	Arabidopsis thaliana	15236768	"fructose-bisphosphate aldolase, class I"	
25	JGP_1_6.10100.10190.3	3	22.76	94.8	4.26E+05	(R)YAIICQENGLVPIVEPEILVDGPHDIDR(C)	C:Carbamidomethylation	1058.8796	3174.614	0.0103	3.2	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
141	JGP_1_6.10102.10202.4	4	19.78	93.9	8.46E+04	(R)YAIICQENGLVPIVEPEILVDGPHDIDR(C)	C:Carbamidomethylation	794.4137	3174.614	0.019	6	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
196	JGP_1_6.3260.3273.2	2	19.13	89	1.34E+05	(K)GDAAADTESLHVK(D)	657.3158	1313.633	-0.0089	-6.7	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
496	JGP_1_6.1029.1029.2	2	16.83	72	5.22E+04	(K)ETTTQGHDDLGKR(C)	729.3544	1457.698	0.0036	2.5	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
570	JGP_1_6.8051.8136.2	2	16.38	73.3	1.47E+06	(K)IGPNEPSQLAIDLNAQGLAR(Y)		1039.0602	2077.104	0.0095	4.6	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
783	JGP_1_6.2989.3097.2	2	15.26	77.2	2.92E+06	(K)NAAYIGTPGK(G)	496.266	991.521	0.004	4	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
815	JGP_1_6.6560.6564.4	4	15.1	87.3	7.68E+05	(K)ALNEHHVLLEGTLLKPNmVTPGSDSK(K)	m:Oxidized methionine	704.875	2800.466	16.012	6.1	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
840	JGP_1_6.4839.4844.3	3	15.01	74.8	1.51E+06	(R)LSSINVENVEENRR(A)	553.624	1658.846	0.0118	7.1	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
1084	JGP_1_6.3174.3268.2	2	14	75.8	1.42E+06	(K)ANSEATLGTYK(G)	577.7898	1154.569	0.0035	3.1	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
1102	JGP_1_6.8055.8055.2	2	13.95	63.4	1.12E+06	(K)IGPNEPSQLAIDLNAQGLAR(Y)		1039.0602	2077.104	0.0095	4.6	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
1200	JGP_1_5.2875.2875.2	2	13.57	72.4	2.09E+05	(K)NAAYIGTPGK(G)	496.2689	991.521	0.0098	9.9	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
1284	JGP_1_6.6165.6263.3	3	13.34	88.2	1.25E+06	(K)DGKPFVDVLK(E)	373.2151	1117.625	0.0056	5	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
1323	JGP_1_2.4131.4137.3	3	13.19	81	1.86E+05	(R)LSSINVENVEENRR(A)	553.6233	1658.846	0.0097	5.9	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
1677	JGP_1_4.2844.2853.2	2	12.18	74.2	1.60E+05	(K)NAAYIGTPGK(G)	496.2653	991.521	0.0026	2.6	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
1682	JGP_1_6.8178.8262.3	3	12.17	76	4.15E+05	(K)KPWSLSFSFGR(A)	437.9026	1311.684	0.0088	6.7	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
1828	JGP_1_1.4295.4300.3	3	11.73	72.6	2.27E+05	(R)LSSINVENVEENRR(A)	553.6247	1658.846	0.0139	8.4	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
2190	JGP_1_3.4408.4413.3	3	10.77	75.2	2.06E+05	(R)LSSINVENVEENRR(A)	553.6222	1658.846	0.0064	3.9	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
2235	JGP_1_1.2763.2768.2	2	10.68	67	3.06E+05	(K)NAAYIGTPGK(G)	496.2645	991.521	0.001	1	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
2507	JGP_1_2.2734.2742.2	2	10.05	72.2	1.77E+05	(K)NAAYIGTPGK(G)	496.2649	991.521	0.0018	1.8	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
2512	JGP_1_2.5292.5298.3	3	10.04	77.8	1.24E+05	(K)DGKPFVDVLK(E)	373.2151	1117.625	0.0056	5	Zea mays	162462282	"fructose-bisphosphate aldolase, cytoplasmic isozyme"	
2085	JGP_1_3.3688.3781.2	2	11.04	68.3	1.69E+06	(K)EGIPIR(M)	342.7063	684.404	0.0014	2.1	Arabidopsis thaliana	9279669	FUSCA3	
1576	JGP_1_7.5980.6082.2	2	12.43	79.5	7.84E+06	(K)SIVVDLR(V)	401.2465	801.483	0.0028	3.5	Solanum tuberosum	77745452	G protein beta subunit-like protein	
712	JGP_1_5.1864.1886.2	2	15.65	71.2	2.59E+05	(K)VCGVTSEGETAK(C)	C:Carbamidomethylation	619.2935	1237.573	0.0068	5.5	Solanum tuberosum	82623395	GDP dissociation inhibitor 1-like
2504	JGP_1_5.7498.7498.2	2	10.06	61.3	2.04E+04	(K)FFIYVQDYK(E)	611.8122	1222.614	0.0028	2.3	Solanum tuberosum	82623395	GDP dissociation inhibitor 1-like	
1303	JGP_1_5.6670.6685.4	4	13.28	75.1	4.18E+05	(R)AIAImSHPIPNTAESHSVQIIIPQK(Q)	m:Oxidized methionine	678.6221	2695.46	16.0066	4.3	Hordeum vulgare	37983041	GDP dissociation inhibitor protein
1545	JGP_1_5.9969.10048.3	3	12.5	66.6	3.19E+05	(R)FQGGSPYIYPLYGLGELPQGFAR(L)		844.1048	2530.276	0.0233	9.2	Hordeum vulgare	37983041	GDP dissociation inhibitor protein
1973	JGP_1_5.8519.8589.2	2	11.32	74.1	1.85E+05	(K)ECILSGLLSVDR(L)	C:Carbamidomethylation	681.3609	1361.709	0.0052	3.8	Hordeum vulgare	37983041	GDP dissociation inhibitor protein
2329	JGP_1_5.3075.3081.3	3	10.43	64.5	8.73E+05	(R)VLIHTGVTK(Y)	323.2042	967.593	0.0046	4.7	Hordeum vulgare	37983041	GDP dissociation inhibitor protein	
1039	JGP_1_5.3845.3855.2	2	14.17	74	3.31E+05	(K)DYNVDmVPK(F)	m:Oxidized methionine	548.7557	1080.503	16.0011	5.6	Oryza sativa	2384760	GDP dissociation inhibitor protein OsGDI2
819	JGP_1_4.6319.6330.3	3	15.08	60.4	3.87E+05	(K)YVFWDEYHPTDK(A)	533.9181	1599.711	0.0283	17.7	Arabidopsis thaliana	15221260	GDSL esterase/lipase	
333	JGP_1_7.10261.10329.4	4	17.92	88.4	5.97E+05	(K)RPGVPVEVFLFDLYDEDGKPGPEFER(H)		752.6313	3007.484	0.0198	6.6	Zea mays	195637392	"glucan endo-1,3-beta-glucosidase, acidic isoform precursor"
487	JGP_1_7.1377.1382.2	2	16.88	74.9	3.53E+05	(K)IGICHGR(V)	C:Carbamidomethylation	406.713	812.42	-0.0008	-1	Zea mays	195637392	"glucan endo-1,3-beta-glucosidase, acidic isoform precursor"
1997	JGP_1_6.10410.10423.4	4	11.24	63.2	3.23E+05	(K)RPGVPVEVFLFDLYDEDGKPGPEFER(H)		752.631	3007.484	0.0186	6.2	Zea mays	195637392	"glucan endo-1,3-beta-glucosidase, acidic isoform precursor"
2057	JGP_1_6.7656.7662.2	2	11.1	72.8	3.19E+05	(R)VGSNLPPPSAAAALLK(R)	753.4409	1505.869	0.0059	3.9	Zea mays	195637392	"glucan endo-1,3-beta-glucosidase, acidic isoform precursor"	
2254	JGP_1_7.7384.7464.2	2	10.64	72.6	5.98E+05	(R)VGSNLPPPSAAAALLK(R)	753.4413	1505.869	0.0067	4.5	Zea mays	195637392	"glucan endo-1,3-beta-glucosidase, acidic isoform precursor"	

2079	JGP_1_1.8647.8722.2	2	11.05	65.4	1.50E+05	(K)SAEPLLEGLLEAR(V)		699.3863	1397.764	0.0019	1.3	Triticum aestivum	295687224	glucan water dikinase
2193	JGP_1_1.6579.6583.2	2	10.76	71	1.90E+05	(R)GGSAATLSALLNR(F)		615.8455	1230.68	0.0036	3	Triticum aestivum	295687224	glucan water dikinase
2216	JGP_1_4.6135.6217.2	2	10.72	65	6.01E+05	(R)AILPYSQALEK(F)		616.8494	1232.689	0.003	2.4	Arabidopsis thaliana	15239045	glucose-6-phosphate isomerase
241	JGP_1_4.7354.7433.2	2	18.62	84.7	3.72E+05	(R)VIPCDFIGVVK(S)	C:Carbamidomethylation	623.8481	1246.686	0.0025	2	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
354	JGP_1_4.8155.8160.2	2	17.73	84.8	1.30E+05	(R)DAVINSDGVNVVPEVWSVK(D)		1014.0257	2027.044	-0.0003	-0.1	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
1156	JGP_1_4.9985.9985.3	3	13.71	73	2.49E+05	(R)YSVCSAVGVLPLSLQYGFPIVQK(F)	C:Carbamidomethylation	842.4598	2525.347	0.0176	7	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
1347	JGP_1_4.9989.9989.3	3	13.11	67.5	2.49E+05	(R)YSVCSAVGVLPLSLQYGFPIVQK(F)	C:Carbamidomethylation	842.4598	2525.347	0.0176	7	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
1425	JGP_1_4.7875.7882.2	2	12.89	70.8	2.03E+05	(K)DLDPETTLVVVVSK(T)		757.9211	1514.831	0.0037	2.4	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
1478	JGP_1_4.8130.8137.3	3	12.72	77.9	1.43E+05	(R)DAVINSDGVNVVPEVWSVK(D)			676.3575	2027.044	0.0136	6.7	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
1506	JGP_1_4.1034.1108.3	3	12.62	81.2	3.23E+05	(K)TPEQLHSEK(V)		356.8511	1068.532	0.0067	6.3	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
1547	JGP_1_4.6429.6515.2	2	12.49	76.3	6.99E+05	(R)FLANVDPVDVAR(S)		658.3576	1315.7	0.0074	5.7	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
2303	JGP_1_4.7215.7235.2	2	10.5	69.3	2.22E+05	(K)EWIVSSLGPQAVAK(H)		742.9104	1484.811	0.0028	1.9	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
2341	JGP_1_6.7034.7034.2	2	10.42	63.2	7.94E+04	(R)FLANVDPVDVAR(S)		658.3564	1315.7	0.005	3.8	Zea mays	162460322	"glucose-6-phosphate isomerase, cytosolic"
565	JGP_1_6.3335.3344.2	2	16.39	85.5	4.36E+05	(R)TLSGPVTDPSK(L)		551.2948	1101.579	0.0037	3.4	Zea mays	162463755	glutamine synthetase root isozyme 3
351	JGP_1_8.7424.7431.2	2	17.77	90.7	1.46E+05	(K)LYGAVMSWNVTR(C)		698.8595	1396.704	0.0075	5.4	Zea mays	168489	glutathione S-transferase I
676	JGP_1_8.9750.9821.3	3	15.85	76.4	5.39E+05	(R)NPFGQVPALQDGDLYLFESR(A)			756.0457	2266.114	0.0087	3.8	Zea mays	168489	glutathione S-transferase I
1072	JGP_1_8.6284.6360.2	2	14.05	67.9	2.59E+05	(K)LYGAVmSWNVTR(C)	m:Oxidized methionine	706.8598	1396.704	16.0081	9.4	Zea mays	168489	glutathione S-transferase I
1409	JGP_1_7.9670.9760.3	3	12.96	68.3	5.68E+05	(R)NPFGQVPALQDGDLYLFESR(A)			756.0423	2266.114	-0.0015	-0.7	Zea mays	168489	glutathione S-transferase I
1645	JGP_1_7.2167.2292.2	2	12.24	76.2	2.08E+06	(K)VVDENLEK(L)		473.2504	945.489	0.0048	5	Zea mays	168489	glutathione S-transferase I
2364	JGP_1_8.9751.9822.2	2	10.39	71.1	5.04E+05	(R)NPFGQVPALQDGDLYLFESR(A)			1133.5568	2266.114	-0.0076	-3.3	Zea mays	168489	glutathione S-transferase I
2497	JGP_1_1.8881.8896.3	3	10.07	66.2	7.84E+04	(R)NPFGQVPALQDGDLYLFESR(A)			756.0454	2266.114	0.0078	3.4	Zea mays	168489	glutathione S-transferase I
2511	JGP_1_7.9675.9678.2	2	10.05	73.5	1.99E+05	(R)NPFGQVPALQDGDLYLFESR(A)			1133.553	2266.114	-0.0152	-6.7	Zea mays	168489	glutathione S-transferase I
1562	JGP_1_8.4297.4304.2	2	12.46	72.2	1.45E+06	(K)VLEVYEAR(L)		489.7684	978.525	0.0041	4.1	Triticum aestivum	23504741	glutathione transferase F3
2093	JGP_1_7.4289.4386.2	2	11.02	62.6	7.94E+05	(K)VLEVYEAR(L)		489.7677	978.525	0.0027	2.7	Triticum aestivum	23504741	glutathione transferase F3
1129	JGP_1_6.10135.10210.4	4	13.84	78.2	7.46E+05	(K)VIHDNFGIIEGLmTTVHAITATQK(T)	m:Oxidized methionine	657.1018	2609.376	16.0098	5.7	Zea mays	162461501	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2"
1413	JGP_1_6.11336.11395.4	4	12.93	69.4	1.27E+05	(K)VIHDNFGIIEGLMTTVHAITATQK(T)		653.1031	2609.376	0.015	5.7	Zea mays	162461501	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2"
207	JGP_1_6.10782.10851.3	3	19.05	82.4	4.01E+05	(K)FGIVEGLMTTVHAITATQK(T)		673.0355	2017.079	0.0133	6.6	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
290	JGP_1_6.7481.7501.2	2	18.19	91.8	1.60E+05	(K)SDINIVSNASCTTNCLAPLAK(V)	C:Carbamidomethylation	1125.0504	2249.09	0.0035	1.5	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
435	JGP_1_6.9415.9486.3	3	17.26	74.4	9.85E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	678.3665	2017.079	16.0063	5.6	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
501	JGP_1_5.9064.9075.3	3	16.8	77.5	1.22E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	678.3653	2017.079	16.0027	3.8	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
555	JGP_1_1.8584.8655.3	3	16.46	78.2	8.60E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	678.3657	2017.079	16.0039	4.4	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
603	JGP_1_6.5598.5598.2	2	16.19	84.8	9.49E+05	(K)TLLFGEK(E)		404.2351	807.461	0.0018	2.3	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
701	JGP_1_6.2994.3003.2	2	15.69	68.5	1.79E+04	(K)YDTVHGQWK(H)		567.2743	1133.537	0.0039	3.4	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
741	JGP_1_6.5898.5994.2	2	15.46	73.6	7.38E+05	(K)DAPmFVVGVNEK(E)	m:Oxidized methionine	661.3289	1305.651	15.9998	3.7	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
872	JGP_1_6.7801.7806.2	2	14.9	77.4	3.33E+05	(K)LVSWYDNEWGYSTR(V)		888.409	1775.802	0.0083	4.7	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
1027	JGP_1_3.8535.8609.3	3	14.2	69	3.67E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	678.3673	2017.079	16.0087	6.8	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
1099	JGP_1_8.10777.10777.3	3	13.96	71.9	7.91E+04	(K)FGIVEGLMTTVHAITATQK(T)		673.0356	2017.079	0.0136	6.7	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
1377	JGP_1_6.2718.2823.2	2	13.02	67.8	1.30E+06	(K)SATYDEIK(A)		463.7283	926.447	0.0028	3	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
1438	JGP_1_2.8070.8143.3	3	12.85	73.6	3.60E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	678.3665	2017.079	16.0063	5.6	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
1551	JGP_1_1.8715.8720.3	3	12.47	69.9	5.81E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	678.3659	2017.079	16.0045	4.7	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
1588	JGP_1_7.5398.5404.2	2	12.41	76.4	2.09E+05	(K)TLLFGEK(E)		404.234	807.461	-0.0004	-0.4	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
1683	JGP_1_7.2581.2597.2	2	12.17	69.4	2.12E+05	(K)SATYDEIK(A)		463.7325	926.447	0.0112	12.1	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
2083	JGP_1_6.5530.5693.2	2	11.05	75.2	1.09E+06	(K)TLLFGEK(E)		404.2344	807.461	0.0004	0.5	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
2244	JGP_1_3.5192.5198.2	2	10.66	80	1.11E+05	(K)TLLFGEK(E)		404.2357	807.461	0.003	3.8	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
2250	JGP_1_1.5077.5161.2	2	10.64	76.6	4.09E+05	(K)TLLFGEK(E)		404.2351	807.461	0.0018	2.3	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"
2390	JGP_1_7.9335.9346.3	3	10.33	62.9	1.69E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	678.367	2017.079	16.0078	6.3	Zea mays	162462949	"glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3"

1768	JGP_1_8.8685.8691.2	2	11.93	68.3	1.30E+04	(R)GFGFVTFSTEEAMR(N)		789.8711	1578.726	0.0092	5.8	Zea mays	195609654	glycine-rich RNA-binding protein 2
296	JGP_1_3.5479.5488.2	2	18.13	82.1	2.05E+05	(K)IEDCYIVSGDDCVAVK(S)	C:Carbamidomethylation	921.9187	1842.825	0.0053	2.9	Zea mays	226508288	"glycoside hydrolase, family 28 precursor"
352	JGP_1_3.2578.2656.2	2	17.76	89.5	9.92E+04	(R)VTEYGAVGDGR(T)		562.274	1123.538	0.0029	2.6	Zea mays	226508288	"glycoside hydrolase, family 28 precursor"
393	JGP_1_4.2586.2671.2	2	17.44	88.6	1.10E+06	(R)VTEYGAVGDGR(T)		562.2742	1123.538	0.0033	2.9	Zea mays	226508288	"glycoside hydrolase, family 28 precursor"
581	JGP_1_4.5662.5700.2	2	16.29	77.9	2.40E+05	(K)IEDCYIVSGDDCVAVK(S)	C:Carbamidomethylation	921.9188	1842.825	0.0055	3	Zea mays	226508288	"glycoside hydrolase, family 28 precursor"
607	JGP_1_3.4216.4343.3	3	16.18	72.6	1.66E+06	(R)FNmPSQHIVIR(R)	m:Oxidized methionine	453.2421	1341.71	16.0021	5.3	Zea mays	226508288	"glycoside hydrolase, family 28 precursor"
1101	JGP_1_4.5754.5759.3	3	13.95	69	4.14E+05	(R)FNMPSQHIVIR(R)		447.91	1341.71	0.0058	4.4	Zea mays	226508288	"glycoside hydrolase, family 28 precursor"
1635	JGP_1_3.5577.5659.3	3	12.26	60.2	3.60E+05	(R)FNMPSQHIVIR(R)		447.9102	1341.71	0.0064	4.8	Zea mays	226508288	"glycoside hydrolase, family 28 precursor"
1898	JGP_1_6.1818.1917.2	2	11.54	74.9	1.89E+06	(K)GEPIPK(A)		320.6887	640.366	0.0037	5.7	Arabidopsis thaliana	42567365	Glycosyl hydrolase family 10 protein
2328	JGP_1_5.1725.1818.2	2	10.43	64.6	1.13E+06	(K)GEPIPK(A)		320.6883	640.366	0.0029	4.5	Arabidopsis thaliana	42567365	Glycosyl hydrolase family 10 protein
2288	JGP_1_8.1925.1931.2	2	10.54	66.8	1.52E+05	(K)GYPDAPR(C)		388.1955	775.373	0.0104	13.4	Zea mays	195607296	Grx_S15.1 - glutaredoxin subgroup II
1188	JGP_1_1.7665.7674.3	3	13.6	66.1	3.37E+05	(K)SNYNFEKPFLYLAR(K)		587.9753	1761.896	0.0155	8.8	Arabidopsis thaliana	15241243	GTP-binding nuclear protein Ran-1
1393	JGP_1_1.4832.4838.2	2	12.97	77.4	2.59E+05	(K)NLQYYEISAK(S)		614.8144	1228.621	0.0007	0.6	Arabidopsis thaliana	15241243	GTP-binding nuclear protein Ran-1
1609	JGP_1_8.10211.10211.2	2	12.35	66.1	9.08E+04	(R)FADDSYIDSYISTIGVDFK(I)			1078.5046	2156.007	-0.0051	-2.4	Pisum sativum	303734	GTP-binding protein
2019	JGP_1_8.5933.5940.2	2	11.19	72.3	2.72E+05	(K)LQIWDTAGQER(F)		658.8418	1316.659	0.017	12.9	Zea mays	162458854	GTP-binding protein YPTM2
2120	JGP_1_3.2934.3021.2	2	10.94	77.2	9.55E+05	(K)YEIVK(K)	326.1908	651.371	0.0031	4.8	Arabidopsis thaliana	15229126	H(+)-ATPase 8	
2396	JGP_1_4.2944.3043.2	2	10.31	71.3	4.97E+05	(K)YEIVK(K)	326.1902	651.371	0.0019	2.9	Arabidopsis thaliana	15229126	H(+)-ATPase 8	
2403	JGP_1_5.2986.2990.2	2	10.29	63.4	2.43E+05	(K)YEIVK(K)	326.191	651.371	0.0035	5.4	Arabidopsis thaliana	15229126	H(+)-ATPase 8	
2383	JGP_1_7.8899.8921.2	2	10.34	73.8	4.11E+04	(R)NIILSLPIR(K)		519.8386	1038.667	0.0029	2.8	Arabidopsis thaliana	30697234	haloacid dehalogenase-like hydrolase domain-containing protein
1613	JGP_1_4.5705.5710.3	3	12.32	68	1.88E+05	(K)VIPGSGDKPmIGVQFR(G)	m:Oxidized methionine	572.978	1700.915	16.0042	5.4	Zea mays	226500092	heat shock cognate 70 kDa protein 2
94	JGP_1_4.5290.5290.2	2	20.76	86	1.52E+05	(R)TTPSYVAFTDSER(L)		737.3541	1473.686	0.0153	10.4	Arabidopsis thaliana	15241847	heat shock protein 70
99	JGP_1_3.5107.5112.2	2	20.62	87.8	2.76E+05	(R)TTPSYVAFTDSER(L)		737.3557	1473.686	0.0185	12.6	Arabidopsis thaliana	15241847	heat shock protein 70
2225	JGP_1_3.3164.3169.2	2	10.7	74.9	3.37E+05	(R)VEIIANDQGNR(T)		614.8164	1228.628	-0.0025	-2	Arabidopsis thaliana	15241847	heat shock protein 70
2485	JGP_1_4.3192.3196.2	2	10.11	69.4	1.80E+05	(R)VEIIANDQGNR(T)		614.815	1228.628	-0.0053	-4.3	Arabidopsis thaliana	15241847	heat shock protein 70
1823	JGP_1_3.6838.6838.2	2	11.74	69.5	1.17E+05	(K)GIVDSEDLPLNISR(E)		764.4052	1527.801	0.0018	1.2	Arabidopsis thaliana	15241115	heat shock protein 81-2
2395	JGP_1_1.5338.5341.2	2	10.31	62	1.04E+05	(K)AVLFVPK(R)		387.2472	773.492	-0.0049	-6.3	Triticum aestivum	86439735	heat shock protein 90
1736	JGP_1_3.5196.5203.3	3	12	65.7	1.95E+05	(R)LVNHFVQEFK(R)		420.8983	1260.674	0.0068	5.4	Zea mays	11182068	hsp70 protein
261	JGP_1_6.2970.2974.2	2	18.46	87.5	4.68E+05	(K)SSGGGSDFGYGSASK(E)		682.2966	1363.576	0.0099	7.2	Zea mays	195656945	hypothetical protein
549	JGP_1_7.9260.9263.4	4	16.51	86.4	1.70E+04	(K)mAIVHDIAEAIVGDITPSDGVPKEEK(S)	m:Oxidized methionine	688.3543	2734.397	15.9986	1.3	Arabidopsis thaliana	12321182	hypothetical protein
944	JGP_1_5.2810.2815.2	2	14.6	74.8	3.12E+05	(K)SSGGGSDFGYGSASK(E)		682.2958	1363.576	0.0083	6.1	Zea mays	195656945	hypothetical protein
1059	JGP_1_7.5593.5604.2	2	14.12	68.1	3.05E+05	(R)VSFGENFSPAR(A)		605.8001	1210.585	0.0078	6.5	Oryza sativa	14192878	Hypothetical protein
1349	JGP_1_8.1840.1850.2	2	13.11	76.3	2.95E+05	(R)LGQQQPDGSYK(V)		610.8004	1220.591	0.0029	2.4	Zea mays	195618412	hypothetical protein
1361	JGP_1_7.9625.9640.3	3	13.07	77.7	7.19E+04	(K)mAIVHDIAEAIVGDITPSDGVPK(E)	m:Oxidized methionine	788.7467	2348.217	16.0089	5.9	Arabidopsis thaliana	12321182	hypothetical protein
1485	JGP_1_7.9804.9804.4	4	12.7	84	6.10E+04	(K)MAIVHDIAEAIVGDITPSDGVPKEEK(S)		684.3593	2734.397	0.0186	6.8	Arabidopsis thaliana	12321182	hypothetical protein
1599	JGP_1_8.9727.9727.3	3	12.37	70.9	1.00E+04	(K)mAIVHDIAEAIVGDITPSDGVPK(E)	m:Oxidized methionine	788.7413	2348.217	15.9927	-0.9	Arabidopsis thaliana	12321182	hypothetical protein
2094	JGP_1_7.4303.4306.2	2	11.02	81.5	2.40E+05	(K)FIISK(-)	304.1948	607.381	0.0009	1.6	Arabidopsis thaliana	62198774	hypothetical protein	
2201	JGP_1_4.5179.5184.2	2	10.75	63.5	4.79E+05	(K)LGEAFERIEGK(K)		624.8351	1248.658	0.0046	3.7	Arabidopsis thaliana	12321891	hypothetical protein 14486-13072
2370	JGP_1_6.5554.5655.2	2	10.37	79.9	5.50E+05	(R)LLEEHPK(I)		433.2382	865.478	-0.0087	-10	Zea mays	195626808	hypothetical protein
2407	JGP_1_3.2813.2813.2	2	10.28	60.7	1.91E+05	(K)SSGGGSDFGYGSASK(E)		682.2983	1363.576	0.0133	9.7	Zea mays	195656945	hypothetical protein
2075	JGP_1_8.6946.7029.3	3	11.07	80.6	1.29E+06	(R)LELDPQQNSTVVVQHDKF(-)			699.6812	2097.061	-0.0321	-15.3	Arabidopsis thaliana	13449377	hypothetical protein ArthMp092
357	JGP_1_7.10705.10769.3	3	17.71	87.9	3.04E+05	(K)IPTVGVVFNPImNELFTAVR(G)	m:Oxidized methionine	745.0778	2217.21	16.0088	6.2	Zea mays	226493279	inositol monophosphatase 3
422	JGP_1_7.11930.11993.3	3	17.33	92.6	2.19E+05	(K)IPTVGVVFNPIMNELFTAVR(G)		739.7443	2217.21	0.0083	3.8	Zea mays	226493279	inositol monophosphatase 3
1040	JGP_1_7.12048.12053.3	3	14.17	80.9	1.08E+05	(K)IPTVGVVFNPIMNELFTAVR(G)		739.7443	2217.21	0.0083	3.8	Zea mays	226493279	inositol monophosphatase 3
2036	JGP_1_7.12004.12004.2	2	11.15	73.5	7.77E+04	(K)IPTVGVVFNPIMNELFTAVR(G)		1109.1089	2217.21	0.0005	0.2	Zea mays	226493279	inositol monophosphatase 3
2091	JGP_1_7.11994.12018.2	2	11.03	73.2	8.43E+04	(K)IPTVGVVFNPIMNELFTAVR(G)		1109.1089	2217.21	0.0005	0.2	Zea mays	226493279	inositol monophosphatase 3
2272	JGP_1_7.1351.1355.2	2	10.6	73.2	3.96E+05	(K)ATLDDTTNR(I)		503.7454	1006.48	0.0035	3.5	Arabidopsis thaliana	79312679	inositol-phosphate phosphatase
2435	JGP_1_7.4057.4057.2	2	10.23	63.9	2.02E+05	(K)GQVDLVTETDK(G)		602.8105	1204.606	0.0082	6.8	Arabidopsis thaliana	79312679	inositol-phosphate phosphatase
767	JGP_1_6.9926.9938.4	4	15.35	81.6	1.05E+05	(K)LRPPLVLQEFVNHGGVIFK(V)			541.5695	2163.244	0.0125	5.8	Zea mays	162459062	inositol-tetrakisphosphate 1-kinase 1
1927	JGP_1_3.1187.1256.2	2	11.45	81.9	3.00E+05	(K)LSQERDK(T)		438.2276	875.458	-0.0102	-11.6	Arabidopsis thaliana	42572655	interactor of constitutive active ROPs 5
1003	JGP_1_3.7619.7704.2	2	14.33	76.3	3.19E+05	(R)FDLASVLCR(G)	C:Carbamidomethylation	540.7823	1080.551	0.0067	6.2	Solanum tuberosum	27728149	isoamylase isoform 3
1814	JGP_1_6.4210.4307.2	2	11.77	77.9	1.54E+06	(K)VLLPTPPTK(R)		483.3003	965.603	-0.0097	-10	Pisum sativum	73698629	isoamylase isoform 3

2378	JGP_1_5.3873.3878.2	2	10.35	70.9	5.11E+05	(K)VLLPTPPTK(R)		483.2994	965.603	-0.0115	-11.9	Pisum sativum	73698629	isoamylase isoform 3
240	JGP_1_3.8528.8536.3	3	18.63	90.9	1.63E+05	(K)TGDIWHVSVEGLPASGVLYGYR(I)			792.7406	2376.198	0.009	3.8	Zea mays	162458751 isoamylase-type starch debranching enzyme ISO3
543	JGP_1_3.7860.7866.2	2	16.53	83.9	1.48E+05	(R)FDDSVILLDPYAK(L)		748.3892	1495.768	0.0032	2.2	Zea mays	162458751	isoamylase-type starch debranching enzyme ISO3
1273	JGP_1_3.2039.2043.2	2	13.36	75.6	1.55E+05	(R)YASAGGGPVAASK(E)		568.2927	1135.574	0.0039	3.4	Zea mays	162458751	isoamylase-type starch debranching enzyme ISO3
1313	JGP_1_1.2026.2026.2	2	13.23	72.7	6.50E+03	(R)YASAGGGPVAASK(E)		568.2888	1135.574	-0.0039	-3.4	Zea mays	162458751	isoamylase-type starch debranching enzyme ISO3
1368	JGP_1_3.3073.3083.2	2	13.03	70.3	2.48E+05	(R)VVDTNLESPK(D)		551.2934	1101.579	0.0009	0.8	Zea mays	162458751	isoamylase-type starch debranching enzyme ISO3
368	JGP_1_1.2681.2691.3	3	17.61	86.6	1.34E+05	(K)TIEAEAAHGTVTR(H)		452.57	1355.691	0.0041	3	Solanum tuberosum	940877	isocitrate dehydrogenase (NADP+)
443	JGP_1_6.7011.7016.3	3	17.22	72.1	2.41E+05	(R)LVPGWTKPICIGR(H)	C:Carbamidomethylation	499.6215	1496.841	0.0093	6.2	Solanum tuberosum	940877	isocitrate dehydrogenase (NADP+)
597	JGP_1_6.2923.2929.3	3	16.21	73.4	7.29E+05	(K)TIEAEAAHGTVTR(H)		452.5715	1355.691	0.0086	6.3	Solanum tuberosum	940877	isocitrate dehydrogenase (NADP+)
1020	JGP_1_5.6650.6650.3	3	14.24	71.5	1.20E+05	(R)LVPGWTKPICIGR(H)	C:Carbamidomethylation	499.619	1496.841	0.0018	1.2	Solanum tuberosum	940877	isocitrate dehydrogenase (NADP+)
1397	JGP_1_5.2775.2781.3	3	12.97	75.1	3.10E+05	(K)TIEAEAAHGTVTR(H)		452.5703	1355.691	0.005	3.7	Solanum tuberosum	940877	isocitrate dehydrogenase (NADP+)
1878	JGP_1_6.2298.2302.2	2	11.59	71.8	3.01E+05	(R)HAFGDQYR(A)		497.2331	993.454	0.0052	5.3	Solanum tuberosum	940877	isocitrate dehydrogenase (NADP+)
820	JGP_1_5.10633.10664.2	2	15.08	80.6	3.04E+03	(K)LIFPFVDLDIK(Y)		660.3849	1319.761	0.0016	1.2	Zea mays	226499486	isocitrate dehydrogenase2
1511	JGP_1_7.6703.6709.2	2	12.61	66.8	1.06E+05	(K)GDLYDQASLVSAVK(G)		733.382	1465.753	0.0034	2.3	Zea mays	162461348	isoflavone reductase homolog IRL
1957	JGP_1_7.2679.2692.2	2	11.38	70.5	4.54E+05	(K)AVVLGDGDTK(A)		487.7652	974.515	0.0078	8	Zea mays	162461348	isoflavone reductase homolog IRL
1895	JGP_1_7.6546.6551.2	2	11.55	80.5	2.04E+05	(R)ILVVGGTGYIGR(H)		602.8575	1204.705	0.0029	2.4	Oryza sativa	18250364	isoflavone reductase-like protein
1298	JGP_1_7.8951.8960.2	2	13.29	72.5	1.14E+05	(R)AFSVFLFNSK(Y)		580.3151	1159.615	0.0083	7.2	Nicotiana tabacum	13603408	isopentenyl diphosphate isomerase 2
2505	JGP_1_6.3415.3560.2	2	10.06	65.9	2.11E+06	(K)AAFALR(A)		324.6957	648.383	0.0014	2.1	Arabidopsis thaliana	18407646	isoprenoid biosynthesis enzyme domain-containing protein
2492	JGP_1_7.0896.0900.2	2	10.09	70	1.52E+05	(R)ITSETGK(A)		368.1986	735.388	0.0016	2.2	Triticum aestivum	17981573	kinase R-like protein
2348	JGP_1_6.2745.2749.2	2	10.41	64.7	9.69E+04	(K)EGIHINK(G)		405.7288	810.447	0.0035	4.3	Arabidopsis thaliana	10177316	kinesin-like protein
578	JGP_1_4.4817.4908.3	3	16.31	78.3	9.56E+05	(R)AAGAYGLISVHSR(D)		434.5733	1301.696	0.0093	7.1	Zea mays	226500290	L-ascorbate oxidase precursor
932	JGP_1_4.4827.4832.2	2	14.64	69.5	4.60E+05	(R)AAGAYGLISVHSR(D)		651.3546	1301.696	0.0059	4.5	Zea mays	226500290	L-ascorbate oxidase precursor
1497	JGP_1_4.1119.1186.2	2	12.64	84	2.49E+05	(K)DHAVLAK(N)		377.217	753.425	0.0014	1.8	Zea mays	226500290	L-ascorbate oxidase precursor
2149	JGP_1_3.1168.1228.2	2	10.87	75.3	8.44E+04	(K)DHAVLAK(N)		377.2154	753.425	-0.0018	-2.4	Zea mays	226500290	L-ascorbate oxidase precursor
824	JGP_1_7.1334.1401.3	3	15.07	72.8	5.12E+06	(R)EDKPQPPPEGR(L)		417.2121	1249.617	0.0046	3.7	Arabidopsis thaliana	15223049	L-ascorbate peroxidase
1045	JGP_1_8.1041.1153.3	3	14.15	65.1	5.79E+06	(R)EDKPQPPPEGR(L)		417.2113	1249.617	0.0022	1.8	Arabidopsis thaliana	15223049	L-ascorbate peroxidase
1495	JGP_1_7.1106.1229.3	3	12.65	62.1	4.76E+06	(R)EDKPQPPPEGR(L)		417.2114	1249.617	0.0025	2	Arabidopsis thaliana	15223049	L-ascorbate peroxidase
1644	JGP_1_7.1255.1266.2	2	12.24	68.9	7.42E+05	(R)EDKPQPPPEGR(L)		625.3105	1249.617	-0.0034	-2.7	Arabidopsis thaliana	15223049	L-ascorbate peroxidase
2332	JGP_1_8.1155.1166.2	2	10.43	67.2	3.96E+05	(R)EDKPQPPPEGR(L)		625.3119	1249.617	-0.0006	-0.5	Arabidopsis thaliana	15223049	L-ascorbate peroxidase
1603	JGP_1_7.6353.6359.2	2	12.36	79	5.41E+06	(K)VTEREVQVEK(D)		608.8291	1216.653	-0.0023	-1.9	Arabidopsis thaliana	15227965	late embryogenesis abundant domain-containing protein
2074	JGP_1_8.6493.6578.2	2	11.07	78.2	3.93E+06	(K)VTEREVQVEK(D)		608.8283	1216.653	-0.0039	-3.2	Arabidopsis thaliana	15227965	late embryogenesis abundant domain-containing protein
1514	JGP_1_7.6167.6265.2	2	12.6	87.3	9.74E+06	(R)LSIEIAR(K)		401.2475	801.483	0.0048	6	Pisum sativum	30313913	LEGCYC
18	JGP_1_6.11083.11135.3	3	22.96	89.5	5.86E+05	(K)IADASGmEWFSIITTPNPIFSHLAGK(T)	m:Oxidized methionine	940.4791	2803.412	16.0104	5.5	Zea mays	162459030	legumin-like protein
76	JGP_1_6.7946.7951.2	2	21.12	92.2	5.64E+05	(K)VAYVLQGTGTCGIVLPEATK(E)	C:Carbamidomethylation	1039.0592	2077.1	0.0113	5.4	Zea mays	162459030	legumin-like protein
171	JGP_1_6.11078.11140.3	3	19.4	87.3	5.86E+05	(K)IADASGmEWFSIITTPNPIFSHLAGK(T)	m:Oxidized methionine	940.4791	2803.412	16.0104	5.5	Zea mays	162459030	legumin-like protein
205	JGP_1_6.11102.11163.4	4	19.06	82.5	1.57E+05	(K)IADASGmEWFSIITTPNPIFSHLAGK(T)	m:Oxidized methionine	705.6124	2803.412	16.0154	7.3	Zea mays	162459030	legumin-like protein
816	JGP_1_6.8012.8012.2	2	15.1	77.4	6.21E+04	(K)LSLAAGGLALPSYSDSAK(V)			860.9652	1720.912	0.0115	6.7	Zea mays	162459030 legumin-like protein
892	JGP_1_6.11631.11631.3	3	14.81	70.3	2.09E+05	(K)IADASGMEWFSIITTPNPIFSHLAGK(T)			935.1463	2803.412	0.012	4.3	Zea mays	162459030 legumin-like protein
917	JGP_1_6.7928.8005.3	3	14.71	77.3	9.72E+05	(K)VAYVLQGTGTCGIVLPEATK(E)	C:Carbamidomethylation		693.0431	2077.1	0.0149	7.2	Zea mays	162459030 legumin-like protein
1135	JGP_1_6.8007.8090.2	2	13.82	81.3	2.59E+06	(K)LSLAAGGLALPSYSDSAK(V)			860.9652	1720.912	0.0115	6.7	Zea mays	162459030 legumin-like protein
1183	JGP_1_6.11697.11697.3	3	13.62	70.3	2.43E+05	(K)IADASGMEWFSIITTPNPIFSHLAGK(T)			935.1463	2803.412	0.012	4.3	Zea mays	162459030 legumin-like protein
1706	JGP_1_6.11690.11690.3	3	12.1	64.8	2.51E+05	(K)IADASGMEWFSIITTPNPIFSHLAGK(T)			935.1463	2803.412	0.012	4.3	Zea mays	162459030 legumin-like protein
2298	JGP_1_6.11628.11628.3	3	10.51	65.5	1.95E+05	(K)IADASGMEWFSIITTPNPIFSHLAGK(T)			935.1463	2803.412	0.012	4.3	Zea mays	162459030 legumin-like protein
1982	JGP_1_5.3986.4096.2	2	11.29	77.5	2.43E+06	(K)YLNFK(H)	342.6913	684.371	0.0038	5.5	Arabidopsis thaliana	15242920	leucine rich repeat family protein	
2360	JGP_1_4.2049.2131.2	2	10.39	67.4	9.83E+05	(R)FLCQNK(K)	C:Carbamidomethylation	405.2037	809.397	0.0027	3.3	Arabidopsis thaliana	15218385	leucine-rich receptor-like protein kinase
1843	JGP_1_3.5327.5333.2	2	11.7	72.7	2.22E+05	(K)FGEAVGFK(A)		427.726	854.441	0.004	4.7	Zea mays	162461878	light harvesting chlorophyll a /b binding protein
362	JGP_1_4.8432.8437.2	2	17.65	86.2	9.18E+04	(K)LIGFLGGSDGLLAQR(T)		758.9283	1516.848	0.0011	0.7	Zea mays	226530941	LOC100280449

1357	JGP_1_1.8251.8257.2	2	13.08	70.4	1.41E+04	(K)LIGFLGGSDGLLAQR(T)		758.9297	1516.848	0.0039	2.6	Zea mays	226530941	LOC100280449		
2247	JGP_1_2.5044.5047.2	2	10.65	70.3	1.24E+05	(R)LYLDELQK(I)		511.2847	1021.556	0.0057	5.6	Zea mays	226493536	LOC100280907		
13	JGP_1_8.8036.8104.2	2	23.32	96.8	2.62E+05	(R)LPDATLSYFDTSSPDGELK(T)			1028.4928	2055.976	0.0026	1.3	Zea mays	226502632	LOC100282052	
114	JGP_1_8.8677.8680.3	3	20.33	91.2	1.86E+05	(K)TIAVGDRLPDATLSYFDTSSPDGELK(T)			923.4624	2768.363	0.0102	3.7	Zea mays	226502632	LOC100282052	
876	JGP_1_8.3859.3966.2	2	14.89	87.9	1.29E+06	(K)HLPGFVAK(A)		434.7572	868.504	0.0032	3.7	Zea mays	226502632	LOC100282052		
1400	JGP_1_8.9102.9105.3	3	12.97	72	1.71E+05	(K)VVLFAVPGAFTPTCTQK(H) C:Carbamidomethylation			612.6656	1835.972	0.0098	5.4	Zea mays	226502632	LOC100282052	
1463	JGP_1_8.7699.7712.3	3	12.78	60.6	1.86E+05	(R)AMGVELDLSDKPVGLGVR(S)			619.3401	1855.995	0.0111	6	Zea mays	226502632	LOC100282052	
1605	JGP_1_8.9096.9117.2	2	12.36	81.1	7.53E+04	(K)VVLFAVPGAFTPTCTQK(H) C:Carbamidomethylation			918.4903	1835.972	0.0009	0.5	Zea mays	226502632	LOC100282052	
189	JGP_1_4.4453.4470.2	2	19.23	84.8	1.52E+05	(K)IYSEmIGNVmTDAR(S)	m:Oxidized methionine		816.38	1599.751	32.0022	7.6	Zea mays	226505720	LOC100282190	
492	JGP_1_4.9606.9675.3	3	16.85	85.3	2.65E+05	(K)LIAELNEILAHDVVDEAGAWK(S)			769.4094	2306.203	0.011	4.8	Zea mays	226505720	LOC100282190	
1657	JGP_1_4.8036.8104.2	2	12.22	71.4	2.10E+05	(R)ELFEFLPK(T)		511.7832	1022.556	0.0034	3.3	Zea mays	226505720	LOC100282190		
1753	JGP_1_4.9576.9582.3	3	11.96	73.5	1.86E+05	(K)VGVVLSGGQAPGGHNVICGIFDYLQER(A)	C:Carbamidomethylation		948.152	2842.43	0.011	3.9	Zea mays	226505720	LOC100282190	
2304	JGP_1_4.9574.9586.4	4	10.5	65.8	8.92E+04	(K)VGVVLSGGQAPGGHNVICGIFDYLQER(A)	C:Carbamidomethylation		711.3673	2842.43	0.0169	5.9	Zea mays	226505720	LOC100282190	
799	JGP_1_8.3977.3989.4	4	15.19	79.2	3.55E+05	(R)AHLKPEPFDRPLR(D)		394.7251	1575.875	0.0031	2	Zea mays	226528336	LOC100282202		
1626	JGP_1_7.9035.9035.3	3	12.29	70.4	1.33E+05	(R)VFFHDCFVSGCDASVLIASTQFQK(S)	C:Carbamidomethylation		921.7711	2763.291	0.0082	3	Zea mays	226510262	LOC100282284 precursor	
1652	JGP_1_6.9103.9210.3	3	12.23	67.8	6.32E+05	(R)VFFHDCFVSGCDASVLIASTQFQK(S)	C:Carbamidomethylation		921.7735	2763.291	0.0154	5.6	Zea mays	226510262	LOC100282284 precursor	
1352	JGP_1_8.2916.2916.2	2	13.1	63.2	3.18E+05	(R)ATmGmAAQDmQNCDEQFR(Q)	C:Carbamidomethylation	m:Oxidized methionine		1076.4179	2103.835	47.9934	4	Zea mays	226494668	LOC100283356
2279	JGP_1_8.5000.5000.2	2	10.58	64.3	2.67E+05	(K)LGLPEASSmANVR(E)	m:Oxidized methionine		680.8505	1344.694	15.9997	3.5	Zea mays	226495607	LOC100283718	
668	JGP_1_6.4350.4365.2	2	15.9	80.2	1.82E+05	(K)AISSSSAYDDQFK(Q)		709.8288	1418.643	0.0069	4.9	Zea mays	226506764	LOC100284080		
2488	JGP_1_6.6316.6325.2	2	10.11	68.6	1.99E+05	(R)LLWASTGVK(N)		487.7878	974.567	0.0014	1.4	Zea mays	226506764	LOC100284080		
842	JGP_1_1.6305.6309.3	3	15	74.4	9.32E+04	(K)LAYIALDYDQEmETAK(T)	m:Oxidized methionine		630.6371	1873.889	16.0079	6.9	Zea mays	226492795	LOC100284092	
1819	JGP_1_5.4028.4030.2	2	11.75	76.7	4.33E+05	(R)LIADLGK(T)		365.2298	729.451	0.0018	2.5	Zea mays	226532026	LOC100284551		
154	JGP_1_1.8976.9040.3	3	19.53	89.5	2.16E+05	(R)SGAFGSYDYEPLLDSLEGNSGFGR(G)			846.724	2538.142	0.0155	6.1	Zea mays	226494853	LOC100285259	
403	JGP_1_1.8216.8221.2	2	17.4	80.3	1.73E+04	(R)EEVGEDNFFLFGAK(A)		801.3869	1601.748	0.0183	11.4	Zea mays	226494853	LOC100285259		
996	JGP_1_1.9631.9637.3	3	14.36	87.8	9.25E+04	(K)HVLDVTGVTIDPTSLFDIQIK(R)			771.0938	2311.254	0.0125	5.4	Zea mays	226494853	LOC100285259	
1094	JGP_1_1.8872.8875.3	3	13.97	67.5	9.42E+04	(R)GDYFLVGYDFPSYIDAQDR(V)			747.6843	2241.014	0.0249	11.1	Zea mays	226494853	LOC100285259	
1104	JGP_1_1.8622.8690.2	2	13.94	70.4	2.62E+05	(K)SDQWTSNLDLLTGLR(K)		859.942	1718.871	0.0059	3.5	Zea mays	226494853	LOC100285259		
1144	JGP_1_3.5839.5849.3	3	13.76	77.1	1.85E+05	(R)TISYTNHTVLPEALEK(W)		605.9908	1815.949	0.0091	5	Zea mays	226494853	LOC100285259		
1205	JGP_1_1.8646.8651.3	3	13.56	80.4	1.53E+05	(K)SDQWTSNLDLLTGLR(K)		573.6318	1718.871	0.0101	5.9	Zea mays	226494853	LOC100285259		
1206	JGP_1_2.8469.8488.3	3	13.56	69.6	7.61E+04	(R)SGAFGSYDYEPLLDSLEGNSGFGR(G)			846.7246	2538.142	0.0173	6.8	Zea mays	226494853	LOC100285259	
1464	JGP_1_1.6604.6619.2	2	12.77	71.9	2.15E+05	(K)FGYELEALAGQEK(D)		727.8637	1454.716	0.0039	2.7	Zea mays	226494853	LOC100285259		
2243	JGP_1_1.9005.9005.2	2	10.66	71	6.42E+04	(R)SGAFGSYDYEPLLDSLEGNSGFGR(G)			1269.5758	2538.142	0.0024	0.9	Zea mays	226494853	LOC100285259	
457	JGP_1_1.3230.3235.2	2	17.1	83.3	2.43E+05	(K)INEQTQQVVVDR(L)		714.8763	1428.744	0.0012	0.8	Zea mays	226495867	LOC100285352		
600	JGP_1_3.3257.3257.2	2	16.2	78.7	1.32E+05	(K)INEQTQQVVVDR(L)		714.8782	1428.744	0.005	3.5	Zea mays	226495867	LOC100285352		
609	JGP_1_8.3547.3652.2	2	16.18	82.8	1.29E+06	(K)INEQTQQVVVDR(L)		714.8797	1428.744	0.008	5.6	Zea mays	226495867	LOC100285352		
745	JGP_1_2.3103.3119.2	2	15.44	76.1	1.14E+05	(K)INEQTQQVVVDR(L)		714.8747	1428.744	-0.002	-1.4	Zea mays	226495867	LOC100285352		
1961	JGP_1_8.3582.3599.3	3	11.36	73.4	2.38E+04	(K)INEQTQQVVVDR(L)		476.9221	1428.744	0.0076	5.3	Zea mays	226495867	LOC100285352		
358	JGP_1_7.9041.9054.3	3	17.69	91.9	2.05E+05	(K)VPIPPGQVYAINDALSAEGAADDYEACLK(Q)	C:Carbamidomethylation		1016.4977	3047.467	0.0119	3.9	Zea mays	226493090	LOC100285843	
698	JGP_1_7.9690.9811.4	4	15.71	82.5	6.26E+05	(R)FDLQLLGmGPDGHIASLFPGHPLVNEK(E)	m:Oxidized methionine		730.3809	2902.492	16.0098	5.1	Zea mays	226493090	LOC100285843	
1362	JGP_1_7.9751.9751.2	2	13.07	68.9	3.43E+04	(K)LLIFDSEEDLAVSLAK(Y)		881.981	1762.947	0.0074	4.2	Zea mays	226493090	LOC100285843		
1583	JGP_1_7.7225.7229.3	3	12.42	69.5	2.76E+05	(R)KLTEPPYLDSVDWSK(W)		593.3086	1777.901	0.0106	5.9	Zea mays	226493090	LOC100285843		
1756	JGP_1_7.9716.9716.3	3	11.96	67	1.40E+05	(R)FDLQLLGmGPDGHIASLFPGHPLVNEK(E)	m:Oxidized methionine		973.5016	2902.492	15.9982	1.1	Zea mays	226493090	LOC100285843	
1811	JGP_1_7.10246.10318.4	4	11.79	72.6	4.34E+05	(R)FDLQLLGMGPDGHIASLFPGHPLVNEK(E)			726.3836	2902.492	0.0206	7.1	Zea mays	226493090	LOC100285843	
166	JGP_1_3.10757.10762.3	3	19.44	83.6	3.31E+05	(R)NIWADDLAASLSTLQSLEAVAGK(D)			791.7536	2373.23	0.0166	7	Zea mays	226531522	LOC100286153	
180	JGP_1_3.8929.8993.2	2	19.33	88.4	1.11E+06	(K)TLTSLSGVTAYGFDLIR(G)		907.493	1813.969	0.0093	5.1	Zea mays	226531522	LOC100286153		
203	JGP_1_6.9381.9386.3	3	19.09	75.1	3.05E+04	(K)WFDTNYHFIVPELGPSTK(F)			717.6934	2151.055	0.0111	5.2	Zea mays	226531522	LOC100286153	
215	JGP_1_3.7770.7844.2	2	18.94	90.4	6.71E+05	(K)AAGASWIQFDEPTLVK(D)		866.9529	1732.891	0.0081	4.7	Zea mays	226531522	LOC100286153		
432	JGP_1_3.10406.10411.4	4	17.27	84.4	1.98E+05	(K)ALGIDTVPVLVGPVSYLLLSKPAK(G)			613.3768	2450.463	0.0221	9	Zea mays	226531522	LOC100286153	
448	JGP_1_3.5562.5649.2	2	17.15	83.7	2.63E+05	(K)ISEEEYISAIK(E)		641.3354	1281.657	0.0062	4.9	Zea mays	226531522	LOC100286153		
497	JGP_1_3.7788.7871.3	3	16.82	80.5	1.79E+05	(K)AAGASWIQFDEPTLVK(D)		578.3059	1732.891	0.0127	7.3	Zea mays	226531522	LOC100286153		
510	JGP_1_3.8410.8484.3	3	16.73	67.5	6.62E+05	(K)WFDTNYHFIVPELGPSTK(F)			717.6943	2151.055	0.0138	6.4	Zea mays	226531522	LOC100286153	
519	JGP_1_6.9932.9996.2	2	16.69	84.2	2.53E+05	(K)TLTSLSGVTAYGFDLIR(G)		907.4917	1813.969	0.0067	3.7	Zea mays	226531522	LOC100286153		
541	JGP_1_4.9225.9290.3	3	16.54	81.5	1.83E+05	(K)TLTSLSGVTAYGFDLIR(G)		605.3311	1813.969	0.0093	5.1	Zea mays	226531522	LOC100286153		
544	JGP_1_3.8933.8998.3	3	16.53	78.9	1.00E+06	(K)TLTSLSGVTAYGFDLIR(G)		605.3324	1813.969	0.0132	7.3	Zea mays	226531522	LOC100286153		
614	JGP_1_4.9219.9284.2	2	16.16	83.7	2.25E+05	(K)TLTSLSGVTAYGFDLIR(G)		907.4901	1813.969	0.0035	1.9	Zea mays	226531522	LOC100286153		
620	JGP_1_3.7278.7403.3	3	16.15	79.8	8.70E+05	(K)ISEEEYISAIKEEISK(V)		623.3268	1867.954	0.0123	6.6	Zea mays	226531522	LOC100286153		
746	JGP_1_3.7250.7255.3	3	15.44	76.8	2.21E+04	(K)IQEELDIDVLVHGEPER(N)		664.3434	1991.008	0.0076	3.8	Zea mays	226531522	LOC100286153		
771	JGP_1_5.11487.11494.3	3	15.33	76.7	4.87E+04	(R)NIWADDLAASLSTLQSLEAVAGK(D)			791.7451	2373.23	-0.0089	-3.7	Zea mays	226531522	LOC100286153	
922	JGP_1_5.9554.9554.2	2	14.68	70.4	1.06E+05	(K)TLTSLSGVTAYGFDLIR(G)		907.4898	1813.969	0.0029	1.6	Zea mays	226531522	LOC100286153		
980	JGP_1_3.8418.8418.3	3	14.45	61.7	3.88E+05	(K)WFDTNYHFIVPELGPSTK(F)			717.6943	2151.055	0.0138	6.4	Zea mays	226531522	LOC100286153	
1022	JGP_1_3.10697.10702.3	3	14.23	62.3	2.09E+05	(R)NIWADDLAASLSTLQSLEAVAGK(D)			791.7536	2373.23	0.0166	7	Zea mays	226531522	LOC100286153	
1030	JGP_1_6.9948.9950.3	3	14.19	74.3	1.29E+05	(K)TLTSLSGVTAYGFDLIR(G)		605.331	1813.969	0.009	5	Zea mays	226531522	LOC100286153		

1212	JGP_1_3.9056.9124.3	3	13.55	67.8	4.49E+05	(K)EVEDLEAAGIQVIQIDEAALR(E)		761.4038	2282.187	0.0094	4.1	Zea mays	226531522	LOC100286153
1279	JGP_1_3.9064.9120.3	3	13.35	83.1	4.45E+05	(K)EVEDLEAAGIQVIQIDEAALR(E)		761.4038	2282.187	0.0094	4.1	Zea mays	226531522	LOC100286153
1446	JGP_1_6.11477.11541.3	3	12.83	79.1	2.87E+05	(K)ALGIDTVPVLVGPVSYLLLSKPAK(G)		817.4974	2450.463	0.0144	5.9	Zea mays	226531522	LOC100286153
1516	JGP_1_3.4929.5071.2	2	12.59	88.5	1.76E+06	(K)TLDLIR(S)		365.7282	730.446	0.0034	4.6	Zea mays	226531522	LOC100286153
1884	JGP_1_4.9227.9227.2	2	11.57	68.7	1.58E+05	(K)TLTSLSGVTAYGFDLIR(G)		907.4901	1813.969	0.0035	1.9	Zea mays	226531522	LOC100286153
1917	JGP_1_3.10421.10481.3	3	11.46	76.4	1.33E+06	(K)ALGIDTVPVLVGPVSYLLLSKPAK(G)			817.4992	2450.463	0.0198	8.1	Zea mays	226531522	LOC100286153
2027	JGP_1_1.9016.9025.3	3	11.16	64.6	7.05E+04	(K)TLTSLSGVTAYGFDLIR(G)		605.3314	1813.969	0.0102	5.6	Zea mays	226531522	LOC100286153
2058	JGP_1_1.10420.10420.3	3	11.09	74.3	7.84E+04	(K)ALGIDTVPVLVGPVSYLLLSKPAK(G)			817.5027	2450.463	0.0303	12.4	Zea mays	226531522	LOC100286153
2118	JGP_1_2.8487.8552.3	3	10.95	71.6	1.04E+05	(K)TLTSLSGVTAYGFDLIR(G)		605.3308	1813.969	0.0084	4.6	Zea mays	226531522	LOC100286153
520	JGP_1_8.6951.6966.2	2	16.69	79	3.38E+04	(R)GLPEDFGGWK(Q)		553.2731	1105.531	0.0076	6.9	Zea mays	226498210	LOC100286263
899	JGP_1_8.9621.9636.3	3	14.78	72.7	1.88E+05	(K)LmDSDTGTADDFVGEATIPLEAVYTER(S)	m:Oxidized methionine		978.1251	2916.345	16.0152	6.9	Zea mays	226498210	LOC100286263
1312	JGP_1_8.9861.9865.3	3	13.24	77.4	2.73E+04	(K)LMDSDTGTADDFVGEATIPLEAVYTER(S)			972.7943	2916.345	0.0228	7.8	Zea mays	226498210	LOC100286263
1223	JGP_1_1.7481.7484.3	3	13.51	74.5	2.24E+05	(R)VETGIIKPGmVVTFGPSGLTTEVK(S)	m:Oxidized methionine		826.1197	2460.342	16.0027	3.2	Zea mays	226494632	LOC100286309
2374	JGP_1_2.7019.7019.3	3	10.36	62.2	1.11E+05	(R)VETGIIKPGmVVTFGPSGLTTEVK(S)	m:Oxidized methionine		826.1169	2460.342	15.9943	-0.2	Zea mays	226494632	LOC100286309
1747	JGP_1_7.5960.5969.2	2	11.98	68.6	9.90E+04	(K)ISPWFR(L)		403.224	805.436	0.0052	6.4	Zea mays	162461852	LOC541901
72	JGP_1_8.5598.5603.2	2	21.18	88.8	1.22E+05	(K)GWDEGVmTmQVGEVAR(I)	m:Oxidized methionine		898.9063	1764.804	32.001	6.2	Zea mays	162462456	LOC542519
445	JGP_1_6.7349.7349.3	3	17.21	75.3	3.01E+05	(R)IDAHSmCSPGFSCDSAYQVTYIVR(G)	C:Carbamidomethylation	m:Oxidized methionine	927.4186	2764.216	16.0249	10.8	Zea mays	162458978	LOC542653
687	JGP_1_6.4164.4267.2	2	15.79	93.1	3.33E+06	(R)LVSSQPASGIVK(L)		593.3486	1185.684	0.0062	5.2	Zea mays	162458978	LOC542653
1970	JGP_1_1.8319.8397.2	2	11.33	71.9	1.44E+05	(R)VVVLNTANLPLVR(E)		704.4494	1407.868	0.0233	16.6	Zea mays	162458978	LOC542653
2293	JGP_1_7.4084.4087.2	2	10.52	77.9	6.99E+05	(R)LVSSQPASGIVK(L)		593.3429	1185.684	-0.0052	-4.4	Zea mays	162458978	LOC542653
21	JGP_1_1.5340.5425.2	2	22.88	93	1.19E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7955	1342.577	0.0071	5.3	Zea mays	162459584	LOC732771 precursor
67	JGP_1_7.5787.5937.2	2	21.22	90.4	2.89E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7975	1342.577	0.0111	8.3	Zea mays	162459584	LOC732771 precursor
74	JGP_1_6.6107.6189.2	2	21.13	86.3	3.41E+06	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7952	1342.577	0.0065	4.9	Zea mays	162459584	LOC732771 precursor
75	JGP_1_5.5821.5826.2	2	21.12	89.1	1.83E+06	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7948	1342.577	0.0057	4.3	Zea mays	162459584	LOC732771 precursor
107	JGP_1_1.5501.5506.2	2	20.46	86.7	2.89E+06	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7954	1342.577	0.0069	5.2	Zea mays	162459584	LOC732771 precursor
182	JGP_1_8.6005.6144.2	2	19.3	85.3	2.19E+06	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7966	1342.577	0.0093	6.9	Zea mays	162459584	LOC732771 precursor
224	JGP_1_2.5106.5204.2	2	18.87	82.4	2.62E+06	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7949	1342.577	0.0059	4.4	Zea mays	162459584	LOC732771 precursor
232	JGP_1_7.6769.6853.2	2	18.77	94.5	1.22E+07	(K)AGIIDMQFR(R)		525.7776	1050.54	0.0078	7.5	Zea mays	162459584	LOC732771 precursor
244	JGP_1_4.5617.5698.2	2	18.6	82.9	2.29E+06	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7956	1342.577	0.0073	5.5	Zea mays	162459584	LOC732771 precursor
320	JGP_1_7.5942.6078.2	2	17.98	76.2	2.42E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7971	1342.577	0.0103	7.7	Zea mays	162459584	LOC732771 precursor
452	JGP_1_3.5436.5534.2	2	17.13	75.7	2.17E+06	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation		671.7948	1342.577	0.0057	4.3	Zea mays	162459584	LOC732771 precursor
970	JGP_1_4.6590.6593.2	2	14.48	79.3	4.27E+05	(K)AGIIDMQFR(R)		525.7759	1050.54	0.0044	4.2	Zea mays	162459584	LOC732771 precursor
1107	JGP_1_7.5302.5307.2	2	13.93	68.4	1.22E+07	(K)AGIIDmQFR(R)	m:Oxidized methionine		533.7755	1050.54	16.0036	8.2	Zea mays	162459584	LOC732771 precursor
1285	JGP_1_6.7111.7199.2	2	13.34	79.4	8.92E+05	(K)AGIIDMQFR(R)		525.7755	1050.54	0.0036	3.5	Zea mays	162459584	LOC732771 precursor
1391	JGP_1_2.6024.6118.2	2	12.98	77.2	3.57E+05	(K)AGIIDMQFR(R)		525.7755	1050.54	0.0036	3.5	Zea mays	162459584	LOC732771 precursor
1695	JGP_1_7.5743.5837.2	2	12.14	80.6	2.55E+06	(R)KAGIIDMQFR(R)		589.8235	1178.635	0.0047	4	Zea mays	162459584	LOC732771 precursor
1727	JGP_1_7.0816.0820.3	3	12.03	65.2	6.32E+04	(K)KGEEEKLR(K)		330.1859	988.542	0.001	1	Zea mays	162459584	LOC732771 precursor
1787	JGP_1_3.6359.6448.2	2	11.85	78.1	3.65E+05	(K)AGIIDMQFR(R)		525.7762	1050.54	0.005	4.8	Zea mays	162459584	LOC732771 precursor
1800	JGP_1_7.6369.6459.2	2	11.83	75.1	5.42E+05	(K)AGIIDMQFR(R)		525.7766	1050.54	0.0058	5.6	Zea mays	162459584	LOC732771 precursor
1978	JGP_1_7.5807.5812.3	3	11.3	76.5	3.75E+06	(R)KAGIIDMQFR(R)		393.5524	1178.635	0.0076	6.5	Zea mays	162459584	LOC732771 precursor
2114	JGP_1_1.6378.6478.2	2	10.96	69.8	7.66E+05	(K)AGIIDMQFR(R)		525.7751	1050.54	0.0028	2.7	Zea mays	162459584	LOC732771 precursor
2430	JGP_1_5.6719.6815.2	2	10.23	67	3.86E+05	(K)AGIIDMQFR(R)		525.7749	1050.54	0.0024	2.3	Zea mays	162459584	LOC732771 precursor
2385	JGP_1_3.2893.2971.2	2	10.33	87.9	4.54E+06	(K)LSGEIPR(L)		386.224	771.436	0.0048	6.2	Arabidopsis thaliana	15225286	LRR receptor-like serine/threonine-protein kinase ERECTA
547	JGP_1_3.6814.6903.2	2	16.51	85.5	4.47E+05	(R)IINEPTAAAIAYGLDK(K)		830.4534	1659.895	0.0043	2.6	Arabidopsis thaliana	1695719	luminal binding protein
640	JGP_1_3.2397.2493.2	2	16.05	88.8	4.15E+05	(R)LSQEEIDR(M)		495.2521	989.49	0.0071	7.2	Arabidopsis thaliana	1695719	luminal binding protein
987	JGP_1_3.6826.6826.2	2	14.42	77.5	3.84E+05	(R)IINEPTAAAIAYGLDK(K)		830.4534	1659.895	0.0043	2.6	Arabidopsis thaliana	1695719	luminal binding protein
1610	JGP_1_3.6229.6234.3	3	12.34	67.1	1.54E+05	(R)ARFEELNNDLFR(K)		508.5941	1523.76	0.0076	5	Arabidopsis thaliana	1695719	luminal binding protein
1735	JGP_1_3.1872.1992.2	2	12	75.3	4.14E+05	(R)LIGEAAK(N)		351.2119	701.419	-0.0027	-3.8	Arabidopsis thaliana	1695719	luminal binding protein
2325	JGP_1_3.2359.2424.2	2	10.44	72.3	3.20E+05	(K)ITITNEK(G)		409.7356	818.462	0.0021	2.6	Arabidopsis thaliana	1695719	luminal binding protein
88	JGP_1_3.8450.8518.2	2	20.83	85.7	3.54E+05	(K)VFSPEEISAmILGK(M)	m:Oxidized methionine		768.9073	1520.803	16.0044	6.2	Zea mays	162457903	luminal-binding protein 3 precursor
97	JGP_1_3.6894.6898.2	2	20.67	92.1	1.91E+05	(R)ITPSWVAFTDSER(L)		754.8753	1508.738	0.0053	3.5	Zea mays	162457903	luminal-binding protein 3 precursor
187	JGP_1_3.8681.8753.2	2	19.25	84.1	3.24E+05	(R)VEIESLFDGTDFSEPLTR(A)			1028.0027	2054.992	0.0064	3.1	Zea mays	162457903	luminal-binding protein 3 precursor
695	JGP_1_3.8500.8500.3	3	15.72	73.8	1.39E+05	(K)VFSPEEISAmILGK(M)	m:Oxidized methionine		512.9407	1520.803	16.0047	6.3	Zea mays	162457903	luminal-binding protein 3 precursor
1703	JGP_1_3.5121.5127.3	3	12.12	79.6	3.33E+05	(K)SQIHEIVLVGGSTR(I)		499.2811	1495.823	0.006	4	Zea mays	162457903	luminal-binding protein 3 precursor
1761	JGP_1_4.8750.8750.2	2	11.94	64.6	9.31E+04	(K)VFSPEEISAmILGK(M)	m:Oxidized methionine		768.908	1520.803	16.0058	7.1	Zea mays	162457903	luminal-binding protein 3 precursor
1996	JGP_1_3.2589.2592.3	3	11.24	71.8	7.34E+04	(K)LADKLEAEEK(E)		382.5407	1145.605	0.0027	2.4	Zea mays	162457903	luminal-binding protein 3 precursor

2491	JGP_1_4.8947.8947.2	2	10.09	67	1.66E+05	(R)VEIESLFDGTDFSEPLTR(A)		1028.0058	2054.992	0.0126	6.1	Zea mays	162457903	luminal-binding protein 3 precursor
22	JGP_1_7.7714.7788.3	3	22.84	90.2	5.54E+05	(R)VLYSSVVYPHNYGFIPR(T)	671.024	2011.044	0.0138	6.9	Solanum tuberosum		2706450	magnesium dependent soluble inorganic pyrophosphatase
116	JGP_1_8.7622.7624.3	3	20.32	85.7	7.66E+05	(R)VLYSSVVYPHNYGFIPR(T)	671.0228	2011.044	0.0102	5.1	Solanum tuberosum		2706450	magnesium dependent soluble inorganic pyrophosphatase
274	JGP_1_6.11161.11245.3	3	18.33	83	7.81E+04	(K)GLNGVPDVVECSFVQSTVTELPFFASK(V)	C:Carbamidomethylation	976.4915	2927.45	0.0104	3.6	Glycine max	5929964	malate dehydrogenase
450	JGP_1_6.5115.5118.3	3	17.14	70.4	4.99E+05	(K)LSSALSAASSACDHIR(D)	C:Carbamidomethylation	549.2742	1645.796	0.0118	7.2	Arabidopsis thaliana	15219721	malate dehydrogenase
513	JGP_1_6.6200.6210.3	3	16.72	82.3	2.62E+05	(K)NVIIWGNHSSTQYPDVNHATVK(T)		827.4189	2480.232	0.0104	4.2	Arabidopsis thaliana	15239843	malate dehydrogenase
906	JGP_1_6.9211.9285.3	3	14.77	69.8	5.33E+05	(R)VLVTGAAGQIGYALVPmIAR(G)	m:Oxidized methionine	672.7186	2000.136	16.0051	5.1	Arabidopsis thaliana	15219721	malate dehydrogenase
1070	JGP_1_6.8015.8105.2	2	14.06	83.9	1.32E+06	(K)VLVVANPANTNALILK(E)	825.5067	1649.995	0.0113	6.8	Arabidopsis thaliana		15219721	malate dehydrogenase
1153	JGP_1_6.6168.6310.4	4	13.72	66.1	8.38E+05	(K)NVIIWGNHSSTQYPDVNHATVK(T)		620.8168	2480.232	0.0137	5.5	Arabidopsis thaliana	15239843	malate dehydrogenase
1664	JGP_1_6.2942.2949.2	2	12.2	80.9	1.35E+06	(R)ALGQISER(L)	437.245	873.479	0.0039	4.4	Arabidopsis thaliana		15219721	malate dehydrogenase
1751	JGP_1_7.7926.7931.2	2	11.97	76.9	7.44E+04	(K)VLVVANPANTNALILK(E)	825.4927	1649.995	-0.0167	-10.1	Arabidopsis thaliana		15219721	malate dehydrogenase
2018	JGP_1_6.5145.5149.2	2	11.19	75.1	4.00E+05	(K)EFAPSIPEK(N)	509.2687	1017.525	0.005	4.9	Arabidopsis thaliana		15219721	malate dehydrogenase
2089	JGP_1_6.8010.8021.3	3	11.03	76.7	5.76E+05	(K)VLVVANPANTNALILK(E)	550.6732	1649.995	0.0102	6.2	Arabidopsis thaliana		15219721	malate dehydrogenase
1350	JGP_1_5.5672.5672.3	3	13.1	75.7	1.02E+05	(R)RPQGLYISLK(E)	392.2374	1174.694	0.0034	2.9	Arabidopsis thaliana		15239517	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)
1468	JGP_1_4.5510.5597.3	3	12.75	82.3	5.74E+05	(R)RPQGLYISLK(E)	392.2385	1174.694	0.0067	5.7	Arabidopsis thaliana		15239517	malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+)
234	JGP_1_6.8368.8445.2	2	18.75	93.4	1.60E+06	(K)LFGVTTLDVVR(A)	610.3595	1219.705	0.0072	5.9	Arabidopsis thaliana		18404382	malate dehydrogenase 1
478	JGP_1_6.8526.8531.2	2	16.93	88.6	7.83E+05	(K)LFGVTTLDVVR(A)	610.3591	1219.705	0.0064	5.3	Arabidopsis thaliana		18404382	malate dehydrogenase 1
926	JGP_1_6.8185.8260.2	2	14.67	79.9	9.53E+05	(R)DDLFNINAGIVK(N)	659.857	1318.7	0.0066	5	Arabidopsis thaliana		18404382	malate dehydrogenase 1
1055	JGP_1_2.7213.7219.2	2	14.12	79.4	1.64E+05	(K)LFGVTTLDVVR(A)	610.3561	1219.705	0.0004	0.3	Arabidopsis thaliana		18404382	malate dehydrogenase 1
1096	JGP_1_6.7552.7636.3	3	13.97	70.5	8.18E+05	(K)KLFGVTTLDVVR(A)	449.9408	1347.8	0.0084	6.2	Arabidopsis thaliana		18404382	malate dehydrogenase 1
1275	JGP_1_6.2119.2212.2	2	13.36	68	1.58E+06	(R)TQDGGTEVVEAK(A)	617.3035	1233.596	0.004	3.2	Arabidopsis thaliana		18404382	malate dehydrogenase 1
1476	JGP_1_1.7697.7700.2	2	12.72	80.2	1.77E+05	(K)LFGVTTLDVVR(A)	610.3558	1219.705	-0.0002	-0.1	Arabidopsis thaliana		18404382	malate dehydrogenase 1
1535	JGP_1_6.1750.1759.2	2	12.52	85.4	2.42E+05	(K)RTQDGGTEVVEAK(A)	695.355	1389.697	0.0059	4.2	Arabidopsis thaliana		18404382	malate dehydrogenase 1
1563	JGP_1_6.1997.2083.2	2	12.45	77.1	1.83E+06	(R)TFYAGK(A)	343.6833	686.351	0.0085	12.4	Arabidopsis thaliana		18404382	malate dehydrogenase 1
1625	JGP_1_6.7583.7587.2	2	12.29	70.7	1.81E+05	(K)KLFGVTTLDVVR(A)	674.4039	1347.8	0.0011	0.8	Arabidopsis thaliana		18404382	malate dehydrogenase 1
2312	JGP_1_7.8261.8276.2	2	10.48	74.5	8.60E+04	(K)LFGVTTLDVVR(A)	610.3527	1219.705	-0.0064	-5.2	Arabidopsis thaliana		18404382	malate dehydrogenase 1
2330	JGP_1_6.1737.1744.3	3	10.43	67.1	7.14E+05	(K)RTQDGGTEVVEAK(A)	463.9058	1389.697	0.006	4.3	Arabidopsis thaliana		18404382	malate dehydrogenase 1
220	JGP_1_6.9136.9205.2	2	18.92	86.3	3.65E+05	(K)mELVDAAFPLLK(G)	m:Oxidized methionine	681.8733	1346.739	16.0005	4.1	Zea mays	162464321	"malate dehydrogenase, cytoplasmic"
235	JGP_1_6.7681.7765.2	2	18.73	93.8	7.15E+05	(K)IVQGLPIDEFSR(K)	687.3782	1373.742	0.0068	4.9	Zea mays	162464321	"malate dehydrogenase, cytoplasmic"
1057	JGP_1_6.9638.9638.3	3	14.12	67.7	2.11E+04	(R)GVmLGADQPVILHmLDIPPAAEALNGVK(M)	m:Oxidized methionine	967.8468	2869.531	31.9944	1.6	Zea mays	162464321	"malate dehydrogenase, cytoplasmic"
1643	JGP_1_6.9882.9960.2	2	12.24	68.4	1.96E+05	(K)MELVDAAFPLLK(G)	673.8756	1346.739	0.0051	3.8	Zea mays	162464321	"malate dehydrogenase, cytoplasmic"
1892	JGP_1_1.8361.8371.2	2	11.55	61.9	1.08E+05	(K)mELVDAAFPLLK(G)	m:Oxidized methionine	681.8744	1346.739	16.0027	5.7	Zea mays	162464321	"malate dehydrogenase, cytoplasmic"
1488	JGP_1_3.4134.4142.2	2	12.67	68.2	1.62E+05	(R)LSVQVSDVK(N)	487.7828	974.552	0.0066	6.8	Solanum tuberosum		83283965	malate dehydrogenase-like protein
214	JGP_1_7.7889.7895.2	2	18.96	84.8	1.88E+05	(K)DLEEFFQSTAGK(F)	686.3287	1371.643	0.0074	5.4	Arabidopsis thaliana		42570897	Metal-dependent phosphohydrolase
112	JGP_1_3.8955.9024.3	3	20.39	91.6	9.02E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	989.8108	2951.413	16.0047	3.3	Zea mays	17017263	methionine synthase
231	JGP_1_3.9094.9163.2	2	18.77	92	2.01E+05	(K)mLAVLDTNILWVNPDCGLK(T)	C:Carbamidomethylation	m:Oxidized methionine	1094.561	2172.119	15.9956	0.3	Zea mays	17017263	methionine synthase
268	JGP_1_3.5078.5082.3	3	18.37	87.7	2.32E+05	(K)ALAGQKDEAYFAANAAAQASR(K)		708.6904	2124.047	0.0098	4.6	Zea mays	17017263	methionine synthase
312	JGP_1_3.9084.9154.3	3	18.02	86.5	3.39E+05	(K)mLAVLDTNILWVNPDCGLK(T)	C:Carbamidomethylation	m:Oxidized methionine	730.0463	2172.119	16.0052	4.7	Zea mays	17017263	methionine synthase
420	JGP_1_3.6804.6881.3	3	17.33	82.9	1.08E+06	(K)LVVSTSCSLmHTAVDLVNETK(L)	C:Carbamidomethylation	m:Oxidized methionine	774.0603	2304.157	16.009	6.1	Zea mays	3747048	methionine synthase
467	JGP_1_3.3629.3727.2	2	17.05	84.8	7.89E+05	(R)IPSTEEIADR(V)	565.7903	1130.569	0.0045	4	Solanum tuberosum		8439545	methionine synthase
596	JGP_1_4.9277.9277.3	3	16.21	74.9	1.29E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	989.8109	2951.413	16.005	3.4	Zea mays	17017263	methionine synthase
838	JGP_1_3.7134.7147.4	4	15.01	67.9	1.36E+04	(R)CVKPPIIYGDVSRPNPmTVFWSK(T)	C:Carbamidomethylation	m:Oxidized methionine	677.6023	2691.379	16.0088	5.1	Zea mays	17017263	methionine synthase
863	JGP_1_3.1537.1617.2	2	14.92	77.1	2.07E+05	(K)STAEDLEK(V)	446.7182	892.426	0.0033	3.7	Zea mays	17017263	methionine synthase	
984	JGP_1_3.7148.7153.2	2	14.43	68.7	1.80E+05	(R)FETCYQIALAIK(K)	C:Carbamidomethylation	728.8819	1456.751	0.0061	4.2	Zea mays	17017263	methionine synthase
1229	JGP_1_3.4728.4728.2	2	13.49	74.2	9.03E+04	(K)DEAYFAANAAAQASR(K)		778.3651	1555.714	0.0094	6	Zea mays	17017263	methionine synthase
1474	JGP_1_6.10026.10048.3	3	12.73	69.2	2.50E+04	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	989.8127	2951.413	16.0104	5.2	Zea mays	17017263	methionine synthase
1697	JGP_1_3.6469.6469.2	2	12.13	64.2	2.35E+05	(R)GTQTLGLVTSAGFPAGK(Y)	802.9381	1604.864	0.0047	2.9	Zea mays	17017263	methionine synthase	
1938	JGP_1_3.6457.6552.2	2	11.42	72.2	4.73E+05	(R)GTQTLGLVTSAGFPAGK(Y)	802.9381	1604.864	0.0047	2.9	Zea mays	17017263	methionine synthase	

2226	JGP_1_3.8975.9003.4	4	10.7	62.7	1.76E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	742.6124	2951.413	16.0146	6.6	Zea mays	17017263	methionine synthase	
2292	JGP_1_3.9004.9004.2	2	10.52	71.6	1.28E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	1484.2073	2951.413	15.9942	-0.3	Zea mays	17017263	methionine synthase	
2322	JGP_1_3.1544.1686.2	2	10.45	73.3	7.68E+05	(K)SSFPSGK(Y)	355.1805	709.351	0.0022	3.1	Solanum tuberosum		8439545	methionine synthase	
2387	JGP_1_3.9050.9050.2	2	10.33	63.8	1.13E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	1484.2096	2951.413	15.9988	1.3	Zea mays	17017263	methionine synthase	
2418	JGP_1_2.1843.1968.2	2	10.25	73	7.46E+05	(K)LDSEIK(S)	352.6953	704.383	0.0008	1.2	Zea mays	17017263	methionine synthase		
2476	JGP_1_4.3734.3734.2	2	10.12	63.6	4.76E+04	(R)IPSTEEIADR(V)	565.7856	1130.569	-0.0049	-4.3	Solanum tuberosum		8439545	methionine synthase	
516	JGP_1_3.10812.10882.3	3	16.69	91.2	2.43E+06	(K)ALGVETVPVLVGPVSYLLLSK(L)		718.7689	2154.278	0.0137	6.4	Arabidopsis thaliana	15228634	methionine synthase 2	
878	JGP_1_2.10458.10523.3	3	14.88	80.3	2.74E+05	(K)ALGVETVPVLVGPVSYLLLSK(L)		718.7653	2154.278	0.0029	1.4	Arabidopsis thaliana	15228634	methionine synthase 2	
1498	JGP_1_6.12050.12115.3	3	12.64	77.6	1.76E+05	(K)ALGVETVPVLVGPVSYLLLSK(L)		718.7682	2154.278	0.0116	5.4	Arabidopsis thaliana	15228634	methionine synthase 2	
1797	JGP_1_5.11647.11652.3	3	11.83	74.3	9.24E+04	(K)ALGVETVPVLVGPVSYLLLSK(L)		718.7686	2154.278	0.0128	6	Arabidopsis thaliana	15228634	methionine synthase 2	
2067	JGP_1_3.4372.4504.2	2	11.08	65	1.23E+06	(K)VVEVDALAK(A)	472.2741	943.546	-0.005	-5.2	Arabidopsis thaliana		15228634	methionine synthase 2	
2105	JGP_1_3.10851.10854.2	2	10.99	71.7	9.13E+05	(K)ALGVETVPVLVGPVSYLLLSK(L)		1077.6462	2154.278	0.0067	3.1	Arabidopsis thaliana	15228634	methionine synthase 2	
2429	JGP_1_3.10940.11016.3	3	10.23	69.7	1.54E+06	(K)ALGVETVPVLVGPVSYLLLSK(L)		718.7692	2154.278	0.0146	6.8	Arabidopsis thaliana	15228634	methionine synthase 2	
1986	JGP_1_5.1640.1728.2	2	11.27	88.4	6.69E+06	(R)TIADVK(A)	323.6937	646.377	0.0031	4.8	Nicotiana tabacum		262192735	metyltransferase	
2048	JGP_1_5.1814.1819.2	2	11.12	86	4.76E+06	(R)TIADVK(A)	323.6939	646.377	0.0035	5.4	Nicotiana tabacum		262192735	metyltransferase	
2109	JGP_1_4.1722.1801.2	2	10.98	86.6	9.37E+05	(R)TIADVK(A)	323.6931	646.377	0.0019	2.9	Nicotiana tabacum		262192735	metyltransferase	
2189	JGP_1_3.1789.1888.2	2	10.77	79.5	2.93E+05	(R)TIADVK(A)	323.6932	646.377	0.0021	3.3	Nicotiana tabacum		262192735	metyltransferase	
2198	JGP_1_6.1789.1882.2	2	10.76	78.1	7.86E+05	(R)TIADVK(A)	323.6929	646.377	0.0015	2.3	Nicotiana tabacum		262192735	metyltransferase	
2224	JGP_1_2.1733.1806.2	2	10.7	76.9	2.73E+05	(R)TIADVK(A)	323.6928	646.377	0.0013	2	Nicotiana tabacum		262192735	metyltransferase	
2442	JGP_1_1.1705.1778.2	2	10.2	80.7	5.25E+05	(R)TIADVK(A)	323.6927	646.377	0.0011	1.7	Nicotiana tabacum		262192735	metyltransferase	
1013	JGP_1_3.3606.3708.2	2	14.28	82.1	4.96E+06	(K)AAGEVLTGLK(M)	479.7841	958.557	0.0042	4.3	Arabidopsis thaliana		15226146	minichromosome maintenance protein 5 (cell division control protein 46)	
1194	JGP_1_6.5193.5198.2	2	13.59	80.7	2.18E+05	(R)IAAVQALSGTGACR(L)	C:Carbamidomethylation	687.8631	1374.716	0.0031	2.3	Glycine max	710596	mitochondrial aspartate aminotransferase	
2122	JGP_1_1.4936.5065.2	2	10.93	67.7	1.51E+05	(R)IPIFK(R)	309.2052	617.402	0.001	1.6	Arabidopsis thaliana		9294271	mitochondrial protein-like	
2493	JGP_1_7.2659.2659.2	2	10.08	61.3	5.22E+05	(K)IEFGSK(E)	340.6853	680.361	0.002	2.9	Arabidopsis thaliana		12049600	mitochondrial succinate dehydrogenase iron-sulphur subunit	
1364	JGP_1_8.1815.1923.2	2	13.06	86	4.89E+06	(K)ICISK(E) C:Carbamidomethylation	310.677	620.344	0.0031	5	Arabidopsis thaliana		15224823	MLO-like protein 15	
1666	JGP_1_6.4177.4182.3	3	12.2	73.8	8.87E+05	(K)EAVAPYERPALSK(G)	477.5952	1430.764	0.0072	5.1	Arabidopsis thaliana		15231702	monodehydroascorbate reductase (NADH)	
2090	JGP_1_6.9076.9081.2	2	11.03	77.7	1.35E+05	(K)GIELILSTEIVK(A)	657.8964	1314.788	-0.0024	-1.8	Arabidopsis thaliana		15231702	monodehydroascorbate reductase (NADH)	
245	JGP_1_5.4482.4572.3	3	18.6	82.3	7.52E+05	(R)LPGFHTCVGSGGER(L)	C:Carbamidomethylation	491.9046	1473.69	0.0089	6.1	Pisum sativum		51860738	monodehydroascorbate reductase I
1274	JGP_1_5.6252.6346.2	2	13.36	80.8	9.50E+05	(R)LLPEWYSEK(G)	582.8031	1164.594	0.0054	4.6	Pisum sativum		51860738	monodehydroascorbate reductase I	
1538	JGP_1_3.4368.4368.3	3	12.51	65.2	1.40E+05	(R)LPGFHTCVGSGGER(L)	C:Carbamidomethylation	491.9053	1473.69	0.011	7.5	Pisum sativum		51860738	monodehydroascorbate reductase I
1594	JGP_1_4.6155.6159.2	2	12.39	76.5	1.96E+05	(R)LLPEWYSEK(G)	582.8051	1164.594	0.0094	8	Pisum sativum		51860738	monodehydroascorbate reductase I	
1638	JGP_1_1.4236.4311.3	3	12.25	66.7	2.92E+05	(R)LPGFHTCVGSGGER(L)	C:Carbamidomethylation	491.9051	1473.69	0.0104	7.1	Pisum sativum		51860738	monodehydroascorbate reductase I
1689	JGP_1_6.4657.4763.3	3	12.15	63.7	1.15E+06	(R)LPGFHTCVGSGGER(L)	C:Carbamidomethylation	491.9041	1473.69	0.0074	5	Pisum sativum		51860738	monodehydroascorbate reductase I
1830	JGP_1_3.5949.5956.2	2	11.73	77	8.43E+04	(R)LLPEWYSEK(G)	582.805	1164.594	0.0092	7.9	Pisum sativum		51860738	monodehydroascorbate reductase I	
1891	JGP_1_1.5897.5990.2	2	11.55	71	5.25E+05	(R)LLPEWYSEK(G)	582.8034	1164.594	0.006	5.1	Pisum sativum		51860738	monodehydroascorbate reductase I	
2252	JGP_1_2.5614.5718.2	2	10.64	65.9	3.11E+05	(R)LLPEWYSEK(G)	582.8029	1164.594	0.005	4.3	Pisum sativum		51860738	monodehydroascorbate reductase I	
2459	JGP_1_4.5022.5107.2	2	10.17	80.5	6.92E+05	(R)IIEVIK(R)	357.7433	714.476	0.0033	4.6	Arabidopsis thaliana		9294577	multidrug resistance p-glycoprotein ABC transporter-like protein	
2472	JGP_1_7.8930.9010.2	2	10.14	69.5	3.86E+05	(R)LSIGVGLHEHR(G)	609.3427	1217.675	0.0032	2.6	Arabidopsis thaliana		15238770	myb-related protein 1	
159	JGP_1_4.5774.5857.2	2	19.5	93.9	5.25E+05	(K)SIQVIVVTDGER(I)	658.3658	1315.722	0.0027	2.1	Zea mays	162463047	NADP malic enzyme4		
577	JGP_1_4.3392.3499.2	2	16.32	60.3	1.69E+04	(R)YIAmmDLQER(N)	m:Oxidized methionine	651.3007	1269.597	31.9975	5.9	Triticum aestivum		158701881	NADP-dependent malic enzyme
588	JGP_1_4.8884.8884.3	3	16.26	77.1	6.24E+05	(K)VLTQFEDFANHNAFDLLEK(Y)		751.0436	2251.103	0.0133	5.9	Zea mays	226510109	NADP-dependent malic enzyme	
827	JGP_1_4.10310.10310.3	3	15.06	67.3	7.75E+04	(R)ATEEQLITPWAFSVASGYTLLR(D)		818.4325	2453.271	0.0118	4.8	Zea mays	226510109	NADP-dependent malic enzyme	
1480	JGP_1_4.9099.9105.2	2	12.71	81.3	3.92E+05	(K)GLIFPPFTNIR(K)	637.8682	1274.726	0.0036	2.8	Triticum aestivum		158701881	NADP-dependent malic enzyme	
1985	JGP_1_4.8971.9039.2	2	11.27	78.4	4.99E+05	(K)GLIFPPFTNIR(K)	637.8685	1274.726	0.0042	3.3	Triticum aestivum		158701881	NADP-dependent malic enzyme	
2384	JGP_1_2.9444.9444.3	3	10.33	62	4.15E+04	(K)LLIDNVEELLPVVYTPTVGEACQK(Y)	C:Carbamidomethylation	900.8183	2700.416	0.0239	8.9	Oryza sativa	415315	NADP-dependent malic enzyme	
161	JGP_1_5.6063.6074.2	2	19.49	86.7	2.47E+05	(K)IFQGDYSTGLPVDK(A)	770.3905	1539.769	0.0048	3.1	Zea mays	162463282	NADPH producing dehydrogenase of the oxidative pentose phosphate pathway		
1560	JGP_1_5.6324.6348.2	2	12.46	80.9	1.26E+05	(R)VVIMLVK(A)	401.2647	801.527	-0.0045	-5.7	Zea mays	162463282	NADPH producing dehydrogenase of the oxidative pentose phosphate pathway		

2281	JGP_1_5.5613.5618.2	2	10.57	68.8	2.02E+05	(R)VVImLVK(A)	m:Oxidized methionine	409.2652	801.527	15.9965	1.9	Zea mays	162463282	NADPH producing dehydrogenase of the oxidative pentose phosphate pathway
2352	JGP_1_6.4388.4497.2	2	10.4	78.6	4.68E+06	(K)ILEDSFK(E)		426.2317	851.451	0.0052	6.1	Hordeum vulgare	28555884	NBS-LRR disease resistance protein homologue
2515	JGP_1_1.8020.8086.4	4	10.02	72	1.85E+05	(K)LDYFYWLmCVLSAANFLHYLFWAMRYK(Y)	C:Carbamidomethylation m:Oxidized methionine		885.1773	3521.704	15.9838	-3.2	Arabidopsis thaliana	17064754 nitrate transporter (NTL1)
202	JGP_1_6.10698.10772.3	3	19.09	93.1	5.12E+05	(R)LIDVDVPVVGGHAGITILPLLSK(T)		776.1336	2326.374	0.0118	5.1	Pisum sativum	3377762	nodule-enhanced malate dehydrogenase
1048	JGP_1_6.7513.7613.2	2	14.14	88.6	3.75E+05	(K)GVDVVVIPAGVPR(K)		639.3839	1277.758	0.0029	2.3	Pisum sativum	3377762	nodule-enhanced malate dehydrogenase
1217	JGP_1_6.3363.3367.2	2	13.54	77.5	4.58E+05	(R)IQNAGTEVVEAK(A)		629.8366	1258.664	0.0022	1.7	Pisum sativum	3377762	nodule-enhanced malate dehydrogenase
1342	JGP_1_2.9215.9228.3	3	13.13	80.3	6.55E+04	(R)LIDVDVPVVGGHAGITILPLLSK(T)		776.1278	2326.374	-0.0056	-2.4	Pisum sativum	3377762	nodule-enhanced malate dehydrogenase
2294	JGP_1_1.8047.8052.3	3	10.51	68.8	1.45E+05	(K)mSPLISDLHLYDIANVK(G)	m:Oxidized methionine	649.012	1929.015	16.0064	5.9	Glycine max	3273828	nodule-enhanced malate dehydrogenase
208	JGP_1_8.5178.5184.3	3	19.04	89.7	1.45E+05	(R)TFIAIKPDGVQR(G)		448.9294	1344.763	0.0102	7.6	Arabidopsis thaliana	18416233	nucleoside diphosphate kinase IV
2102	JGP_1_7.3005.3010.2	2	11	75.7	1.57E+06	(R)VAINALK(V)		364.7374	728.467	0.001	1.4	Arabidopsis thaliana	15229223	nucleoside-triphosphatase
2278	JGP_1_8.2991.3099.2	2	10.58	74.4	2.74E+06	(R)VAINALK(V)		364.7368	728.467	-0.0002	-0.2	Arabidopsis thaliana	15229223	nucleoside-triphosphatase
2159	JGP_1_8.5170.5174.2	2	10.86	63.4	5.46E+05	(R)IEATEPASFTVK(E)		646.8461	1292.673	0.0117	9	Zea mays	226507244	OB-fold nucleic acid binding domain containing protein
1482	JGP_1_4.1694.1776.2	2	12.7	76.3	8.03E+05	(K)APIPTK(E)		313.6981	626.387	0.0017	2.8	Zea mays	99866719	Opie3 gag protein
1760	JGP_1_2.1738.1821.2	2	11.94	74.1	1.96E+05	(K)APIPTK(E)		313.6976	626.387	0.0007	1.2	Zea mays	99866719	Opie3 gag protein
1975	JGP_1_3.1763.1868.2	2	11.3	62.9	3.25E+05	(K)APIPTK(E)		313.6972	626.387	-0.0001	-0.1	Zea mays	99866719	Opie3 gag protein
319	JGP_1_6.11555.11621.3	3	18.01	84.6	3.88E+05	(R)GILAGNIFDLGSAQLAEVFAK(D)			712.0607	2134.154	0.0133	6.2	Zea mays	226494919 pantothenate kinase 4
641	JGP_1_6.3375.3385.2	2	16.04	86.8	3.38E+05	(R)AENDPTVPDAPAK(A)		662.8249	1324.638	0.0046	3.5	Zea mays	226494919	pantothenate kinase 4
1555	JGP_1_6.4339.4344.2	2	12.47	70.5	3.79E+05	(R)AIETNLYAQmK(C)	m:Oxidized methionine	649.3283	1281.651	15.9986	2.8	Zea mays	226494919	pantothenate kinase 4
1904	JGP_1_6.10501.10501.3	3	11.52	70.5	2.02E+05	(K)DGmSFLASCQNLVSRPWVIDDLDAFK(S)	C:Carbamidomethylation m:Oxidized methionine		1000.8188	2984.428	16.0138	6.3	Zea mays	226494919 pantothenate kinase 4
1233	JGP_1_8.1975.2083.2	2	13.48	90.7	1.12E+07	(R)DAVTIR(A)		337.6977	674.383	0.005	7.4	Zea mays	226501590	pectinesterase inhibitor domain containing protein precursor
1227	JGP_1_1.7955.7967.2	2	13.5	69.8	7.93E+04	(R)TIYIQNDIGGFIDPK(G)		847.4442	1693.88	0.0016	0.9	Zea mays	226508982	pectinesterase-1 precursor
1286	JGP_1_6.8723.8803.2	2	13.34	77.4	3.25E+05	(R)TIYIQNDIGGFIDPK(G)		847.4464	1693.88	0.006	3.5	Zea mays	226508982	pectinesterase-1 precursor
1574	JGP_1_6.3434.3537.2	2	12.43	82.8	1.33E+06	(R)AVVAALSK(G)		379.7426	758.477	0.0009	1.1	Triticum aestivum	300681506	"pepsin A, putative, expressed"
1614	JGP_1_5.3214.3311.2	2	12.32	77.5	9.45E+05	(R)AVVAALSK(G)		379.7423	758.477	0.0003	0.3	Triticum aestivum	300681506	"pepsin A, putative, expressed"
655	JGP_1_8.9550.9620.2	2	15.96	84.9	1.22E+05	(K)VFFDILIGK(M)		526.3149	1051.619	0.0039	3.7	Arabidopsis thaliana	15228814	Peptidyl-prolyl cis-trans isomerase CYP19-3
2229	JGP_1_8.1551.1736.2	2	10.7	63.1	3.62E+06	(R)HVVFGK(V)		343.7042	686.398	0.0027	3.9	Arabidopsis thaliana	15227674	Peptidyl-prolyl cis-trans isomerase CYP19-4
1123	JGP_1_8.7116.7212.2	2	13.86	70.7	4.85E+05	(R)IVMGLFGK(T)		432.755	864.501	0.0016	1.8	Arabidopsis thaliana	15237739	Peptidyl-prolyl cis-trans isomerase CYP20-1
1198	JGP_1_8.5414.5420.2	2	13.58	72.6	5.57E+05	(R)IVmGLFGK(T)	m:Oxidized methionine	440.7526	864.501	15.9968	2.1	Arabidopsis thaliana	15237739	Peptidyl-prolyl cis-trans isomerase CYP20-1
2125	JGP_1_6.1330.1339.2	2	10.93	79.2	9.82E+03	(K)DAAPNKNSVR(G)		536.2877	1071.554	0.014	13	Arabidopsis thaliana	15224497	peroxidase 23
297	JGP_1_3.4403.4538.3	3	18.12	86.9	2.23E+06	(K)EDFGGGHPDPNLTYAK(E)		573.2693	1717.782	0.0117	6.8	Arabidopsis thaliana	2829893	phosphoglucomutase
313	JGP_1_4.6374.6457.2	2	18.02	95.4	3.53E+06	(K)LVSVEDIVR(Q)		515.3043	1029.594	0.0074	7.2	Arabidopsis thaliana	2829893	phosphoglucomutase
330	JGP_1_4.4494.4587.3	3	17.93	83.8	1.84E+06	(K)EDFGGGHPDPNLTYAK(E)		573.2698	1717.782	0.0132	7.7	Arabidopsis thaliana	2829893	phosphoglucomutase
444	JGP_1_3.7014.7129.2	2	17.21	82.3	1.95E+06	(K)FFEVPTGWK(F)		555.787	1110.562	0.0049	4.4	Arabidopsis thaliana	2829893	phosphoglucomutase
466	JGP_1_4.7306.7311.3	3	17.06	85.4	7.45E+05	(K)ATGAFILTASHNPGGPTEDFGIK(Y)			767.7271	2301.151	0.0158	6.8	Arabidopsis thaliana	2829893 phosphoglucomutase
645	JGP_1_4.4515.4523.2	2	16	87.3	2.51E+05	(K)EDFGGGHPDPNLTYAK(E)		859.3977	1717.782	0.0065	3.8	Arabidopsis thaliana	2829893	phosphoglucomutase
677	JGP_1_3.6151.6231.2	2	15.84	91.7	4.64E+06	(K)LVSVEDIVR(Q)		515.3039	1029.594	0.0066	6.4	Arabidopsis thaliana	2829893	phosphoglucomutase
710	JGP_1_4.4947.5032.2	2	15.66	61.7	1.70E+06	(R)SmPTSAALDVVAK(N)	m:Oxidized methionine	653.3426	1289.677	16.001	4.6	Arabidopsis thaliana	15223226	phosphoglucomutase
750	JGP_1_3.7057.7063.3	3	15.41	78.1	5.02E+05	(K)ATGAFILTASHNPGGPTEDFGIK(Y)			767.7289	2301.151	0.0212	9.2	Arabidopsis thaliana	2829893 phosphoglucomutase
791	JGP_1_4.7269.7348.2	2	15.22	78.1	1.34E+06	(K)FFEVPTGWK(F)		555.7857	1110.562	0.0023	2	Arabidopsis thaliana	2829893	phosphoglucomutase
797	JGP_1_3.4788.4872.2	2	15.19	68.4	2.54E+06	(R)SmPTSAALDVVAK(N)	m:Oxidized methionine	653.343	1289.677	16.0018	5.2	Arabidopsis thaliana	15223226	phosphoglucomutase
855	JGP_1_5.6575.6597.2	2	14.95	76.9	4.46E+05	(K)LVSVEDIVR(Q)		515.3028	1029.594	0.0044	4.3	Arabidopsis thaliana	2829893	phosphoglucomutase
907	JGP_1_3.4434.4437.2	2	14.75	81.7	2.88E+05	(K)EDFGGGHPDPNLTYAK(E)		859.3973	1717.782	0.0057	3.3	Arabidopsis thaliana	2829893	phosphoglucomutase
953	JGP_1_3.5773.5827.2	2	14.54	80.5	3.59E+05	(R)SMPTSAALDVVAK(N)		645.3387	1289.677	-0.0068	-5.3	Arabidopsis thaliana	15223226	phosphoglucomutase
955	JGP_1_6.6901.6998.2	2	14.54	89.9	5.89E+05	(K)LVSVEDIVR(Q)		515.3027	1029.594	0.0042	4.1	Arabidopsis thaliana	2829893	phosphoglucomutase
1331	JGP_1_4.2598.2602.2	2	13.18	66.8	1.90E+05	(R)QHWATYGR(H)		509.7472	1018.485	0.0018	1.8	Arabidopsis thaliana	2829893	phosphoglucomutase
1484	JGP_1_5.6141.6141.2	2	12.7	73.4	1.02E+04	(R)SMPTSAALDVVAK(N)		645.3432	1289.677	0.0022	1.7	Arabidopsis thaliana	15223226	phosphoglucomutase
1509	JGP_1_4.0857.0887.2	2	12.61	79.7	7.37E+04	(R)HYYTR(Y)	370.1808	739.352	0.0021	2.9	Arabidopsis thaliana	2829893	phosphoglucomutase	
1971	JGP_1_4.5948.6039.2	2	11.33	64.6	3.44E+05	(R)SMPTSAALDVVAK(N)		645.3387	1289.677	-0.0068	-5.3	Arabidopsis thaliana	15223226	phosphoglucomutase

2457	JGP_1_2.5859.5869.2	2	10.17	68.2	1.09E+05	(K)LVSVEDIVR(Q)		515.3012	1029.594	0.0012	1.2	Arabidopsis thaliana	2829893	phosphoglucomutase
15	JGP_1_5.7505.7583.3	3	23.12	86.8	3.57E+05	(K)FTFCYDALHGVAGAYAK(H)	C:Carbamidomethylation	630.9718	1890.884	0.0165	8.7	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
38	JGP_1_4.6971.6981.3	3	22.27	85.8	4.77E+04	(K)FFGNLmDAGmCSICGEESFGTGSDHIR(E)	C:Carbamidomethylation	m:Oxidized methionine	1009.7547	2995.248	32.0018	4	Zea mays	162463106
63	"phosphoglucomutase, cytoplasmic 1" JGP_1_3.7064.7141.3	3	21.42	79.4	2.24E+06	(K)FTFCYDALHGVAGAYAK(H)	C:Carbamidomethylation	630.9702	1890.884	0.0117	6.2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
73	JGP_1_3.6707.6734.3	3	21.15	81.3	3.09E+05	(K)FFGNLmDAGmCSICGEESFGTGSDHIR(E)	C:Carbamidomethylation	m:Oxidized methionine	1009.7537	2995.248	31.9988	3	Zea mays	162463106
79	"phosphoglucomutase, cytoplasmic 1" JGP_1_4.6545.6640.3	3	21.06	87.1	1.00E+06	(R)SDVSEVVAADEFEYKDPVDGSVSK(H)		858.0738	2572.194	0.0131	5.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
91	JGP_1_3.6299.6387.3	3	20.78	93	1.39E+06	(R)SDVSEVVAADEFEYKDPVDGSVSK(H)		858.0731	2572.194	0.011	4.3	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
118	JGP_1_3.3421.3426.2	2	20.31	86	1.95E+06	(R)YDYENVDAGAAK(E)		658.2966	1315.58	0.0058	4.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
127	JGP_1_3.12052.12113.3	3	20.05	97	1.88E+06	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)			971.8558	2913.54	0.0132	4.5	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
145	JGP_1_3.4803.4807.3	3	19.65	88.6	2.64E+05	(K)SSSNVEPPEFGAAADGDADR(N)			664.6255	1991.858	0.0042	2.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
155	JGP_1_3.2799.2937.2	2	19.53	84.9	1.41E+05	(K)YNmGNGGPAPESVTDK(I)	m:Oxidized methionine		826.8658	1636.727	15.9972	1.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
165	JGP_1_6.12756.12818.3	3	19.45	94.8	3.26E+05	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)			971.8502	2913.54	-0.0036	-1.2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
174	JGP_1_3.4784.4796.2	2	19.36	88.1	3.17E+05	(K)SSSNVEPPEFGAAADGDADR(N)			996.4348	1991.858	0.0046	2.3	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
225	JGP_1_4.7329.7403.3	3	18.86	69.7	1.51E+06	(K)FTFCYDALHGVAGAYAK(H)	C:Carbamidomethylation	630.9706	1890.884	0.0129	6.8	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
227	JGP_1_4.11993.12063.3	3	18.82	92.6	3.03E+06	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)			971.8564	2913.54	0.015	5.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
243	JGP_1_3.11944.11944.2	2	18.61	82	1.32E+04	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)			1457.2756	2913.54	0.0043	1.5	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
246	JGP_1_5.12324.12392.3	3	18.59	92.1	2.63E+05	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)			971.8556	2913.54	0.0126	4.3	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
255	JGP_1_4.12128.12130.3	3	18.5	90.9	1.33E+06	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)			971.8564	2913.54	0.015	5.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
281	JGP_1_4.2799.2948.2	2	18.27	75.5	1.93E+05	(K)YNmGNGGPAPESVTDK(I)	m:Oxidized methionine		826.8664	1636.727	15.9984	2.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
286	JGP_1_4.3407.3506.2	2	18.24	81.1	1.59E+06	(R)YDYENVDAGAAK(E)		658.2968	1315.58	0.0062	4.7	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
306	JGP_1_4.6644.6733.3	3	18.04	87.9	1.81E+06	(K)TIFDFEAIKK(L)		404.5623	1211.667	0.0053	4.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
309	JGP_1_3.3197.3341.2	2	18.03	83	1.63E+06	(R)YDYENVDAGAAK(E)		658.2966	1315.58	0.0058	4.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
363	JGP_1_4.8526.8589.2	2	17.65	88.8	9.43E+05	(R)DSQDALAPLVDVALK(L)		777.927	1554.837	0.0094	6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
388	JGP_1_3.8041.8108.3	3	17.49	88.3	2.11E+06	(K)HIFVEELGADESSLLNCVPK(E)	C:Carbamidomethylation		753.0486	2257.117	0.0143	6.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
401	JGP_1_7.7819.7831.3	3	17.41	74.7	1.92E+05	(K)FTFCYDALHGVAGAYAK(H)	C:Carbamidomethylation	630.9742	1890.884	0.0237	12.5	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
417	JGP_1_3.5382.5467.2	2	17.34	91.5	6.09E+05	(K)ELmANLVSmQSSLSDVNK(L)	m:Oxidized methionine		999.4825	1965.962	31.9957	3	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
425	JGP_1_4.8331.8399.3	3	17.3	90.4	7.10E+05	(K)HIFVEELGADESSLLNCVPK(E)	C:Carbamidomethylation		753.0486	2257.117	0.0143	6.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
429	JGP_1_3.8238.8308.2	2	17.28	91.4	3.36E+06	(R)DSQDALAPLVDVALK(L)		777.9277	1554.837	0.0108	6.9	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
459	JGP_1_3.8243.8303.2	2	17.09	93	3.18E+06	(R)DSQDALAPLVDVALK(L)		777.9277	1554.837	0.0108	6.9	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
472	JGP_1_3.7104.7104.2	2	16.98	72.4	2.15E+05	(K)FTFCYDALHGVAGAYAK(H)	C:Carbamidomethylation	945.9478	1890.884	0.004	2.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
495	JGP_1_3.3697.3704.2	2	16.83	86.7	1.24E+06	(R)LSGTGSVGATIR(V)		559.8142	1118.616	0.0047	4.2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
502	JGP_1_4.4912.4940.2	2	16.78	87.8	2.28E+05	(K)SSSNVEPPEFGAAADGDADR(N)			996.4353	1991.858	0.0056	2.8	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
512	JGP_1_3.8250.8318.3	3	16.72	87.3	1.06E+06	(R)DSQDALAPLVDVALK(L)		518.9543	1554.837	0.011	7.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
525	JGP_1_3.6458.6541.3	3	16.64	84	2.03E+06	(K)TIFDFEAIKK(L)		404.5629	1211.667	0.0071	5.9	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
585	JGP_1_4.5605.5609.2	2	16.28	83.6	3.65E+05	(K)ELmANLVSmQSSLSDVNK(L)	m:Oxidized methionine		999.4832	1965.962	31.9971	3.7	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
650	JGP_1_4.3558.3666.2	2	15.97	86.2	2.77E+06	(R)LSGTGSVGATIR(V)		559.8144	1118.616	0.0051	4.6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
656	JGP_1_4.12116.12116.2	2	15.95	72.9	4.53E+03	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)			1457.2635	2913.54	-0.0199	-6.8	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
679	JGP_1_3.11885.11973.3	3	15.82	87.5	5.32E+06	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)			971.8558	2913.54	0.0132	4.5	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
689	JGP_1_4.3091.3097.2	2	15.78	86	2.25E+06	(R)GATIVVSGDGR(Y)		516.2808	1031.548	0.0063	6.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
737	JGP_1_3.8378.8491.3	3	15.48	81.5	6.34E+05	(R)DSQDALAPLVDVALK(L)		518.9543	1554.837	0.011	7.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
756	JGP_1_3.3936.4036.2	2	15.38	87.6	2.31E+06	(K)DAVQIITK(M)		444.2647	887.52	0.0025	2.8	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
764	JGP_1_5.6840.6935.3	3	15.35	83.4	2.76E+05	(K)TIFDFEAIKK(L)		404.5623	1211.667	0.0053	4.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
780	JGP_1_6.9238.9296.2	2	15.27	85	2.02E+05	(R)DSQDALAPLVDVALK(L)		777.925	1554.837	0.0054	3.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
781	JGP_1_3.3508.3607.2	2	15.26	78.1	3.15E+06	(R)LSGTGSVGATIR(V)		559.8141	1118.616	0.0045	4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
801	JGP_1_4.4980.4980.3	3	15.18	70.7	1.58E+05	(K)SSSNVEPPEFGAAADGDADR(N)			664.627	1991.858	0.0087	4.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
802	JGP_1_3.8174.8174.3	3	15.17	83	8.49E+05	(K)HIFVEELGADESSLLNCVPK(E)	C:Carbamidomethylation		753.048	2257.117	0.0125	5.6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"

806	JGP_1_4.2918.3008.2	2	15.16	85.3	2.69E+06	(R)GATIVVSGDGR(Y)	516.2807	1031.548	0.0061	5.9	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
814	JGP_1_6.12776.12776.4	4	15.1	76.8	5.92E+04	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)		729.1448	2913.54	0.0177	6.1	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
847	JGP_1_4.2809.2863.3	3	14.98	77	1.09E+05	(K)YNmGNGGPAPESVTDK(I) m:Oxidized methionine	551.5821	1636.727	16.0046	5.9	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
851	JGP_1_3.12027.12027.2	2	14.96	65.2	1.32E+04	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)		1457.2756	2913.54	0.0043	1.5	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
901	JGP_1_5.3632.3635.2	2	14.77	78.2	3.71E+05	(R)LSGTGSVGATIR(V)	559.8132	1118.616	0.0027	2.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
910	JGP_1_4.8534.8599.3	3	14.75	79.4	3.25E+05	(R)DSQDALAPLVDVALK(L)	518.9544	1554.837	0.0113	7.3	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
924	JGP_1_4.12014.12117.4	4	14.67	77	6.01E+05	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)		729.1434	2913.54	0.0121	4.2	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
936	JGP_1_3.8368.8494.2	2	14.63	88.6	2.21E+06	(R)DSQDALAPLVDVALK(L)	777.9277	1554.837	0.0108	6.9	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1038	JGP_1_3.5813.5813.3	3	14.17	78	1.22E+06	(K)SSSNVEPPEFGAAADGDADRNmILGK(R)	m:Oxidized methionine	888.7482	2648.226	16.0044	3.5	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
1052	JGP_1_6.3972.3978.2	2	14.13	78.5	5.63E+05	(R)LSGTGSVGATIR(V)	559.8108	1118.616	-0.0021	-1.9	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1083	JGP_1_4.6686.6771.2	2	14	74.6	4.58E+05	(K)TIFDFEAIKK(L)	606.3382	1211.667	0.0021	1.7	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1185	JGP_1_5.3505.3519.2	2	13.61	65.3	2.76E+05	(R)YDYENVDAGAAK(E)	658.2981	1315.58	0.0088	6.7	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1192	JGP_1_3.2903.2981.2	2	13.59	82.1	2.52E+06	(R)GATIVVSGDGR(Y)	516.2795	1031.548	0.0037	3.6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1197	JGP_1_5.8844.8849.2	2	13.58	84.3	1.10E+05	(R)DSQDALAPLVDVALK(L)	777.9239	1554.837	0.0032	2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1236	JGP_1_7.4279.4284.2	2	13.47	74.8	3.16E+05	(K)DAVQIITK(M)	444.2636	887.52	0.0003	0.3	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1241	JGP_1_7.6905.6920.3	3	13.46	79.2	1.93E+04	(K)TIFDFEAIKK(L)	404.5612	1211.667	0.002	1.6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1320	JGP_1_3.11894.12025.4	4	13.2	77	8.76E+05	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)		729.1465	2913.54	0.0245	8.4	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
1365	JGP_1_4.4009.4106.2	2	13.05	74.5	1.84E+06	(K)DAVQIITK(M)	444.2649	887.52	0.0029	3.2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1366	JGP_1_3.7097.7097.2	2	13.04	67.1	2.09E+05	(K)FTFCYDALHGVAGAYAK(H) C:Carbamidomethylation	945.9478	1890.884	0.004	2.1	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1416	JGP_1_3.3374.3378.3	3	12.92	68.9	1.94E+05	(R)YDYENVDAGAAK(E)	439.2018	1315.58	0.0108	8.2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1429	JGP_1_4.4330.4423.2	2	12.88	84.6	1.99E+06	(R)YLFGDGSR(L)	457.7244	914.437	0.0049	5.3	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1650	JGP_1_5.4067.4071.2	2	12.23	73.7	2.36E+05	(K)DAVQIITK(M)	444.2634	887.52	-0.0001	-0.2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1660	JGP_1_3.3056.3061.2	2	12.2	77.9	2.90E+06	(R)GATIVVSGDGR(Y)	516.2801	1031.548	0.0049	4.8	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1661	JGP_1_3.4253.4336.2	2	12.2	79	2.38E+06	(R)YLFGDGSR(L)	457.725	914.437	0.0061	6.6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1765	JGP_1_4.12120.12120.2	2	11.93	63.2	4.53E+03	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)		1457.2635	2913.54	-0.0199	-6.8	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
1767	JGP_1_8.3164.3169.2	2	11.93	73.9	4.01E+05	(R)GATIVVSGDGR(Y)	516.281	1031.548	0.0067	6.5	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1796	JGP_1_3.2817.2857.3	3	11.83	75.7	1.08E+05	(K)YNmGNGGPAPESVTDK(I) m:Oxidized methionine	551.5814	1636.727	16.0025	4.6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
1935	JGP_1_6.7252.7256.3	3	11.43	76.4	1.86E+05	(K)TIFDFEAIKK(L)	404.5623	1211.667	0.0053	4.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
2044	JGP_1_8.9257.9261.2	2	11.13	70.4	9.99E+04	(R)DSQDALAPLVDVALK(L)	777.924	1554.837	0.0034	2.2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
2045	JGP_1_3.4417.4513.2	2	11.12	74.9	1.61E+06	(R)YLFGDGSR(L)	457.7244	914.437	0.0049	5.3	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
2069	JGP_1_5.6146.6146.3	3	11.08	66.1	2.08E+05	(K)SSSNVEPPEFGAAADGDADRNmILGK(R)	m:Oxidized methionine	888.7486	2648.226	16.0056	4	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
2099	JGP_1_4.6017.6024.3	3	11	66.2	1.04E+06	(K)SSSNVEPPEFGAAADGDADRNmILGK(R)	m:Oxidized methionine	888.7489	2648.226	16.0065	4.3	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
2148	JGP_1_3.10963.10963.3	3	10.88	63.4	1.84E+04	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)		971.8558	2913.54	0.0132	4.5	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
2167	JGP_1_3.1429.1507.2	2	10.82	73.8	1.16E+05	(K)MQEYTGR(S)	442.7016	884.393	0.0028	3.2	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
2245	JGP_1_3.5451.5451.3	3	10.66	75.3	1.19E+06	(K)ELmANLVSmQSSLSDVNK(L)	m:Oxidized methionine	666.6588	1965.962	31.9999	5	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
2307	JGP_1_3.5362.5456.3	3	10.49	70.1	1.23E+06	(K)ELmANLVSmQSSLSDVNK(L)	m:Oxidized methionine	666.6588	1965.962	31.9999	5	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
2317	JGP_1_3.6424.6424.3	3	10.46	68	1.02E+05	(K)ELMANLVSmQSSLSDVNK(L)	m:Oxidized methionine	661.3334	1965.962	16.0237	14.5	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
2323	JGP_1_4.5600.5679.3	3	10.45	64.6	6.91E+05	(K)ELmANLVSmQSSLSDVNK(L)	m:Oxidized methionine	666.6596	1965.962	32.0023	6.2	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
2326	JGP_1_4.4964.4964.3	3	10.44	64.1	1.53E+05	(K)SSSNVEPPEFGAAADGDADR(N)		664.627	1991.858	0.0087	4.4	Zea mays	162463106 "phosphoglucomutase, cytoplasmic 1"
2327	JGP_1_4.8649.8649.2	2	10.43	68.9	4.51E+05	(R)DSQDALAPLVDVALK(L)	777.927	1554.837	0.0094	6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
2349	JGP_1_6.4410.4412.2	2	10.41	61.9	3.96E+05	(K)DAVQIITK(M)	444.2686	887.52	0.0103	11.6	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
2434	JGP_1_7.3762.3762.2	2	10.23	63.8	2.35E+04	(R)YDYENVDAGAAK(E)	658.3008	1315.58	0.0142	10.8	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
2445	JGP_1_6.9286.9286.2	2	10.2	63.7	1.85E+05	(R)DSQDALAPLVDVALK(L)	777.925	1554.837	0.0054	3.4	Zea mays	162463106	"phosphoglucomutase, cytoplasmic 1"
35	JGP_1_3.9308.9424.3	3	22.31	95	8.30E+05	(K)VTVFQQPHYLQNFVQSTFNALPADQVK(G)		1040.5393	3119.595	0.0085	2.7	Zea mays	162459678 "phosphoglucomutase, cytoplasmic 2"
46	JGP_1_4.9589.9695.3	3	22.07	95.2	8.19E+05	(K)VTVFQQPHYLQNFVQSTFNALPADQVK(G)		1040.5388	3119.595	0.007	2.2	Zea mays	162459678 "phosphoglucomutase, cytoplasmic 2"
550	JGP_1_4.3758.3856.2	2	16.5	80.1	2.29E+06	(R)VYIEQYEK(D)	536.2751	1071.536	0.0072	6.7	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"

671	JGP_1_3.9304.9304.3	3	15.88	77.2	7.22E+05	(K)VTVFQQPHYLQNFVQSTFNALPADQVK(G)		1040.5393	3119.595	0.0085	2.7	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
738	JGP_1_4.4037.4141.3	3	15.48	69.5	1.46E+06	(K)ATTPFEGQKPGTSGLR(K)	549.6248	1646.85	0.0102	6.2	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
811	JGP_1_4.9141.9147.4	4	15.13	88.4	2.80E+05	(K)KVTVFQQPHYLQNFVQSTFNALPADQVK(G)		812.6814	3247.69	0.0139	4.3	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
960	JGP_1_3.4047.4051.3	3	14.5	69.7	1.84E+06	(K)ATTPFEGQKPGTSGLR(K)	549.6247	1646.85	0.0099	6	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
1146	JGP_1_3.8861.8920.4	4	13.74	81.2	1.60E+05	(K)KVTVFQQPHYLQNFVQSTFNALPADQVK(G)		812.6829	3247.69	0.0199	6.1	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
1345	JGP_1_3.3713.3811.2	2	13.11	75.9	3.32E+06	(R)VYIEQYEK(D)	536.2752	1071.536	0.0074	6.9	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
1500	JGP_1_3.9295.9401.4	4	12.63	74	1.19E+06	(K)VTVFQQPHYLQNFVQSTFNALPADQVK(G)		780.6579	3119.595	0.0149	4.8	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
2168	JGP_1_3.3489.3588.4	4	10.82	69.3	1.07E+06	(K)KATTPFEGQKPGTSGLR(K)	444.4945	1774.945	0.0115	6.5	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
2397	JGP_1_4.9585.9687.4	4	10.31	66.4	1.06E+06	(K)VTVFQQPHYLQNFVQSTFNALPADQVK(G)		780.6589	3119.595	0.0189	6.1	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
2416	JGP_1_6.4149.4153.2	2	10.26	70.4	5.07E+05	(R)VYIEQYEK(D)	536.2763	1071.536	0.0096	9	Zea mays	162459678	"phosphoglucomutase, cytoplasmic 2"
105	JGP_1_6.5489.5582.2	2	20.49	94.2	2.35E+06	(K)YSLKPLVPR(L)	536.8317	1072.651	0.0048	4.5	Arabidopsis thaliana	15219412	phosphoglycerate kinase
271	JGP_1_6.4389.4498.2	2	18.34	90.5	6.33E+06	(K)KPFAAIVGGSK(V)	537.8221	1074.631	0.0063	5.9	Arabidopsis thaliana	15219412	phosphoglycerate kinase
463	JGP_1_5.6768.6852.2	2	17.07	85.6	1.27E+06	(K)ELDYLVGAVANPK(K)	694.8782	1388.742	0.0071	5.1	Arabidopsis thaliana	15219412	phosphoglycerate kinase
621	JGP_1_6.7150.7244.2	2	16.15	84.6	5.74E+06	(K)ELDYLVGAVANPK(K)	694.879	1388.742	0.0087	6.3	Arabidopsis thaliana	15219412	phosphoglycerate kinase
629	JGP_1_5.4038.4042.2	2	16.1	80.5	7.77E+05	(K)KPFAAIVGGSK(V)	537.8208	1074.631	0.0037	3.5	Arabidopsis thaliana	15219412	phosphoglycerate kinase
630	JGP_1_6.4384.4494.3	3	16.1	90.6	4.10E+06	(K)KPFAAIVGGSK(V)	358.8842	1074.631	0.0074	6.9	Arabidopsis thaliana	15219412	phosphoglycerate kinase
643	JGP_1_6.5478.5572.3	3	16.02	80.2	7.13E+06	(K)YSLKPLVPR(L)	358.2247	1072.651	0.0082	7.6	Arabidopsis thaliana	15219412	phosphoglycerate kinase
646	JGP_1_6.7326.7411.2	2	16	84.2	1.13E+05	(K)ELDYLVGAVANPK(K)	694.8793	1388.742	0.0093	6.7	Arabidopsis thaliana	15219412	phosphoglycerate kinase
648	JGP_1_5.5318.5396.3	3	15.99	75.5	2.50E+06	(K)YSLKPLVPR(L)	358.224	1072.651	0.0061	5.7	Arabidopsis thaliana	15219412	phosphoglycerate kinase
749	JGP_1_6.5670.5672.2	2	15.42	80.7	1.36E+06	(K)YSLKPLVPR(L)	536.8316	1072.651	0.0046	4.3	Arabidopsis thaliana	15219412	phosphoglycerate kinase
788	JGP_1_6.5662.5750.3	3	15.23	74.5	5.46E+06	(K)YSLKPLVPR(L)	358.2248	1072.651	0.0085	7.9	Arabidopsis thaliana	15219412	phosphoglycerate kinase
1110	JGP_1_7.6936.7015.2	2	13.92	83.1	2.82E+05	(K)ELDYLVGAVANPK(K)	694.875	1388.742	0.0007	0.5	Arabidopsis thaliana	15219412	phosphoglycerate kinase
1293	JGP_1_5.5323.5411.2	2	13.31	70.6	6.63E+05	(K)YSLKPLVPR(L)	536.8304	1072.651	0.0022	2	Arabidopsis thaliana	15219412	phosphoglycerate kinase
1671	JGP_1_7.4171.4177.2	2	12.2	64.6	3.42E+05	(K)KPFAAIVGGSK(V)	537.8191	1074.631	0.0003	0.3	Arabidopsis thaliana	15219412	phosphoglycerate kinase
1921	JGP_1_6.7176.7265.3	3	11.46	68.4	1.05E+06	(K)ELDYLVGAVANPK(K)	463.5881	1388.742	0.0077	5.6	Arabidopsis thaliana	15219412	phosphoglycerate kinase
1988	JGP_1_7.5322.5327.3	3	11.27	67.3	4.33E+05	(K)YSLKPLVPR(L)	358.2232	1072.651	0.0037	3.5	Arabidopsis thaliana	15219412	phosphoglycerate kinase
2132	JGP_1_6.3724.3858.2	2	10.91	68.5	1.44E+06	(K)FAAGTEAVAK(Q)	482.76	964.51	0.0029	3	Arabidopsis thaliana	15219412	phosphoglycerate kinase
633	JGP_1_5.1125.1140.2	2	16.08	75.6	5.95E+04	(R)FYKEEEK(N)	486.7404	972.467	0.0062	6.4	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
807	JGP_1_6.6384.6473.3	3	15.16	75.5	1.77E+06	(K)GVTTIIGGGDSVAAVEK(V)	525.2892	1573.843	0.0099	6.3	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
1261	JGP_1_6.6343.6443.2	2	13.39	76.8	5.60E+06	(K)GVTTIIGGGDSVAAVEK(V)	787.4293	1573.843	0.0081	5.2	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
1269	JGP_1_6.1145.1148.2	2	13.37	75.6	1.98E+05	(R)FYKEEEK(N)	486.7387	972.467	0.0028	2.9	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
1532	JGP_1_6.0863.0867.2	2	12.53	72.2	5.79E+04	(R)AHASTEGVTK(F)	500.7568	1000.506	0.0005	0.5	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
1564	JGP_1_6.6528.6534.2	2	12.45	76.9	3.79E+06	(K)GVTTIIGGGDSVAAVEK(V)	787.4301	1573.843	0.0097	6.2	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
1742	JGP_1_5.6087.6167.2	2	11.99	76.5	1.47E+06	(K)GVTTIIGGGDSVAAVEK(V)	787.4292	1573.843	0.0079	5	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
1820	JGP_1_6.9016.9095.2	2	11.75	78.6	5.96E+05	(K)GVSLLLPTDVVVADK(F)	763.4485	1525.884	0.0061	4	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
1839	JGP_1_7.6239.6243.2	2	11.71	72.4	3.29E+05	(K)GVTTIIGGGDSVAAVEK(V)	787.4196	1573.843	-0.0113	-7.2	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
2388	JGP_1_6.0882.0887.3	3	10.33	77.8	2.49E+05	(R)AHASTEGVTK(F)	334.1751	1000.506	0.0049	4.9	Arabidopsis thaliana	15230595	phosphoglycerate kinase 1
365	JGP_1_5.3380.3389.3	3	17.63	84.9	4.30E+05	(R)FYKEEEKNEPEFAK(K)	596.6238	1787.849	0.0082	4.6	Solanum tuberosum	82621134	phosphoglycerate kinase precursor-like
398	JGP_1_6.3665.3668.3	3	17.42	86.5	1.60E+06	(R)FYKEEEKNEPEFAK(K)	596.6245	1787.849	0.0103	5.8	Solanum tuberosum	82621134	phosphoglycerate kinase precursor-like
1755	JGP_1_6.3634.3757.4	4	11.96	66.4	5.10E+06	(R)FYKEEEKNEPEFAK(K)	447.721	1787.849	0.0135	7.6	Solanum tuberosum	82621134	phosphoglycerate kinase precursor-like
146	JGP_1_6.3749.3857.2	2	19.63	89.6	7.46E+06	(K)FAAGTEAIAK(K)	489.7699	978.525	0.0071	7.2	Solanum tuberosum	82400156	phosphoglycerate kinase precursor-like protein
1133	JGP_1_5.3463.3576.2	2	13.82	81.8	2.34E+06	(K)FAAGTEAIAK(K)	489.7691	978.525	0.0055	5.6	Solanum tuberosum	82400156	phosphoglycerate kinase precursor-like protein
1536	JGP_1_7.3716.3723.2	2	12.52	67	3.75E+05	(K)FAAGTEAIAK(K)	489.7679	978.525	0.0031	3.1	Solanum tuberosum	82400156	phosphoglycerate kinase precursor-like protein
17	JGP_1_4.9064.9070.3	3	22.96	90.1	9.21E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		771.0657	2311.168	0.0148	6.4	Zea mays	551288	phosphoglycerate mutase
24	JGP_1_4.8910.8984.4	4	22.78	86.1	5.62E+06	(K)ESFESGTLHLIGLLSDGGVHSR(L)		578.5521	2311.168	0.0189	8.2	Zea mays	551288	phosphoglycerate mutase
111	JGP_1_4.8931.9004.3	3	20.4	87.3	1.57E+06	(K)ESFESGTLHLIGLLSDGGVHSR(L)		771.0657	2311.168	0.0148	6.4	Zea mays	551288	phosphoglycerate mutase

190	JGP_1_3.8740.8803.4	4	19.21	79.8	2.67E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		578.5519	2311.168	0.0181	7.8	Zea mays	551288	phosphoglycerate mutase
221	JGP_1_4.8861.8935.3	3	18.91	89.2	8.33E+05	(K)IILDAVEQVGGIYLVTADHGNAEDmVK(R)	m:Oxidized methionine	962.8276	2870.46	16.0078	4.5	Zea mays	551288	phosphoglycerate mutase
303	JGP_1_1.8806.8869.4	4	18.05	78.6	1.86E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		578.5521	2311.168	0.0189	8.2	Zea mays	551288	phosphoglycerate mutase
337	JGP_1_5.9225.9297.4	4	17.89	73.6	5.91E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		578.5506	2311.168	0.0129	5.6	Zea mays	551288	phosphoglycerate mutase
430	JGP_1_4.9044.9117.4	4	17.28	75.5	5.11E+06	(K)ESFESGTLHLIGLLSDGGVHSR(L)		578.552	2311.168	0.0185	8	Zea mays	551288	phosphoglycerate mutase
473	JGP_1_4.4543.4682.4	4	16.98	84.3	4.09E+06	(K)AHGTAVGLPSDDDmGNSEVGHNALGAGR(I)	m:Oxidized methionine	681.0662	2705.233	16.0097	5.4	Zea mays	551288	phosphoglycerate mutase
572	JGP_1_4.2638.2726.2	2	16.36	86.3	3.38E+06	(R)TFACSETVK(F)	C:Carbamidomethylation	521.75	1042.487	0.0054	5.1	Zea mays	551288	phosphoglycerate mutase
595	JGP_1_4.5955.5960.2	2	16.21	87.5	1.94E+05	(K)RGWDAQVLGEAPYK(F)		795.409	1589.807	0.0037	2.3	Zea mays	551288	phosphoglycerate mutase
772	JGP_1_4.8662.8730.4	4	15.31	72.5	2.48E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		578.5512	2311.168	0.0153	6.6	Zea mays	551288	phosphoglycerate mutase
857	JGP_1_4.5929.6013.3	3	14.93	83	7.95E+05	(K)RGWDAQVLGEAPYK(F)		530.6101	1589.807	0.0087	5.5	Zea mays	551288	phosphoglycerate mutase
873	JGP_1_4.2292.2381.2	2	14.89	87.4	3.65E+06	(K)SALEAVK(T)		359.2123	717.414	0.0032	4.4	Zea mays	551288	phosphoglycerate mutase
889	JGP_1_4.8632.8635.4	4	14.83	77.7	3.26E+04	(K)IILDAVEQVGGIYLVTADHGNAEDmVKR(N)	m:Oxidized methionine	761.3988	3026.561	16.0118	5.6	Zea mays	551288	phosphoglycerate mutase
897	JGP_1_4.5050.5133.2	2	14.78	72.8	6.27E+05	(R)YENDWDVVK(R)		584.274	1167.532	0.009	7.7	Zea mays	551288	phosphoglycerate mutase
900	JGP_1_4.6398.6482.2	2	14.77	80.2	1.23E+06	(R)GWDAQVLGEAPYK(F)		717.3617	1433.706	0.0102	7.1	Zea mays	551288	phosphoglycerate mutase
994	JGP_1_2.8274.8337.4	4	14.37	69.6	1.79E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)			578.5514	2311.168	0.0161	7	Zea mays	551288	phosphoglycerate mutase
1330	JGP_1_3.2398.2407.2	2	13.18	81.8	1.90E+05	(K)SALEAVK(T)		359.2114	717.414	0.0014	1.9	Zea mays	551288	phosphoglycerate mutase
1332	JGP_1_4.9159.9172.3	3	13.18	73	1.36E+05	(K)IILDAVEQVGGIYLVTADHGNAEDMVK(R)			957.4946	2870.46	0.0088	3.1	Zea mays	551288	phosphoglycerate mutase
1403	JGP_1_4.5200.5255.4	4	12.96	62.9	6.28E+05	(K)AHGTAVGLPSDDDMGNSEVGHNALGAGR(I)			677.0699	2705.233	0.0245	9.1	Zea mays	551288	phosphoglycerate mutase
1698	JGP_1_5.4748.4752.4	4	12.13	66.8	1.98E+05	(K)AHGTAVGLPSDDDmGNSEVGHNALGAGR(I)	m:Oxidized methionine	681.0655	2705.233	16.0069	4.4	Zea mays	551288	phosphoglycerate mutase
1738	JGP_1_6.9632.9702.4	4	12	65.5	2.25E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		578.5512	2311.168	0.0153	6.6	Zea mays	551288	phosphoglycerate mutase
1860	JGP_1_6.2468.2468.2	2	11.65	78.4	4.06E+05	(K)SALEAVK(T)		359.2139	717.414	0.0064	8.9	Zea mays	551288	phosphoglycerate mutase
2042	JGP_1_5.6625.6635.2	2	11.13	70.7	1.92E+05	(R)GWDAQVLGEAPYK(F)		717.3633	1433.706	0.0134	9.3	Zea mays	551288	phosphoglycerate mutase
920	JGP_1_8.4168.4177.2	2	14.69	84.2	4.34E+05	(K)DVDLSTYK(G)		470.7365	940.462	0.0035	3.7	Hordeum vulgare	27544804	phospholipid hydroperoxide glutathione peroxidase-like protein
1116	JGP_1_8.5310.5325.2	2	13.89	67.2	3.18E+05	(R)YAPTTSPLSIEK(D)		653.8482	1306.689	0.0002	0.2	Hordeum vulgare	27544804	phospholipid hydroperoxide glutathione peroxidase-like protein
2389	JGP_1_7.1674.1681.2	2	10.33	69.7	4.37E+05	(R)VSIDGK(I)		309.6721	618.346	-0.0088	-14.2	Arabidopsis thaliana	15234859	phytochrome D
2165	JGP_1_1.4054.4154.2	2	10.83	82.5	4.06E+07	(K)VAKGKSPR(K)		421.7614	842.521	-0.0051	-6.1	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2182	JGP_1_2.4036.4116.2	2	10.78	81.9	4.11E+07	(K)VAKGKSPR(K)		421.7625	842.521	-0.0029	-3.5	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2187	JGP_1_2.3872.3966.2	2	10.77	81.6	4.58E+07	(K)VAKGKSPR(K)		421.7624	842.521	-0.0031	-3.7	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2195	JGP_1_3.4144.4236.2	2	10.76	81.6	3.83E+07	(K)VAKGKSPR(K)		421.7625	842.521	-0.0029	-3.5	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2203	JGP_1_7.4377.4477.2	2	10.75	81.5	1.71E+07	(K)VAKGKSPR(K)		421.7611	842.521	-0.0057	-6.8	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2208	JGP_1_6.4550.4652.2	2	10.74	81.4	3.76E+07	(K)VAKGKSPR(K)		421.7618	842.521	-0.0043	-5.1	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2221	JGP_1_1.4224.4304.2	2	10.71	81.1	3.61E+07	(K)VAKGKSPR(K)		421.7618	842.521	-0.0043	-5.1	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2228	JGP_1_5.4307.4406.2	2	10.7	80.3	2.96E+07	(K)VAKGKSPR(K)		421.7622	842.521	-0.0035	-4.2	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2237	JGP_1_3.4311.4401.2	2	10.68	80.8	3.25E+07	(K)VAKGKSPR(K)		421.7624	842.521	-0.0031	-3.7	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2280	JGP_1_4.4219.4322.2	2	10.57	80.3	3.42E+07	(K)VAKGKSPR(K)		421.762	842.521	-0.0039	-4.7	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2289	JGP_1_8.4384.4559.2	2	10.54	79.7	1.26E+07	(K)VAKGKSPR(K)		421.7614	842.521	-0.0051	-6.1	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2300	JGP_1_7.4562.4567.2	2	10.51	79.9	1.53E+07	(K)VAKGKSPR(K)		421.7617	842.521	-0.0045	-5.4	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
2409	JGP_1_4.4407.4507.2	2	10.27	78.2	2.54E+07	(K)VAKGKSPR(K)		421.7623	842.521	-0.0033	-4	Arabidopsis thaliana	15224020	P-loop containing nucleoside triphosphate hydrolase-like protein
151	JGP_1_8.8319.8399.2	2	19.6	87	8.87E+06	(R)YANPIAFFR(K)		549.7939	1098.573	0.0074	6.8	Zea mays	226505364	pollen allergen Phl p 11 precursor
249	JGP_1_8.1426.1528.2	2	18.58	88.9	3.77E+06	(R)VYCDPCR(A)	C:Carbamidomethylation	485.2013	969.392	0.0036	3.7	Zea mays	226505364	pollen allergen Phl p 11 precursor
335	JGP_1_8.8466.8590.2	2	17.9	81.5	2.08E+06	(R)YANPIAFFR(K)		549.7932	1098.573	0.006	5.5	Zea mays	226505364	pollen allergen Phl p 11 precursor
339	JGP_1_8.4649.4747.2	2	17.88	89.1	4.08E+06	(R)SVAGATVEVVCR(H)	C:Carbamidomethylation	624.3264	1247.641	0.0043	3.4	Zea mays	226505364	pollen allergen Phl p 11 precursor
402	JGP_1_8.8174.8249.2	2	17.41	80.5	5.18E+06	(R)YANPIAFFR(K)		549.7938	1098.573	0.0072	6.6	Zea mays	226505364	pollen allergen Phl p 11 precursor
605	JGP_1_7.8096.8175.2	2	16.19	81.9	1.18E+06	(R)YANPIAFFR(K)		549.793	1098.573	0.0056	5.1	Zea mays	226505364	pollen allergen Phl p 11 precursor
693	JGP_1_2.7274.7357.2	2	15.73	71.6	4.12E+05	(R)YANPIAFFR(K)		549.7928	1098.573	0.0052	4.8	Zea mays	226505364	pollen allergen Phl p 11 precursor
758	JGP_1_8.3757.3762.2	2	15.38	81.7	3.05E+06	(K)AGGFVVTGR(V)		432.2425	863.473	0.0043	5	Zea mays	226505364	pollen allergen Phl p 11 precursor
883	JGP_1_3.7666.7756.2	2	14.87	69.9	6.24E+05	(R)YANPIAFFR(K)		549.7921	1098.573	0.0038	3.5	Zea mays	226505364	pollen allergen Phl p 11 precursor
915	JGP_1_1.7870.7880.2	2	14.72	70.8	5.51E+05	(R)YANPIAFFR(K)		549.793	1098.573	0.0056	5.1	Zea mays	226505364	pollen allergen Phl p 11 precursor
993	JGP_1_1.1685.1758.2	2	14.37	78.9	2.53E+05	(R)VYCDPCR(A)	C:Carbamidomethylation	485.2014	969.392	0.0038	3.9	Zea mays	226505364	pollen allergen Phl p 11 precursor
1046	JGP_1_1.7706.7794.2	2	14.14	75.9	1.38E+06	(R)YANPIAFFR(K)		549.7931	1098.573	0.0058	5.3	Zea mays	226505364	pollen allergen Phl p 11 precursor

1073	JGP_1_7.3702.3800.2	2	14.04	77.8	8.04E+05	(K)AGGFVVTGR(V)		432.2417	863.473	0.0027	3.2	Zea mays	226505364	pollen allergen Phl p 11 precursor
1098	JGP_1_4.7922.8009.2	2	13.96	72.8	3.29E+05	(R)YANPIAFFR(K)		549.7922	1098.573	0.004	3.7	Zea mays	226505364	pollen allergen Phl p 11 precursor
1159	JGP_1_8.3195.3317.2	2	13.71	88.9	2.14E+06	(R)VPLTSNNGIK(Q)		521.8003	1042.589	0.0042	4	Zea mays	226505364	pollen allergen Phl p 11 precursor
1288	JGP_1_7.1602.1705.2	2	13.33	72.8	6.07E+05	(R)VYCDPCR(A)	C:Carbamidomethylation	485.2015	969.392	0.004	4.2	Zea mays	226505364	pollen allergen Phl p 11 precursor
1450	JGP_1_7.3361.3364.2	2	12.81	78.8	4.09E+05	(R)VPLTSNNGIK(Q)		521.7966	1042.589	-0.0032	-3.1	Zea mays	226505364	pollen allergen Phl p 11 precursor
1600	JGP_1_2.1743.1748.2	2	12.36	68.5	6.99E+04	(R)VYCDPCR(A)	C:Carbamidomethylation	485.202	969.392	0.005	5.2	Zea mays	226505364	pollen allergen Phl p 11 precursor
1624	JGP_1_5.8054.8154.2	2	12.29	69.2	2.48E+05	(R)YANPIAFFR(K)		549.792	1098.573	0.0036	3.3	Zea mays	226505364	pollen allergen Phl p 11 precursor
1901	JGP_1_7.8239.8245.2	2	11.53	62.4	1.83E+05	(R)YANPIAFFR(K)		549.7912	1098.573	0.002	1.8	Zea mays	226505364	pollen allergen Phl p 11 precursor
2086	JGP_1_8.4698.4703.3	3	11.04	65.7	3.76E+05	(R)SVAGATVEVVCR(H)	C:Carbamidomethylation	416.5536	1247.641	0.005	4	Zea mays	226505364	pollen allergen Phl p 11 precursor
2200	JGP_1_2.4098.4129.2	2	10.75	62.6	1.60E+04	(R)SVAGATVEVVCR(H)	C:Carbamidomethylation	624.3282	1247.641	0.0079	6.3	Zea mays	226505364	pollen allergen Phl p 11 precursor
389	JGP_1_8.4159.4266.2	2	17.49	89.3	5.80E+06	(K)EPIKGPISVR(F)		548.3333	1095.652	0.0073	6.6	Zea mays	226510546	pollen allergen Phl p 2 precursor
458	JGP_1_8.2409.2509.2	2	17.1	98.2	4.72E+07	(K)GPISVR(F)		314.6954	628.378	0.0058	9.3	Zea mays	226510546	pollen allergen Phl p 2 precursor
593	JGP_1_8.3656.3751.2	2	16.23	92.8	4.51E+07	(K)TFTLDSK(E)		406.217	811.42	0.0071	8.8	Zea mays	226510546	pollen allergen Phl p 2 precursor
651	JGP_1_8.3458.3651.2	2	15.97	93.4	5.06E+07	(K)TFTLDSK(E)		406.2166	811.42	0.0063	7.8	Zea mays	226510546	pollen allergen Phl p 2 precursor
685	JGP_1_1.3416.3578.2	2	15.8	90	2.87E+06	(K)TFTLDSK(E)		406.214	811.42	0.0011	1.4	Zea mays	226510546	pollen allergen Phl p 2 precursor
846	JGP_1_8.2204.2324.2	2	14.99	95.7	5.04E+07	(K)GPISVR(F)		314.6954	628.378	0.0058	9.3	Zea mays	226510546	pollen allergen Phl p 2 precursor
1244	JGP_1_1.2484.2563.2	2	13.44	89.7	1.74E+06	(K)GPISVR(F)		314.6935	628.378	0.002	3.2	Zea mays	226510546	pollen allergen Phl p 2 precursor
1343	JGP_1_7.3663.3760.2	2	13.12	79.8	1.99E+06	(K)TFTLDSK(E)		406.2149	811.42	0.0029	3.6	Zea mays	226510546	pollen allergen Phl p 2 precursor
1653	JGP_1_7.2336.2449.2	2	12.23	90.2	6.96E+06	(K)GPISVR(F)		314.6947	628.378	0.0044	7.1	Zea mays	226510546	pollen allergen Phl p 2 precursor
1802	JGP_1_1.4037.4042.2	2	11.81	74.7	2.41E+05	(K)EPIKGPISVR(F)		548.3284	1095.652	-0.0025	-2.3	Zea mays	226510546	pollen allergen Phl p 2 precursor
2164	JGP_1_8.4148.4342.3	3	10.84	69	1.88E+07	(K)EPIKGPISVR(F)		365.8922	1095.652	0.01	9.1	Zea mays	226510546	pollen allergen Phl p 2 precursor
2305	JGP_1_1.3663.3668.2	2	10.49	62.5	1.29E+06	(K)TFTLDSK(E)		406.2147	811.42	0.0025	3.1	Zea mays	226510546	pollen allergen Phl p 2 precursor
2347	JGP_1_5.2486.2491.2	2	10.41	80.2	3.35E+05	(K)GPISVR(F)		314.6933	628.378	0.0016	2.6	Zea mays	226510546	pollen allergen Phl p 2 precursor
2498	JGP_1_2.2474.2541.2	2	10.07	78.5	4.34E+05	(K)GPISVR(F)		314.6932	628.378	0.0014	2.3	Zea mays	226510546	pollen allergen Phl p 2 precursor
10	JGP_1_8.10271.10339.2	2	23.45	100	8.30E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5208	2022.022	0.0125	6.2	Zea mays	162464215	pollen profilin variant 4
34	JGP_1_1.9321.9439.2	2	22.31	98.3	2.69E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5164	2022.022	0.0037	1.8	Zea mays	162464215	pollen profilin variant 4
36	JGP_1_5.9903.9972.2	2	22.31	98.3	9.34E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5193	2022.022	0.0095	4.7	Zea mays	162464215	pollen profilin variant 4
43	JGP_1_8.10399.10469.2	2	22.11	98.5	1.18E+07	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5231	2022.022	0.0171	8.4	Zea mays	162464215	pollen profilin variant 4
49	JGP_1_2.8917.8922.2	2	21.98	96.4	1.38E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5181	2022.022	0.0071	3.5	Zea mays	162464215	pollen profilin variant 4
60	JGP_1_4.9565.9634.2	2	21.51	97.1	2.55E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5179	2022.022	0.0067	3.3	Zea mays	162464215	pollen profilin variant 4
61	JGP_1_2.8789.8857.2	2	21.47	96.8	1.68E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5172	2022.022	0.0053	2.6	Zea mays	162464215	pollen profilin variant 4
62	JGP_1_3.9398.9480.2	2	21.44	95.9	2.27E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5174	2022.022	0.0057	2.8	Zea mays	162464215	pollen profilin variant 4
80	JGP_1_8.10285.10354.3	3	21.06	95.5	4.91E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			674.6844	2022.022	0.0168	8.3	Zea mays	162464215	pollen profilin variant 4
106	JGP_1_2.8802.8862.3	3	20.47	91.6	1.06E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			674.6832	2022.022	0.0132	6.5	Zea mays	162464215	pollen profilin variant 4
122	JGP_1_3.9271.9338.2	2	20.18	95.6	2.48E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5187	2022.022	0.0083	4.1	Zea mays	162464215	pollen profilin variant 4
183	JGP_1_4.9699.9706.2	2	19.27	88.3	3.21E+04	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5189	2022.022	0.0087	4.3	Zea mays	162464215	pollen profilin variant 4
184	JGP_1_1.9320.9440.3	3	19.26	90.7	1.66E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			674.6821	2022.022	0.0099	4.9	Zea mays	162464215	pollen profilin variant 4
185	JGP_1_1.9445.9510.2	2	19.26	93.9	2.06E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5175	2022.022	0.0059	2.9	Zea mays	162464215	pollen profilin variant 4
211	JGP_1_8.10529.10594.2	2	19.02	93.3	6.75E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5187	2022.022	0.0083	4.1	Zea mays	162464215	pollen profilin variant 4
288	JGP_1_7.10204.10328.2	2	18.22	92.1	1.63E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5188	2022.022	0.0085	4.2	Zea mays	162464215	pollen profilin variant 4
311	JGP_1_8.10414.10484.3	3	18.03	86.6	5.25E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			674.6841	2022.022	0.0159	7.9	Zea mays	162464215	pollen profilin variant 4
413	JGP_1_6.10308.10375.2	2	17.36	85.3	3.37E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5179	2022.022	0.0067	3.3	Zea mays	162464215	pollen profilin variant 4
436	JGP_1_7.10333.10445.2	2	17.26	86	1.34E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			1011.5189	2022.022	0.0087	4.3	Zea mays	162464215	pollen profilin variant 4
462	JGP_1_3.9281.9348.3	3	17.07	86.8	1.69E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)			674.6825	2022.022	0.0111	5.5	Zea mays	162464215	pollen profilin variant 4
468	JGP_1_5.9913.9984.3	3	17.05	87.5	5.12E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)			674.6831	2022.022	0.0129	6.4	Zea mays	162464215	pollen profilin variant 4
522	JGP_1_6.10321.10395.3	3	16.67	82.6	4.65E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)			674.6832	2022.022	0.0132	6.5	Zea mays	162464215	pollen profilin variant 4

680	JGP_1_7.10234.10298.3	3	15.82	82.1	9.44E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)		674.6833	2022.022	0.0135	6.7	Zea mays	162464215	pollen profilin variant 4
1224	JGP_1_3.9411.9411.3	3	13.51	79.2	2.65E+04	(K)DFDEPGFLAPTGLFLGPTK(Y)		674.6828	2022.022	0.012	5.9	Zea mays	162464215	pollen profilin variant 4
1251	JGP_1_1.9444.9444.3	3	13.42	72.8	1.05E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)		674.6822	2022.022	0.0102	5	Zea mays	162464215	pollen profilin variant 4
1424	JGP_1_4.9567.9635.3	3	12.9	73.9	1.41E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)		674.6822	2022.022	0.0102	5	Zea mays	162464215	pollen profilin variant 4
1620	JGP_1_7.10216.10303.3	3	12.31	68.1	9.51E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)		674.683	2022.022	0.0126	6.2	Zea mays	162464215	pollen profilin variant 4
1717	JGP_1_5.10044.10044.2	2	12.07	69.2	4.11E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)		1011.5195	2022.022	0.0099	4.9	Zea mays	162464215	pollen profilin variant 4
2350	JGP_1_2.8797.8867.3	3	10.4	67.3	1.06E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)		674.6833	2022.022	0.0135	6.7	Zea mays	162464215	pollen profilin variant 4
2481	JGP_1_2.8930.8930.3	3	10.11	67.5	1.52E+04	(K)DFDEPGFLAPTGLFLGPTK(Y)		674.6828	2022.022	0.012	5.9	Zea mays	162464215	pollen profilin variant 4
345	JGP_1_8.3512.3612.2	2	17.83	97.4	4.03E+06	(R)AGVLLTR(N)	365.2362	729.462	0.0034	4.6	Zea mays	162458188	pollen-specific protein C13 precursor	
524	JGP_1_8.8742.8819.2	2	16.66	90.4	1.93E+06	(K)DVPLPVCAALLK(Q)	C:Carbamidomethylation	648.376	1295.739	0.0056	4.3	Zea mays	162458188	pollen-specific protein C13 precursor
894	JGP_1_7.7165.7168.2	2	14.81	73.5	9.92E+04	(R)AIDGVTDATGTYTIELK(D)	884.4524	1767.901	-0.0036	-2	Zea mays	162458188	pollen-specific protein C13 precursor	
1199	JGP_1_8.7220.7317.2	2	13.58	75.3	6.42E+05	(R)AIDGVTDATGTYTIELK(D)	884.4574	1767.901	0.0064	3.6	Zea mays	162458188	pollen-specific protein C13 precursor	
1410	JGP_1_8.0958.0964.2	2	12.96	74.7	1.59E+05	(R)VYCDTCR(A)	C:Carbamidomethylation	487.1985	973.387	0.0031	3.2	Zea mays	162458188	pollen-specific protein C13 precursor
1518	JGP_1_7.8779.8784.2	2	12.58	74.7	3.01E+05	(K)DVPLPVCAALLK(Q)	C:Carbamidomethylation	648.3753	1295.739	0.0042	3.2	Zea mays	162458188	pollen-specific protein C13 precursor
1604	JGP_1_8.8885.8891.2	2	12.36	74.4	1.60E+04	(K)DVPLPVCAALLK(Q)	C:Carbamidomethylation	648.376	1295.739	0.0056	4.3	Zea mays	162458188	pollen-specific protein C13 precursor
1782	JGP_1_8.8811.8811.3	3	11.87	73.2	5.23E+04	(K)DVPLPVCAALLK(Q)	C:Carbamidomethylation	432.5844	1295.739	-0.0005	-0.4	Zea mays	162458188	pollen-specific protein C13 precursor
2158	JGP_1_7.3686.3791.2	2	10.86	67.4	2.12E+06	(R)AGVLLTR(N)	365.2356	729.462	0.0022	3	Zea mays	162458188	pollen-specific protein C13 precursor	
509	JGP_1_4.9936.9951.3	3	16.74	81.1	2.93E+05	(R)LLIPVPFDQPPPENDHVVLIGDWYTK(D)		1001.5315	3002.566	0.0137	4.6	Zea mays	226529445	pollen-specific protein NTP303 precursor
732	JGP_1_4.9952.10022.4	4	15.52	77.9	2.17E+05	(R)LLIPVPFDQPPPENDHVVLIGDWYTK(D)		751.4021	3002.566	0.0203	6.8	Zea mays	226529445	pollen-specific protein NTP303 precursor
1528	JGP_1_1.9706.9710.4	4	12.54	73.2	9.33E+03	(R)LLIPVPFDQPPPENDHVVLIGDWYTK(D)		751.4028	3002.566	0.0231	7.7	Zea mays	226529445	pollen-specific protein NTP303 precursor
1729	JGP_1_4.8241.8322.2	2	12.02	70	2.49E+05	(R)TFIEIVFENPEK(S)	733.3867	1465.757	0.0088	6	Zea mays	226506544	pollen-specific protein NTP303 precursor	
1764	JGP_1_4.1073.1082.2	2	11.93	72.7	5.51E+04	(R)FIHDAK(S)	365.6981	730.388	0.0007	0.9	Zea mays	226506544	pollen-specific protein NTP303 precursor	
2130	JGP_1_1.9711.9711.3	3	10.91	69.9	1.62E+04	(R)LLIPVPFDQPPPENDHVVLIGDWYTK(D)		1001.5156	3002.566	-0.034	-11.3	Zea mays	226529445	pollen-specific protein NTP303 precursor
2361	JGP_1_4.6956.7075.2	2	10.39	66.1	1.69E+05	(K)VILINGEFPGPR(I)	656.3725	1311.742	-0.0042	-3.2	Zea mays	226506544	pollen-specific protein NTP303 precursor	
71	JGP_1_5.14201.14205.2	2	21.19	95	1.72E+05	(K)GDVTIQVDGNLLATTDLSQYK(D)		1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
129	JGP_1_5.2256.2358.2	2	20.03	88.8	9.31E+06	(K)IHYENIK(M)	458.7511	916.489	0.0062	6.8	Zea mays	22424	polygalacturonase	
169	JGP_1_5.2444.2448.2	2	19.41	86.2	5.69E+06	(K)IHYENIK(M)	458.751	916.489	0.006	6.6	Zea mays	22424	polygalacturonase	
239	JGP_1_2.3886.3956.2	2	18.64	91.1	9.88E+06	(R)VDNLVITGK(G)	479.7854	958.557	0.0068	7	Zea mays	22426	polygalacturonase	
250	JGP_1_5.3215.3308.2	2	18.56	85.8	2.75E+06	(R)YKDEKDVTDINVK(D)	783.908	1566.801	0.0077	4.9	Zea mays	22426	polygalacturonase	
276	JGP_1_1.4059.4172.2	2	18.31	91.6	8.40E+06	(R)VDNLVITGK(G)	479.7848	958.557	0.0056	5.8	Zea mays	22426	polygalacturonase	
278	JGP_1_5.4185.4275.2	2	18.3	90.9	3.63E+07	(R)VDNLVITGK(G)	479.7863	958.557	0.0086	8.9	Zea mays	22426	polygalacturonase	
359	JGP_1_3.3952.4131.2	2	17.68	93.1	8.31E+06	(R)VDNLVITGK(G)	479.7832	958.557	0.0024	2.5	Zea mays	22426	polygalacturonase	
442	JGP_1_4.4186.4327.2	2	17.22	91.2	1.09E+07	(R)VDNLVITGK(G)	479.7855	958.557	0.007	7.3	Zea mays	22426	polygalacturonase	
449	JGP_1_2.3094.3098.2	2	17.14	78	1.86E+05	(R)YKDEKDVTDINVK(D)	783.9059	1566.801	0.0035	2.3	Zea mays	22426	polygalacturonase	
460	JGP_1_2.7392.7392.2	2	17.08	79.2	2.16E+05	(K)GDVTIQVDGNLLATTDLSQYK(D)		1126.0772	2251.145	0.0019	0.8	Zea mays	22426	polygalacturonase
530	JGP_1_1.3878.3969.2	2	16.6	84.2	6.29E+06	(R)VDNLVITGK(G)	479.7817	958.557	-0.0006	-0.7	Zea mays	22426	polygalacturonase	
558	JGP_1_2.2446.2451.2	2	16.44	79.9	1.47E+06	(K)IHYENIK(M)	458.7493	916.489	0.0026	2.9	Zea mays	22424	polygalacturonase	
580	JGP_1_5.4000.4105.2	2	16.3	88.9	2.37E+07	(R)VDNLVITGK(G)	479.7856	958.557	0.0072	7.5	Zea mays	22426	polygalacturonase	
590	JGP_1_4.3163.3261.2	2	16.25	85.6	2.13E+06	(R)YKDEKDVTDINVK(D)	783.9067	1566.801	0.0051	3.3	Zea mays	22426	polygalacturonase	
625	JGP_1_3.4136.4269.2	2	16.13	87.1	7.71E+06	(R)VDNLVITGK(G)	479.7852	958.557	0.0064	6.6	Zea mays	22426	polygalacturonase	
652	JGP_1_2.3197.3306.2	2	15.96	90.5	4.10E+06	(K)DVTDINVK(D)	452.2453	903.478	0.0051	5.7	Zea mays	22426	polygalacturonase	
658	JGP_1_5.3573.3681.2	2	15.95	89.8	1.54E+07	(K)DVTDINVK(D)	452.2463	903.478	0.0071	7.9	Zea mays	22426	polygalacturonase	
663	JGP_1_4.2397.2487.2	2	15.92	78	1.73E+06	(K)IHYENIK(M)	458.7494	916.489	0.0028	3.1	Zea mays	22424	polygalacturonase	
703	JGP_1_4.3383.3517.2	2	15.68	89.3	1.48E+07	(K)DVTDINVK(D)	452.246	903.478	0.0065	7.2	Zea mays	22426	polygalacturonase	
725	JGP_1_5.3565.3569.3	3	15.57	81.9	8.02E+05	(R)YKDEKDVTDINVK(D)	522.9413	1566.801	0.0084	5.3	Zea mays	22426	polygalacturonase	
739	JGP_1_2.3718.3801.2	2	15.47	80.4	8.06E+06	(R)VDNLVITGK(G)	479.7828	958.557	0.0016	1.6	Zea mays	22426	polygalacturonase	
763	JGP_1_1.3336.3418.2	2	15.35	87	2.74E+06	(K)DVTDINVK(D)	452.2443	903.478	0.0031	3.5	Zea mays	22426	polygalacturonase	
765	JGP_1_5.8563.8615.2	2	15.35	81.2	3.48E+05	(K)GDVTIQVDGNLLATTDLSQYK(D)		1126.075	2251.145	-0.0025	-1.1	Zea mays	22426	polygalacturonase
831	JGP_1_6.2474.2572.2	2	15.04	78.4	1.09E+06	(K)IHYENIK(M)	458.7493	916.489	0.0026	2.9	Zea mays	22424	polygalacturonase	
860	JGP_1_6.3595.3595.2	2	14.93	72.3	2.79E+05	(R)YKDEKDVTDINVK(D)	783.9056	1566.801	0.0029	1.9	Zea mays	22426	polygalacturonase	
880	JGP_1_3.3346.3477.2	2	14.88	87.8	3.52E+06	(K)DVTDINVK(D)	452.245	903.478	0.0045	5	Zea mays	22426	polygalacturonase	
939	JGP_1_5.8410.8505.2	2	14.63	76.6	3.90E+05	(K)GDVTIQVDGNLLATTDLSQYK(D)		1126.0747	2251.145	-0.0031	-1.4	Zea mays	22426	polygalacturonase
959	JGP_1_3.3946.4046.2	2	14.5	75.1	5.44E+06	(R)VDNLVITGK(G)	479.7829	958.557	0.0018	1.8	Zea mays	22426	polygalacturonase	
961	JGP_1_4.2932.3028.3	3	14.5	71.6	5.68E+05	(R)YKDEKDVTDINVK(D)	522.9439	1566.801	0.0162	10.3	Zea mays	22426	polygalacturonase	
991	JGP_1_5.2998.3061.3	3	14.39	72.1	5.07E+05	(R)YKDEKDVTDINVK(D)	522.9421	1566.801	0.0108	6.9	Zea mays	22426	polygalacturonase	
1000	JGP_1_5.14510.14510.2	2	14.34	74.8	9.50E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)		1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
1018	JGP_1_5.13999.14109.3	3	14.25	79	4.15E+05	(K)GDVTIQVDGNLLATTDLSQYK(D)		751.0562	2251.145	0.0088	3.9	Zea mays	22426	polygalacturonase
1044	JGP_1_4.3874.3966.2	2	14.15	82.3	2.14E+06	(K)DVTDINVK(D)	452.2446	903.478	0.0037	4.1	Zea mays	22426	polygalacturonase	
1085	JGP_1_6.3780.3882.2	2	14	84.3	1.83E+06	(K)DVTDINVK(D)	452.2453	903.478	0.0051	5.7	Zea mays	22426	polygalacturonase	
1111	JGP_1_6.4373.4483.2	2	13.91	77.8	5.38E+06	(R)VDNLVITGK(G)	479.7855	958.557	0.007	7.3	Zea mays	22426	polygalacturonase	
1130	JGP_1_6.4582.4588.2	2	13.84	80.6	4.38E+06	(R)VDNLVITGK(G)	479.7851	958.557	0.0062	6.4	Zea mays	22426	polygalacturonase	

1248	JGP_1_5.14580.14580.2	2	13.43	75.5	8.20E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)			1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
1395	JGP_1_4.3532.3537.3	3	12.97	64	5.63E+05	(R)YKDEKDVTDINVK(D)		522.9419	1566.801	0.0102	6.5	Zea mays	22426	polygalacturonase
1453	JGP_1_5.14707.14707.2	2	12.8	66.1	7.30E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)			1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
1457	JGP_1_5.14682.14682.2	2	12.79	75.5	7.37E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)			1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
1530	JGP_1_5.13929.13994.3	3	12.53	73.7	1.73E+05	(K)GDVTIQVDGNLLATTDLSQYK(D)			751.0566	2251.145	0.01	4.4	Zea mays	22426	polygalacturonase
1531	JGP_1_5.14087.14087.2	2	12.53	67.3	9.66E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)			1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
1629	JGP_1_5.14059.14169.3	3	12.28	70.1	5.27E+05	(K)GDVTIQVDGNLLATTDLSQYK(D)			751.0562	2251.145	0.0088	3.9	Zea mays	22426	polygalacturonase
1633	JGP_1_3.2507.2507.2	2	12.27	69.6	1.04E+06	(K)IHYENIK(M)		458.7494	916.489	0.0028	3.1	Zea mays	22424	polygalacturonase	
1723	JGP_1_4.3152.3299.2	2	12.04	73.3	9.10E+05	(K)DVTDINVK(D)		452.2425	903.478	-0.0005	-0.5	Zea mays	22426	polygalacturonase	
1832	JGP_1_5.2348.2443.3	3	11.73	78.5	4.18E+07	(K)IHYENIK(M)		306.1709	916.489	0.0095	10.3	Zea mays	22424	polygalacturonase	
1852	JGP_1_8.4336.4341.2	2	11.68	66.1	6.42E+05	(R)VDNLVITGK(G)		479.7829	958.557	0.0018	1.8	Zea mays	22426	polygalacturonase	
1864	JGP_1_5.14692.14692.2	2	11.63	64.9	7.29E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)			1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
1876	JGP_1_4.2332.2336.2	2	11.59	87.3	1.13E+07	(K)DVTFK(N)	305.1683	609.324	0.0051	8.3	Zea mays	22424	polygalacturonase	
1894	JGP_1_5.2071.2228.2	2	11.55	86.5	6.28E+06	(K)DVTFK(N)	305.1678	609.324	0.0041	6.7	Zea mays	22424	polygalacturonase	
1949	JGP_1_5.14514.14514.2	2	11.4	70.5	9.45E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)			1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
1955	JGP_1_4.4734.4734.3	3	11.38	62.5	1.11E+05	(K)VTCGPGHGISVGSLGR(Y)	C:Carbamidomethylation	518.6016	1553.785	0.005	3.2	Arabidopsis thaliana	2982583	polygalacturonase
1958	JGP_1_5.14570.14570.2	2	11.37	62.4	8.80E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)			1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
1972	JGP_1_5.12720.12720.3	3	11.33	73.4	8.58E+03	(K)GDVTIQVDGNLLATTDLSQYK(D)			751.0566	2251.145	0.01	4.4	Zea mays	22426	polygalacturonase
1994	JGP_1_5.13784.13874.3	3	11.25	72.2	1.59E+05	(K)GDVTIQVDGNLLATTDLSQYK(D)			751.0566	2251.145	0.01	4.4	Zea mays	22426	polygalacturonase
2059	JGP_1_4.2176.2306.2	2	11.09	87	2.40E+07	(K)DVTFK(N)	305.1681	609.324	0.0047	7.7	Zea mays	22424	polygalacturonase	
2065	JGP_1_1.2433.2513.3	3	11.08	74.2	5.26E+06	(K)IHYENIK(M)		306.1697	916.489	0.0059	6.4	Zea mays	22424	polygalacturonase	
2080	JGP_1_2.2207.2281.2	2	11.05	85.9	3.37E+06	(K)DVTFK(N)	305.1671	609.324	0.0027	4.4	Zea mays	22424	polygalacturonase	
2081	JGP_1_3.2191.2297.2	2	11.05	85.9	4.05E+06	(K)DVTFK(N)	305.1669	609.324	0.0023	3.7	Zea mays	22424	polygalacturonase	
2087	JGP_1_1.4589.4721.2	2	11.03	74.7	1.94E+06	(K)QTILIPK(G)		406.7673	812.524	0.0033	4.1	Zea mays	22426	polygalacturonase	
2119	JGP_1_4.4637.4722.2	2	10.95	77	3.81E+06	(K)QTILIPK(G)		406.7675	812.524	0.0037	4.6	Zea mays	22426	polygalacturonase	
2140	JGP_1_4.2391.2522.3	3	10.89	71.6	7.87E+06	(K)IHYENIK(M)		306.1701	916.489	0.0071	7.7	Zea mays	22424	polygalacturonase	
2154	JGP_1_5.4180.4187.2	2	10.86	66.3	5.40E+05	(K)DVTDINVK(D)		452.2443	903.478	0.0031	3.5	Zea mays	22426	polygalacturonase	
2169	JGP_1_5.4693.4781.2	2	10.82	79.5	1.82E+07	(K)QTILIPK(G)		406.7692	812.524	0.0071	8.7	Zea mays	22426	polygalacturonase	
2176	JGP_1_5.3174.3278.4	4	10.8	67.9	2.62E+07	(R)YKDEKDVTDINVK(D)		392.4594	1566.801	0.0148	9.4	Zea mays	22426	polygalacturonase	
2253	JGP_1_7.4288.4411.2	2	10.64	61.2	8.00E+05	(R)VDNLVITGK(G)		479.7815	958.557	-0.001	-1.1	Zea mays	22426	polygalacturonase	
2290	JGP_1_4.4802.4958.2	2	10.53	73	2.53E+06	(K)QTILIPK(G)		406.7678	812.524	0.0043	5.3	Zea mays	22426	polygalacturonase	
2291	JGP_1_3.4696.4827.2	2	10.52	79.3	1.23E+06	(K)QTILIPK(G)		406.768	812.524	0.0047	5.8	Zea mays	22426	polygalacturonase	
2296	JGP_1_5.3993.4101.2	2	10.51	75.6	1.63E+06	(K)DVTDINVK(D)		452.2442	903.478	0.0029	3.2	Zea mays	22426	polygalacturonase	
2320	JGP_1_5.14635.14635.2	2	10.46	66	7.81E+04	(K)GDVTIQVDGNLLATTDLSQYK(D)			1126.0767	2251.145	0.0009	0.4	Zea mays	22426	polygalacturonase
2351	JGP_1_4.4003.4102.2	2	10.4	60.1	6.84E+06	(R)VDNLVITGK(G)		479.7836	958.557	0.0032	3.3	Zea mays	22426	polygalacturonase	
2499	JGP_1_2.4401.4531.2	2	10.07	73.8	2.68E+06	(K)QTILIPK(G)		406.7681	812.524	0.0049	6	Zea mays	22426	polygalacturonase	
2503	JGP_1_5.4866.5024.2	2	10.06	74	1.30E+07	(K)QTILIPK(G)		406.7694	812.524	0.0075	9.2	Zea mays	22426	polygalacturonase	
1163	JGP_1_5.4528.4533.3	3	13.69	74.7	1.64E+06	(K)CGPGHGISVGSLGR(Y)	C:Carbamidomethylation	451.8976	1353.669	0.0091	6.7	Arabidopsis thaliana	2832691	polygalacturonase-like protein
1065	JGP_1_3.6307.6396.2	2	14.07	95.8	6.91E+06	(K)LVILLK(K)		349.765	698.518	0.0052	7.5	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
1420	JGP_1_1.6415.6430.2	2	12.91	85.5	1.68E+05	(K)LVILLK(K)		349.7631	698.518	0.0014	2.1	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
1462	JGP_1_7.6595.6678.2	2	12.78	86.4	5.18E+05	(K)LVILLK(K)		349.7634	698.518	0.002	2.9	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
1477	JGP_1_4.6530.6623.2	2	12.72	92.8	2.45E+06	(K)LVILLK(K)		349.7642	698.518	0.0036	5.2	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
1493	JGP_1_3.6476.6481.2	2	12.65	90.6	3.92E+06	(K)LVILLK(K)		349.765	698.518	0.0052	7.5	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
1504	JGP_1_8.6740.6814.2	2	12.63	89.6	3.00E+05	(K)LVILLK(K)		349.7634	698.518	0.002	2.9	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
1549	JGP_1_6.7026.7109.2	2	12.49	84.5	5.71E+05	(K)LVILLK(K)		349.7635	698.518	0.0022	3.2	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
1718	JGP_1_5.6664.6758.2	2	12.07	88.2	7.04E+05	(K)LVILLK(K)		349.7636	698.518	0.0024	3.5	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
1740	JGP_1_2.6063.6082.2	2	11.99	79.2	1.45E+05	(K)LVILLK(K)		349.7628	698.518	0.0008	1.2	Arabidopsis thaliana	15221225	"polynucleotidyl transferase, ribonuclease H-like protein"
862	JGP_1_8.4067.4073.2	2	14.93	86.8	7.12E+05	(R)TLADYNIQK(E)		533.284	1065.557	0.0032	3	Arabidopsis thaliana	30679302	polyubiquitin 14
1283	JGP_1_6.5885.5885.3	3	13.34	65.3	1.00E+05	(K)ESTLHLVLR(L)		356.5466	1067.621	0.0045	4.2	Arabidopsis thaliana	30679302	polyubiquitin 14
1886	JGP_1_8.5324.5329.3	3	11.57	65.8	4.29E+05	(K)ESTLHLVLR(L)		356.5472	1067.621	0.0063	5.9	Arabidopsis thaliana	30679302	polyubiquitin 14
2393	JGP_1_8.4169.4171.2	2	10.32	71.9	1.17E+06	(R)LIFAGK(Q)		324.7088	648.408	0.0024	3.7	Arabidopsis thaliana	30679302	polyubiquitin 14
2157	JGP_1_7.3583.3695.2	2	10.86	72.4	1.58E+06	(R)FGNVVSAR(V)		425.2341	849.458	0.0032	3.8	Glycine max	356520229	"PREDICTED: 28 kDa ribonucleoprotein, chloroplastic-like"
2479	JGP_1_8.3423.3531.2	2	10.12	77.8	1.03E+07	(R)FGNVVSAR(V)		425.2358	849.458	0.0066	7.8	Glycine max	356520229	"PREDICTED: 28 kDa ribonucleoprotein, chloroplastic-like"
2367	JGP_1_5.4553.4557.3	3	10.38	72.1	1.83E+05	(R)ERVPANLVQAQR(D)		460.929	1380.771	0.0018	1.3	Glycine max	356573789	"PREDICTED: 6-phosphogluconate dehydrogenase, decarboxylating-like isoform 1"
2234	JGP_1_1.2744.2889.2	2	10.68	72.2	1.16E+06	(K)IEVAGR(M)		322.6917	644.373	0.0035	5.5	Glycine max	356552270	PREDICTED: 70 kDa peptidyl-prolyl isomerase-like
551	JGP_1_5.4078.4167.2	2	16.5	85.1	5.14E+05	(R)IVGVSEETTTGVK(R)		660.3567	1319.705	0.0008	0.6	Glycine max	356540099	PREDICTED: adenosylhomocysteinase-like
2379	JGP_1_6.5550.5553.2	2	10.35	68.7	2.04E+05	(K)SIKPPLVR(K)		455.2984	909.588	0.0015	1.7	Glycine max	356495631	PREDICTED: armadillo repeat-containing kinesin-like protein 3-like
2495	JGP_1_8.7640.7724.2	2	10.08	64	1.43E+06	(R)VLGLGLFK(S)		423.7776	846.545	0.0032	3.7	Glycine max	356517680	PREDICTED: choline/ethanolamine kinase-like

1557	JGP_1_7.4152.4168.2	2	12.47	73	2.64E+05	(R)FHVEK(E)	330.1811	659.351	0.0038	5.7	Glycine max	356513667	PREDICTED: cyclin-dependent kinase G-2-like
1699	JGP_1_7.2894.2989.2	2	12.13	77.7	1.15E+06	(R)FHVEK(E)	330.1855	659.351	0.0126	19.1	Glycine max	356513667	PREDICTED: cyclin-dependent kinase G-2-like
2451	JGP_1_1.4217.4221.2	2	10.18	76.5	1.50E+05	(R)IAEIIR(G)		357.7297	714.451	0.0013	1.8	Glycine max	356548407 PREDICTED: F-box/kelch-repeat protein At1g22040-like
2264	JGP_1_8.9320.9324.2	2	10.63	74.7	9.44E+04	(K)LWQVPETLPEEVLGK(M)		869.4753	1737.942	0.0012	0.7	Glycine max	356543333 PREDICTED: flavoprotein wrbA-like
1433	JGP_1_6.4119.4232.2	2	12.87	89.3	4.89E+06	(K)IYNFR(E)	356.6947	712.378	0.0044	6.2	Glycine max	356505023	PREDICTED: glycinin G1
2410	JGP_1_4.6900.6968.2	2	10.27	77.5	2.80E+05	(R)LVSGQEIAVK(R)		522.31	1043.61	0.0032	3.1	Glycine max	356545219 PREDICTED: G-type lectin S-receptor-like serine/threonine-protein kinase At4g27290-like
2301	JGP_1_8.5104.5112.2	2	10.51	73.8	2.61E+05	(K)GTVEFLR(A)		411.231	821.452	0.0031	3.8	Glycine max	356539100 PREDICTED: interactor of constitutive active ROPs 3-like
852	JGP_1_4.3641.3746.2	2	14.96	93.6	6.60E+06	(K)LVPVPPK(V)		375.2513	749.492	0.0033	4.5	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
973	JGP_1_5.3491.3599.2	2	14.47	93.9	7.35E+06	(K)LVPVPPK(V)		375.2519	749.492	0.0045	6.1	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1028	JGP_1_4.3448.3546.2	2	14.2	93.3	4.14E+06	(K)LVPVPPK(V)		375.251	749.492	0.0027	3.7	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1034	JGP_1_3.3612.3711.2	2	14.18	92.2	3.91E+06	(K)LVPVPPK(V)		375.2509	749.492	0.0025	3.4	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1240	JGP_1_4.3837.3936.2	2	13.46	87.4	2.45E+06	(K)LVPVPPK(V)		375.2508	749.492	0.0023	3.1	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1280	JGP_1_5.3705.3806.2	2	13.35	90.1	7.22E+06	(K)LVPVPPK(V)		375.252	749.492	0.0047	6.3	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1290	JGP_1_3.3423.3526.2	2	13.32	90.1	2.94E+06	(K)LVPVPPK(V)		375.2508	749.492	0.0023	3.1	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1319	JGP_1_1.3451.3554.2	2	13.21	86.8	8.17E+05	(K)LVPVPPK(V)		375.2487	749.492	-0.0019	-2.5	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1359	JGP_1_6.4047.4152.2	2	13.08	84.5	1.48E+06	(K)LVPVPPK(V)		375.2449	749.492	-0.0095	-12.6	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1479	JGP_1_5.3895.4016.2	2	12.72	86.7	2.99E+06	(K)LVPVPPK(V)		375.2509	749.492	0.0025	3.4	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1487	JGP_1_3.3798.3887.2	2	12.68	85.9	1.33E+06	(K)LVPVPPK(V)		375.2508	749.492	0.0023	3.1	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1640	JGP_1_2.3471.3553.2	2	12.24	78.3	4.31E+05	(K)LVPVPPK(V)		375.2478	749.492	-0.0037	-4.9	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1954	JGP_1_3.3983.3989.2	2	11.38	76.5	3.75E+05	(K)LVPVPPK(V)		375.2506	749.492	0.0019	2.6	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
2016	JGP_1_4.4034.4059.2	2	11.19	78.9	5.44E+05	(K)LVPVPPK(V)		375.2507	749.492	0.0021	2.9	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
2113	JGP_1_6.3847.3952.2	2	10.97	80.2	1.19E+06	(K)LVPVPPK(V)		375.25	749.492	0.0007	1	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
2181	JGP_1_2.3308.3391.2	2	10.78	78.3	3.91E+05	(K)LVPVPPK(V)		375.249	749.492	-0.0013	-1.7	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
2205	JGP_1_1.3680.3794.2	2	10.74	76.6	5.07E+05	(K)LVPVPPK(V)		375.2484	749.492	-0.0025	-3.3	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
2274	JGP_1_5.4110.4220.2	2	10.59	75.9	7.85E+05	(K)LVPVPPK(V)		375.2505	749.492	0.0017	2.3	Glycine max	356558077 PREDICTED: LOW QUALITY PROTEIN: reticuline oxidase-like protein-like
1580	JGP_1_4.6440.6523.2	2	12.42	68.6	3.68E+06	(K)DRAYGSKDILGMR(S)		741.3782	1481.753	-0.0038	-2.6	Glycine max	356496533 PREDICTED: monosaccharide-sensing protein 3-like
1678	JGP_1_5.6604.6697.2	2	12.18	66.1	4.14E+06	(K)DRAYGSKDILGMR(S)		741.3774	1481.753	-0.0054	-3.6	Glycine max	356496533 PREDICTED: monosaccharide-sensing protein 3-like
1918	JGP_1_3.6219.6296.2	2	11.46	63.7	2.63E+06	(K)DRAYGSKDILGMR(S)		741.3765	1481.753	-0.0072	-4.9	Glycine max	356496533 PREDICTED: monosaccharide-sensing protein 3-like
971	JGP_1_5.10594.10599.3	3	14.48	75.5	1.69E+04	(K)LLINNVEELLPVVYTPTVGEACQK(Y)		C:Carbamidomethylation	900.4912	2699.432	0.0266	9.9	Glycine max 356515635 PREDICTED: NADP-dependent malic enzyme-like
2033	JGP_1_4.3178.3189.2	2	11.15	72.3	1.36E+05	(R)VLIRGPQSK(A)		499.305	997.615	-0.0126	-12.6	Glycine max	356533509 PREDICTED: paladin-like
854	JGP_1_6.8983.8986.3	3	14.96	79.4	1.98E+05	(K)TVPASSIPDGWmGLDIGPDSIK(T)		m:Oxidized methionine	758.0495	2256.122	16.0123	7.6	Glycine max 356525744 "PREDICTED: phosphoglycerate kinase, cytosolic-like"
2020	JGP_1_2.3158.3277.2	2	11.18	75.2	4.76E+05	(K)FLSVAK(I)		332.7036	664.403	-0.0029	-4.4	Glycine max	356529344 PREDICTED: probable aminotransferase ACS12-like
2128	JGP_1_4.5987.6079.2	2	10.92	71.7	2.41E+06	(R)VAAVLSIPR(V)		463.2977	925.583	0.0052	5.6	Glycine max	356550364 PREDICTED: probable E3 ubiquitin-protein ligase ARI7-like
2420	JGP_1_5.5988.6122.2	2	10.25	60.9	4.44E+06	(R)VAAVLSIPR(V)		463.2985	925.583	0.0068	7.3	Glycine max	356550364 PREDICTED: probable E3 ubiquitin-protein ligase ARI7-like
2334	JGP_1_8.3192.3198.2	2	10.43	69.7	5.32E+05	(K)FTTEKSPLGEK(H)		618.8285	1236.647	0.0027	2.2	Glycine max	356557921 PREDICTED: probable F-box protein At4g22030-like
2055	JGP_1_5.8924.8990.2	2	11.11	86.5	2.71E+05	(K)IVIPRSSTKTPTLER(K)		849.4985	1697.991	-0.0011	-0.7	Glycine max	356525726 PREDICTED: probable GMP synthase [glutamine-hydrolyzing]-like
2358	JGP_1_3.5913.5999.2	2	10.39	77	2.39E+05	(R)LEVLDLSR(N)		472.7748	944.541	0.0012	1.3	Glycine max	356498764 PREDICTED: probable LRR receptor-like serine/threonine-protein kinase At2g24230-like
1355	JGP_1_6.2684.2689.2	2	13.09	77.2	8.23E+05	(K)IAELTAK(V)		373.2273	745.445	0.0019	2.5	Glycine max	356520513 PREDICTED: protein CASP-like
2141	JGP_1_4.3602.3606.2	2	10.89	73.6	4.40E+05	(R)LGDAELDELK(R)		551.7802	1102.563	-0.0095	-8.6	Glycine max	356543582 PREDICTED: protein HIRA-like
2142	JGP_1_5.1409.1483.2	2	10.89	73.9	2.45E+05	(K)IEETNGK(L)		395.6977	790.394	-0.006	-7.6	Glycine max	356522331 PREDICTED: protein TIF31 homolog
2468	JGP_1_2.5949.5964.2	2	10.15	66.2	1.95E+05	(K)FALDVAVK(T)		431.757	862.503	0.0034	4	Glycine max	356507019 PREDICTED: puromycin-sensitive aminopeptidase-like
2152	JGP_1_3.7601.7603.5	5	10.86	64.6	6.83E+05	(R)TVISWNAMLVGYSKHGEGREVLELFNLmIDENK(V)		m:Oxidized methionine	762.5758	3792.909	15.9411	-14.1	Glycine max 356498444 "PREDICTED: putative pentatricopeptide repeat-containing protein At3g13770, mitochondrial-like"
1964	JGP_1_2.6838.6913.4	4	11.34	73.3	5.88E+05	(R)LLVYDYmENGSLAQNLDSSSNVLDWSK(R)		m:Oxidized methionine	770.1173	3061.446	16.0015	2.1	Glycine max 356523097 PREDICTED: putative receptor protein kinase ZmPK1-like
1913	JGP_1_8.4459.4562.3	3	11.5	69	3.49E+06	(R)LSALCLMQK(F)		C:Carbamidomethylation	355.1945	1063.564	0.0051	4.8	Glycine max 356534382 PREDICTED: putative transcription elongation factor SPT5 homolog 2-like
601	JGP_1_5.3827.3920.2	2	16.19	94.3	4.44E+06	(K)IYAESLAR(F)		461.7561	922.499	0.0057	6.1	Glycine max	356521229 PREDICTED: rab GDP dissociation inhibitor alpha-like
1783	JGP_1_4.3834.3938.2	2	11.86	74	6.96E+05	(K)IYAESLAR(F)		461.7544	922.499	0.0023	2.5	Glycine max	356521229 PREDICTED: rab GDP dissociation inhibitor alpha-like
1784	JGP_1_5.6423.6427.2	2	11.86	67.3	2.85E+05	(K)LNILEVTGK(A)		493.8003	986.588	0.0053	5.3	Glycine max	356507844 PREDICTED: ribonuclease H2 subunit B-like

1124	JGP_1_4.3588.3696.2	2	13.85	80.1	2.09E+06	(K)LQELQLK(T)		436.2676	871.525	0.0032	3.6	Glycine max	356519367	PREDICTED: RNA-dependent RNA polymerase 1-like			
1335	JGP_1_3.3544.3636.2	2	13.16	81.4	4.27E+06	(K)LQELQLK(T)		436.268	871.525	0.004	4.6	Glycine max	356519367	PREDICTED: RNA-dependent RNA polymerase 1-like			
1684	JGP_1_3.3099.3176.2	2	12.16	81.5	1.28E+06	(R)IQVNEIK(G)		422.2516	843.493	0.0025	2.9	Glycine max	356503073	PREDICTED: serine/threonine-protein kinase OXI1-like			
2060	JGP_1_4.3134.3154.2	2	11.09	74.6	5.21E+05	(R)IQVNEIK(G)		422.251	843.493	0.0013	1.5	Glycine max	356503073	PREDICTED: serine/threonine-protein kinase OXI1-like			
2066	JGP_1_1.3044.3138.2	2	11.08	79.5	1.87E+06	(R)IQVNEIK(G)		422.2512	843.493	0.0017	2	Glycine max	356503073	PREDICTED: serine/threonine-protein kinase OXI1-like			
2199	JGP_1_6.3374.3483.2	2	10.76	77.3	2.43E+06	(R)IQVNEIK(G)		422.2524	843.493	0.0041	4.8	Glycine max	356503073	PREDICTED: serine/threonine-protein kinase OXI1-like			
2463	JGP_1_7.3340.3345.2	2	10.16	65.2	6.47E+05	(R)IQVNEIK(G)		422.2517	843.493	0.0027	3.2	Glycine max	356503073	PREDICTED: serine/threonine-protein kinase OXI1-like			
1980	JGP_1_3.4844.4923.3	3	11.29	70.6	3.85E+05	(K)TLHPNWSPAAIK(S)		445.5813	1334.722	0.0078	5.8	Glycine max	356566983	PREDICTED: subtilisin-like protease-like			
2423	JGP_1_3.2108.2197.2	2	10.24	71.1	2.37E+05	(K)SLQVEDAK(V)		445.2361	889.462	0.0024	2.7	Glycine max	356541541	PREDICTED: U-box domain-containing protein 43-like			
2026	JGP_1_7.7583.7671.2	2	11.17	69.4	6.60E+05	(R)LVQVLFK(D)		423.7773	846.545	0.0026	3	Glycine max	356552569	"PREDICTED: uncharacterized aarF domain-containing protein kinase At4g31390, chloroplastic-like"			
1597	JGP_1_5.1380.1458.2	2	12.37	70.1	2.35E+06	(K)LGmEAVK(V)	m:Oxidized methionine	382.2059	747.407	15.9976	3.5	Glycine max	356502900	PREDICTED: uncharacterized protein C24B11.05-like			
2315	JGP_1_5.2928.2935.2	2	10.47	79	9.83E+05	(K)LGMEAVK(V)		374.2083	747.407	0.0024	3.2	Glycine max	356502900	PREDICTED: uncharacterized protein C24B11.05-like			
1346	JGP_1_4.4422.4522.2	2	13.11	84.6	1.24E+07	(R)LSIASIPR(F)		428.7694	856.525	0.0064	7.5	Glycine max	356532972	PREDICTED: uncharacterized protein LOC100779146			
1443	JGP_1_1.4249.4399.2	2	12.84	84	1.36E+07	(R)LSIASIPR(F)		428.7688	856.525	0.0052	6.1	Glycine max	356532972	PREDICTED: uncharacterized protein LOC100779146			
1512	JGP_1_3.4411.4502.2	2	12.6	84.5	1.44E+07	(R)LSIASIPR(F)		428.7695	856.525	0.0066	7.8	Glycine max	356532972	PREDICTED: uncharacterized protein LOC100779146			
1713	JGP_1_2.4136.4216.2	2	12.08	83.6	1.45E+07	(R)LSIASIPR(F)		428.7693	856.525	0.0062	7.3	Glycine max	356532972	PREDICTED: uncharacterized protein LOC100779146			
1724	JGP_1_5.4433.4531.2	2	12.04	82.6	8.24E+06	(R)LSIASIPR(F)		428.7683	856.525	0.0042	5	Glycine max	356532972	PREDICTED: uncharacterized protein LOC100779146			
2282	JGP_1_6.4772.4872.2	2	10.57	82.7	1.00E+07	(R)LSIASIPR(F)		428.769	856.525	0.0056	6.6	Glycine max	356532972	PREDICTED: uncharacterized protein LOC100779146			
2413	JGP_1_8.4492.4607.2	2	10.27	80.2	3.99E+06	(R)LSIASIPR(F)		428.7686	856.525	0.0048	5.7	Glycine max	356532972	PREDICTED: uncharacterized protein LOC100779146			
1294	JGP_1_6.6808.6808.2	2	13.31	82.2	3.51E+06	(K)AVGDWFYDR(R)		564.7622	1128.511	0.0062	5.5	Glycine max	356559067	PREDICTED: uncharacterized protein LOC100781246			
2268	JGP_1_8.4334.4339.2	2	10.62	74.6	1.21E+05	(R)IGGVEGDQIVR(R)		571.8037	1142.616	-0.0163	-14.3	Glycine max	356554697	PREDICTED: uncharacterized protein LOC100782858			
1861	JGP_1_8.7372.7464.2	2	11.65	71.4	6.03E+06	(R)LGPFGLFLK(E)		496.2969	991.597	-0.011	-11.1	Glycine max	356502428	PREDICTED: uncharacterized protein LOC100786283			
1866	JGP_1_7.7271.7348.2	2	11.63	70.5	3.34E+06	(R)LGPFGLFLK(E)		496.2977	991.597	-0.0094	-9.5	Glycine max	356502428	PREDICTED: uncharacterized protein LOC100786283			
2470	JGP_1_4.7552.7581.3	3	10.14	68.1	2.60E+05	(K)LEPIFSPVSLEDMSYmK(Q)	m:Oxidized methionine	667.9886	1985.96	15.9914	-1.8	Glycine max	356534402	PREDICTED: uncharacterized protein LOC100793513			
2428	JGP_1_2.2728.2827.2	2	10.23	76.8	3.76E+05	(K)IDLAGR(M)		322.6928	644.373	0.0057	8.9	Glycine max	356573400	"PREDICTED: uncharacterized protein LOC100796021, partial"			
2123	JGP_1_2.3683.3766.2	2	10.93	69.8	6.80E+05	(R)LLICIADGSDSNK(L)	C:Carbamidomethylation	703.3547	1405.699	0.003	2.1	Glycine max	356500376	PREDICTED: uncharacterized protein LOC100796864			
2509	JGP_1_5.2656.2763.2	2	10.05	76.4	8.20E+06	(K)DAAISELNQK(L)		544.7731	1088.558	-0.0193	-17.7	Glycine max	356507578	PREDICTED: uncharacterized protein LOC100807704			
1306	JGP_1_8.4512.4517.2	2	13.26	67.4	3.01E+05	(K)SCIILR(C)	C:Carbamidomethylation	381.2212	761.434	0.0013	1.7	Glycine max	356568232	PREDICTED: uncharacterized protein LOC100809661			
919	JGP_1_8.2971.3074.2	2	14.7	87.7	8.89E+05	(R)SFGLSK(K)		319.6803	638.351	0.0025	3.9	Glycine max	356507300	PREDICTED: uncharacterized protein LOC100813790			
1258	JGP_1_1.2996.3085.2	2	13.4	83.7	5.83E+05	(R)SFGLSK(K)		319.6798	638.351	0.0015	2.4	Glycine max	356507300	PREDICTED: uncharacterized protein LOC100813790			
1289	JGP_1_2.2957.3037.2	2	13.32	82.5	3.96E+05	(R)SFGLSK(K)		319.6801	638.351	0.0021	3.3	Glycine max	356507300	PREDICTED: uncharacterized protein LOC100813790			
1386	JGP_1_6.3214.3313.2	2	12.99	78.4	9.69E+05	(R)SFGLSK(K)		319.6798	638.351	0.0015	2.4	Glycine max	356507300	PREDICTED: uncharacterized protein LOC100813790			
1526	JGP_1_5.3019.3123.2	2	12.55	87.5	5.76E+06	(R)SFGLSK(K)		319.6808	638.351	0.0035	5.5	Glycine max	356507300	PREDICTED: uncharacterized protein LOC100813790			
2077	JGP_1_4.3053.3164.2	2	11.06	82.4	5.08E+05	(R)SFGLSK(K)		319.68	638.351	0.0019	3	Glycine max	356507300	PREDICTED: uncharacterized protein LOC100813790			
2150	JGP_1_4.2244.2343.2	2	10.87	79.5	3.48E+05	(K)LFAEQK(E)		368.2068	735.404	0.0028	3.7	Glycine max	356564668	PREDICTED: uncharacterized protein LOC100817801			
2402	JGP_1_8.4244.4364.2	2	10.3	85	7.42E+05	(K)IIEPLK(E)		356.7346	712.46	0.0016	2.2	Glycine max	356528879	PREDICTED: uncharacterized protein LOC100820110			
2449	JGP_1_7.4268.4373.2	2	10.19	81.5	7.72E+05	(K)IIEPLK(E)		356.734	712.46	0.0004	0.5	Glycine max	356528879	PREDICTED: uncharacterized protein LOC100820110			
2061	JGP_1_4.5340.5348.2	2	11.09	69.4	2.77E+05	(R)HALmAFAEEWK(N)	m:Oxidized methionine	674.8128	1332.641	15.9778	-12.7	Glycine max	356519100	PREDICTED: zinc finger Ran-binding domain-containing protein 3-like			
2506	JGP_1_7.3292.3297.2	2	10.06	65.8	7.85E+05	(R)YAFPIK(C)		369.7074	738.418	-0.011	-14.8	Arabidopsis thaliana	25293277	probable glutaminyl-tRNA synthetase (glnrs) [imported]			
6	JGP_1_8.8195.8201.3	3	23.78	97.2	3.12E+05	(K)KTGQALVIGIYDEPMTPGQCNMVVER(L)	C:Carbamidomethylation	969.4831	2906.421	0.0139	4.8	Zea mays	162461525	profilin-3			
117	JGP_1_8.8722.8796.3	3	20.32	98	4.18E+05	(K)TGQALVIGIYDEPMTPGQCNMVVER(L)	C:Carbamidomethylation	926.7862	2778.326	0.0181	6.5	Zea mays	162461525	profilin-3			
265	JGP_1_8.7010.7015.3	3	18.41	86.5	5.80E+05	(K)KTGQALVIGIYDEPmTPGQCNmVVER(L)	C:Carbamidomethylation	m:Oxidized methionine	980.1458	2906.421	32.002	4.1	Zea mays	162461525	profilin-3		
304	JGP_1_8.7507.7520.3	3	18.05	84.2	3.70E+05	(K)KTGQALVIGIYDEPmTPGQCNMVVER(L)	C:Carbamidomethylation	m:Oxidized methionine	974.8146	2906.421	16.0084	4.6	Zea mays	162461525	profilin-3		
348	JGP_1_8.6591.6678.2	2	17.82	90.6	9.20E+06	(K)YMVIQGEPGAVIR(G)		716.8899	1432.762	0.0108	7.6	Zea mays	162461525	profilin-3			
392	JGP_1_7.6434.6523.2	2	17.47	88.4	9.45E+05	(K)YMVIQGEPGAVIR(G)		716.8877	1432.762	0.0064	4.5	Zea mays	162461525	profilin-3			
523	JGP_1_8.8172.8239.3	3	16.66	84.3	7.44E+05	(K)TGQALVIGIYDEPmTPGQCNMVVER(L)	C:Carbamidomethylation	m:Oxidized methionine	932.1164	2778.326	16.0087	4.9	Zea mays	162461525	profilin-3		
539	JGP_1_6.6705.6721.2	2	16.56	86.8	3.51E+05	(K)YMVIQGEPGAVIR(G)		716.8863	1432.762	0.0036	2.5	Zea mays	162461525	profilin-3			
626	JGP_1_8.6620.6704.3	3	16.12	85.7	1.38E+06	(K)YMVIQGEPGAVIR(G)		478.2612	1432.762	0.0074	5.1	Zea mays	162461525	profilin-3			

821	JGP_1_2.6369.6506.2	2	15.07	86.9	1.59E+06	(R)LGDYLVEQGL(-)		553.7926	1106.573	0.0051	4.6	Zea mays	162461525	profilin-3				
884	JGP_1_8.8307.8309.3	3	14.87	77.6	1.25E+05	(K)TGQALVIGIYDEPMTPGQCNmVVER(L)	C:Carbamidomethylation	m:Oxidized methionine	932.1166	2778.326	16.0093	5.2	Zea mays	162461525	profilin-3			
921	JGP_1_8.5893.6009.2	2	14.69	71.3	7.49E+06	(K)YmVIQGEPGAVIR(G)	m:Oxidized methionine		724.8873	1432.762	16.0056	7.4	Zea mays	162461525	profilin-3			
1033	JGP_1_8.1320.1481.2	2	14.19	74	9.80E+06	(K)GSGGITVK(K)			359.7104	718.409	0.0041	5.8	Zea mays	162461525	profilin-3			
1049	JGP_1_2.1637.1734.2	2	14.13	74.5	8.48E+05	(K)GSGGITVK(K)			359.7091	718.409	0.0015	2.1	Zea mays	162461525	profilin-3			
1080	JGP_1_8.7564.7575.2	2	14.01	87	4.15E+05	(K)TGQALVIGIYDEPmTPGQCNmVVER(L)	C:Carbamidomethylation	m:Oxidized methionine	1405.6672	2778.326	32.0012	4	Zea mays	162461525	profilin-3			
1087	JGP_1_1.6769.6848.2	2	13.99	89.1	2.57E+06	(R)LGDYLVEQGL(-)		553.7925	1106.573	0.0049	4.4	Zea mays	162461525	profilin-3				
1125	JGP_1_4.6173.6269.2	2	13.85	80.4	4.75E+05	(K)YMVIQGEPGAVIR(G)		716.8874	1432.762	0.0058	4.1	Zea mays	162461525	profilin-3				
1145	JGP_1_5.6372.6379.2	2	13.76	82.5	3.66E+05	(K)YMVIQGEPGAVIR(G)		716.8867	1432.762	0.0044	3.1	Zea mays	162461525	profilin-3				
1324	JGP_1_3.6766.6841.2	2	13.19	87.7	1.87E+06	(R)LGDYLVEQGL(-)		553.7932	1106.573	0.0063	5.7	Zea mays	162461525	profilin-3				
1372	JGP_1_8.5870.5988.3	3	13.03	76.9	1.90E+06	(K)YmVIQGEPGAVIR(G)	m:Oxidized methionine		483.5932	1432.762	16.0034	5.8	Zea mays	162461525	profilin-3			
1469	JGP_1_7.7619.7698.2	2	12.75	82	7.99E+05	(R)LGDYLVEQGL(-)		553.7915	1106.573	0.0029	2.6	Zea mays	162461525	profilin-3				
1486	JGP_1_8.8192.8294.2	2	12.7	83.6	6.73E+04	(K)TGQALVIGIYDEPMTPGQCNmVVER(L)	C:Carbamidomethylation	m:Oxidized methionine	1397.6656	2778.326	15.998	1.1	Zea mays	162461525	profilin-3			
1566	JGP_1_8.7631.7719.2	2	12.45	78.1	4.75E+06	(R)LGDYLVEQGL(-)		553.7928	1106.573	0.0055	5	Zea mays	162461525	profilin-3				
1608	JGP_1_7.1507.1639.2	2	12.35	70.5	3.77E+06	(K)GSGGITVK(K)		359.7095	718.409	0.0023	3.3	Zea mays	162461525	profilin-3				
1721	JGP_1_8.6754.6839.2	2	12.06	73.6	1.07E+05	(K)YMVIQGEPGAVIR(G)		716.8906	1432.762	0.0122	8.5	Zea mays	162461525	profilin-3				
1979	JGP_1_8.8737.8746.2	2	11.3	79.2	2.57E+05	(K)TGQALVIGIYDEPMTPGQCNMVVER(L)	C:Carbamidomethylation		1389.6688	2778.326	0.0044	1.6	Zea mays	162461525	profilin-3			
2179	JGP_1_2.5644.5657.2	2	10.79	77.1	1.72E+05	(K)YMVIQGEPGAVIR(G)		716.8859	1432.762	0.0028	2	Zea mays	162461525	profilin-3				
2220	JGP_1_1.1609.1678.2	2	10.71	66.6	1.14E+06	(K)GSGGITVK(K)		359.7091	718.409	0.0015	2.1	Zea mays	162461525	profilin-3				
2295	JGP_1_3.5974.6053.2	2	10.51	70.4	2.71E+05	(K)YMVIQGEPGAVIR(G)		716.8858	1432.762	0.0026	1.8	Zea mays	162461525	profilin-3				
2318	JGP_1_4.1631.1706.2	2	10.46	65.9	1.27E+06	(K)GSGGITVK(K)		359.709	718.409	0.0013	1.9	Zea mays	162461525	profilin-3				
2355	JGP_1_8.8197.8197.2	2	10.4	74.4	1.94E+05	(K)TGQALVIGIYDEPmTPGQCNMVVER(L)	C:Carbamidomethylation	m:Oxidized methionine	1397.6666	2778.326	16	1.8	Zea mays	162461525	profilin-3			
2432	JGP_1_6.7686.7772.2	2	10.23	66.3	7.23E+05	(R)LGDYLVEQGL(-)		553.7932	1106.573	0.0063	5.7	Zea mays	162461525	profilin-3				
1775	JGP_1_5.4906.5007.2	2	11.9	75.4	5.66E+05	(K)VVRVDLK(E)		414.7649	828.53	-0.0076	-9.2	Arabidopsis thaliana	15217929	prolyl oligopeptidase-like protein				
2108	JGP_1_2.4416.4486.2	2	10.98	68.8	1.04E+06	(K)VVRVDLK(E)		414.7612	828.53	-0.015	-18.2	Arabidopsis thaliana	15217929	prolyl oligopeptidase-like protein				
2192	JGP_1_6.5085.5182.2	2	10.77	77.8	3.03E+06	(K)VVRVDLK(E)		414.7649	828.53	-0.0076	-9.2	Arabidopsis thaliana	15217929	prolyl oligopeptidase-like protein				
2427	JGP_1_1.4564.4644.2	2	10.23	69.2	3.05E+06	(K)VVRVDLK(E)		414.7642	828.53	-0.009	-10.9	Arabidopsis thaliana	15217929	prolyl oligopeptidase-like protein				
1466	JGP_1_6.8918.8926.2	2	12.77	67.4	5.27E+04	(K)YGVSGYPTIQWFPK(G)		821.9214	1642.826	0.0091	5.6	Arabidopsis thaliana	15226610	protein disulfide-isomerase A6				
2344	JGP_1_2.2657.2724.2	2	10.41	71.7	6.52E+04	(K)LGASFK(K)		311.6827	622.356	0.0022	3.6	Arabidopsis thaliana	15226610	protein disulfide-isomerase A6				
1308	JGP_1_3.6508.6524.2	2	13.24	74	1.76E+05	(K)NQVAmNPINTVFDAK(R)	m:Oxidized methionine		839.4197	1661.832	16.0006	3.4	Arabidopsis thaliana	15232682	protein heat shock protein 70-3			
1872	JGP_1_8.2326.2330.2	2	11.61	83.9	1.93E+06	(R)TTILAK(Y)		323.7119	646.413	0.0031	4.8	Glycine max	351727631	protein kinase				
1879	JGP_1_7.2312.2419.2	2	11.59	79.7	3.68E+06	(R)TTILAK(Y)		323.7115	646.413	0.0023	3.6	Glycine max	351727631	protein kinase				
2039	JGP_1_5.3927.3931.2	2	11.14	60.8	5.75E+05	(R)SGSRDSEVSK(E)		526.2585	1051.501	0.0083	7.9	Arabidopsis thaliana	42563202	protein kinase domain-containing protein				
2313	JGP_1_1.8526.8532.2	2	10.47	73.9	6.27E+03	(K)LVLPITGGSSSEPANKK(Q)		849.4864	1697.943	0.0223	13.1	Zea mays	18568275	prpol				
1627	JGP_1_3.6164.6174.2	2	12.28	82.5	1.88E+05	(K)NAVVTVPAYFNDSQR(Q)		840.9226	1680.834	0.0039	2.3	Pisum sativum	562006	PsHSP71.2				
1649	JGP_1_4.3509.3538.3	3	12.23	62.2	1.25E+05	(K)ATAGDTHLGGEDFDNR(M)		559.2556	1675.731	0.0216	12.9	Pisum sativum	562006	PsHSP71.2				
1716	JGP_1_3.3471.3504.3	3	12.07	63.4	3.14E+05	(K)ATAGDTHLGGEDFDNR(M)		559.2565	1675.731	0.0243	14.5	Pisum sativum	562006	PsHSP71.2				
1803	JGP_1_3.2176.2253.2	2	11.81	63.9	3.57E+05	(K)ITITNDK(G)		402.7271	804.446	0.0008	0.9	Pisum sativum	562006	PsHSP71.2				
1981	JGP_1_3.6189.6192.3	3	11.29	65.9	7.28E+04	(K)NAVVTVPAYFNDSQR(Q)		560.9559	1680.834	0.0191	11.4	Pisum sativum	562006	PsHSP71.2				
2052	JGP_1_3.1857.1863.2	2	11.11	79.1	2.44E+05	(R)LIGDAAK(N)		344.206	687.404	0.0012	1.7	Pisum sativum	562006	PsHSP71.2				
2311	JGP_1_4.1753.1753.2	2	10.48	77.1	1.45E+05	(R)LIGDAAK(N)		344.2039	687.404	-0.003	-4.4	Pisum sativum	562006	PsHSP71.2				
1694	JGP_1_7.4732.4838.2	2	12.14	80.5	3.19E+06	(K)LIAEWK(T)		380.2252	759.44	0.0032	4.2	Triticum aestivum	40644788	putative anther endoxylanase				
1925	JGP_1_8.4663.4762.2	2	11.46	83	8.36E+05	(K)LIAEWK(T)		380.2246	759.44	0.002	2.6	Triticum aestivum	40644788	putative anther endoxylanase				
798	JGP_1_4.6105.6192.2	2	15.19	83.7	1.14E+06	(R)FSISWSR(I)		441.7287	882.447	0.0033	3.7	Arabidopsis thaliana	26450684	putative beta-glucosidase				
1960	JGP_1_7.5598.5695.2	2	11.36	69.3	6.68E+05	(K)YWIVK(N)	354.7092	708.408	0.0032	4.5	Arabidopsis thaliana	18423124	putative cysteine proteinase					
1154	JGP_1_6.6396.6535.2	2	13.72	83.9	5.50E+06	(R)LLFAIAEK(G)		452.7821	904.55	0.0067	7.4	Arabidopsis thaliana	15227209	putative F-box protein				
1739	JGP_1_7.6100.6192.2	2	12	84.2	1.89E+06	(R)LLFAIAEK(G)		452.7799	904.55	0.0023	2.5	Arabidopsis thaliana	15227209	putative F-box protein				
1743	JGP_1_1.5799.5884.2	2	11.98	73.4	2.71E+05	(R)LLFAIAEK(G)		452.779	904.55	0.0005	0.5	Arabidopsis thaliana	15227209	putative F-box protein				
1818	JGP_1_2.5492.5573.2	2	11.75	78.7	3.79E+05	(R)LLFAIAEK(G)		452.7792	904.55	0.0009	1	Arabidopsis thaliana	15227209	putative F-box protein				
1937	JGP_1_3.5809.5896.2	2	11.42	82	2.97E+05	(R)LLFAIAEK(G)		452.7804	904.55	0.0033	3.6	Arabidopsis thaliana	15227209	putative F-box protein				
1968	JGP_1_8.6251.6334.2	2	11.34	74.3	5.49E+05	(R)LLFAIAEK(G)		452.7802	904.55	0.0029	3.2	Arabidopsis thaliana	15227209	putative F-box protein				
2421	JGP_1_5.6123.6209.2	2	10.25	70.5	2.58E+05	(R)LLFAIAEK(G)		452.7796	904.55	0.0017	1.9	Arabidopsis thaliana	15227209	putative F-box protein				
1467	JGP_1_4.4628.4770.2	2	12.75	77.2	1.64E+06	(K)LPCSQLSCIEK(G)	C:Carbamidomethylation		667.8289	1334.644	0.0062	4.7	Arabidopsis thaliana	334185830	putative F-box/FBD/LRR-repeat protein			
1788	JGP_1_4.4837.4842.2	2	11.85	76.7	1.78E+06	(K)LPCSQLSCIEK(G)	C:Carbamidomethylation		667.83	1334.644	0.0084	6.3	Arabidopsis thaliana	334185830	putative F-box/FBD/LRR-repeat protein			
1920	JGP_1_5.4984.4986.2	2	11.46	74.3	7.17E+05	(K)LPCSQLSCIEK(G)	C:Carbamidomethylation		667.834	1334.644	0.0164	12.3	Arabidopsis thaliana	334185830	putative F-box/FBD/LRR-repeat protein			
1772	JGP_1_8.2421.2520.2	2	11.91	80.2	1.20E+06	(R)NITVNEAQSR(G)		566.2936	1131.575	0.0046	4.1	Solanum tuberosum	82623423	putative glycine-rich RNA binding protein-like				
2003	JGP_1_1.2396.2399.2	2	11.22	74.2	2.06E+05	(R)NITVNEAQSR(G)		566.2922	1131.575	0.0018	1.6	Solanum tuberosum	82623423	putative glycine-rich RNA binding protein-like				
2337	JGP_1_5.1253.1388.2	2	10.42	60.5	1.77E+06	(R)ASVWENFK(N)		490.7413	980.484	-0.0083	-8.4	Triticum aestivum	150246869	putative glycosyltransferase family 47				
446	JGP_1_6.9697.9765.2	2	17.2	84.2	1.23E+06	(K)VAILGAAGGIGQPLSLLmK(L)	m:Oxidized methionine		913.0395	1809.067	16.0051	5.6	Solanum tuberosum	21388550	putative mitochondrial NAD-dependent malate dehydrogenase			
786	JGP_1_6.10566.10635.2	2	15.25	83.7	6.88E+05	(K)VAILGAAGGIGQPLSLLMK(L)			905.0388	1809.067	0.0037	2	Solanum tuberosum	21388550	putative mitochondrial NAD-dependent malate dehydrogenase			

812	JGP_1_6.10552.10641.2	2	15.13	74.6	6.88E+05	(K)VAILGAAGGIGQPLSLLMK(L)		905.0388	1809.067	0.0037	2	Solanum tuberosum	21388550	putative mitochondrial NAD-dependent malate dehydrogenase
1690	JGP_1_6.9693.9766.3	3	12.15	70.8	1.19E+06	(K)VAILGAAGGIGQPLSLLmK(L)	m:Oxidized methionine	609.0291	1809.067	16.0061	6.1	Solanum tuberosum	21388550	putative mitochondrial NAD-dependent malate dehydrogenase
1923	JGP_1_6.9172.9237.3	3	11.46	74	2.51E+05	(R)KVAILGAAGGIGQPLSLLmK(L)	m:Oxidized methionine	651.7228	1937.162	15.9922	-1.4	Solanum tuberosum	21388550	putative mitochondrial NAD-dependent malate dehydrogenase
2131	JGP_1_6.10583.10587.3	3	10.91	67	2.23E+05	(K)VAILGAAGGIGQPLSLLMK(L)		603.6958	1809.067	0.0062	3.4	Solanum tuberosum	21388550	putative mitochondrial NAD-dependent malate dehydrogenase
1109	JGP_1_6.5982.6073.2	2	13.92	89.3	2.11E+06	(R)FVIYVK(A)	384.7375	768.465	0.0023	3	Arabidopsis thaliana	15238729	Putative pectinesterase/pectinesterase inhibitor 61	
1318	JGP_1_1.5378.5471.2	2	13.22	78.6	1.20E+06	(R)FVIYVK(A)	384.7378	768.465	0.0029	3.8	Arabidopsis thaliana	15238729	Putative pectinesterase/pectinesterase inhibitor 61	
1451	JGP_1_8.5573.5664.2	2	12.81	84.6	2.72E+05	(R)FVIYVK(A)	384.7369	768.465	0.0011	1.4	Arabidopsis thaliana	15238729	Putative pectinesterase/pectinesterase inhibitor 61	
1471	JGP_1_6.6148.6153.2	2	12.74	85.4	1.25E+06	(R)FVIYVK(A)	384.7377	768.465	0.0027	3.5	Arabidopsis thaliana	15238729	Putative pectinesterase/pectinesterase inhibitor 61	
1499	JGP_1_7.5725.5728.2	2	12.64	79.1	6.82E+05	(R)FVIYVK(A)	384.7378	768.465	0.0029	3.8	Arabidopsis thaliana	15238729	Putative pectinesterase/pectinesterase inhibitor 61	
1946	JGP_1_1.5551.5558.2	2	11.4	76.5	6.48E+05	(R)FVIYVK(A)	384.7377	768.465	0.0027	3.5	Arabidopsis thaliana	15238729	Putative pectinesterase/pectinesterase inhibitor 61	
1983	JGP_1_5.5803.5808.2	2	11.29	69.9	1.48E+05	(R)FVIYVK(A)	384.7372	768.465	0.0017	2.2	Arabidopsis thaliana	15238729	Putative pectinesterase/pectinesterase inhibitor 61	
2139	JGP_1_2.5169.5248.2	2	10.89	67.6	1.91E+05	(R)FVIYVK(A)	384.7376	768.465	0.0025	3.2	Arabidopsis thaliana	15238729	Putative pectinesterase/pectinesterase inhibitor 61	
1618	JGP_1_3.3068.3213.2	2	12.31	75.9	2.59E+06	(K)AFKEAK(K)	347.2014	693.393	0.0025	3.6	Arabidopsis thaliana	15227876	putative phosphoserine aminotransferase	
1659	JGP_1_7.2970.3131.2	2	12.22	82.9	1.87E+07	(K)AFKEAK(K)	347.2024	693.393	0.0045	6.5	Arabidopsis thaliana	15227876	putative phosphoserine aminotransferase	
1822	JGP_1_2.2956.3091.2	2	11.74	76	2.62E+06	(K)AFKEAK(K)	347.2015	693.393	0.0027	3.9	Arabidopsis thaliana	15227876	putative phosphoserine aminotransferase	
1932	JGP_1_7.3149.3332.2	2	11.44	77.3	1.14E+07	(K)AFKEAK(K)	347.2024	693.393	0.0045	6.5	Arabidopsis thaliana	15227876	putative phosphoserine aminotransferase	
2028	JGP_1_4.3069.3166.2	2	11.16	68.3	1.94E+06	(K)AFKEAK(K)	347.2013	693.393	0.0023	3.3	Arabidopsis thaliana	15227876	putative phosphoserine aminotransferase	
2417	JGP_1_1.4761.4770.2	2	10.25	71.2	7.57E+04	(K)TAVFFR(Q)	370.7097	740.409	0.0031	4.2	Arabidopsis thaliana	18408327	putative protease Do-like 3	
1561	JGP_1_6.5570.5575.4	4	12.46	70.3	3.52E+05	(K)IEDLSNQVPFDQSAVmSSAQAEK(F)	m:Oxidized methionine	628.2964	2494.177	15.9872	-3.1	Arabidopsis thaliana	3080423	putative protein
2342	JGP_1_8.8894.8960.3	3	10.42	71.9	5.44E+06	(K)ILSLVPTKLAAATSVLSK(R)		604.7045	1812.121	-0.0215	-11.9	Arabidopsis thaliana	17064772	putative protein
1271	JGP_1_7.2072.2081.2	2	13.37	81.6	2.80E+05	(K)GGQAIAVSR(D)	429.7432	858.479	-0.0001	-0.1	Zea mays	40744586	putative protein phosphatase	
1461	JGP_1_4.3767.3868.2	2	12.78	74.5	1.23E+06	(K)IYDFAGK(L)	407.2128	813.414	0.0042	5.2	Arabidopsis thaliana	7523670	putative retroelement pol polyprotein	
2392	JGP_1_6.6614.6614.3	3	10.32	65	5.45E+05	(K)TGLPYIWHSK(A)	401.221	1201.636	0.012	10	Arabidopsis thaliana	26452371	putative reversibly glycosylated polypeptide-3 RGP	
173	JGP_1_1.8285.8360.2	2	19.38	91.9	2.20E+05	(K)IAVLGFAFK(K)	483.2955	965.582	0.0019	1.9	Arabidopsis thaliana	15228687	putative UDP-glucose 6-dehydrogenase 1	
400	JGP_1_5.8684.8760.2	2	17.41	85	9.41E+04	(K)IAVLGFAFK(K)	483.2964	965.582	0.0037	3.8	Arabidopsis thaliana	15228687	putative UDP-glucose 6-dehydrogenase 1	
1314	JGP_1_2.7798.7802.2	2	13.23	82.5	5.55E+04	(K)IAVLGFAFK(K)	483.2966	965.582	0.0041	4.2	Arabidopsis thaliana	15228687	putative UDP-glucose 6-dehydrogenase 1	
44	JGP_1_5.8442.8550.2	2	22.1	93.1	2.01E+06	(K)IFNTNNLWVNLK(A)	738.4071	1475.801	0.0064	4.3	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
45	JGP_1_5.7929.8017.2	2	22.08	97.4	3.51E+06	(K)SIPSIVELDSLK(V)	650.8752	1300.736	0.0073	5.6	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
132	JGP_1_6.8762.8835.2	2	19.99	80.8	3.10E+05	(K)IFNTNNLWVNLK(A)	738.4045	1475.801	0.0012	0.8	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
217	JGP_1_5.7490.7494.2	2	18.93	91	2.50E+05	(K)SIPSIVELDSLK(V)	650.8743	1300.736	0.0055	4.2	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
253	JGP_1_5.7968.7980.3	3	18.51	86.8	1.11E+05	(K)SIPSIVELDSLK(V)	434.2515	1300.736	0.0041	3.1	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
291	JGP_1_1.7992.8055.2	2	18.18	86.4	5.71E+05	(K)IFNTNNLWVNLK(A)	738.3986	1475.801	-0.0106	-7.2	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
294	JGP_1_4.8161.8231.2	2	18.17	79.7	3.85E+05	(K)IFNTNNLWVNLK(A)	738.4036	1475.801	-0.0006	-0.4	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
332	JGP_1_5.6466.6574.2	2	17.92	94.5	1.08E+06	(K)VLQLETAAGAAIR(F)	656.8843	1312.758	0.003	2.3	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
342	JGP_1_5.6293.6386.2	2	17.85	90.2	3.15E+06	(K)VLQLETAAGAAIR(F)	656.8865	1312.758	0.0074	5.6	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
356	JGP_1_2.7092.7166.2	2	17.71	81.4	7.08E+05	(K)SIPSIVELDSLK(V)	650.8741	1300.736	0.0051	3.9	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
369	JGP_1_1.5918.6002.2	2	17.59	85.1	5.78E+05	(K)VLQLETAAGAAIR(F)	656.8836	1312.758	0.0016	1.2	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
373	JGP_1_4.7757.7825.2	2	17.58	88.5	1.00E+06	(K)SIPSIVELDSLK(V)	650.8744	1300.736	0.0057	4.4	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
486	JGP_1_3.5959.5961.2	2	16.88	87.7	1.73E+05	(K)VLQLETAAGAAIR(F)	656.8845	1312.758	0.0034	2.6	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
538	JGP_1_1.7556.7635.2	2	16.56	84	1.54E+06	(K)SIPSIVELDSLK(V)	650.8742	1300.736	0.0053	4	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
729	JGP_1_2.5612.5616.2	2	15.55	90	2.49E+05	(K)VLQLETAAGAAIR(F)	656.884	1312.758	0.0024	1.8	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
742	JGP_1_7.8164.8176.2	2	15.46	79	5.86E+03	(K)SIPSIVELDSLK(V)	650.8777	1300.736	0.0123	9.4	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
776	JGP_1_5.6311.6407.3	3	15.29	77.6	9.32E+05	(K)VLQLETAAGAAIR(F)	438.26	1312.758	0.0071	5.4	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
858	JGP_1_5.8388.8469.3	3	14.93	76.1	3.53E+05	(K)IFNTNNLWVNLK(A)	492.607	1475.801	0.0059	4	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
952	JGP_1_6.6650.6730.2	2	14.55	73.8	4.97E+05	(K)VLQLETAAGAAIR(F)	656.8745	1312.758	-0.0166	-12.6	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	
1076	JGP_1_2.5638.5641.3	3	14.02	80.3	1.39E+05	(K)VLQLETAAGAAIR(F)	438.2586	1312.758	0.0029	2.2	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2	

1187	JGP_1_7.8699.8699.2	2	13.61	63.5	1.18E+04	(K)IFNTNNLWVNLK(A)		738.4046	1475.801	0.0014	0.9	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2
1534	JGP_1_4.6142.6147.2	2	12.52	72.4	6.50E+05	(K)VLQLETAAGAAIR(F)		656.8834	1312.758	0.0012	0.9	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2
1546	JGP_1_6.8327.8333.2	2	12.5	79.1	2.02E+05	(K)SIPSIVELDSLK(V)		650.8746	1300.736	0.0061	4.7	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2
1752	JGP_1_4.7339.7339.2	2	11.96	66.5	3.40E+04	(K)SIPSIVELDSLK(V)		650.8716	1300.736	0.0001	0	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2
1757	JGP_1_4.6158.6164.3	3	11.95	69.1	2.22E+05	(K)VLQLETAAGAAIR(F)		438.2595	1312.758	0.0056	4.3	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2
2056	JGP_1_3.7520.7594.2	2	11.1	64.6	4.55E+05	(K)SIPSIVELDSLK(V)		650.8743	1300.736	0.0055	4.2	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2
2111	JGP_1_5.8093.8100.2	2	10.98	65.7	5.57E+04	(K)SIPSIVELDSLK(V)		650.8752	1300.736	0.0073	5.6	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2
2436	JGP_1_5.7225.7293.2	2	10.22	63	1.42E+05	(K)SGFISLVSR(Y)		483.2772	965.542	0.0057	5.9	Arabidopsis thaliana	15228498	putative UTP--glucose-1-phosphate uridylyltransferase 2
1351	JGP_1_6.9951.9957.2	2	13.1	76.1	4.46E+04	(R)DVTTTPAELVTFFR(D)		798.9191	1596.827	0.0041	2.6	Zea mays	3851005	pyruvate dehydrogenase E1 alpha subunit
440	JGP_1_5.5762.5767.3	3	17.23	87	4.68E+05	(R)LSAVYGGTYMLNKPECK(V)	C:Carbamidomethylation	644.3211	1930.94	0.0086	4.5	Arabidopsis thaliana	15232210	RAB GDP dissociation inhibitor 2
822	JGP_1_5.5073.5073.2	2	15.07	64	2.80E+05	(R)LSAVYGGTYmLNKPECK(V)	C:Carbamidomethylation m:Oxidized methionine	973.9709	1930.94	15.9944	-0.3	Arabidopsis thaliana	15232210	RAB GDP dissociation inhibitor 2
828	JGP_1_5.5052.5158.3	3	15.06	79.5	8.04E+05	(R)LSAVYGGTYmLNKPECK(V)	C:Carbamidomethylation m:Oxidized methionine	649.6546	1930.94	16.0091	7.3	Arabidopsis thaliana	15232210	RAB GDP dissociation inhibitor 2
3	JGP_1_5.9303.9377.3	3	24.93	88.3	1.31E+06	(K)YGLEDDTVDFIGHALALHR(D)		714.6968	2142.061	0.0144	6.7	Zea mays	226502766	rab GDP dissociation inhibitor alpha
4	JGP_1_6.9706.9780.4	4	24.45	86.8	6.43E+05	(K)YGLEDDTVDFIGHALALHR(D)		536.275	2142.061	0.0167	7.8	Zea mays	226502766	rab GDP dissociation inhibitor alpha
7	JGP_1_4.9005.9074.4	4	23.7	86.8	8.16E+05	(K)YGLEDDTVDFIGHALALHR(D)		536.275	2142.061	0.0167	7.8	Zea mays	226502766	rab GDP dissociation inhibitor alpha
31	JGP_1_5.9283.9357.4	4	22.48	79.3	4.58E+06	(K)YGLEDDTVDFIGHALALHR(D)		536.2754	2142.061	0.0183	8.6	Zea mays	226502766	rab GDP dissociation inhibitor alpha
37	JGP_1_5.8863.8975.4	4	22.3	84.2	8.65E+04	(K)YGLEDDTVDFIGHALALHR(D)		536.2732	2142.061	0.0095	4.4	Zea mays	226502766	rab GDP dissociation inhibitor alpha
54	JGP_1_5.9417.9422.4	4	21.76	83.1	3.17E+06	(K)YGLEDDTVDFIGHALALHR(D)		536.2757	2142.061	0.0195	9.1	Zea mays	226502766	rab GDP dissociation inhibitor alpha
156	JGP_1_5.4997.5003.3	3	19.53	78.4	4.50E+05	(R)KSDmYVFCCSYAHNVAPK(G)	C:Carbamidomethylation m:Oxidized methionine	731.6615	2176.961	16.0087	6.3	Zea mays	226502766	rab GDP dissociation inhibitor alpha
233	JGP_1_7.9571.9634.4	4	18.77	74.5	2.40E+05	(K)YGLEDDTVDFIGHALALHR(D)		536.2756	2142.061	0.0191	8.9	Zea mays	226502766	rab GDP dissociation inhibitor alpha
299	JGP_1_5.5554.5654.3	3	18.11	88	1.02E+06	(R)DDSYLDEPAIDTVKR(M)		579.6195	1736.834	0.0102	5.9	Zea mays	226502766	rab GDP dissociation inhibitor alpha
350	JGP_1_5.6064.6156.2	2	17.77	91	1.08E+06	(R)DDSYLDEPAIDTVK(R)		790.8732	1580.733	0.0065	4.1	Zea mays	226502766	rab GDP dissociation inhibitor alpha
372	JGP_1_6.9737.9741.3	3	17.59	72	1.87E+05	(K)YGLEDDTVDFIGHALALHR(D)		714.697	2142.061	0.015	7	Zea mays	226502766	rab GDP dissociation inhibitor alpha
381	JGP_1_5.5462.5468.3	3	17.54	80.8	5.13E+05	(K)SDmYVFCCSYAHNVAPK(G)	C:Carbamidomethylation m:Oxidized methionine	688.9656	2048.866	16.0159	10.2	Zea mays	226502766	rab GDP dissociation inhibitor alpha
498	JGP_1_5.2341.2433.2	2	16.82	88.5	2.77E+06	(K)AYGVTSEGETAK(C)		606.7942	1212.574	0.0069	5.6	Zea mays	226502766	rab GDP dissociation inhibitor alpha
711	JGP_1_1.8855.8916.4	4	15.65	67.1	1.09E+05	(K)YGLEDDTVDFIGHALALHR(D)		536.2738	2142.061	0.0119	5.6	Zea mays	226502766	rab GDP dissociation inhibitor alpha
752	JGP_1_5.4847.4851.2	2	15.4	71.2	4.10E+05	(K)EYNVDMVPK(F)		547.7668	1094.519	0.0077	7	Zea mays	226502766	rab GDP dissociation inhibitor alpha
848	JGP_1_3.8793.8836.4	4	14.97	73	8.20E+04	(K)YGLEDDTVDFIGHALALHR(D)		536.2742	2142.061	0.0135	6.3	Zea mays	226502766	rab GDP dissociation inhibitor alpha
849	JGP_1_5.5402.5574.2	2	14.97	85.1	1.59E+06	(K)DVLALYNK(I)		468.2656	935.52	0.0043	4.6	Zea mays	226502766	rab GDP dissociation inhibitor alpha
938	JGP_1_5.2298.2398.2	2	14.63	78.3	2.30E+06	(K)VEFDESGK(A)		455.7168	910.415	0.0111	12.2	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1257	JGP_1_5.1043.1118.2	2	13.41	82.7	1.43E+06	(K)HPIPDTK(D)		404.2233	807.436	0.0034	4.2	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1282	JGP_1_5.2488.2494.2	2	13.34	80.7	1.35E+06	(K)VEFDESGK(A)		455.7162	910.415	0.0099	10.8	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1354	JGP_1_5.9027.9104.2	2	13.09	77.2	2.27E+06	(K)ECIISGLLSVDGLK(V)	C:Carbamidomethylation	752.4114	1503.809	0.0068	4.5	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1360	JGP_1_6.2498.2599.2	2	13.07	69.8	2.44E+05	(K)VEFDESGK(A)		455.7162	910.415	0.0099	10.8	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1376	JGP_1_5.5714.5801.3	3	13.02	73	2.24E+06	(K)DSHSVQIILPK(K)		412.9049	1236.695	0.0055	4.4	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1430	JGP_1_5.5741.5832.2	2	12.88	78.2	1.11E+06	(K)DSHSVQIILPK(K)		618.8522	1236.695	0.0025	2	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1515	JGP_1_7.9615.9615.3	3	12.6	60.9	1.07E+04	(K)YGLEDDTVDFIGHALALHR(D)		714.6984	2142.061	0.0192	9	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1527	JGP_1_5.9055.9128.3	3	12.55	71.4	3.65E+05	(K)ECIISGLLSVDGLK(V)	C:Carbamidomethylation	501.944	1503.809	0.0087	5.8	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1591	JGP_1_4.5905.5910.2	2	12.4	82	1.98E+05	(R)DDSYLDEPAIDTVK(R)		790.8744	1580.733	0.0089	5.6	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1612	JGP_1_4.5855.5938.2	2	12.33	73	3.36E+05	(K)SNLmGLFEK(R)	m:Oxidized methionine	527.7672	1038.529	15.9983	3.2	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1663	JGP_1_5.3592.3706.2	2	12.2	76	1.88E+06	(K)EYNVDmVPK(F)	m:Oxidized methionine	555.7629	1094.519	15.9999	4.4	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1686	JGP_1_5.5876.5967.3	3	12.16	77.9	2.43E+04	(K)DSHSVQIILPK(K)		412.905	1236.695	0.0058	4.7	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1692	JGP_1_5.7538.7545.2	2	12.14	69.4	2.25E+05	(K)FFIYVQDYEEDDPK(S)		904.4246	1807.806	0.0358	19.8	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1734	JGP_1_4.5599.5682.3	3	12.01	71.9	4.39E+05	(K)DSHSVQIILPK(K)		412.9053	1236.695	0.0067	5.4	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1845	JGP_1_5.5584.5584.2	2	11.7	72.5	2.29E+05	(R)DDSYLDEPAIDTVKR(M)		868.9216	1736.834	0.0022	1.3	Zea mays	226502766	rab GDP dissociation inhibitor alpha
1899	JGP_1_6.5730.5732.2	2	11.54	72.9	2.20E+05	(K)DVLALYNK(I)		468.2643	935.52	0.0017	1.8	Zea mays	226502766	rab GDP dissociation inhibitor alpha

1907	JGP_1_5.2574.2688.2	2	11.51	71.3	2.56E+06	(R)AICImK(H)	C:Carbamidomethylation m:Oxidized methionine	376.1972	735.389	15.9979	4	Zea mays	226502766	rab GDP dissociation inhibitor alpha	
2144	JGP_1_6.6426.6426.2	2	10.89	70.6	1.95E+05	(R)DDSYLDEPAIDTVK(R)	790.8764	1580.733	0.0129	8.2	Zea mays	226502766	rab GDP dissociation inhibitor alpha		
2175	JGP_1_4.5305.5352.2	2	10.8	63.8	3.49E+05	(K)DVLALYNK(I)	468.269	935.52	0.0111	11.8	Zea mays	226502766	rab GDP dissociation inhibitor alpha		
2223	JGP_1_5.5963.6082.2	2	10.71	66.4	1.76E+06	(K)SNLmGLFEK(R)	m:Oxidized methionine	527.7681	1038.529	16.0001	4.9	Zea mays	226502766	rab GDP dissociation inhibitor alpha	
2287	JGP_1_6.2549.2555.2	2	10.54	67.5	4.17E+05	(K)AYGVTSEGETAK(C)	606.7923	1212.574	0.0031	2.5	Zea mays	226502766	rab GDP dissociation inhibitor alpha		
2381	JGP_1_5.4968.4974.4	4	10.34	61.8	5.67E+05	(R)KSDmYVFCCSYAHNVAPK(G)	C:Carbamidomethylation m:Oxidized methionine	548.9989	2176.961	16.0125	8	Zea mays	226502766	rab GDP dissociation inhibitor alpha	
2411	JGP_1_4.8790.8794.2	2	10.27	66.1	1.35E+05	(K)ECIISGLLSVDGLK(V)	C:Carbamidomethylation	752.4089	1503.809	0.0018	1.2	Zea mays	226502766	rab GDP dissociation inhibitor alpha	
2412	JGP_1_5.3893.3918.2	2	10.27	75.5	5.33E+05	(R)AICIMK(H)	C:Carbamidomethylation	368.1997	735.389	0.0029	4	Zea mays	226502766	rab GDP dissociation inhibitor alpha	
2439	JGP_1_5.6989.6999.3	3	10.21	63.7	1.80E+05	(R)KFFIYVQDYEEDDPK(S)	645.9768	1935.901	0.0148	7.6	Zea mays	226502766	rab GDP dissociation inhibitor alpha		
14	JGP_1_5.10439.10559.3	3	23.17	100	1.30E+06	(R)FQGGSPYIYPLYGLGELPQAFAR(L)	848.7754	2544.292	0.0195	7.7	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
135	JGP_1_4.10062.10130.3	3	19.97	90.1	2.34E+05	(R)FQGGSPYIYPLYGLGELPQAFAR(L)	848.7737	2544.292	0.0144	5.6	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
188	JGP_1_5.10450.10563.2	2	19.24	91.3	5.51E+05	(R)FQGGSPYIYPLYGLGELPQAFAR(L)	1272.6553	2544.292	0.0112	4.4	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
273	JGP_1_5.10562.10578.3	3	18.33	79.3	3.63E+05	(R)FQGGSPYIYPLYGLGELPQAFAR(L)	848.7754	2544.292	0.0195	7.7	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
476	JGP_1_7.10735.10776.3	3	16.96	79.7	1.70E+05	(R)FQGGSPYIYPLYGLGELPQAFAR(L)	848.7732	2544.292	0.0129	5.1	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
886	JGP_1_8.4417.4423.2	2	14.86	68.8	1.25E+05	(K)VPATDVEALK(S)	521.7929	1042.578	0.0006	0.6	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
1014	JGP_1_6.10878.10945.3	3	14.28	71.4	6.81E+04	(R)FQGGSPYIYPLYGLGELPQAFAR(L)	848.7742	2544.292	0.0159	6.2	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
1218	JGP_1_7.10740.10740.3	3	13.53	67.2	1.46E+05	(R)FQGGSPYIYPLYGLGELPQAFAR(L)	848.7732	2544.292	0.0129	5.1	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
1315	JGP_1_5.4257.4356.2	2	13.23	67.3	5.64E+06	(K)VPATDVEALK(S)	521.7958	1042.578	0.0064	6.2	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
1681	JGP_1_6.10881.10881.2	2	12.17	63.9	1.32E+04	(R)FQGGSPYIYPLYGLGELPQAFAR(L)	1272.6444	2544.292	-0.0106	-4.2	Arabidopsis thaliana	145357818	RAB GDP-dissociation inhibitor		
2046	JGP_1_3.5139.5147.2	2	11.12	71.4	8.55E+04	(K)AFLHK(R)	308.1859	615.361	0.0032	5.2	Arabidopsis thaliana	7269299	Rab geranylgeranyl transferase like protein (fragment)		
1778	JGP_1_8.6755.6828.2	2	11.89	78.5	3.75E+05	(K)IILLGDSGVGK(T)	536.3238	1071.641	-0.0005	-0.5	Arabidopsis thaliana	18421886	RAB GTPase homolog G1		
1639	JGP_1_8.6683.6764.2	2	12.25	80.3	1.84E+05	(R)SLIPSYIR(D)	474.7805	948.551	0.0024	2.6	Arabidopsis thaliana	15224916	Ras-related protein RABH1B		
236	JGP_1_7.7014.7105.3	3	18.72	78.2	4.22E+05	(K)AAQDIALAELAPTHPIR(L)	596.3326	1786.981	0.0022	1.3	MAIZE	1345588	RecName: Full=14-3-3-like protein GF14-12		
262	JGP_1_7.3185.3367.3	3	18.46	83.7	1.01E+06	(R)IISSIEQKEEGR(G)	463.5866	1388.738	0.0073	5.2	MAIZE	1345588	RecName: Full=14-3-3-like protein GF14-12		
493	JGP_1_7.7021.7021.3	3	16.85	76.2	2.57E+05	(K)AAQDIALAELAPTHPIR(L)	596.3326	1786.981	0.0022	1.3	MAIZE	1345588	RecName: Full=14-3-3-like protein GF14-12		
986	JGP_1_8.3116.3121.3	3	14.43	75.2	9.84E+04	(R)IISSIEQKEEGR(G)	463.5857	1388.738	0.0046	3.3	MAIZE	1345588	RecName: Full=14-3-3-like protein GF14-12		
2404	JGP_1_7.3251.3251.2	2	10.29	63.9	1.46E+05	(R)IISSIEQKEEGR(G)	694.8754	1388.738	0.0055	4	MAIZE	1345588	RecName: Full=14-3-3-like protein GF14-12		
1641	JGP_1_5.3545.3651.2	2	12.24	81.5	9.63E+05	(R)TVLLDTK(T)	395.2397	789.472	0.0005	0.6	MAIZE	1352468	RecName: Full=Beta-fructofuranosidase 1	AltName: Full=Invertase 1	AltName: Full=Sucrose 1	Flags: Precursor
16	JGP_1_5.8509.8583.2	2	23.12	89.9	3.61E+05	(K)YIGIELWQVK(S)	624.8553	1248.699	0.0046	3.7	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor	
210	JGP_1_5.2560.2659.2	2	19.03	81.9	8.17E+05	(K)LDCGGGYVK(L)	C:Carbamidomethylation	484.731	968.451	0.0041	4.3	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor
503	JGP_1_5.8715.8787.3	3	16.77	82.6	4.57E+05	(K)APmIDNPDFKDDPYIYAFDSLK(Y)	m:Oxidized methionine	864.4089	2575.206	16.006	4.3	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor
759	JGP_1_5.2304.2403.2	2	15.36	85	6.86E+05	(K)GIQTSEDYR(F)	534.7554	1068.496	0.0079	7.4	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor	
868	JGP_1_5.5849.5852.5	5	14.91	86.3	3.70E+05	(K)KPEDWDDKEYIPDPEDKKPEGYDDIPK(E)	653.1132	3261.511	0.0259	7.9	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor	
912	JGP_1_5.7269.7342.2	2	14.74	84.9	3.24E+05	(K)TLVLQFSVK(H)	517.8168	1034.624	0.0019	1.8	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor	
1128	JGP_1_5.3121.3126.2	2	13.84	79.2	1.59E+05	(K)KPEGYDDIPK(E)	581.2945	1161.579	0.0031	2.7	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor	
1595	JGP_1_5.1173.1248.3	3	12.39	67.7	3.86E+05	(K)IKNPNYQGK(W)	354.5312	1061.574	0.0052	4.9	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor	
1658	JGP_1_5.8720.8720.3	3	12.22	63.6	3.66E+05	(K)APmIDNPDFKDDPYIYAFDSLK(Y)	m:Oxidized methionine	864.4089	2575.206	16.006	4.3	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor
1672	JGP_1_5.2390.2498.2	2	12.19	76	1.15E+06	(K)EIPDPDAK(K)	442.7237	884.436	0.0041	4.7	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor	
2010	JGP_1_5.4614.4623.2	2	11.21	66.9	5.15E+05	(K)TFAEETWGK(H)	534.7563	1068.5	0.0057	5.3	MAIZE	11131840	RecName: Full=Calreticulin	Flags: Precursor	
41	JGP_1_5.5217.5301.2	2	22.14	92.5	1.98E+06	(K)AYEDAASVLTASK(I)	663.3365	1325.658	0.0074	5.6	MAIZE	548493	RecName: Full=Exopolygalacturonase	Short=ExoPG	"
AltName: Full=Galacturan 1,4-alpha-galacturonidase"					AltName: Full=Pectinase		Flags: Precursor								
81	JGP_1_5.3970.4080.2	2	21.04	89.9	5.49E+06	(K)GKLDGQGPAVWSK(N)	671.8632	1342.711	0.0077	5.8	MAIZE	548493	RecName: Full=Exopolygalacturonase	Short=ExoPG	"
AltName: Full=Galacturan 1,4-alpha-galacturonidase"					AltName: Full=Pectinase		Flags: Precursor								
85	JGP_1_2.4611.4691.2	2	20.96	89.8	8.96E+05	(K)AYEDAASVLTASK(I)	663.3359	1325.658	0.0062	4.7	MAIZE	548493	RecName: Full=Exopolygalacturonase	Short=ExoPG	"
AltName: Full=Galacturan 1,4-alpha-galacturonidase"					AltName: Full=Pectinase		Flags: Precursor								
101	JGP_1_1.4818.4905.2	2	20.58	85.5	1.02E+06	(K)AYEDAASVLTASK(I)	663.3346	1325.658	0.0036	2.7	MAIZE	548493	RecName: Full=Exopolygalacturonase	Short=ExoPG	"
AltName: Full=Galacturan 1,4-alpha-galacturonidase"					AltName: Full=Pectinase		Flags: Precursor								
103	JGP_1_3.4904.4986.2	2	20.56	85.9	5.96E+05	(K)AYEDAASVLTASK(I)	663.3359	1325.658	0.0062	4.7	MAIZE	548493	RecName: Full=Exopolygalacturonase	Short=ExoPG	"
AltName: Full=Galacturan 1,4-alpha-galacturonidase"					AltName: Full=Pectinase		Flags: Precursor								
175	JGP_1_5.3942.4107.3	3	19.36	72.6	1.66E+07	(K)GKLDGQGPAVWSK(N)	448.246	1342.711	0.0121	9	MAIZE	548493	RecName: Full=Exopolygalacturonase	Short=ExoPG	"
AltName: Full=Galacturan 1,4-alpha-galacturonidase"					AltName: Full=Pectinase		Flags: Precursor								
195	JGP_1_5.4160.4165.2	2	19.13	88.8	2.05E+06	(K)GKLDGQGPAVWSK(N)	671.8631	1342.711	0.0075	5.6	MAIZE	548493	RecName: Full=Exopolygalacturonase	Short=ExoPG	"
AltName: Full=Galacturan 1,4-alpha-galacturonidase"					AltName: Full=Pectinase		Flags: Precursor								

366	JGP_1_3.4167.4256.2	2	17.62	82.8	1.60E+06	(K)LDGQGPAVWSK(N)		579.3039	1157.595	0.0056	4.8	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
370	JGP_1_4.5060.5142.2	2	17.59	80.7	6.64E+05	(K)AYEDAASVLTASK(I)		663.3355	1325.658	0.0054	4.1	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
602	JGP_1_5.4526.4532.2	2	16.19	86.9	1.03E+07	(K)LDGQGPAVWSK(N)		579.3051	1157.595	0.008	6.9	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
653	JGP_1_5.4338.4441.2	2	15.96	82.7	1.20E+07	(K)LDGQGPAVWSK(N)		579.3024	1157.595	0.0026	2.2	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
664	JGP_1_4.4245.4344.2	2	15.91	82.5	2.70E+06	(K)LDGQGPAVWSK(N)		579.3036	1157.595	0.005	4.3	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
715	JGP_1_4.4016.4122.3	3	15.64	60.6	2.00E+06	(K)GKLDGQGPAVWSK(N)		448.2446	1342.711	0.0079	5.9	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
782	JGP_1_3.3963.4062.3	3	15.26	64.8	1.33E+06	(K)GKLDGQGPAVWSK(N)		448.2445	1342.711	0.0076	5.6	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
835	JGP_1_2.3868.3992.2	2	15.02	76.2	2.89E+06	(K)LDGQGPAVWSK(N)		579.3024	1157.595	0.0026	2.2	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
981	JGP_1_6.5429.5517.2	2	14.45	72.3	6.66E+05	(K)AYEDAASVLTASK(I)		663.3369	1325.658	0.0082	6.2	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1002	JGP_1_1.4084.4180.2	2	14.33	77.2	1.21E+06	(K)LDGQGPAVWSK(N)		579.3018	1157.595	0.0014	1.2	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1108	JGP_1_2.3732.3821.3	3	13.92	64.3	8.22E+05	(K)GKLDGQGPAVWSK(N)		448.2447	1342.711	0.0082	6.1	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1113	JGP_1_3.4333.4357.2	2	13.89	66.8	6.42E+05	(K)LDGQGPAVWSK(N)		579.304	1157.595	0.0058	5	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1208	JGP_1_5.5269.5272.3	3	13.56	70.5	1.81E+05	(K)AYEDAASVLTASK(I)		442.5628	1325.658	0.0155	11.7	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1252	JGP_1_2.4062.4067.2	2	13.42	74.2	1.30E+06	(K)LDGQGPAVWSK(N)		579.3036	1157.595	0.005	4.3	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1297	JGP_1_4.4428.4428.2	2	13.29	72.5	1.33E+06	(K)LDGQGPAVWSK(N)		579.3038	1157.595	0.0054	4.6	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1396	JGP_1_4.4424.4424.2	2	12.97	74.3	1.42E+06	(K)LDGQGPAVWSK(N)		579.3038	1157.595	0.0054	4.6	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1628	JGP_1_5.1280.1375.2	2	12.28	70.8	4.62E+05	(K)TMAVCK(N)	C:Carbamidomethylation	355.1743	709.337	0.0042	5.9	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG
" AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1634	JGP_1_6.4353.4353.2	2	12.27	75.8	8.56E+05	(K)GKLDGQGPAVWSK(N)		671.8624	1342.711	0.0061	4.6	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1807	JGP_1_7.4505.4520.2	2	11.8	62.7	3.16E+05	(K)LDGQGPAVWSK(N)		579.2995	1157.595	-0.0032	-2.8	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
1902	JGP_1_1.4250.4255.2	2	11.52	73.2	4.75E+05	(K)LDGQGPAVWSK(N)		579.302	1157.595	0.0018	1.5	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
2035	JGP_1_6.4358.4358.2	2	11.15	66.7	8.56E+05	(K)GKLDGQGPAVWSK(N)		671.8624	1342.711	0.0061	4.6	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
2172	JGP_1_2.4647.4656.3	3	10.81	64.6	1.28E+05	(K)AYEDAASVLTASK(I)		442.5622	1325.658	0.0137	10.3	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
2260	JGP_1_6.4598.4692.2	2	10.63	68.5	1.51E+06	(K)LDGQGPAVWSK(N)		579.3028	1157.595	0.0034	2.9	MAIZE	548493	RecName: Full=Exopolygalacturonase Short=ExoPG "
AltName: Full=Galacturan 1,4-alpha-galacturonidase"				AltName: Full=Pectinase		Flags: Precursor								
109	JGP_1_2.7072.7148.2	2	20.44	94.5	4.14E+05	(R)VPTVDVSVVDLTVR(I)		749.9299	1498.848	0.005	3.3	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
124	JGP_1_1.7530.7604.2	2	20.16	88.7	1.16E+06	(R)VPTVDVSVVDLTVR(I)		749.9308	1498.848	0.0068	4.5	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
298	JGP_1_3.7486.7565.2	2	18.12	88.9	3.05E+05	(R)VPTVDVSVVDLTVR(I)		749.9302	1498.848	0.0056	3.7	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
427	JGP_1_4.7759.7764.2	2	17.29	89.1	1.80E+05	(R)VPTVDVSVVDLTVR(I)		749.9312	1498.848	0.0076	5.1	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
773	JGP_1_6.7968.7973.2	2	15.31	75	2.09E+05	(R)VPTVDVSVVDLTVR(I)		749.9299	1498.848	0.005	3.3	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
1265	JGP_1_6.3145.3244.2	2	13.38	88.9	1.29E+06	(K)VVISAPSK(D)		400.7491	800.488	0.0033	4.1	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
1665	JGP_1_6.3979.4082.2	2	12.2	81.6	1.94E+06	(R)SSIFDAK(A)		384.2016	767.393	0.0025	3.3	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
2040	JGP_1_6.2700.2804.3	3	11.14	68.6	1.22E+06	(K)KVVISAPSK(D)		310.2002	928.583	0.0035	3.7	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
2112	JGP_1_1.2566.2575.3	3	10.97	69.8	2.06E+05	(K)KVVISAPSK(D)		310.1999	928.583	0.0026	2.8	MAIZE	120670	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase,
cytosolic 1"														
179	JGP_1_2.5229.5313.2	2	19.35	87.9	3.23E+05	(R)VFFDmTVGGAPAGR(I)	m:Oxidized methionine	720.8527	1424.699	15.999	2.9	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
199	JGP_1_6.5784.5788.2	2	19.1	87.5	3.70E+05	(R)IVmELYANEVPK(T)	m:Oxidized methionine	711.3714	1405.74	15.996	0.7	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
213	JGP_1_7.6084.6103.2	2	18.97	84.5	4.10E+05	(R)VFFDmTVGGAPAGR(I)	m:Oxidized methionine	720.8533	1424.699	16.0002	3.7	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
229	JGP_1_1.5517.5612.2	2	18.79	85.5	8.17E+05	(R)VFFDmTVGGAPAGR(I)	m:Oxidized methionine	720.8526	1424.699	15.9988	2.7	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
242	JGP_1_8.7001.7107.2	2	18.62	87	1.15E+06	(R)IVMELYANEVPK(T)		703.376	1405.74	0.0052	3.7	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
295	JGP_1_8.6160.6253.2	2	18.14	84.2	1.37E+06	(R)VFFDmTVGGAPAGR(I)	m:Oxidized methionine	720.8539	1424.699	16.0014	4.5	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
328	JGP_1_5.5503.5506.2	2	17.95	86.5	2.85E+05	(R)IVmELYANEVPK(T)	m:Oxidized methionine	711.3726	1405.74	15.9984	2.4	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
418	JGP_1_4.5315.5318.2	2	17.34	87.1	3.36E+05	(R)IVmELYANEVPK(T)	m:Oxidized methionine	711.3728	1405.74	15.9988	2.7	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
610	JGP_1_4.5773.5779.2	2	16.17	74.9	2.71E+05	(R)VFFDmTVGGAPAGR(I)	m:Oxidized methionine	720.8538	1424.699	16.0012	4.4	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
611	JGP_1_8.7412.7499.3	3	16.17	83.3	1.31E+06	(K)HVVFGQVVEGMDVVK(A)		548.295	1642.862	0.0083	5.1	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
619	JGP_1_3.5148.5232.2	2	16.15	76.7	5.56E+05	(R)IVmELYANEVPK(T)	m:Oxidized methionine	711.3729	1405.74	15.999	2.8	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
744	JGP_1_6.0928.0935.3	3	15.45	75.6	3.57E+05	(K)SGKPLHYK(G)		310.5126	929.52	0.0029	3.1	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
789	JGP_1_1.5493.5497.2	2	15.22	69	3.34E+05	(K)HVVFGQVVEGmDVVK(A)	m:Oxidized methionine	829.9329	1642.862	15.9964	0.9	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									
803	JGP_1_5.0914.0959.3	3	15.17	85.5	2.55E+05	(K)SGKPLHYK(G)		310.5128	929.52	0.0035	3.8	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase
Short=PPIase	AltName: Full=Cyclophilin		AltName: Full=Cyclosporin A-binding protein		AltName: Full=Rotamase									

867	JGP_1_3.5557.5646.2	2	14.91	83.9	3.64E+05	(R)VFFDmTVGGAPAGR(I)	m:Oxidized methionine	720.8534	1424.699	16.0004	3.8	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1026	JGP_1_7.0859.0864.3	3	14.21	71.3	8.52E+05	(K)SGKPLHYK(G)		310.5131	929.52	0.0044	4.8	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1056	JGP_1_6.6256.6265.2	2	14.12	69	2.83E+05	(R)VFFDmTVGGAPAGR(I)	m:Oxidized methionine	720.8527	1424.699	15.999	2.9	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1086	JGP_1_8.7512.7600.2	2	14	70.3	1.30E+06	(R)VFFDMTVGGAPAGR(I)		712.8577	1424.699	0.009	6.3	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1164	JGP_1_1.0934.1013.3	3	13.68	76.4	2.02E+05	(K)SGKPLHYK(G)		310.513	929.52	0.0041	4.4	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1336	JGP_1_3.5532.5543.2	2	13.16	70.8	1.60E+05	(K)HVVFGQVVEGmDVVK(A)	m:Oxidized methionine	829.934	1642.862	15.9986	2.2	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1356	JGP_1_7.7400.7404.2	2	13.09	63.5	2.20E+05	(R)VFFDMTVGGAPAGR(I)		712.8569	1424.699	0.0074	5.2	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1445	JGP_1_1.5455.5541.3	3	12.83	75.8	2.12E+06	(K)HVVFGQVVEGmDVVK(A)	m:Oxidized methionine	553.6265	1642.862	16.0028	4.8	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1447	JGP_1_8.7426.7504.2	2	12.83	77.1	6.04E+05	(K)HVVFGQVVEGMDVVK(A)		821.9366	1642.862	0.0038	2.3	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1456	JGP_1_8.6226.6236.3	3	12.8	73.2	3.11E+05	(R)VFFDmTVGGAPAGR(I)	m:Oxidized methionine	480.9056	1424.699	16.0032	5.7	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1540	JGP_1_5.5894.5899.2	2	12.51	67.1	2.82E+04	(K)HVVFGQVVEGmDVVK(A)	m:Oxidized methionine	829.9341	1642.862	15.9988	2.3	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1794	JGP_1_7.0947.0952.2	2	11.84	70.4	3.30E+05	(R)ALCTGEK(G)	C:Carbamidomethylation	389.6937	778.376	0.0038	4.8	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1858	JGP_1_8.7531.7547.3	3	11.66	69.8	2.39E+05	(R)VFFDMTVGGAPAGR(I)		475.5737	1424.699	0.0075	5.2	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1933	JGP_1_8.0903.0907.2	2	11.44	63.2	5.68E+05	(R)ALCTGEK(G)	C:Carbamidomethylation	389.6932	778.376	0.0028	3.5	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1951	JGP_1_3.1337.1411.2	2	11.39	80.7	3.76E+05	(K)TAENFR(A)		369.1849	737.358	0.0048	6.6	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1967	JGP_1_7.7351.7354.2	2	11.34	72	6.02E+04	(K)HVVFGQVVEGMDVVK(A)		821.9311	1642.862	-0.0072	-4.4	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1989	JGP_1_8.6905.6923.3	3	11.27	67.6	1.51E+05	(K)HVVFGQVVEGMDVVK(A)		548.2949	1642.862	0.008	4.9	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2051	JGP_1_8.7057.7072.3	3	11.12	76.1	8.48E+04	(R)IVMELYANEVPK(T)		469.2527	1405.74	0.004	2.8	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2103	JGP_1_8.0844.0854.3	3	11	68.3	2.61E+05	(K)SGKPLHYK(G)		310.5127	929.52	0.0032	3.5	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2161	JGP_1_2.1353.1467.2	2	10.84	81.1	1.79E+05	(K)TAENFR(A)		369.1843	737.358	0.0036	4.9	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2185	JGP_1_2.1471.1539.2	2	10.77	73	1.17E+05	(K)TAENFR(A)		369.1838	737.358	0.0026	3.6	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2248	JGP_1_2.5218.5224.2	2	10.65	65.9	1.36E+05	(K)HVVFGQVVEGmDVVK(A)	m:Oxidized methionine	829.9343	1642.862	15.9992	2.6	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2255	JGP_1_8.1110.1146.2	2	10.64	75.8	1.47E+06	(K)TAENFR(A)		369.1845	737.358	0.004	5.5	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2284	JGP_1_3.1016.1038.3	3	10.55	67.8	3.76E+05	(K)SGKPLHYK(G)		310.5133	929.52	0.005	5.4	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2419	JGP_1_2.5107.5177.3	3	10.25	63.8	6.58E+05	(K)HVVFGQVVEGmDVVK(A)	m:Oxidized methionine	553.6179	1642.862	15.977	-10.8	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2441	JGP_1_8.5788.5788.3	3	10.21	60.3	1.08E+05	(R)IVmELYANEVPK(T)	m:Oxidized methionine	474.5869	1405.74	16.0066	8.2	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
2469	JGP_1_5.1301.1390.2	2	10.15	71.1	2.84E+05	(K)TAENFR(A)		369.1898	737.358	0.0146	19.9	MAIZE	118104	RecName: Full=Peptidyl-prolyl cis-trans isomerase Short=PPIase AltName: Full=Cyclophilin AltName: Full=Cyclosporin A-binding protein AltName: Full=Rotamase
1847	JGP_1_4.7246.7246.2	2	11.69	71.5	1.19E+04	(R)TADDIVDFIK(K)		568.7978	1136.583	0.0049	4.3	MAIZE	1709619	RecName: Full=Protein disulfide-isomerase Short=PDI Flags: Precursor
556	JGP_1_3.5808.5814.2	2	16.46	81.5	1.23E+05	(R)FLAIDAVEK(A)		503.2852	1005.562	0.0016	1.6	MAIZE	75140229	"RecName: Full=Transketolase, chloroplastic" Short=TK
1449	JGP_1_3.2318.2318.2	2	12.81	63.7	1.33E+05	(K)YTPESPGDATR(N)		597.281	1193.543	0.0114	9.6	MAIZE	75140229	"RecName: Full=Transketolase, chloroplastic" Short=TK
1812	JGP_1_1.8884.8889.2	2	11.78	72.6	1.59E+05	(R)LVSQVISSLTASLR(F)		737.4284	1473.863	-0.014	-9.5	MAIZE	135398	RecName: Full=Tubulin alpha-1 chain AltName: Full=Alpha-1-tubulin
2239	JGP_1_8.7576.7605.3	3	10.68	73.8	1.16E+05	(K)IESLRAILEK(S)		391.239	1171.705	-0.0021	-1.8	Solanum tuberosum	164598916	resistance protein PSH-RGH6
317	JGP_1_5.5379.5471.2	2	18.01	97	7.41E+06	(R)FPELGVK(Q)		395.2321	789.451	0.0064	8.1	Zea mays	226496241	reticuline oxidase precursor
361	JGP_1_4.5245.5417.2	2	17.65	94	5.96E+06	(R)FPELGVK(Q)		395.2318	789.451	0.0058	7.4	Zea mays	226496241	reticuline oxidase precursor
491	JGP_1_5.7333.7412.2	2	16.86	91.4	1.11E+06	(K)DLLPLMASR(F)		508.2862	1015.561	0.0046	4.6	Zea mays	226496241	reticuline oxidase precursor
574	JGP_1_5.5556.5561.2	2	16.35	86.6	4.91E+06	(R)FPELGVK(Q)		395.2317	789.451	0.0056	7.1	Zea mays	226496241	reticuline oxidase precursor
618	JGP_1_3.5131.5236.2	2	16.15	92.9	4.74E+06	(R)FPELGVK(Q)		395.2314	789.451	0.005	6.3	Zea mays	226496241	reticuline oxidase precursor
714	JGP_1_7.5405.5493.2	2	15.65	85.7	2.96E+05	(R)FPELGVK(Q)		395.2282	789.451	-0.0014	-1.8	Zea mays	226496241	reticuline oxidase precursor
967	JGP_1_3.5714.5797.2	2	14.48	74.3	2.66E+06	(K)DLLPLmASR(F)	m:Oxidized methionine	516.2835	1015.561	15.9992	4.2	Zea mays	226496241	reticuline oxidase precursor
974	JGP_1_6.5635.5728.2	2	14.47	70.6	1.24E+06	(R)FPELGVK(Q)		395.2305	789.451	0.0032	4.1	Zea mays	226496241	reticuline oxidase precursor
1004	JGP_1_2.4858.4941.2	2	14.32	85.4	7.95E+05	(R)FPELGVK(Q)		395.2307	789.451	0.0036	4.6	Zea mays	226496241	reticuline oxidase precursor
1082	JGP_1_4.5923.6015.2	2	14	79	3.51E+06	(K)DLLPLmASR(F)	m:Oxidized methionine	516.2838	1015.561	15.9998	4.8	Zea mays	226496241	reticuline oxidase precursor
1095	JGP_1_6.5817.5822.2	2	13.97	82.4	7.85E+05	(R)FPELGVK(Q)		395.2305	789.451	0.0032	4.1	Zea mays	226496241	reticuline oxidase precursor
1161	JGP_1_4.5423.5423.2	2	13.7	80.6	7.50E+04	(R)FPELGVK(Q)		395.2318	789.451	0.0058	7.4	Zea mays	226496241	reticuline oxidase precursor
1373	JGP_1_1.5068.5155.2	2	13.02	68.8	1.38E+06	(R)FPELGVK(Q)		395.2317	789.451	0.0056	7.1	Zea mays	226496241	reticuline oxidase precursor
1415	JGP_1_6.7758.7841.2	2	12.93	80.5	2.84E+05	(K)DLLPLMASR(F)		508.2871	1015.561	0.0064	6.3	Zea mays	226496241	reticuline oxidase precursor

1428	JGP_1_3.6923.7001.2	2	12.88	80.8	6.61E+05	(K)DLLPLMASR(F)		508.2866	1015.561	0.0054	5.4	Zea mays	226496241	reticuline oxidase precursor
1581	JGP_1_4.7146.7233.2	2	12.42	87.1	9.84E+05	(K)DLLPLMASR(F)		508.2864	1015.561	0.005	5	Zea mays	226496241	reticuline oxidase precursor
1616	JGP_1_5.7488.7492.2	2	12.32	82.5	6.43E+05	(K)DLLPLMASR(F)		508.286	1015.561	0.0042	4.2	Zea mays	226496241	reticuline oxidase precursor
1758	JGP_1_5.6084.6196.2	2	11.95	70.8	4.32E+06	(K)DLLPLmASR(F)	m:Oxidized methionine	516.2841	1015.561	16.0004	5.4	Zea mays	226496241	reticuline oxidase precursor
1859	JGP_1_4.6082.6087.2	2	11.65	71.1	2.55E+06	(K)DLLPLmASR(F)	m:Oxidized methionine	516.2838	1015.561	15.9998	4.8	Zea mays	226496241	reticuline oxidase precursor
2196	JGP_1_4.7304.7309.2	2	10.76	74.6	4.57E+05	(K)DLLPLMASR(F)		508.2864	1015.561	0.005	5	Zea mays	226496241	reticuline oxidase precursor
898	JGP_1_6.6733.6738.2	2	14.78	71.6	6.35E+05	(K)VPEGFDYELYNR(N)		751.3528	1501.696	0.0025	1.7	Triticum aestivum	4158232	reversibly glycosylated polypeptide
1510	JGP_1_6.5284.5290.2	2	12.61	66.6	2.78E+05	(K)DINALEQHIK(N)		590.8194	1180.632	-0.0005	-0.5	Triticum aestivum	4158232	reversibly glycosylated polypeptide
1667	JGP_1_6.5288.5292.3	3	12.2	69.9	2.75E+05	(K)DINALEQHIK(N)		394.2188	1180.632	0.0098	8.3	Triticum aestivum	4158232	reversibly glycosylated polypeptide
1725	JGP_1_6.5589.5698.3	3	12.04	62.9	6.06E+05	(K)VICDHLSLGVK(T)	C:Carbamidomethylation	414.2307	1240.672	0.0057	4.6	Triticum aestivum	4158232	reversibly glycosylated polypeptide
1246	JGP_1_6.7267.7272.2	2	13.44	75	2.81E+05	(K)YIYTIDDDCFVAK(D)	C:Carbamidomethylation	811.8776	1622.741	0.0072	4.5	Arabidopsis thaliana	15241258	reversibly glycosylated polypeptide 4
869	JGP_1_7.8518.8546.2	2	14.91	74.7	1.72E+05	(R)FSFTVSNNIVSGLK(Y)		756.9081	1512.806	0.0033	2.2	Zea mays	226529012	rho GDP-dissociation inhibitor 1
1578	JGP_1_8.5175.5180.2	2	12.43	77.6	1.43E+05	(K)DGSLYSFR(F)		472.7311	944.447	0.0077	8.2	Zea mays	226529012	rho GDP-dissociation inhibitor 1
2454	JGP_1_7.5232.5239.2	2	10.18	66	2.12E+05	(K)DGSLYSFR(F)		472.7312	944.447	0.0079	8.4	Zea mays	226529012	rho GDP-dissociation inhibitor 1
1676	JGP_1_1.5147.5240.2	2	12.18	70	3.82E+06	(R)AAGTNAKILK(E)		493.7996	986.599	-0.0074	-7.5	Arabidopsis thaliana	18406440	ribosomal protein L2-like protein
1849	JGP_1_4.5360.5443.2	2	11.68	67.1	7.31E+05	(R)AAGTNAKILK(E)		493.7986	986.599	-0.0094	-9.5	Arabidopsis thaliana	18406440	ribosomal protein L2-like protein
1914	JGP_1_3.5216.5301.2	2	11.49	69.3	2.59E+06	(R)AAGTNAKILK(E)		493.8002	986.599	-0.0062	-6.3	Arabidopsis thaliana	18406440	ribosomal protein L2-like protein
1976	JGP_1_6.5709.5802.2	2	11.3	69.4	3.02E+06	(R)AAGTNAKILK(E)		493.7993	986.599	-0.008	-8.1	Arabidopsis thaliana	18406440	ribosomal protein L2-like protein
1990	JGP_1_6.5892.5897.2	2	11.26	71.9	2.37E+06	(R)AAGTNAKILK(E)		493.8	986.599	-0.0066	-6.7	Arabidopsis thaliana	18406440	ribosomal protein L2-like protein
2197	JGP_1_5.5502.5602.2	2	10.76	64.6	6.92E+05	(R)AAGTNAKILK(E)		493.7989	986.599	-0.0088	-8.9	Arabidopsis thaliana	18406440	ribosomal protein L2-like protein
2031	JGP_1_2.4222.4301.2	2	11.15	80.9	8.18E+05	(K)LELSDIAGR(V)		487.2711	973.531	0.0036	3.7	Arabidopsis thaliana	9293981	RNA binding protein-like
1507	JGP_1_5.6323.6326.2	2	12.62	71.6	2.93E+05	(R)DSAAVFAWK(G)		497.7552	994.499	0.0039	3.9	Arabidopsis thaliana	3242075	S-adenosyl-L-homocysteine hydrolase
2005	JGP_1_5.2545.2644.3	3	11.22	81.6	1.08E+06	(R)ITIKPQTDR(W)		357.8784	1071.616	0.005	4.6	Arabidopsis thaliana	3242075	S-adenosyl-L-homocysteine hydrolase
2023	JGP_1_5.9295.9302.3	3	11.17	71.7	2.77E+05	(K)NNAIVCNIGHFDNEIDmLGLETYPGVK(R)	C:Carbamidomethylation m:Oxidized methionine		1017.1575	3033.445	16.0135	6.1	Arabidopsis thaliana	3242075 S-adenosyl-L-homocysteine hydrolase
2054	JGP_1_4.2572.2589.3	3	11.11	69.5	1.89E+05	(R)ITIKPQTDR(W)		357.8778	1071.616	0.0032	3	Arabidopsis thaliana	3242075	S-adenosyl-L-homocysteine hydrolase
1587	JGP_1_6.4734.4832.2	2	12.41	85.7	2.99E+06	(K)FIIEK(E)	325.2009	649.392	0.0026	4	Nicotiana tabacum	198444876	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase 1	
1745	JGP_1_5.4449.4541.2	2	11.98	80.9	9.97E+05	(K)FIIEK(E)	325.2011	649.392	0.003	4.6	Nicotiana tabacum	198444876	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase 1	
2455	JGP_1_8.4524.4529.2	2	10.18	75.8	2.64E+05	(K)FIIEK(E)	325.2008	649.392	0.0024	3.7	Nicotiana tabacum	198444876	S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase 1	
415	JGP_1_1.4970.5023.3	3	17.35	79.7	2.44E+05	(R)FVIGGPHGDAGLTGR(K)		485.2598	1453.755	0.0102	7	Arabidopsis thaliana	15234354	S-adenosylmethionine synthase 2
504	JGP_1_2.4759.4762.3	3	16.76	79	2.03E+05	(R)FVIGGPHGDAGLTGR(K)		485.2595	1453.755	0.0093	6.4	Arabidopsis thaliana	15234354	S-adenosylmethionine synthase 2
546	JGP_1_1.4742.4755.3	3	16.51	83.4	3.26E+05	(K)TIFHLNPSGR(F)		381.2107	1141.611	0.0063	5.5	Arabidopsis thaliana	15234354	S-adenosylmethionine synthase 2
573	JGP_1_6.5585.5587.3	3	16.36	77	3.01E+05	(R)FVIGGPHGDAGLTGR(K)		485.2597	1453.755	0.0099	6.8	Arabidopsis thaliana	15234354	S-adenosylmethionine synthase 2
1105	JGP_1_5.5334.5336.3	3	13.93	72.8	2.75E+05	(R)FVIGGPHGDAGLTGR(K)		485.2589	1453.755	0.0075	5.2	Arabidopsis thaliana	15234354	S-adenosylmethionine synthase 2
1370	JGP_1_6.5259.5263.3	3	13.03	74.8	2.22E+05	(K)TIFHLNPSGR(F)		381.2116	1141.611	0.009	7.9	Arabidopsis thaliana	15234354	S-adenosylmethionine synthase 2
1392	JGP_1_5.5031.5038.3	3	12.98	72.1	1.43E+05	(K)TIFHLNPSGR(F)		381.2101	1141.611	0.0045	3.9	Arabidopsis thaliana	15234354	S-adenosylmethionine synthase 2
2366	JGP_1_2.4554.4554.3	3	10.38	72.9	1.29E+05	(K)TIFHLNPSGR(F)		381.2102	1141.611	0.0048	4.2	Arabidopsis thaliana	15234354	S-adenosylmethionine synthase 2
2309	JGP_1_2.1443.1506.2	2	10.48	79	1.64E+05	(K)ADPVPR(G)		327.6824	654.357	0.0006	0.9	Arabidopsis thaliana	15225432	SAUR-like auxin-responsive protein
2489	JGP_1_4.1414.1482.2	2	10.1	74.7	1.64E+05	(K)ADPVPR(G)		327.6827	654.357	0.0012	1.8	Arabidopsis thaliana	15225432	SAUR-like auxin-responsive protein
965	JGP_1_8.2068.2074.2	2	14.49	91.4	5.12E+06	(K)GAVTPIK(N)		343.2177	685.424	0.0038	5.6	Arabidopsis thaliana	18422605	senescence-associated protein 12
727	JGP_1_8.9291.9302.2	2	15.57	77.4	7.53E+04	(R)IWVFSGDTDSVVPLTATR(Y)			982.5137	1964.012	0.0078	3.9	Zea mays	226500300	serine carboxypeptidase K10B2.2 precursor
1012	JGP_1_8.8557.8560.2	2	14.29	80.1	1.37E+05	(R)YSIDALSLPTITK(W)		711.3997	1421.789	0.0035	2.5	Zea mays	226500300	serine carboxypeptidase K10B2.2 precursor
557	JGP_1_5.6019.6023.2	2	16.46	84.1	1.45E+05	(K)NAVFGDSSALAPGGVR(I)		759.391	1517.771	0.004	2.7	Arabidopsis thaliana	15236375	serine hydroxymethyltransferase 4
2308	JGP_1_5.7965.7965.2	2	10.49	60.7	7.52E+04	(K)ISATSIYFESLPYK(V)		809.9257	1618.836	0.0078	4.8	Arabidopsis thaliana	15236375	serine hydroxymethyltransferase 4
2398	JGP_1_5.1671.1680.2	2	10.31	68.4	1.96E+05	(R)IGAPAmTSR(G)	m:Oxidized methionine	460.2377	903.472	15.9965	1.7	Arabidopsis thaliana	15236375	serine hydroxymethyltransferase 4
1572	JGP_1_5.5843.5932.2	2	12.43	77.7	1.83E+05	(R)FIVFK(I)	327.2054	653.402	0.0014	2.2	Arabidopsis thaliana	3047107	Similar to actin binding protein	F6N23.12
1945	JGP_1_1.5473.5562.2	2	11.4	83	1.27E+06	(R)FIVFK(I)	327.2056	653.402	0.0018	2.8	Arabidopsis thaliana	3047107	Similar to actin binding protein	F6N23.12

1992	JGP_1_8.5744.5750.2	2	11.26	81.8	3.90E+05	(R)FIVFK(I)	327.206	653.402	0.0026	4	Arabidopsis thaliana	3047107	Similar to actin binding protein F6N23.12
2000	JGP_1_2.5232.5316.2	2	11.23	79.8	3.75E+05	(R)FIVFK(I)	327.2055	653.402	0.0016	2.5	Arabidopsis thaliana	3047107	Similar to actin binding protein F6N23.12
2024	JGP_1_6.6093.6190.2	2	11.17	81.1	2.43E+05	(R)FIVFK(I)	327.2057	653.402	0.002	3.1	Arabidopsis thaliana	3047107	Similar to actin binding protein F6N23.12
2319	JGP_1_4.5699.5783.2	2	10.46	79.9	3.23E+05	(R)FIVFK(I)	327.2056	653.402	0.0018	2.8	Arabidopsis thaliana	3047107	Similar to actin binding protein F6N23.12
2210	JGP_1_4.8347.8349.2	2	10.73	62.9	7.93E+04	(K)FDLQDLLK(A)		496.2784	991.546	0.0036	3.7	Arabidopsis thaliana	3047095 "similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 72.39)"
1394	JGP_1_3.1866.1881.2	2	12.97	87	1.16E+06	(R)VAESLR(R)		337.6967	674.383	0.003	4.4	Zea mays	226493309 small multi-drug export protein
1384	JGP_1_7.5195.5195.2	2	13	72.4	1.44E+05	(K)IIAVCADDPEYR(H)	C:Carbamidomethylation	711.3428	1421.673	0.0054	3.8	Zea mays	162458198 soluble inorganic pyrophosphatase
706	JGP_1_7.0985.0997.2	2	15.68	87.5	1.01E+05	(K)IPDGKPANR(F)		484.2696	967.532	0	0	Arabidopsis thaliana	15242465 soluble inorganic pyrophosphatase 1
804	JGP_1_7.5792.5799.2	2	15.17	86.3	3.20E+05	(K)IVAISLDDPK(A)		535.8084	1070.609	0.0003	0.3	Arabidopsis thaliana	15242465 soluble inorganic pyrophosphatase 1
247	JGP_1_4.4759.4853.2	2	18.58	84.6	1.10E+06	(R)YAGmLQYDGELK(L)	m:Oxidized methionine	702.333	1387.656	16.0025	5.4	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
423	JGP_1_4.5872.5877.2	2	17.32	90.5	3.80E+06	(R)YLVSPPEIDR(T)		594.8198	1188.626	0.0064	5.4	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
533	JGP_1_4.6064.6064.3	3	16.59	75.5	5.19E+05	(R)YAGmLQYDGELKLPSR(Y)	m:Oxidized methionine	619.6482	1840.926	16.0039	4.8	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
552	JGP_1_4.5712.5792.2	2	16.49	89	3.61E+06	(R)YLVSPPEIDR(T)		594.8194	1188.626	0.0056	4.7	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
567	JGP_1_4.4929.5040.2	2	16.38	80.6	7.64E+05	(R)YAGmLQYDGELK(L)	m:Oxidized methionine	702.3325	1387.656	16.0015	4.7	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
736	JGP_1_4.5988.6000.2	2	15.49	75.5	3.46E+05	(R)YAGMLQYDGELK(L)		694.3337	1387.656	0.0039	2.8	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
1001	JGP_1_5.5952.5956.2	2	14.34	82.7	4.73E+05	(R)YLVSPPEIDR(T)		594.8179	1188.626	0.0026	2.2	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
1358	JGP_1_4.7121.7203.3	3	13.08	66.4	5.40E+05	(K)FGHVTFFWNGNR(S)		494.5771	1481.707	0.0095	6.4	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
1763	JGP_1_6.6285.6288.2	2	11.94	66.9	2.11E+05	(R)YLVSPPEIDR(T)		594.8192	1188.626	0.0052	4.4	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
1870	JGP_1_3.5624.5629.2	2	11.61	72	1.84E+05	(R)YLVSPPEIDR(T)		594.8166	1188.626	0	0	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
2127	JGP_1_4.1379.1456.2	2	10.92	79.4	1.35E+06	(K)FDQVR(V)	332.6751	664.341	0.0016	2.4	Arabidopsis thaliana	2160168	"Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
2267	JGP_1_4.2539.2641.2	2	10.62	81.5	2.76E+06	(R)DAILSGK(F)		352.2038	703.399	0.0018	2.6	Arabidopsis thaliana	2160168 "Strong similarity to R. communis phosphoglycerate mutase (gb|X70652). ESTs gb|T41853,gb|T76648 come from this gene"
949	JGP_1_3.2679.2842.2	2	14.55	86.6	8.39E+05	(R)SPIVVK(L)		321.7133	642.418	0.0008	1.3	Arabidopsis thaliana	3695019 subtilisin-like protease
2156	JGP_1_6.7231.7237.4	4	10.86	68.3	3.49E+05	(K)KGGTEHLGLPVFNSVAEAK(A)			489.269	1954.039	0.0149	7.6	Arabidopsis thaliana 15241592 Succinyl-CoA ligase [GDP-forming] subunit alpha-1
162	JGP_1_6.5574.5664.3	3	19.49	85.7	6.67E+05	(R)LIGPNCPGIIKPGECK(I)	C:Carbamidomethylation	584.9789	1752.914	0.0086	4.9	Arabidopsis thaliana	15237260 Succinyl-CoA ligase [GDP-forming] subunit alpha-2
1051	JGP_1_6.2852.2857.2	2	14.13	73.9	9.41E+05	(R)VICQGITGK(N)	C:Carbamidomethylation	488.2688	975.529	0.0011	1.2	Arabidopsis thaliana	15237260 Succinyl-CoA ligase [GDP-forming] subunit alpha-2
464	JGP_1_6.10317.10393.2	2	17.07	87.7	1.47E+05	(K)AILVNIFGGIMK(C)		638.3812	1275.749	0.0058	4.5	Arabidopsis thaliana	15225353 Succinyl-CoA ligase [GDP-forming] subunit beta
623	JGP_1_6.9327.9395.2	2	16.15	82.4	3.21E+05	(K)AILVNIFGGImK(C)	m:Oxidized methionine	646.3764	1275.749	15.9962	1	Arabidopsis thaliana	15225353 Succinyl-CoA ligase [GDP-forming] subunit beta
903	JGP_1_6.2563.2657.2	2	14.77	78.3	8.84E+05	(K)VYLCEK(L)	C:Carbamidomethylation	406.2054	811.402	0.0017	2.1	Arabidopsis thaliana	15225353 Succinyl-CoA ligase [GDP-forming] subunit beta
1687	JGP_1_2.2948.2954.2	2	12.15	73.1	5.99E+04	(K)VPVVVR(L)		334.7267	668.445	0.0008	1.1	Arabidopsis thaliana	15225353 Succinyl-CoA ligase [GDP-forming] subunit beta
1777	JGP_1_6.3223.3327.2	2	11.89	85.1	1.44E+06	(K)VPVVVR(L)		334.7272	668.445	0.0018	2.6	Arabidopsis thaliana	15225353 Succinyl-CoA ligase [GDP-forming] subunit beta
1950	JGP_1_6.6114.6199.2	2	11.4	64.3	7.96E+05	(K)LNFDDNAAFR(Q)		591.7832	1182.554	0.0053	4.5	Arabidopsis thaliana	15225353 Succinyl-CoA ligase [GDP-forming] subunit beta
564	JGP_1_6.6259.6353.2	2	16.4	93.3	1.03E+06	(K)VPIDVFK(G)		409.2458	817.482	0.0025	3.1	Solanum tuberosum	76573373 succinyl-CoA ligase beta subunit-like protein
1272	JGP_1_1.5659.5664.2	2	13.36	70.1	1.03E+05	(K)VPIDVFK(G)		409.2412	817.482	-0.0067	-8.2	Solanum tuberosum	76573373 succinyl-CoA ligase beta subunit-like protein
2022	JGP_1_5.6018.6024.2	2	11.17	61.6	8.59E+04	(K)VPIDVFK(G)		409.245	817.482	0.0009	1.1	Solanum tuberosum	76573373 succinyl-CoA ligase beta subunit-like protein
2283	JGP_1_2.5353.5363.2	2	10.56	64.8	7.80E+04	(K)VPIDVFK(G)		409.243	817.482	-0.0031	-3.8	Solanum tuberosum	76573373 succinyl-CoA ligase beta subunit-like protein
426	JGP_1_6.5522.5625.2	2	17.3	83.2	5.18E+05	(K)TAGPLIIACSK(G)	C:Carbamidomethylation	565.8136	1130.624	-0.0039	-3.4	Zea mays	226500228 succinyl-CoA ligase beta-chain
769	JGP_1_6.8398.8516.3	3	15.34	72.6	1.84E+05	(K)LHGGTPANFLDVGGSASEGQVVEAFK(I)			863.0948	2587.279	-0.0089	-3.4	Zea mays 226500228 succinyl-CoA ligase beta-chain
1118	JGP_1_6.1593.1682.2	2	13.88	73.9	7.15E+05	(K)GITDEDAAK(V)		460.2239	919.437	0.0038	4.1	Zea mays	226500228 succinyl-CoA ligase beta-chain
1883	JGP_1_6.6544.6559.2	2	11.58	61.1	2.58E+05	(K)LYELFCK(C)	C:Carbamidomethylation	486.7495	972.486	0.0058	6	Zea mays	226500228 succinyl-CoA ligase beta-chain
2276	JGP_1_6.4610.4702.2	2	10.58	68.9	9.51E+05	(K)YGINVPR(G)		409.7313	818.452	0.0034	4.2	Zea mays	226500228 succinyl-CoA ligase beta-chain
2490	JGP_1_6.1702.1710.2	2	10.1	68	3.76E+05	(R)LEGTNVDQGK(R)		530.7683	1060.527	0.0024	2.3	Zea mays	226500228 succinyl-CoA ligase beta-chain
1952	JGP_1_5.5652.5656.2	2	11.39	68.4	1.93E+05	(K)DLIHWR(H)		420.2315	839.452	0.0035	4.1	Triticum aestivum	18146823 sucrose:sucrose 1-fructosytransferase
2100	JGP_1_5.2264.2268.2	2	11	70.2	4.66E+05	(R)SPTLYK(E)		354.7009	708.393	0.0019	2.6	Triticum aestivum	12958605 sucrose-6F-phosphate phosphohydrolase SPP1
192	JGP_1_5.7174.7179.2	2	19.16	81.9	1.98E+05	(K)IIYSGGQDLDILPQGAGK(G)			922.9933	1844.975	0.0041	2.2	Zea mays 162463022 sucrose-phosphatase 1
977	JGP_1_5.6869.6873.2	2	14.46	77.5	1.90E+05	(R)FDLWESEGDVR(V)		676.8132	1352.612	0.0074	5.5	Zea mays	162463022 sucrose-phosphatase 1
1201	JGP_1_5.6715.6718.2	2	13.57	70.1	2.22E+05	(K)GQALAYLLK(K)		488.7954	976.583	0.0009	1	Arabidopsis thaliana	15223847 sucrose-phosphatase 1
1296	JGP_1_5.6723.6810.3	3	13.3	77.1	1.64E+05	(K)AESPEGFVLTHIQK(T)		519.2766	1555.812	0.0038	2.4	Zea mays	162463022 sucrose-phosphatase 1

1611	JGP_1_1.6433.6465.2	2	12.33	65.7	2.38E+05	(K)GQALAYLLK(K)		488.7948	976.583	-0.0003	-0.3	Arabidopsis thaliana	15223847	sucrose-phosphatase 1	
2460	JGP_1_5.7170.7173.3	3	10.17	67.1	2.02E+05	(K)IIYSGGQDLDILPQGAGK(G)			615.6669	1844.975	0.0109	5.9	Zea mays	162463022	sucrose-phosphatase 1
1539	JGP_1_5.5884.5979.2	2	12.51	71.3	3.88E+05	(R)FYVLYEK(W)		481.2566	961.503	0.003	3.1	Zea mays	162460308	sucrose-phosphatase 2	
1622	JGP_1_8.4317.4321.2	2	12.3	80.8	1.00E+06	(K)AVAVLGSSEGVK(G)		558.8189	1116.626	0.0046	4.1	Zea mays	162463249	superoxide dismutase [Cu-Zn] 4AP	
2115	JGP_1_2.8015.8082.2	2	10.96	78.9	2.24E+06	(R)SIEVREVDVTR(D)		651.8657	1302.701	0.0229	17.6	Arabidopsis thaliana	8671773	T10O22.24	
2098	JGP_1_8.10222.10224.5	5	11.01	63.4	2.07E+05	(K)SSEIGFYVITPLLPIPNEPNRSGIYSLYAQTK(L)				714.3844	3567.873	0.0195	5.5	Arabidopsis thaliana	8778690	T1N15.12
53	JGP_1_7.10154.10225.4	4	21.83	98	2.10E+05	(K)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	585.0624	2337.212	0.0159	6.8	Triticum aestivum	9798603	TaWIN1	
57	JGP_1_7.10233.10238.3	3	21.62	87.7	1.50E+06	(K)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	779.7469	2337.212	0.0143	6.1	Triticum aestivum	9798603	TaWIN1	
126	JGP_1_7.6919.7003.3	3	20.07	81.1	1.53E+06	(K)AAQDIALADLAPTHPIR(L)		591.6628	1772.965	0.0085	4.8	Triticum aestivum	9798603	TaWIN1	
134	JGP_1_7.10106.10173.3	3	19.98	81.2	1.81E+06	(K)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	779.7475	2337.212	0.0161	6.9	Triticum aestivum	9798603	TaWIN1	
324	JGP_1_7.9744.9748.3	3	17.97	82.9	1.29E+05	(K)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	779.7457	2337.212	0.0107	4.6	Triticum aestivum	9798603	TaWIN1	
334	JGP_1_7.6961.6966.2	2	17.92	86.3	1.97E+05	(K)AAQDIALADLAPTHPIR(L)		886.9926	1772.965	0.0126	7.1	Triticum aestivum	9798603	TaWIN1	
390	JGP_1_2.6169.6172.3	3	17.47	80.6	1.46E+05	(K)AAQDIALADLAPTHPIR(L)		591.6642	1772.965	0.0127	7.2	Triticum aestivum	9798603	TaWIN1	
507	JGP_1_2.8844.8847.3	3	16.74	76.9	1.31E+05	(K)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	779.7449	2337.212	0.0083	3.5	Triticum aestivum	9798603	TaWIN1	
825	JGP_1_1.9369.9376.3	3	15.06	71	2.07E+05	(K)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	779.7449	2337.212	0.0083	3.5	Triticum aestivum	9798603	TaWIN1	
1069	JGP_1_1.6543.6549.3	3	14.06	75	1.95E+05	(K)AAQDIALADLAPTHPIR(L)		591.6609	1772.965	0.0028	1.6	Triticum aestivum	9798603	TaWIN1	
1381	JGP_1_7.11941.11941.3	3	13.01	74.2	7.20E+04	(K)QAFDEAISELDSLGEESYKDSTLImQLLR(D)	m:Oxidized methionine	1106.5356	3301.614	15.9778	-5.2	Triticum aestivum	9798603	TaWIN1	
2151	JGP_1_7.7076.7076.3	3	10.87	61.5	4.38E+05	(K)AAQDIALADLAPTHPIR(L)		591.6635	1772.965	0.0106	6	Triticum aestivum	9798603	TaWIN1	
2478	JGP_1_5.9904.9904.3	3	10.12	60.8	9.68E+04	(K)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	779.743	2337.212	0.0026	1.1	Triticum aestivum	9798603	TaWIN1	
576	JGP_1_8.3837.3841.2	2	16.33	89.4	3.19E+06	(K)VDVDELK(D)		409.2205	817.43	0.0035	4.3	Triticum aestivum	27461140	thioredoxin H	
1926	JGP_1_8.8767.8854.2	2	11.46	71.6	3.30E+05	(R)IMAPIFADLAK(K)		595.3377	1189.665	0.0032	2.7	Triticum aestivum	16517113	thioredoxin H	
416	JGP_1_8.5697.5850.3	3	17.35	86.6	2.63E+06	(R)AIAPLFVEHAK(K)		399.2349	1195.683	0.0068	5.7	Zea mays	162459002	thioredoxin h homolog2	
484	JGP_1_1.5619.5691.3	3	16.89	86.4	3.88E+05	(R)AIAPLFVEHAK(K)		399.2344	1195.683	0.0053	4.4	Zea mays	162459002	thioredoxin h homolog2	
1437	JGP_1_8.5759.5762.2	2	12.86	68.7	5.09E+05	(R)AIAPLFVEHAK(K)		598.3471	1195.683	0.0036	3	Zea mays	162459002	thioredoxin h homolog2	
2450	JGP_1_8.6469.6554.2	2	10.19	69.3	1.18E+06	(R)VEINVLVEK(C)		521.8184	1042.614	0.0152	14.6	Arabidopsis thaliana	15230522	TIR-NBS-LRR class disease resistance protein	
2218	JGP_1_6.7883.7885.2	2	10.72	63.9	3.66E+04	(R)VTSVASFFVSR(V)		600.3277	1199.642	0.0062	5.2	Solanum tuberosum	77999311	transaldolase-like protein	
1268	JGP_1_3.2296.2301.2	2	13.37	87.2	4.96E+05	(K)IDDELK(A)		366.6942	732.377	0.0037	5.1	Arabidopsis thaliana	15233477	"Transcription initiation factor TFIIE, beta subunit"	
1855	JGP_1_5.3451.3465.2	2	11.67	68.4	2.07E+05	(K)VSEIVAK(I)		373.2269	745.445	0.0011	1.5	Arabidopsis thaliana	15232013	transducin/WD40 domain-containing protein	
2508	JGP_1_4.3459.3462.2	2	10.05	75.7	2.12E+05	(K)GIIYDGK(T)		383.2125	765.414	0.0036	4.7	Arabidopsis thaliana	22331145	transducin/WD40 domain-containing protein	
2219	JGP_1_8.4844.4859.2	2	10.72	73.5	2.44E+05	(K)LAPVFK(C)		337.7153	674.424	-0.0002	-0.4	Arabidopsis thaliana	18394746	transducin/WD-40 repeat-containing protein	
1993	JGP_1_1.2725.2731.2	2	11.25	73.2	1.59E+05	(K)TYPQQAGTIR(K)		567.7962	1134.59	-0.0051	-4.5	Arabidopsis thaliana	15223002	translation initiation factor eIF-5A	
1015	JGP_1_8.7042.7134.2	2	14.28	82	1.06E+06	(K)VVDIVDTFR(L)		532.2954	1063.578	0.0053	5	Arabidopsis thaliana	15228276	translationally-controlled tumor protein-like protein	
1696	JGP_1_7.6934.6938.2	2	12.14	68.6	2.84E+05	(K)VVDIVDTFR(L)		532.2868	1063.578	-0.0119	-11.2	Arabidopsis thaliana	15228276	translationally-controlled tumor protein-like protein	
133	JGP_1_7.6047.6052.2	2	19.99	91.9	7.66E+05	(R)AILGESNEFVGDK(V)		689.849	1378.685	0.0058	4.2	Solanum tuberosum	77745458	triose phosphate isomerase cytosolic isoform-like	
226	JGP_1_8.6070.6168.2	2	18.83	89.6	1.55E+06	(R)AILGESNEFVGDK(V)		689.8503	1378.685	0.0084	6.1	Solanum tuberosum	77745458	triose phosphate isomerase cytosolic isoform-like	
437	JGP_1_7.5895.5968.2	2	17.25	83.7	6.31E+05	(R)AILGESNEFVGDK(V)		689.8483	1378.685	0.0044	3.2	Solanum tuberosum	77745458	triose phosphate isomerase cytosolic isoform-like	
529	JGP_1_8.6428.6514.2	2	16.62	81.9	7.07E+05	(K)FFVGGNWK(C)		477.7475	954.483	0.0045	4.7	Arabidopsis thaliana	15226479	triosephosphate isomerase	
12	JGP_1_7.4122.4128.3	3	23.32	94.4	2.70E+06	(K)VATPAQAQEVHASLR(D)		526.6212	1577.839	0.0096	6.1	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
23	JGP_1_8.4143.4252.3	3	22.81	95.6	4.53E+06	(K)VATPAQAQEVHASLR(D)		526.6211	1577.839	0.0093	5.9	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
39	JGP_1_8.4196.4203.2	2	22.23	95	2.89E+05	(K)VATPAQAQEVHASLR(D)		789.4237	1577.839	0.0007	0.4	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
66	JGP_1_7.4173.4194.2	2	21.23	84.2	1.55E+05	(K)VATPAQAQEVHASLR(D)		789.422	1577.839	-0.0027	-1.7	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
98	JGP_1_8.4056.4166.2	2	20.63	89	2.70E+06	(R)IIYGGSVTAANCK(E)	C:Carbamidomethylation	677.3487	1353.683	0.007	5.2	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
128	JGP_1_8.10597.10600.4	4	20.05	97.9	2.57E+05	(K)KGGAFTGEVSAEmLVNLGVPWVILGHSER(R)	m:Oxidized methionine	768.1552	3053.588	16.0113	5.3	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
344	JGP_1_7.4055.4060.2	2	17.84	85.1	1.77E+06	(R)IIYGGSVTAANCK(E)	C:Carbamidomethylation	677.3491	1353.683	0.0078	5.8	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
1008	JGP_1_7.6204.6207.2	2	14.31	70.4	2.41E+05	(R)ALLGESSDFVADK(V)		676.3435	1351.674	0.0057	4.2	Zea mays	226529672	"triosephosphate isomerase, cytosolic"	
1031	JGP_1_7.10485.10491.4	4	14.19	87.1	1.27E+05	(K)KGGAFTGEVSAEmLVNLGVPWVILGHSER(R)	m:Oxidized methionine	768.1553	3053.588	16.0117	5.5	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
1071	JGP_1_7.7860.7865.2	2	14.06	76.6	9.75E+04	(R)LDFAVAAQNCWVR(K)	C:Carbamidomethylation	775.3889	1549.758	0.0125	8.1	Zea mays	226529672	"triosephosphate isomerase, cytosolic"	
1190	JGP_1_8.4278.4281.2	2	13.6	67.9	8.36E+05	(R)EAGSTMEVVAAQTK(A)		711.3546	1421.694	0.0079	5.5	Zea mays	195605636	"triosephosphate isomerase, cytosolic"	
1317	JGP_1_7.4259.4274.2	2	13.23	72.4	4.73E+05	(R)EAGSTMEVVAAQTK(A)		711.3528	1421.694	0.0043	3	Zea mays	195605636	"triosephosphate isomerase, cytosolic"	
2073	JGP_1_8.11084.11084.3	3	11.07	67.7	1.06E+05	(K)GGAFTGEVSAEmLVNLGVPWVILGHSER(R)	m:Oxidized methionine	981.1702	2925.493	16.0033	2.9	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	
2133	JGP_1_8.4963.4967.2	2	10.91	61.1	5.02E+04	(K)VAYALSQGLK(V)		525.3069	1049.599	0.0076	7.2	Zea mays	226495391	"triosephosphate isomerase, cytosolic"	

2484	JGP_1_3.4972.4976.2	2	10.11	76.2	4.86E+05	(R)LGFSLTK(D)		383.2306	765.451	0.0034	4.5	Arabidopsis thaliana	42562367	tRNA nucleotidyltransferase (CCA-adding enzyme)	
2134	JGP_1_1.8587.8587.3	3	10.9	64.8	2.62E+04	(R)AIFVDLEPTVIDEVR(T)		572.6474	1715.921	0.0062	3.6	Zea mays	162458676	tubulin alpha-3 chain	
631	JGP_1_1.8331.8399.3	3	16.09	84.9	2.01E+05	(R)LHFFmVGFAPLTSR(G)	m:Oxidized methionine	546.9571	1622.851	16.0056	6.5	Zea mays	162462765	tubulin beta-5 chain	
1037	JGP_1_1.8266.8339.2	2	14.17	88.2	2.67E+05	(K)LAVNLIPFPR(L)		570.3517	1139.694	0.0026	2.3	Zea mays	162462765	tubulin beta-5 chain	
2365	JGP_1_1.1980.1986.3	3	10.38	75.1	1.02E+05	(K)IREEYPDR(M)		359.8517	1077.532	0.0082	7.6	Zea mays	162462765	tubulin beta-5 chain	
2425	JGP_1_7.7269.7349.3	3	10.24	74.5	1.07E+06	(R)IAVDTVVNAVGAERK(E)		514.6308	1541.865	0.0133	8.6	Arabidopsis thaliana	22331218	ubiquitin carboxyl-terminal hydrolase 14	
895	JGP_1_8.10770.10836.3	3	14.8	82.5	2.65E+05	(K)VLLSICSLLTDPNPDDPLVPEIAHmYK(T)	C:Carbamidomethylation m:Oxidized methionine	1022.8623	3050.558	16.0146	6.4	Arabidopsis thaliana	18423494	ubiquitin-conjugating enzyme E2 10	
1006	JGP_1_8.11227.11265.4	4	14.32	73.5	8.04E+03	(K)VLLSICSLLTDPNPDDPLVPEIAHMYK(T)	C:Carbamidomethylation	763.3999	3050.558	0.0201	6.6	Arabidopsis thaliana	18423494	ubiquitin-conjugating enzyme E2 10	
1813	JGP_1_8.11225.11225.3	3	11.78	71.5	1.36E+05	(K)VLLSICSLLTDPNPDDPLVPEIAHMYK(T)	C:Carbamidomethylation	1017.5252	3050.558	0.0033	1.1	Arabidopsis thaliana	18423494	ubiquitin-conjugating enzyme E2 10	
527	JGP_1_8.9411.9460.2	2	16.63	88.7	1.99E+05	(K)VFSVPEAAPFTAVLK(Y)		788.4449	1575.878	0.0044	2.8	Zea mays	226492858	ubiquitin-fold modifier 1	
2191	JGP_1_5.4048.4063.2	2	10.77	82.8	1.15E+05	(R)LEGLIK(M)		336.7215	672.429	0.0067	9.9	Arabidopsis thaliana	18390863	UDP-apiose/xylose synthase	
805	JGP_1_1.5278.5280.2	2	15.16	74.2	1.89E+05	(K)LAANAFLAQR(I)		537.8054	1074.605	-0.0019	-1.8	Glycine max	351726550	UDP-glucose 6-dehydrogenase	
1165	JGP_1_5.5658.5669.2	2	13.68	71.1	1.69E+05	(K)LAANAFLAQR(I)		537.8066	1074.605	0.0005	0.4	Glycine max	351726550	UDP-glucose 6-dehydrogenase	
1762	JGP_1_5.7600.7610.2	2	11.94	71.9	9.55E+04	(R)IITTNLWSAELSK(L)		738.4086	1475.81	-0.0005	-0.3	Zea mays	226505792	UDP-glucose 6-dehydrogenase	
200	JGP_1_5.3560.3669.2	2	19.09	96.8	6.90E+06	(R)LVEADALK(M)		429.7525	858.493	0.0046	5.4	Nicotiana tabacum	17402533	UDP-glucose pyrophosphorylase	
865	JGP_1_2.3361.3446.2	2	14.91	84.9	4.87E+05	(R)LVEADALK(M)		429.7512	858.493	0.002	2.3	Nicotiana tabacum	17402533	UDP-glucose pyrophosphorylase	
968	JGP_1_4.3544.3647.2	2	14.48	88.4	1.19E+06	(R)LVEADALK(M)		429.7511	858.493	0.0018	2.1	Nicotiana tabacum	17402533	UDP-glucose pyrophosphorylase	
1207	JGP_1_5.3434.3440.3	3	13.56	63.1	2.52E+05	(K)RLVEADALK(M)		338.87	1014.594	0.0012	1.2	Nicotiana tabacum	17402533	UDP-glucose pyrophosphorylase	
1304	JGP_1_7.3837.3856.2	2	13.27	80.2	5.03E+05	(R)LVEADALK(M)		429.7506	858.493	0.0008	0.9	Nicotiana tabacum	17402533	UDP-glucose pyrophosphorylase	
1375	JGP_1_5.2969.3063.2	2	13.02	93.6	6.53E+06	(K)SVIEVR(N)		351.7134	702.414	0.0051	7.2	Nicotiana tabacum	17402533	UDP-glucose pyrophosphorylase	

number	filename	parent_charge	score	percent_scored_peak_intensity	totalIntensity	sequence	modifications	parent_m_over_z	matched_parent_mass	delta_parent_mass	delta_parent_mass_ppm	species	accession_number	entry_name
1317.389655	JGP_1_8.10196.10205.4	2.32771066	13.94472358	77.9030084	2.23E+06	(R)HIEILGYLLYVAK(V)		570.215843	1342.052111	1.802331226	3.548392979	Zea mays	115388117.5	15 kDa zinc-binding protein
1317.443057	JGP_1_7.6050.6055.3	2.327689396	13.94459987	77.90352848	2.23E+06	(K)TVDVEELTVEER(N)		570.1829491	1341.972007	1.802214772	3.54818893	Nicotiana tabacum	115396557.4	14-3-3 e-1 protein
1317.496459	JGP_1_3.6554.6554.4	2.327668131	13.94447616	77.90404855	2.23E+06	(K)AAQDIAVAELAPTHPIR(L)		570.1500552	1341.891903	1.802098318	3.547984882	Solanum tuberosum	115404997.3	14-3-3 protein
1317.549861	JGP_1_8.7176.7176.4	2.327646867	13.94435245	77.90456862	2.23E+06	(K)AAQDIAVAELAPTHPIR(L)		570.1171612	1341.8118	1.801981865	3.547780833	Solanum tuberosum	115413437.3	14-3-3 protein
1317.603263	JGP_1_7.4222.4336.3	2.327625602	13.94422874	77.90508869	2.23E+06	(R)YLAEFK(S)		570.0842673	1341.731696	1.801865411	3.547576784	Arabidopsis thaliana	115421877.2	14-3-3-like protein GF14 kappa
1317.656665	JGP_1_7.5715.5718.3	2.327604338	13.94410503	77.90560876	2.23E+06	(R)NLLSVAYK(N)		570.0513733	1341.651593	1.801748957	3.547372735	Arabidopsis thaliana	115430317.1	14-3-3-like protein GF14 kappa
1317.710067	JGP_1_8.5714.5747.3	2.327583073	13.94398132	77.90612883	2.23E+06	(R)NLLSVAYK(N)		570.0184794	1341.571489	1.801632503	3.547168687	Arabidopsis thaliana	115438757.1	14-3-3-like protein GF14 kappa
1317.763469	JGP_1_2.5133.5144.3	2.327561809	13.94385761	77.9066489	2.23E+06	(R)NLLSVAYK(N)		569.9855855	1341.491386	1.801516049	3.546964638	Arabidopsis thaliana	115447197	14-3-3-like protein GF14 kappa
1317.816871	JGP_1_7.0912.0917.3	2.327540544	13.9437339	77.90716897	2.23E+06	(K)LAEQAER(Y)		569.9526915	1341.411282	1.801399595	3.546760589	Arabidopsis thaliana	115455636.9	14-3-3-like protein GF14 kappa
1317.870273	JGP_1_1.5358.5436.3	2.32751928	13.94361019	77.90768904	2.23E+06	(R)NLLSVAYK(N)		569.9197976	1341.331178	1.801283141	3.54655654	Arabidopsis thaliana	115464076.8	14-3-3-like protein GF14 kappa
1317.923674	JGP_1_7.2236.2239.3	2.327498015	13.94348648	77.90820911	2.24E+06	(R)IVSSIEQK(E)		569.8869037	1341.251075	1.801166688	3.546352491	Arabidopsis thaliana	115472516.8	14-3-3-like protein GF14 kappa
1317.977076	JGP_1_4.7660.7781.3	2.327476751	13.94336277	77.90872918	2.24E+06	(R)LDQLQILLK(G)		569.8540097	1341.170971	1.801050234	3.546148443	Zea mays	115480956.7	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"
1318.030478	JGP_1_1.7442.7531.3	2.327455486	13.94323906	77.90924925	2.24E+06	(R)LDQLQILLK(G)		569.8211158	1341.090868	1.80093378	3.545944394	Zea mays	115489396.6	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"
1318.08388	JGP_1_5.7760.7863.3	2.327434222	13.94311535	77.90976932	2.24E+06	(R)LDQLQILLK(G)		569.7882219	1341.010764	1.800817326	3.545740345	Zea mays	115497836.5	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"
1318.137282	JGP_1_4.7479.7589.3	2.327412957	13.94299164	77.91028939	2.24E+06	(R)LDQLQILLK(G)		569.7553279	1340.930661	1.800700872	3.545536296	Zea mays	115506276.5	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"
1318.190684	JGP_1_2.6983.7052.3	2.327391693	13.94286792	77.91080946	2.24E+06	(R)LDQLQILLK(G)		569.722434	1340.850557	1.800584418	3.545332248	Zea mays	115514716.4	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"
1318.244086	JGP_1_6.8237.8245.3	2.327370428	13.94274421	77.91132953	2.24E+06	(R)LDQLQILLK(G)		569.68954	1340.770453	1.800467964	3.545128199	Zea mays	115523156.3	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"
1318.297488	JGP_1_5.7833.7833.3	2.327349164	13.9426205	77.9118496	2.24E+06	(R)LDQLQILLK(G)		569.6566461	1340.69035	1.800351511	3.54492415	Zea mays	115531596.2	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"
1318.35089	JGP_1_4.7484.7484.3	2.327327899	13.94249679	77.91236967	2.24E+06	(R)LDQLQILLK(G)		569.6237522	1340.610246	1.800235057	3.544720101	Zea mays	115540036.2	"2,3-bisphosphoglycerate-independent phosphoglycerate mutase"
1318.404292	JGP_1_1.7167.7170.4	2.327306635	13.94237308	77.91288974	2.24E+06	(R)IDHILGFFR(I)		569.5908582	1340.530143	1.800118603	3.544516052	Arabidopsis thaliana	115548476.1	4-alpha-glucanotransferase
1318.457693	JGP_1_3.7715.7820.5	2.32728537	13.94224937	77.91340981	2.24E+06	(K)SEHAFYLDWAVHSFR(I)		569.5579643	1340.450039	1.800002149	3.544312004	Arabidopsis thaliana	115556916	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.511095	JGP_1_3.5293.5376.4	2.327264105	13.94212566	77.91392988	2.24E+06	(K)YGAGIGPGVYDIHSPR(I)		569.5250704	1340.369936	1.799885695	3.544107955	Arabidopsis thaliana	115565356	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.564497	JGP_1_3.6204.6281.3	2.327242841	13.94200195	77.91444995	2.24E+06	(K)YLFAGVVDGR(N)		569.4921764	1340.289832	1.799769241	3.543903906	Arabidopsis thaliana	115573795.9	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.617899	JGP_1_4.5523.5529.4	2.327221576	13.94187824	77.91497002	2.24E+06	(K)YGAGIGPGVYDIHSPR(I)		569.4592825	1340.209728	1.799652788	3.543699857	Arabidopsis thaliana	115582235.8	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.671301	JGP_1_3.6556.6561.3	2.327200312	13.94175453	77.91549009	2.24E+06	(K)SWLAFAAQK(V)		569.4263885	1340.129625	1.799536334	3.543495809	Arabidopsis thaliana	115590675.7	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.724703	JGP_1_3.9441.9513.3	2.327179047	13.94163082	77.91601016	2.25E+06	(K)GmLTGPVTILNWSFVR(N)	m:Oxidized methionine	569.3934946	1340.049521	1.79941988	3.54329176	Arabidopsis thaliana	115599115.7	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase

1318.778105	JGP_1_4.6509.6514.3	2.327157783	13.94150711	77.91653023	2.25E+06	(K)YLFAGVVDGR(N)		569.3606007	1339.969418	1.799303426	3.543087711	Arabidopsis thaliana	115607555.6	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.831507	JGP_1_3.8033.8039.3	2.327136518	13.9413834	77.9170503	2.25E+06	(K)FALESFWDGK(S)		569.3277067	1339.889314	1.799186972	3.542883662	Arabidopsis thaliana	115615995.5	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.884909	JGP_1_3.6366.6371.3	2.327115254	13.94125969	77.91757037	2.25E+06	(K)YLFAGVVDGR(N)		569.2948128	1339.809211	1.799070518	3.542679613	Arabidopsis thaliana	115624435.4	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.938311	JGP_1_3.7831.7968.3	2.327093989	13.94113598	77.91809044	2.25E+06	(K)FALESFWDGK(S)		569.2619189	1339.729107	1.798954064	3.542475565	Arabidopsis thaliana	115632875.4	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1318.991712	JGP_1_4.9765.9769.3	2.327072725	13.94101227	77.91861051	2.25E+06	(K)GmLTGPVTILNWSFVR(N)	m:Oxidized methionine	569.2290249	1339.649003	1.798837611	3.542271516	Arabidopsis thaliana	115641315.3	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1319.045114	JGP_1_5.6700.6705.3	2.32705146	13.94088856	77.91913058	2.25E+06	(K)YLFAGVVDGR(N)		569.196131	1339.5689	1.798721157	3.542067467	Arabidopsis thaliana	115649755.2	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1319.098516	JGP_1_1.6315.6329.3	2.327030196	13.94076485	77.91965066	2.25E+06	(K)YLFAGVVDGR(N)		569.1632371	1339.488796	1.798604703	3.541863418	Arabidopsis thaliana	115658195.2	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1319.151918	JGP_1_3.7775.7775.4	2.327008931	13.94064114	77.92017073	2.25E+06	(K)SEHAFYLDWAVHSFR(I)		569.1303431	1339.408693	1.798488249	3.541659369	Arabidopsis thaliana	115666635.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1319.20532	JGP_1_6.7046.7050.3	2.326987667	13.94051743	77.9206908	2.25E+06	(K)YLFAGVVDGR(N)		569.0974492	1339.328589	1.798371795	3.541455321	Arabidopsis thaliana	115675075	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1319.258722	JGP_1_2.5963.5984.3	2.326966402	13.94039372	77.92121087	2.25E+06	(K)YLFAGVVDGR(N)		569.0645552	1339.248486	1.798255341	3.541251272	Arabidopsis thaliana	115683514.9	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1319.312124	JGP_1_3.4013.4111.3	2.326945138	13.94027001	77.92173094	2.25E+06	(K)VVEVNALAK(A)		569.0316613	1339.168382	1.798138888	3.541047223	Arabidopsis thaliana	115691954.9	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
1319.365526	JGP_1_5.6605.6605.3	2.326923873	13.9401463	77.92225101	2.25E+06	(K)GLLYLGmGVSGGEEGAR(N)	m:Oxidized methionine	568.9987674	1339.088279	1.798022434	3.540843174	Arabidopsis thaliana	115700394.8	6-phosphogluconate dehydrogenase
1319.418928	JGP_1_5.5689.5689.3	2.326902609	13.94002259	77.92277108	2.25E+06	(K)VAAQVPDSGPCVTYIGK(G)	C:Carbamidomethylation	568.9658734	1339.008175	1.79790598	3.540639126	Glycine max	115708834.7	6-phosphogluconate dehydrogenase
1319.47233	JGP_1_7.8416.8451.3	2.326881344	13.93989888	77.92329115	2.25E+06	(K)LAEPPYLEAVDWSK(W)		568.9329795	1338.928071	1.797789526	3.540435077	Zea mays	115717274.6	6-phosphogluconolactonase
1319.525731	JGP_1_7.7659.7738.3	2.32686008	13.93977517	77.92381122	2.26E+06	(K)LAFDGFLSK(V)		568.9000856	1338.847968	1.797673072	3.540231028	Arabidopsis thaliana	115725714.6	6-phosphogluconolactonase 4
1319.579133	JGP_1_7.7506.7584.3	2.326838815	13.93965146	77.92433129	2.26E+06	(K)LAFDGFLSK(V)		568.8671916	1338.767864	1.797556618	3.540026979	Arabidopsis thaliana	115734154.5	6-phosphogluconolactonase 4
1319.632535	JGP_1_5.2611.2769.3	2.326817551	13.93952775	77.92485136	2.26E+06	(K)VPIPDK(N)		568.8342977	1338.687761	1.797440164	3.53982293	Arabidopsis thaliana	115742594.4	6-phosphogluconolactonase 5
1319.685937	JGP_1_4.6234.6347.3	2.326796286	13.93940404	77.92537143	2.26E+06	(R)LLPDLPK(I)		568.8014038	1338.607657	1.797323711	3.539618882	Arabidopsis thaliana	115751034.3	ABC transporter-like protein
1319.739339	JGP_1_3.8966.8974.4	2.326775022	13.93928033	77.9258915	2.26E+06	(R)VLLQDFTGVPAVVDLACmR(D)	C:Carbamidomethylation	m:Oxidized methionine	568.7685098	1338.527554	1.797207257	3.539414833	Arabidopsis thaliana	115759474.3	aconitase
1319.792741	JGP_1_2.8473.8533.4	2.326753757	13.93915662	77.92641157	2.26E+06	(R)VLLQDFTGVPAVVDLACmR(D)	C:Carbamidomethylation	m:Oxidized methionine	568.7356159	1338.44745	1.797090803	3.539210784	Arabidopsis thaliana	115767914.2	aconitase
1319.846143	JGP_1_2.5291.5366.3	2.326732493	13.93903291	77.92693164	2.26E+06	(R)ILLESAIR(N)		568.7027219	1338.367346	1.796974349	3.539006735	Arabidopsis thaliana	115776354.1	aconitase
1319.899545	JGP_1_2.7838.7848.3	2.326711228	13.9389092	77.92745171	2.26E+06	(R)SNLVGmGIIPLCFK(A)	C:Carbamidomethylation	m:Oxidized methionine	568.669828	1338.287243	1.796857895	3.538802687	Arabidopsis thaliana	115784794.1	aconitase
1319.952947	JGP_1_4.5810.5823.3	2.326689964	13.93878549	77.92797178	2.26E+06	(R)ILLESAIR(N)		568.6369341	1338.207139	1.796741441	3.538598638	Arabidopsis thaliana	115793234	aconitase
1320.006349	JGP_1_2.8752.8827.4	2.326668699	13.93866178	77.92849185	2.26E+06	(K)INPLVPVDLVIDHSVQVDVAR(S)			568.6040401	1338.127036	1.796624988	3.538394589	Arabidopsis thaliana	115801673.9	aconitate hydratase 1
1320.05975	JGP_1_3.9264.9275.4	2.326647435	13.93853807	77.92901192	2.26E+06	(K)INPLVPVDLVIDHSVQVDVAR(S)			568.5711462	1338.046932	1.796508534	3.53819054	Arabidopsis thaliana	115810113.8	aconitate hydratase 1
1320.113152	JGP_1_6.10246.10251.4	2.32662617	13.93841436	77.92953199	2.26E+06	(K)INPLVPVDLVIDHSVQVDVAR(S)			568.5382523	1337.966829	1.79639208	3.537986491	Arabidopsis thaliana	115818553.8	aconitate hydratase 1
1320.166554	JGP_1_1.9316.9316.4	2.326604906	13.93829064	77.93005206	2.26E+06	(K)INPLVPVDLVIDHSVQVDVAR(S)			568.5053583	1337.886725	1.796275626	3.537782443	Arabidopsis thaliana	115826993.7	aconitate hydratase 1
1320.219956	JGP_1_2.4424.4434.3	2.326583641	13.93816693	77.93057213	2.26E+06	(K)IIDWEK(T)		568.4724644	1337.806621	1.796159172	3.537578394	Arabidopsis thaliana	115835433.6	aconitate hydratase 2
1320.273358	JGP_1_1.8230.8299.5	2.326562376	13.93804322	77.9310922	2.26E+06	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)			568.4395704	1337.726518	1.796042718	3.537374345	Arabidopsis thaliana	115843873.5	actin (ACT3)
1320.32676	JGP_1_2.7732.7754.5	2.326541112	13.93791951	77.93161227	2.27E+06	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)			568.4066765	1337.646414	1.795926264	3.537170296	Arabidopsis thaliana	115852313.5	actin (ACT3)
1320.380162	JGP_1_5.2631.2634.3	2.326519847	13.9377958	77.93213234	2.27E+06	(K)AGFAGDDAPR(A)		568.3737826	1337.566311	1.795809811	3.536966248	Arabidopsis thaliana	115860753.4	actin (ACT3)
1320.433564	JGP_1_4.1994.2004.3	2.326498583	13.93767209	77.93265241	2.27E+06	(K)VVAPPER(K)		568.3408886	1337.486207	1.795693357	3.536762199	Arabidopsis thaliana	115869193.3	actin (ACT3)
1320.486966	JGP_1_5.1865.1865.3	2.326477318	13.93754838	77.93317248	2.27E+06	(K)DAYVGDEAQSK(R)		568.3079947	1337.406104	1.795576903	3.53655815	Arabidopsis thaliana	115877633.2	actin (ACT3)
1320.540368	JGP_1_2.1994.2062.3	2.326456054	13.93742467	77.93369255	2.27E+06	(K)VVAPPER(K)		568.2751008	1337.326	1.795460449	3.536354101	Arabidopsis thaliana	115886073.2	actin (ACT3)
1320.593769	JGP_1_3.2057.2063.3	2.326434789	13.93730096	77.93421262	2.27E+06	(K)VVAPPER(K)		568.2422068	1337.245896	1.795343995	3.536150052	Arabidopsis thaliana	115894513.1	actin (ACT3)
1320.647171	JGP_1_1.1840.1918.3	2.326413525	13.93717725	77.93473269	2.27E+06	(K)DAYVGDEAQSK(R)		568.2093129	1337.165793	1.795227541	3.535946004	Arabidopsis thaliana	115902953	actin (ACT3)
1320.700573	JGP_1_3.8201.8201.5	2.32639226	13.93705354	77.93525277	2.27E+06	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)			568.176419	1337.085689	1.795111088	3.535741955	Arabidopsis thaliana	115911393	actin (ACT3)
1320.753975	JGP_1_1.2511.2594.3	2.326370996	13.93692983	77.93577284	2.27E+06	(K)AGFAGDDAPR(A)		568.143525	1337.005586	1.794994634	3.535537906	Arabidopsis thaliana	115919832.9	actin (ACT3)
1320.807377	JGP_1_6.9102.9102.5	2.326349731	13.93680612	77.93629291	2.27E+06	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)			568.1106311	1336.925482	1.79487818	3.535333857	Arabidopsis thaliana	115928272.8	actin (ACT3)
1320.860779	JGP_1_6.2752.2760.3	2.326328467	13.93668241	77.93681298	2.27E+06	(K)AGFAGDDAPR(A)		568.0777371	1336.845379	1.794761726	3.535129808	Arabidopsis thaliana	115936712.7	actin (ACT3)
1320.914181	JGP_1_5.1930.1936.3	2.326307202	13.9365587	77.93733305	2.27E+06	(K)VVAPPER(K)		568.0448432	1336.765275	1.794645272	3.53492576	Arabidopsis thaliana	115945152.7	actin (ACT3)
1320.967583	JGP_1_1.1960.2033.3	2.326285938	13.93643499	77.93785312	2.27E+06	(K)VVAPPER(K)		568.0119493	1336.685171	1.794528818	3.534721711	Arabidopsis thaliana	115953592.6	actin (ACT3)
1321.020985	JGP_1_6.2055.2143.3	2.326264673	13.93631128	77.93837319	2.27E+06	(K)VVAPPER(K)		567.9790553	1336.605068	1.794412364	3.534517662	Arabidopsis thaliana	115962032.5	actin (ACT3)
1321.074387	JGP_1_2.3324.3337.4	2.326243409	13.93618757	77.93889326	2.27E+06	(K)AEYDESGPSIVHR(K)		567.9461614	1336.524964	1.794295911	3.534313613	Arabidopsis thaliana	115970472.4	actin 3
1321.127788	JGP_1_1.3431.3441.4	2.326222144	13.93606386	77.93941333	2.28E+06	(K)AEYDESGPSIVHR(K)		567.9132675	1336.444861	1.794179457	3.534109565	Arabidopsis thaliana	115978912.4	actin 3
1321.18119	JGP_1_8.1971.2079.3	2.32620088	13.93594015	77.9399334	2.28E+06	(K)MIYASSK(D)		567.8803735	1336.364757	1.794063003	3.533905516	Arabidopsis thaliana	115987352.3	actin depolymerizing factor 5
1321.234592	JGP_1_1.4420.4491.3	2.326179615	13.93581644	77.94045347	2.28E+06	(K)INENVQQVVVDR(L)		567.8474796	1336.284654	1.793946549	3.533701467	Zea mays	115995792.2	actin-depolymerizing factor
1321.287994	JGP_1_1.8566.8634.3	2.326158351	13.93569273	77.94097354	2.28E+06	(K)IFFISWAPDTSR(V)		567.8145856	1336.20455	1.793830095	3.533497418	Zea mays	116004232.2	actin-depolymerizing factor

1321.341396	JGP_1_8.9350.9419.3	2.326137086	13.93556902	77.94149361	2.28E+06	(K)IFFISWAPDTSR(V)		567.7816917	1336.124446	1.793713641	3.533293369	Zea mays	116012672.1 actin-depolymerizing factor
1321.394798	JGP_1_3.4539.4606.3	2.326115822	13.93544531	77.94201368	2.28E+06	(K)INENVQQVVVDR(L)		567.7487978	1336.044343	1.793597187	3.533089321	Zea mays	116021112 actin-depolymerizing factor
1321.4482	JGP_1_4.4643.4648.3	2.326094557	13.9353216	77.94253375	2.28E+06	(K)INENVQQVVVDR(L)		567.7159038	1335.964239	1.793480734	3.532885272	Zea mays	116029551.9 actin-depolymerizing factor
1321.501602	JGP_1_6.9418.9492.3	2.326073293	13.93519789	77.94305382	2.28E+06	(K)IFFISWAPDTSR(V)		567.6830099	1335.884136	1.79336428	3.532681223	Zea mays	116037991.9 actin-depolymerizing factor
1321.555004	JGP_1_7.9314.9393.3	2.326052028	13.93507418	77.94357389	2.28E+06	(K)IFFISWAPDTSR(V)		567.650116	1335.804032	1.793247826	3.532477174	Zea mays	116046431.8 actin-depolymerizing factor
1321.608406	JGP_1_2.8058.8132.3	2.326030764	13.93495047	77.94409396	2.28E+06	(K)IFFISWAPDTSR(V)		567.617222	1335.723929	1.793131372	3.532273126	Zea mays	116054871.7 actin-depolymerizing factor
1321.661808	JGP_1_8.9332.9346.3	2.326009499	13.93482676	77.94461403	2.28E+06	(R)YAVFDFDFVTDENCQK(S)	C:Carbamidomethylation	567.5843281	1335.643825	1.793014918	3.532069077	Zea mays	116063311.6 actin-depolymerizing factor
1321.715209	JGP_1_5.9019.9085.3	2.325988235	13.93470305	77.9451341	2.28E+06	(K)IFFISWAPDTSR(V)		567.5514342	1335.563721	1.792898464	3.531865028	Zea mays	116071751.6 actin-depolymerizing factor
1321.768611	JGP_1_1.8699.8705.3	2.32596697	13.93457934	77.94565417	2.28E+06	(K)IFFISWAPDTSR(V)		567.5185402	1335.483618	1.792782011	3.531660979	Zea mays	116080191.5 actin-depolymerizing factor
1321.822013	JGP_1_7.4973.4979.3	2.325945706	13.93445563	77.94617424	2.28E+06	(K)INENVQQVVVDR(L)		567.4856463	1335.403514	1.792665557	3.53145693	Zea mays	116088631.4 actin-depolymerizing factor
1321.875415	JGP_1_8.4884.4884.3	2.325924441	13.93433192	77.94669431	2.28E+06	(K)INENVQQVVVDR(L)		567.4527523	1335.323411	1.792549103	3.531252882	Zea mays	116097071.3 actin-depolymerizing factor
1321.928817	JGP_1_3.8515.8590.3	2.325903177	13.93420821	77.94721438	2.29E+06	(K)IFFISWAPDTSR(V)		567.4198584	1335.243307	1.792432649	3.531048833	Zea mays	116105511.3 actin-depolymerizing factor
1321.982219	JGP_1_2.4307.4307.3	2.325881912	13.9340845	77.94773445	2.29E+06	(K)INENVQQVVVDR(L)		567.3869645	1335.163204	1.792316195	3.530844784	Zea mays	116113951.2 actin-depolymerizing factor
1322.035621	JGP_1_8.4888.4888.3	2.325860648	13.93396079	77.94825452	2.29E+06	(K)INENVQQVVVDR(L)		567.3540705	1335.0831	1.792199741	3.530640735	Zea mays	116122391.1 actin-depolymerizing factor
1322.089023	JGP_1_4.8751.8816.3	2.325839383	13.93383707	77.94877459	2.29E+06	(K)IFFISWAPDTSR(V)		567.3211766	1335.002996	1.792083287	3.530436687	Zea mays	116130831.1 actin-depolymerizing factor
1322.142425	JGP_1_2.4238.4241.3	2.325818118	13.93371336	77.94929466	2.29E+06	(K)INENVQQVVVDR(L)		567.2882827	1334.922893	1.791966834	3.530232638	Zea mays	116139271 actin-depolymerizing factor
1322.195827	JGP_1_6.5009.5009.3	2.325796854	13.93358965	77.94981473	2.29E+06	(K)INENVQQVVVDR(L)		567.2553887	1334.842789	1.79185038	3.530028589	Zea mays	116147710.9 actin-depolymerizing factor
1322.249228	JGP_1_5.4817.4817.3	2.325775589	13.93346594	77.9503348	2.29E+06	(K)INENVQQVVVDR(L)		567.2224948	1334.762686	1.791733926	3.52982454	Zea mays	116156150.8 actin-depolymerizing factor
1322.30263	JGP_1_1.4436.4440.4	2.325754325	13.93334223	77.95085487	2.29E+06	(K)INENVQQVVVDR(L)		567.1896008	1334.682582	1.791617472	3.529620491	Zea mays	116164590.8 actin-depolymerizing factor
1322.356032	JGP_1_6.5020.5020.3	2.32573306	13.93321852	77.95137495	2.29E+06	(K)INENVQQVVVDR(L)		567.1567069	1334.602479	1.791501018	3.529416443	Zea mays	116173030.7 actin-depolymerizing factor
1322.409434	JGP_1_1.7315.7325.4	2.325711796	13.93309481	77.95189502	2.29E+06	(R)ELDGIQCEIQATDPSEmSLDIVR(S)	C:Carbamidomethylation m:Oxidized methionine	567.123813	1334.522375	1.791384564	3.529212394	Zea mays	116181470.6 actin-depolymerizing factor 1
1322.462836	JGP_1_2.6854.6854.4	2.325690531	13.9329711	77.95241509	2.29E+06	(R)ELDGIQCEIQATDPSEmSLDIVR(S)	C:Carbamidomethylation m:Oxidized methionine	567.090919	1334.442271	1.791268111	3.529008345	Zea mays	116189910.5 actin-depolymerizing factor 1
1322.516238	JGP_1_8.8361.8441.3	2.325669267	13.93284739	77.95293516	2.29E+06	(R)YAIYDLDFTTVENCQK(S)	C:Carbamidomethylation	567.0580251	1334.362168	1.791151657	3.528804296	Zea mays	116198350.5 actin-depolymerizing factor 2
1322.56964	JGP_1_8.6776.6780.3	2.325648002	13.93272368	77.95345523	2.29E+06	(R)LGEPNQGYGDFTDSLPADECR(Y)	C:Carbamidomethylation	567.0251312	1334.282064	1.791035203	3.528600247	Zea mays	116206790.4 actin-depolymerizing factor 2
1322.623042	JGP_1_2.8418.8483.3	2.325626738	13.93259997	77.9539753	2.29E+06	(K)IFFFSWSPDTAR(T)		566.9922372	1334.201961	1.790918749	3.528396199	Zea mays	116215230.3 actin-depolymerizing factor 2
1322.676444	JGP_1_8.9682.9755.3	2.325605473	13.93247626	77.95449537	2.29E+06	(K)IFFFSWSPDTAR(T)		566.9593433	1334.121857	1.790802295	3.52819215	Zea mays	116223670.2 actin-depolymerizing factor 2
1322.729846	JGP_1_8.9814.9820.3	2.325584209	13.93235255	77.95501544	2.30E+06	(K)IFFFSWSPDTAR(T)		566.9264494	1334.041754	1.790685841	3.527988101	Zea mays	116232110.2 actin-depolymerizing factor 2
1322.783247	JGP_1_3.8891.8953.3	2.325562944	13.93222884	77.95553551	2.30E+06	(K)IFFFSWSPDTAR(T)		566.8935554	1333.96165	1.790569387	3.527784052	Zea mays	116240550.1 actin-depolymerizing factor 2
1322.836649	JGP_1_8.6781.6784.4	2.32554168	13.93210513	77.95605558	2.30E+06	(R)LGEPNQGYGDFTDSLPADECR(Y)	C:Carbamidomethylation	566.8606615	1333.881547	1.790452934	3.527580004	Zea mays	116248990 actin-depolymerizing factor 2
1322.890051	JGP_1_7.9695.9763.3	2.325520415	13.93198142	77.95657565	2.30E+06	(K)IFFFSWSPDTAR(T)		566.8277675	1333.801443	1.79033648	3.527375955	Zea mays	116257430 actin-depolymerizing factor 2
1322.943453	JGP_1_4.9149.9214.3	2.325499151	13.93185771	77.95709572	2.30E+06	(K)IFFFSWSPDTAR(T)		566.7948736	1333.721339	1.790220026	3.527171906	Zea mays	116265869.9 actin-depolymerizing factor 2
1322.996855	JGP_1_1.2645.2650.4	2.325477886	13.931734	77.95761579	2.30E+06	(R)IDDKDmEIKVDR(L)	m:Oxidized methionine	566.7619797	1333.641236	1.790103572	3.526967857	Zea mays	116274309.8 actin-depolymerizing factor 2
1323.050257	JGP_1_1.7552.7552.3	2.325456622	13.93161029	77.95813586	2.30E+06	(R)YAIYDLDFTTVENCQK(S)	C:Carbamidomethylation	566.7290857	1333.561132	1.789987118	3.526763808	Zea mays	116282749.7 actin-depolymerizing factor 2
1323.103659	JGP_1_1.8930.9034.3	2.325435357	13.93148658	77.95865593	2.30E+06	(K)IFFFSWSPDTAR(T)		566.6961918	1333.481029	1.789870664	3.52655976	Zea mays	116291189.7 actin-depolymerizing factor 2
1323.157061	JGP_1_2.8543.8550.3	2.325414093	13.93136287	77.959176	2.30E+06	(K)IFFFSWSPDTAR(T)		566.6632979	1333.400925	1.789754211	3.526355711	Zea mays	116299629.6 actin-depolymerizing factor 2
1323.210463	JGP_1_6.9843.9910.3	2.325392828	13.93123916	77.95969607	2.30E+06	(K)IFFFSWSPDTAR(T)		566.6304039	1333.320822	1.789637757	3.526151662	Zea mays	116308069.5 actin-depolymerizing factor 2
1323.263865	JGP_1_1.8941.9049.4	2.325371564	13.93111545	77.96021614	2.30E+06	(K)IFFFSWSPDTAR(T)		566.59751	1333.240718	1.789521303	3.525947613	Zea mays	116316509.4 actin-depolymerizing factor 2
1323.317266	JGP_1_1.2624.2714.5	2.325350299	13.93099174	77.96073621	2.30E+06	(R)IDDKDmEIKVDR(L)	m:Oxidized methionine	566.564616	1333.160614	1.789404849	3.525743565	Zea mays	116324949.4 actin-depolymerizing factor 2
1323.370668	JGP_1_1.9091.9094.3	2.325329035	13.93086803	77.96125628	2.30E+06	(K)IFFFSWSPDTAR(T)		566.5317221	1333.080511	1.789288395	3.525539516	Zea mays	116333389.3 actin-depolymerizing factor 2
1323.42407	JGP_1_1.1658.1749.4	2.32530777	13.93074432	77.96177635	2.30E+06	(R)IDDKDmEIK(V)	m:Oxidized methionine	566.4988282	1333.000407	1.789171941	3.525335467	Zea mays	116341829.2 actin-depolymerizing factor 2
1323.477472	JGP_1_5.9457.9533.3	2.325286506	13.93062061	77.96229642	2.30E+06	(K)IFFFSWSPDTAR(T)		566.4659342	1332.920304	1.789055487	3.525131418	Zea mays	116350269.2 actin-depolymerizing factor 2
1323.530874	JGP_1_2.8458.8464.4	2.325265241	13.9304969	77.96281649	2.30E+06	(K)IFFFSWSPDTAR(T)		566.4330403	1332.8402	1.788939034	3.524927369	Zea mays	116358709.1 actin-depolymerizing factor 2
1323.584276	JGP_1_3.9014.9020.3	2.325243977	13.93037319	77.96333656	2.31E+06	(K)IFFFSWSPDTAR(T)		566.4001464	1332.760097	1.78882258	3.524723321	Zea mays	116367149 actin-depolymerizing factor 2
1323.637678	JGP_1_8.5013.5017.3	2.325222712	13.93024948	77.96385663	2.31E+06	(R)FITFK(M)	566.3672524	1332.679993	1.788706126	3.524519272	Zea mays	116375588.9 actin-depolymerizing factor 3	
1323.69108	JGP_1_1.7011.7091.3	2.325201448	13.93012577	77.9643767	2.31E+06	(K)SYELPDGQVITIGAER(F)		566.3343585	1332.599889	1.788589672	3.524315223	Solanum tuberosum	116384028.9 actin-like
1323.744482	JGP_1_2.6609.6613.3	2.325180183	13.93000206	77.96489677	2.31E+06	(K)SYELPDGQVITIGAER(F)		566.3014646	1332.519786	1.788473218	3.524111174	Solanum tuberosum	116392468.8 actin-like
1323.797884	JGP_1_3.7023.7029.3	2.325158919	13.92987835	77.96541684	2.31E+06	(K)SYELPDGQVITIGAER(F)		566.2685706	1332.439682	1.788356764	3.523907126	Solanum tuberosum	116400908.7 actin-like
1323.851285	JGP_1_6.7868.7887.3	2.325137654	13.92975464	77.96593691	2.31E+06	(K)SYELPDGQVITIGAER(F)		566.2356767	1332.359579	1.788240311	3.523703077	Solanum tuberosum	116409348.6 actin-like
1323.904687	JGP_1_6.8712.8792.3	2.32511639	13.92963093	77.96645698	2.31E+06	(K)VLPYADYIFGNETEAK(I)		566.2027827	1332.279475	1.788123857	3.523499028	Zea mays	116417788.6 adenosine kinase

1323.958089	JGP_1_2.7583.7653.3	2.325095125	13.92950722	77.96697705	2.31E+06	(K)TFPVILLPK(E)		566.1698888	1332.199372	1.788007403	3.523294979	Oryza sativa	116426228.5	adenosine kinase
1324.011491	JGP_1_1.7977.7980.3	2.32507386	13.92938351	77.96749713	2.31E+06	(K)VLPYADYIFGNETEAK(I)		566.1369949	1332.119268	1.787890949	3.52309093	Zea mays	116434668.4	adenosine kinase
1324.064893	JGP_1_6.11627.11695.4	2.325052596	13.92925979	77.9680172	2.31E+06	(K)VFLmNLSAPFICEFFR(D)	C:Carbamidomethylation m:Oxidized methionine	566.1041009	1332.039164	1.787774495	3.522886882	Zea mays	116443108.3	adenosine kinase
1324.118295	JGP_1_6.8811.8885.3	2.325031331	13.92913608	77.96853727	2.31E+06	(K)TFPVILLPK(E)		566.071207	1331.959061	1.787658041	3.522682833	Oryza sativa	116451548.3	adenosine kinase
1324.171697	JGP_1_2.7454.7454.3	2.325010067	13.92901237	77.96905734	2.31E+06	(K)VLPYADYIFGNETEAK(I)		566.0383131	1331.878957	1.787541587	3.522478784	Zea mays	116459988.2	adenosine kinase
1324.225099	JGP_1_6.11626.11696.3	2.324988802	13.92888866	77.96957741	2.31E+06	(K)VFLmNLSAPFICEFFR(D)	C:Carbamidomethylation m:Oxidized methionine	566.0054191	1331.798854	1.787425134	3.522274735	Zea mays	116468428.1	adenosine kinase
1324.278501	JGP_1_6.6919.6925.3	2.324967538	13.92876495	77.97009748	2.31E+06	(R)IAVITQGADPVVVAEDGK(V)		565.9725252	1331.71875	1.78730868	3.522070687	Zea mays	116476868.1	adenosine kinase
1324.331903	JGP_1_6.8952.8958.3	2.324946273	13.92864124	77.97061755	2.31E+06	(K)TFPVILLPK(E)		565.9396313	1331.638647	1.787192226	3.521866638	Oryza sativa	116485308	adenosine kinase
1324.385304	JGP_1_3.8009.8070.3	2.324925009	13.92851753	77.97113762	2.32E+06	(K)TFPVILLPK(E)		565.9067373	1331.558543	1.787075772	3.521662589	Oryza sativa	116493747.9	adenosine kinase
1324.438706	JGP_1_6.5012.5018.3	2.324903744	13.92839382	77.97165769	2.32E+06	(K)ISQLPLASGK(Q)		565.8738434	1331.478439	1.786959318	3.52145854	Oryza sativa	116502187.8	adenosine kinase
1324.492108	JGP_1_1.8096.8164.3	2.32488248	13.92827011	77.97217776	2.32E+06	(K)TFPVILLPK(E)		565.8409494	1331.398336	1.786842864	3.521254491	Oryza sativa	116510627.8	adenosine kinase
1324.54551	JGP_1_1.7995.8012.4	2.324861215	13.9281464	77.97269783	2.32E+06	(K)VLPYADYIFGNETEAK(I)		565.8080555	1331.318232	1.786726411	3.521050443	Zea mays	116519067.7	adenosine kinase
1324.598912	JGP_1_1.4479.4486.3	2.324839951	13.92802269	77.9732179	2.32E+06	(K)ISQLPLASGK(Q)		565.7751616	1331.238129	1.786609957	3.520846394	Oryza sativa	116527507.6	adenosine kinase
1324.652314	JGP_1_4.8281.8285.3	2.324818686	13.92789898	77.97373797	2.32E+06	(K)TFPVILLPK(E)		565.7422676	1331.158025	1.786493503	3.520642345	Oryza sativa	116535947.5	adenosine kinase
1324.705716	JGP_1_5.8480.8483.3	2.324797422	13.92777527	77.97425804	2.32E+06	(K)TFPVILLPK(E)		565.7093737	1331.077922	1.786377049	3.520438296	Oryza sativa	116544387.5	adenosine kinase
1324.759118	JGP_1_6.8743.8747.4	2.324776157	13.92765156	77.97477811	2.32E+06	(K)VLPYADYIFGNETEAK(I)		565.6764798	1330.997818	1.786260595	3.520234247	Zea mays	116552827.4	adenosine kinase
1324.81252	JGP_1_6.6935.6940.4	2.324754893	13.92752785	77.97529818	2.32E+06	(R)IAVITQGADPVVVAEDGK(V)		565.6435858	1330.917714	1.786144141	3.520030199	Zea mays	116561267.3	adenosine kinase
1324.865922	JGP_1_2.4308.4312.3	2.324733628	13.92740414	77.97581825	2.32E+06	(K)ISQLPLASGK(Q)		565.6106919	1330.837611	1.786027687	3.51982615	Oryza sativa	116569707.2	adenosine kinase
1324.919323	JGP_1_2.5832.5839.4	2.324712364	13.92728043	77.97633832	2.32E+06	(R)IAVITQGADPVVVAEDGK(V)		565.5777979	1330.757507	1.785911234	3.519622101	Zea mays	116578147.2	adenosine kinase
1324.972725	JGP_1_6.6696.6699.3	2.324691099	13.92715672	77.97685839	2.32E+06	(R)SLIANLSAANCYK(V)	C:Carbamidomethylation	565.544904	1330.677404	1.78579478	3.519418052	Arabidopsis thaliana	116586587.1	adenosine kinase 2
1325.026127	JGP_1_6.5083.5100.3	2.324669835	13.92703301	77.97737846	2.32E+06	(K)SNVEYIAGGATQNSIR(V)		565.5120101	1330.5973	1.785678326	3.519214004	Nicotiana tabacum	116595027	adenosine kinase isoform 1S
1325.079529	JGP_1_6.4663.4669.3	2.32464857	13.9269093	77.97789853	2.32E+06	(K)HLPmYDELASK(N)	m:Oxidized methionine	565.4791161	1330.517197	1.785561872	3.519009955	Nicotiana tabacum	116603467	adenosine kinase isoform 1T
1325.132931	JGP_1_5.4618.4624.3	2.324627306	13.92678559	77.9784186	2.32E+06	(K)IPDPESTDNAEFK(I)		565.4462222	1330.437093	1.785445418	3.518805906	Zea mays	116611906.9	adenosylhomocysteinase
1325.186333	JGP_1_5.6374.6387.5	2.324606041	13.92666188	77.97893867	2.33E+06	(K)SQADYISVPIEGPYKPAHYR(Y)		565.4133283	1330.356989	1.785328964	3.518601857	Zea mays	116620346.8	adenosylhomocysteinase
1325.239735	JGP_1_4.6616.6626.3	2.324584777	13.92653817	77.97945874	2.33E+06	(K)IVLTIIR(D)		565.3804343	1330.276886	1.78521251	3.518397808	Zea mays	116628786.7	adenosylhomocysteinase
1325.293137	JGP_1_1.6445.6534.3	2.324563512	13.92641446	77.97997881	2.33E+06	(K)IVLTIIR(D)		565.3475404	1330.196782	1.785096057	3.51819376	Zea mays	116637226.7	adenosylhomocysteinase
1325.346539	JGP_1_5.6739.6829.3	2.324542248	13.92629075	77.98049888	2.33E+06	(K)IVLTIIR(D)		565.3146465	1330.116679	1.784979603	3.517989711	Zea mays	116645666.6	adenosylhomocysteinase
1325.399941	JGP_1_4.4505.4505.3	2.324520983	13.92616704	77.98101895	2.33E+06	(K)IPDPESTDNAEFK(I)		565.2817525	1330.036575	1.784863149	3.517785662	Zea mays	116654106.5	adenosylhomocysteinase
1325.453342	JGP_1_5.6600.6600.4	2.324499719	13.92604333	77.98153902	2.33E+06	(R)WCSCNIFSTQDHAAAAIAR(D)	C:Carbamidomethylation	565.2488586	1329.956472	1.784746695	3.517581613	Arabidopsis thaliana	116662546.4	adenosylhomocysteinase 2
1325.506744	JGP_1_5.8835.8839.4	2.324478454	13.92591962	77.98205909	2.33E+06	(R)LYQmQETGALLFPAINVNDSVTK(S)	m:Oxidized methionine	565.2159646	1329.876368	1.784630241	3.517377565	Arabidopsis thaliana	116670986.4	adenosylhomocysteinase 2
1325.560146	JGP_1_8.9922.9930.4	2.32445719	13.92579591	77.98257916	2.33E+06	(K)LGEIVTTIPTIGFNVETVEYK(N)		565.1830707	1329.796264	1.784513787	3.517173516	Arabidopsis thaliana	116679426.3	ADP-ribosylation factor 1
1325.613548	JGP_1_8.8315.8327.3	2.324435925	13.9256722	77.98309923	2.33E+06	(K)NISFTVWDVGGQDK(I)		565.1501768	1329.716161	1.784397334	3.516969467	Arabidopsis thaliana	116687866.2	ADP-ribosylation factor 1
1325.66695	JGP_1_8.6735.6809.3	2.324414661	13.92554849	77.98361931	2.33E+06	(R)ILMVGLDAAGK(T)		565.1172828	1329.636057	1.78428088	3.516765418	Arabidopsis thaliana	116696306.2	ADP-ribosylation factor 1
1325.720352	JGP_1_1.8966.8995.4	2.324393396	13.92542478	77.98413938	2.33E+06	(K)LGEIVTTIPTIGFNVETVEYK(N)		565.0843889	1329.555954	1.784164426	3.516561369	Arabidopsis thaliana	116704746.1	ADP-ribosylation factor 1
1325.773754	JGP_1_1.5362.5466.3	2.324372132	13.92530107	77.98465945	2.33E+06	(K)IIGVDINPDK(C)		565.051495	1329.47585	1.784047972	3.516357321	Zea mays	116713186	alcohol dehydrogenase 2
1325.827156	JGP_1_1.9051.9110.4	2.324350867	13.92517736	77.98517952	2.33E+06	(K)GSTVAIFGLGAVGLAAAEGAR(I)		565.018601	1329.395747	1.783931518	3.516153272	Triticum aestivum	116721625.9	alcohol dehydrogenase ADH1A
1325.880558	JGP_1_2.2899.2982.3	2.324329602	13.92505365	77.98569959	2.33E+06	(R)TFVHEK(V)		564.9857071	1329.315643	1.783815064	3.515949223	Arabidopsis thaliana	116730065.9	aldehyde dehydrogenase 2B4
1325.93396	JGP_1_7.2855.2950.3	2.324308338	13.92492994	77.98621966	2.33E+06	(R)TFVHEK(V)		564.9528131	1329.235539	1.78369861	3.515745174	Arabidopsis thaliana	116738505.8	aldehyde dehydrogenase 2B4
1325.987361	JGP_1_7.2685.2780.3	2.324287073	13.92480623	77.98673973	2.34E+06	(R)TFVHEK(V)		564.9199192	1329.155436	1.783582157	3.515541126	Arabidopsis thaliana	116746945.7	aldehyde dehydrogenase 2B4
1326.040763	JGP_1_3.2992.3086.3	2.324265809	13.92468251	77.9872598	2.34E+06	(R)TFVHEK(V)		564.8870253	1329.075332	1.783465703	3.515337077	Arabidopsis thaliana	116755385.6	aldehyde dehydrogenase 2B4
1326.094165	JGP_1_6.3153.3253.3	2.324244544	13.9245588	77.98777987	2.34E+06	(R)TFVHEK(V)		564.8541313	1328.995229	1.783349249	3.515133028	Arabidopsis thaliana	116763825.6	aldehyde dehydrogenase 2B4
1326.147567	JGP_1_1.2906.2998.3	2.32422328	13.92443509	77.98829994	2.34E+06	(R)TFVHEK(V)		564.8212374	1328.915125	1.783232795	3.514928979	Arabidopsis thaliana	116772265.5	aldehyde dehydrogenase 2B4
1326.200969	JGP_1_5.2991.3088.3	2.324202015	13.92431138	77.98882001	2.34E+06	(R)TFVHEK(V)		564.7883435	1328.835022	1.783116341	3.51472493	Arabidopsis thaliana	116780705.4	aldehyde dehydrogenase 2B4
1326.254371	JGP_1_4.2991.3086.3	2.324180751	13.92418767	77.98934008	2.34E+06	(R)TFVHEK(V)		564.7554495	1328.754918	1.782999887	3.514520882	Arabidopsis thaliana	116789145.3	aldehyde dehydrogenase 2B4
1326.307773	JGP_1_1.3079.3084.3	2.324159486	13.92406396	77.98986015	2.34E+06	(R)TFVHEK(V)		564.7225556	1328.674815	1.782883434	3.514316833	Arabidopsis thaliana	116797585.3	aldehyde dehydrogenase 2B4
1326.361175	JGP_1_7.3035.3135.3	2.324138222	13.92394025	77.99038022	2.34E+06	(R)TFVHEK(V)		564.6896617	1328.594711	1.78276698	3.514112784	Arabidopsis thaliana	116806025.2	aldehyde dehydrogenase 2B4
1326.414577	JGP_1_6.6751.6753.3	2.324116957	13.92381654	77.99090029	2.34E+06	(K)LGDLLAVAR(V)		564.6567677	1328.514607	1.782650526	3.513908735	Zea mays	116814465.1	"aldo-keto reductase family 1, member B1"
1326.467979	JGP_1_6.7282.7321.3	2.324095693	13.92369283	77.99142036	2.34E+06	(K)EPIIISIAEK(L)		564.6238738	1328.434504	1.782534072	3.513704686	Zea mays	116822905.1	"aldo-keto reductase family 1, member B1"
1326.52138	JGP_1_3.6339.6344.4	2.324074428	13.92356912	77.99194043	2.34E+06	(R)FFGHVEILPDGSR(K)		564.5909798	1328.3544	1.782417618	3.513500638	Oryza sativa	116831345	"alpha 1,4-glucan phosphorylase H isozyme"
1326.574782	JGP_1_1.6715.6794.4	2.324053164	13.92344541	77.9924605	2.34E+06	(R)ALTNAVGNLGITGAYAEAVKK(F)		564.5580859	1328.274297	1.782301164	3.513296589	Oryza sativa	116839784.9	"alpha 1,4-glucan phosphorylase H isozyme"
1326.628184	JGP_1_2.5996.6002.4	2.324031899	13.9233217	77.99298057	2.34E+06	(R)FFGHVEILPDGSR(K)		564.525192	1328.194193	1.78218471	3.51309254	Oryza sativa	116848224.8	"alpha 1,4-glucan phosphorylase H isozyme"

1326.681586	JGP_1_1.7235.7235.3	2.324010635	13.92319799	77.99350064	2.34E+06	(R)ALTNAVGNLGITGAYAEAVK(K)		564.492298	1328.11409	1.782068257	3.512888491	Oryza sativa	116856664.8	"alpha 1,4-glucan phosphorylase H isozyme"
1326.734988	JGP_1_2.7975.8064.3	2.32398937	13.92307428	77.99402071	2.34E+06	(R)QLLNILGAVYR(Y)		564.4594041	1328.033986	1.781951803	3.512684443	Oryza sativa	116865104.7	"alpha 1,4-glucan phosphorylase H isozyme"
1326.78839	JGP_1_3.7172.7176.4	2.323968106	13.92295057	77.99454078	2.35E+06	(K)VAVQLNDTHPTLAIPELmR(L)	m:Oxidized methionine	564.4265102	1327.953882	1.781835349	3.512480394	Oryza sativa	116873544.6	"alpha 1,4-glucan phosphorylase H isozyme"
1326.841792	JGP_1_1.6333.6338.4	2.323946841	13.92282686	77.99506085	2.35E+06	(R)FFGHVEILPDGSR(K)		564.3936162	1327.873779	1.781718895	3.512276345	Oryza sativa	116881984.5	"alpha 1,4-glucan phosphorylase H isozyme"
1326.895194	JGP_1_1.8485.8554.3	2.323925577	13.92270315	77.99558092	2.35E+06	(R)QLLNILGAVYR(Y)		564.3607223	1327.793675	1.781602441	3.512072296	Oryza sativa	116890424.5	"alpha 1,4-glucan phosphorylase H isozyme"
1326.948596	JGP_1_1.3061.3071.3	2.323904312	13.92257944	77.99610099	2.35E+06	(K)mSILNTAGSGK(F)	m:Oxidized methionine	564.3278283	1327.713572	1.781485987	3.511868247	Oryza sativa	116898864.4	"alpha 1,4-glucan phosphorylase H isozyme"
1327.001998	JGP_1_2.6789.6789.4	2.323883048	13.92245573	77.99662106	2.35E+06	(R)ALTNAVGNLGITGAYAEAVK(K)		564.2949344	1327.633468	1.781369534	3.511664199	Oryza sativa	116907304.3	"alpha 1,4-glucan phosphorylase H isozyme"
1327.055399	JGP_1_1.7202.7285.4	2.323861783	13.92233202	77.99714113	2.35E+06	(K)VAVQLNDTHPTLAIPELmR(L)	m:Oxidized methionine	564.2620405	1327.553365	1.78125308	3.51146015	Oryza sativa	116915744.2	"alpha 1,4-glucan phosphorylase H isozyme"
1327.108801	JGP_1_2.7992.7992.3	2.323840519	13.92220831	77.9976612	2.35E+06	(R)QLLNILGAVYR(Y)		564.2291465	1327.473261	1.781136626	3.511256101	Oryza sativa	116924184.2	"alpha 1,4-glucan phosphorylase H isozyme"
1327.162203	JGP_1_1.9406.9462.5	2.323819254	13.9220846	77.99818127	2.35E+06	(K)VVFIPNYNVSVAEVLIPGSELSQHISTAGmEASGTSNmK(F)	m:Oxidized methionine	564.1962526	1327.393157	1.781020172	3.511052052	Oryza sativa	116932624.1	"alpha 1,4-glucan phosphorylase H isozyme"
1327.215605	JGP_1_6.7084.7173.3	2.32379799	13.92196089	77.99870134	2.35E+06	(K)LGTIDPYFVK(L)		564.1633587	1327.313054	1.780903718	3.510848004	Zea mays	116941064	"alpha-1,4-glucan-protein synthase [UDP-forming]"
1327.269007	JGP_1_1.2851.2868.3	2.323776725	13.92183718	77.99922141	2.35E+06	(K)AFATYTNAK(R)		564.1304647	1327.23295	1.780787264	3.510643955	Arabidopsis thaliana	116949504	alpha-glucan phosphorylase isozyme H
1327.322409	JGP_1_2.2863.2863.3	2.323755461	13.92171347	77.99974149	2.35E+06	(K)AFATYTNAK(R)		564.0975708	1327.152847	1.78067081	3.510439906	Arabidopsis thaliana	116957943.9	alpha-glucan phosphorylase isozyme H
1327.375811	JGP_1_1.4312.4395.4	2.323734196	13.92158976	78.00026156	2.35E+06	(R)HDVVFPVR(F)		564.0646769	1327.072743	1.780554357	3.510235857	Arabidopsis thaliana	116966383.8	alpha-glucan phosphorylase isozyme H
1327.429213	JGP_1_1.2209.2294.3	2.323712932	13.92146605	78.00078163	2.35E+06	(R)TIAQYAK(E)		564.0317829	1326.99264	1.780437903	3.510031808	Arabidopsis thaliana	116974823.7	alpha-glucan phosphorylase isozyme H
1327.482615	JGP_1_2.4174.4186.4	2.323691667	13.92134234	78.0013017	2.35E+06	(R)HDVVFPVR(F)		563.998889	1326.912536	1.780321449	3.50982776	Arabidopsis thaliana	116983263.7	alpha-glucan phosphorylase isozyme H
1327.536017	JGP_1_1.2546.2590.3	2.323670403	13.92121863	78.00182177	2.35E+06	(R)LWEAK(A)	563.965995	1326.832432	1.780204995	3.509623711	Arabidopsis thaliana	116991703.6	alpha-glucan phosphorylase isozyme H	
1327.589418	JGP_1_4.10017.10017.4	2.323649138	13.92109492	78.00234184	2.36E+06	(R)AmHNVGLAGLTFWSPNINIFR(D)	m:Oxidized methionine	563.9331011	1326.752329	1.780088541	3.509419662	Hordeum vulgare	117000143.5	alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I
1327.64282	JGP_1_4.6119.6119.3	2.323627873	13.92097121	78.00286191	2.36E+06	(R)LGFFDGDPR(Q)		563.9002072	1326.672225	1.779972087	3.509215613	Hordeum vulgare	117008583.4	alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I
1327.696222	JGP_1_3.2691.2691.3	2.323606609	13.9208475	78.00338198	2.36E+06	(R)LTLAEK(V)		563.8673132	1326.592122	1.779855634	3.509011565	Hordeum vulgare	117017023.4	alpha-L-arabinofuranosidase/beta-D-xylosidase isoenzyme ARA-I
1327.749624	JGP_1_6.1437.1575.3	2.323585344	13.92072379	78.00390205	2.36E+06	(R)LIYHGK(Y)		563.8344193	1326.512018	1.77973918	3.508807516	Zea mays	117025463.3	alpha-L-fucosidase 2 precursor
1327.803026	JGP_1_6.7902.7986.3	2.32356408	13.92060008	78.00442212	2.36E+06	(K)ISGVYDDAKDVAR(K)		563.8015254	1326.431915	1.779622726	3.508603467	Arabidopsis thaliana	117033903.2	aluminum-activated malate transporter 9
1327.856428	JGP_1_5.7510.7514.3	2.323542815	13.92047637	78.00494219	2.36E+06	(K)ISGVYDDAKDVAR(K)		563.7686314	1326.351811	1.779506272	3.508399418	Arabidopsis thaliana	117042343.2	aluminum-activated malate transporter 9
1327.90983	JGP_1_6.7428.7512.4	2.323521551	13.92035266	78.00546226	2.36E+06	(K)LIISILAHR(N)		563.7357375	1326.271707	1.779389818	3.508195369	Arabidopsis thaliana	117050783.1	annexin D2
1327.963232	JGP_1_7.6959.6971.4	2.323500286	13.92022895	78.00598233	2.36E+06	(K)LIISILAHR(N)		563.7028436	1326.191604	1.779273364	3.507991321	Arabidopsis thaliana	117059223	annexin D2
1328.016634	JGP_1_7.7156.7164.4	2.323479022	13.92010523	78.0065024	2.36E+06	(R)SLEEDVAAHVTGDFR(K)		563.6699496	1326.1115	1.77915691	3.507787272	Zea mays	117067662.9	annexin2
1328.070036	JGP_1_7.2265.2270.4	2.323457757	13.91998152	78.00702247	2.36E+06	(R)ALGDEIHGK(F)		563.6370557	1326.031397	1.779040457	3.507583223	Zea mays	117076102.9	annexin2
1328.123437	JGP_1_7.8073.8080.3	2.323436493	13.91985781	78.00754254	2.36E+06	(K)LLVPLVSAYR(Y)		563.6041617	1325.951293	1.778924003	3.507379174	Zea mays	117084542.8	annexin2
1328.176839	JGP_1_6.8306.8310.3	2.323415228	13.9197341	78.00806261	2.36E+06	(K)LLVPLVSAYR(Y)		563.5712678	1325.87119	1.778807549	3.507175125	Zea mays	117092982.7	annexin2
1328.230241	JGP_1_6.6494.6500.3	2.323393964	13.91961039	78.00858268	2.36E+06	(R)VALGPSGDLSLTSR(I)		563.5383739	1325.791086	1.778691095	3.506971077	Zea mays	117101422.6	apospory-associated protein C
1328.283643	JGP_1_6.8647.8650.4	2.323372699	13.91948668	78.00910275	2.36E+06	(K)AFVDLILKPSEEDLK(I)		563.5054799	1325.710982	1.778574641	3.506767028	Zea mays	117109862.6	apospory-associated protein C
1328.337045	JGP_1_1.5795.5808.3	2.323351435	13.91936297	78.00962282	2.36E+06	(R)VALGPSGDLSLTSR(I)		563.472586	1325.630879	1.778458187	3.506562979	Zea mays	117118302.5	apospory-associated protein C
1328.390447	JGP_1_8.1958.2063.3	2.32333017	13.91923926	78.01014289	2.37E+06	(R)ALIAEK(N)		563.4396921	1325.550775	1.778341734	3.50635893	Solanum tuberosum	117126742.4	ascorbate peroxidase
1328.443849	JGP_1_7.6314.6436.3	2.323308906	13.91911555	78.01066296	2.37E+06	(K)EGLLQLPSDK(A)		563.4067981	1325.470672	1.77822528	3.506154882	Glycine max	117135182.3	"ascorbate peroxidase 1, cytosolic"
1328.497251	JGP_1_8.6519.6523.3	2.323287641	13.91899184	78.01118303	2.37E+06	(K)EGLLQLPSDK(A)		563.3739042	1325.390568	1.778108826	3.505950833	Glycine max	117143622.3	"ascorbate peroxidase 1, cytosolic"
1328.550653	JGP_1_7.3241.3250.3	2.323266377	13.91886813	78.0117031	2.37E+06	(R)LPDATQGSDHLR(Q)		563.3410102	1325.310465	1.777992372	3.505746784	Zea mays	117152062.2	ascorbate peroxidase2
1328.604055	JGP_1_8.3115.3232.4	2.323245112	13.91874442	78.01222317	2.37E+06	(R)LPDATQGSDHLR(Q)		563.3081163	1325.230361	1.777875918	3.505542735	Zea mays	117160502.1	ascorbate peroxidase2
1328.657456	JGP_1_7.6995.7074.4	2.323223848	13.91862071	78.01274324	2.37E+06	(K)ALLSDPSFRPLVDK(Y)		563.2752224	1325.150257	1.777759464	3.505338686	Zea mays	117168942.1	ascorbate peroxidase2
1328.710858	JGP_1_8.7202.7292.4	2.323202583	13.918497	78.01326331	2.37E+06	(K)ALLSDPSFRPLVDK(Y)		563.2423284	1325.070154	1.77764301	3.505134638	Zea mays	117177382	ascorbate peroxidase2
1328.76426	JGP_1_7.7145.7150.4	2.323181319	13.91837329	78.01378338	2.37E+06	(K)ALLSDPSFRPLVDK(Y)		563.2094345	1324.99005	1.777526557	3.504930589	Zea mays	117185821.9	ascorbate peroxidase2
1328.817662	JGP_1_8.7256.7256.3	2.323160054	13.91824958	78.01430345	2.37E+06	(K)ALLSDPSFRPLVDK(Y)		563.1765406	1324.909947	1.777410103	3.50472654	Zea mays	117194261.8	ascorbate peroxidase2
1328.871064	JGP_1_8.2399.2405.3	2.32313879	13.91812587	78.01482352	2.37E+06	(K)TGGPFGTmK(N)	m:Oxidized methionine	563.1436466	1324.829843	1.777293649	3.504522491	Zea mays	117202701.8	ascorbate peroxidase2
1328.924466	JGP_1_8.2216.2315.3	2.323117525	13.91800216	78.01534359	2.37E+06	(K)TGGPFGTmK(N)	m:Oxidized methionine	563.1107527	1324.74974	1.777177195	3.504318443	Zea mays	117211141.7	ascorbate peroxidase2
1328.977868	JGP_1_6.7580.7586.3	2.323096261	13.91787845	78.01586367	2.37E+06	(R)ISLAGLSLAK(C)		563.0778588	1324.669636	1.777060741	3.504114394	Arabidopsis thaliana	117219581.6	aspartate aminotransferase
1329.03127	JGP_1_8.8124.8199.4	2.323074996	13.91775474	78.01638374	2.37E+06	(K)LLSQLSALLSDIGLNIK(E)		563.0449648	1324.589532	1.776944287	3.503910345	Zea mays	117228021.5	ATP binding protein
1329.084672	JGP_1_1.6562.6572.4	2.323053732	13.91763103	78.01690381	2.37E+06	(R)VGLTGLTVAEHFR(D)		563.0120709	1324.509429	1.776827833	3.503706296	Zea mays	117236461.5	"ATP synthase subunit beta, mitochondrial precursor"
1329.138074	JGP_1_1.5783.5790.3	2.323032467	13.91750732	78.01742388	2.37E+06	(R)VLNTGSPITVPVGR(A)		562.9791769	1324.429325	1.77671138	3.503502247	Zea mays	117244901.4	"ATP synthase subunit beta, mitochondrial precursor"
1329.191476	JGP_1_2.6168.6188.4	2.323011203	13.91738361	78.01794395	2.38E+06	(R)VGLTGLTVAEHFR(D)		562.946283	1324.349222	1.776594926	3.503298199	Zea mays	117253341.3	"ATP synthase subunit beta, mitochondrial precursor"
1329.244877	JGP_1_1.5835.5850.3	2.322989938	13.9172599	78.01846402	2.38E+06	(R)VVDALGVPIDGK(G)		562.9133891	1324.269118	1.776478472	3.50309415	Triticum aestivum	117261781.2	atp2
1329.298279	JGP_1_5.5358.5446.3	2.322968674	13.91713619	78.01898409	2.38E+06	(K)IFIYSK(E)		562.8804951	1324.189015	1.776362018	3.502890101	Arabidopsis thaliana	117270221.2	auxin response factor 14
1329.351681	JGP_1_6.5580.5747.3	2.322947409	13.91701248	78.01950416	2.38E+06	(K)IFIYSK(E)		562.8476012	1324.108911	1.776245564	3.502686052	Arabidopsis thaliana	117278661.1	auxin response factor 14
1329.405083	JGP_1_6.5753.5753.3	2.322926145	13.91688877	78.02002423	2.38E+06	(K)IFIYSK(E)		562.8147073	1324.028808	1.77612911	3.502482004	Arabidopsis thaliana	117287101	auxin response factor 14
1329.458485	JGP_1_6.2750.2759.3	2.32290488	13.91676506	78.0205443	2.38E+06	(R)GQETPGEDPAVSAR(Y)		562.7818133	1323.948704	1.776012657	3.502277955	Zea mays	117295541	auxin-induced beta-glucosidase

1329.511887	JGP_1_5.2580.2584.3	2.322883615	13.91664135	78.02106437	2.38E+06	(R)GQETPGEDPAVSAR(Y)		562.7489194	1323.8686	1.775896203	3.502073906	Zea mays	117303980.9	auxin-induced beta-glucosidase
1329.565289	JGP_1_4.2523.2657.3	2.322862351	13.91651764	78.02158444	2.38E+06	(R)GQETPGEDPAVSAR(Y)		562.7160254	1323.788497	1.775779749	3.501869857	Zea mays	117312420.8	auxin-induced beta-glucosidase
1329.618691	JGP_1_7.2725.2725.3	2.322841086	13.91639393	78.02210451	2.38E+06	(R)GQETPGEDPAVSAR(Y)		562.6831315	1323.708393	1.775663295	3.501665808	Zea mays	117320860.7	auxin-induced beta-glucosidase
1329.672093	JGP_1_4.2541.2554.4	2.322819822	13.91627022	78.02262458	2.38E+06	(R)GQETPGEDPAVSAR(Y)		562.6502376	1323.62829	1.775546841	3.50146176	Zea mays	117329300.7	auxin-induced beta-glucosidase
1329.725495	JGP_1_7.4020.4020.3	2.322798557	13.91614651	78.02314465	2.38E+06	(R)IGFYQR(Y)		562.6173436	1323.548186	1.775430387	3.501257711	Arabidopsis thaliana	117337740.6	basic chitinase
1329.778896	JGP_1_7.4502.4597.4	2.322777293	13.9160228	78.02366472	2.38E+06	(K)AFGSLAKPGLNDK(I)		562.5844497	1323.468083	1.775313933	3.501053662	Zea mays	117346180.5	beta-expansin 1
1329.832298	JGP_1_7.1882.1989.3	2.322756028	13.91589909	78.02418479	2.38E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	562.5515558	1323.387979	1.77519748	3.500849613	Zea mays	117354620.4	beta-expansin 1
1329.8857	JGP_1_4.2018.2141.3	2.322734764	13.91577538	78.02470486	2.38E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	562.5186618	1323.307875	1.775081026	3.500645565	Zea mays	117363060.4	beta-expansin 1
1329.939102	JGP_1_7.4682.4832.4	2.322713499	13.91565167	78.02522493	2.38E+06	(K)AFGSLAKPGLNDK(I)		562.4857679	1323.227772	1.774964572	3.500441516	Zea mays	117371500.3	beta-expansin 1
1329.992504	JGP_1_3.2079.2152.3	2.322692235	13.91552795	78.025745	2.39E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	562.452874	1323.147668	1.774848118	3.500237467	Zea mays	117379940.2	beta-expansin 1
1330.045906	JGP_1_2.2016.2086.3	2.32267097	13.91540424	78.02626507	2.39E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	562.41998	1323.067565	1.774731664	3.500033418	Zea mays	117388380.2	beta-expansin 1
1330.099308	JGP_1_1.2006.2079.3	2.322649706	13.91528053	78.02678514	2.39E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	562.3870861	1322.987461	1.77461521	3.499829369	Zea mays	117396820.1	beta-expansin 1
1330.15271	JGP_1_3.4362.4477.4	2.322628441	13.91515682	78.02730521	2.39E+06	(K)AFGSLAKPGLNDK(I)		562.3541921	1322.907358	1.774498757	3.499625321	Zea mays	117405260	beta-expansin 1
1330.206112	JGP_1_6.2089.2177.3	2.322607177	13.91503311	78.02782528	2.39E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	562.3212982	1322.827254	1.774382303	3.499421272	Zea mays	117413699.9	beta-expansin 1
1330.259514	JGP_1_7.4258.4361.3	2.322585912	13.9149094	78.02834535	2.39E+06	(K)GPFSIR(L)		562.2884043	1322.74715	1.774265849	3.499217223	Zea mays	117422139.9	beta-expansin 1
1330.312915	JGP_1_7.4452.4457.3	2.322564648	13.91478569	78.02886542	2.39E+06	(K)GPFSIR(L)		562.2555103	1322.667047	1.774149395	3.499013174	Zea mays	117430579.8	beta-expansin 1
1330.366317	JGP_1_8.4530.4539.3	2.322543383	13.91466198	78.02938549	2.39E+06	(K)AFGSLAKPGLNDK(I)		562.2226164	1322.586943	1.774032941	3.498809125	Zea mays	117439019.7	beta-expansin 1
1330.419719	JGP_1_7.0729.0735.3	2.322522119	13.91453827	78.02990556	2.39E+06	(R)LTSESGK(K)		562.1897225	1322.50684	1.773916487	3.498605077	Zea mays	117447459.6	beta-expansin 1
1330.473121	JGP_1_7.4514.4607.3	2.322500854	13.91441456	78.03042563	2.39E+06	(K)AFGSLAKPGLNDK(I)		562.1568285	1322.426736	1.773800033	3.498401028	Zea mays	117455899.6	beta-expansin 1
1330.526523	JGP_1_6.4578.4672.3	2.32247959	13.91429085	78.0309457	2.39E+06	(K)GPFSIR(L)		562.1239346	1322.346633	1.77368358	3.498196979	Zea mays	117464339.5	beta-expansin 1
1330.579925	JGP_1_8.4499.4620.4	2.322458325	13.91416714	78.03146577	2.39E+06	(K)AFGSLAKPGLNDK(I)		562.0910406	1322.266529	1.773567126	3.49799293	Zea mays	117472779.4	beta-expansin 1
1330.633327	JGP_1_4.4277.4368.3	2.322437061	13.91404343	78.03198585	2.39E+06	(K)GPFSIR(L)		562.0581467	1322.186425	1.773450672	3.497788882	Zea mays	117481219.3	beta-expansin 1
1330.686729	JGP_1_5.4197.4285.3	2.322415796	13.91391972	78.03250592	2.39E+06	(K)GPFSIR(L)		562.0252528	1322.106322	1.773334218	3.497584833	Zea mays	117489659.3	beta-expansin 1
1330.740131	JGP_1_7.8854.8949.3	2.322394532	13.91379601	78.03302599	2.39E+06	(K)NVNLPPFSAMTSCGNQPLFK(D)		C:Carbamidomethylation	561.9923588	1322.026218	1.773217764	3.497380784	Zea mays	117498099.2 beta-expansin 1a precursor
1330.793533	JGP_1_2.7614.7708.3	2.322373267	13.9136723	78.03354606	2.40E+06	(K)NVNLPPFSAMTSCGNEPLFK(D)		C:Carbamidomethylation	561.9594649	1321.946115	1.77310131	3.497176735	Zea mays	117506539.1 beta-expansin 7 precursor
1330.846934	JGP_1_4.8392.8485.3	2.322352003	13.91354859	78.03406613	2.40E+06	(K)NVNLPPFSAMTSCGNEPLFK(D)		C:Carbamidomethylation	561.926571	1321.866011	1.772984857	3.496972686	Zea mays	117514979.1 beta-expansin 7 precursor
1330.900336	JGP_1_7.5547.5648.3	2.322330738	13.91342488	78.0345862	2.40E+06	(R)HSWGAIWR(M)		561.893677	1321.785908	1.772868403	3.496768638	Triticum aestivum	117523419	beta-expansin TaEXPB4
1330.953738	JGP_1_6.5850.5943.3	2.322309474	13.91330117	78.03510627	2.40E+06	(R)HSWGAIWR(M)		561.8607831	1321.705804	1.772751949	3.496564589	Triticum aestivum	117531858.9	beta-expansin TaEXPB4
1331.00714	JGP_1_7.5354.5462.3	2.322288209	13.91317746	78.03562634	2.40E+06	(R)HSWGAIWR(M)		561.8278892	1321.6257	1.772635495	3.49636054	Triticum aestivum	117540298.8	beta-expansin TaEXPB4
1331.060542	JGP_1_2.5089.5161.4	2.322266945	13.91305375	78.03614641	2.40E+06	(R)HSWGAIWR(M)		561.7949952	1321.545597	1.772519041	3.496156491	Triticum aestivum	117548738.8	beta-expansin TaEXPB4
1331.113944	JGP_1_4.5487.5492.3	2.32224568	13.91293004	78.03666648	2.40E+06	(R)HSWGAIWR(M)		561.7621013	1321.465493	1.772402587	3.495952443	Triticum aestivum	117557178.7	beta-expansin TaEXPB4
1331.167346	JGP_1_4.5582.5587.4	2.322224416	13.91280633	78.03718655	2.40E+06	(R)HSWGAIWR(M)		561.7292073	1321.38539	1.772286133	3.495748394	Triticum aestivum	117565618.6	beta-expansin TaEXPB4
1331.220748	JGP_1_6.5843.5939.4	2.322203151	13.91268262	78.03770662	2.40E+06	(R)HSWGAIWR(M)		561.6963134	1321.305286	1.77216968	3.495544345	Triticum aestivum	117574058.5	beta-expansin TaEXPB4
1331.27415	JGP_1_7.5548.5649.4	2.322181887	13.91255891	78.03822669	2.40E+06	(R)HSWGAIWR(M)		561.6634195	1321.225183	1.772053226	3.495340296	Triticum aestivum	117582498.5	beta-expansin TaEXPB4
1331.327552	JGP_1_7.5367.5467.4	2.322160622	13.9124352	78.03874676	2.40E+06	(R)HSWGAIWR(M)		561.6305255	1321.145079	1.771936772	3.495136247	Triticum aestivum	117590938.4	beta-expansin TaEXPB4
1331.380953	JGP_1_3.6242.6332.3	2.322139357	13.91231149	78.03926683	2.40E+06	(K)YFVGSVLSGGGSVPAEK(A)		561.5976316	1321.064975	1.771820318	3.494932199	Zea mays	117599378.3	beta-glucanase precursor
1331.434355	JGP_1_4.6493.6506.3	2.322118093	13.91218778	78.0397869	2.40E+06	(K)YFVGSVLSGGGSVPAEK(A)		561.5647377	1320.984872	1.771703864	3.49472815	Zea mays	117607818.2	beta-glucanase precursor
1331.487757	JGP_1_3.2046.2121.3	2.322096828	13.91206407	78.04030697	2.40E+06	(K)IGQmSQIER(A)	m:Oxidized methionine	561.5318437	1320.904768	1.77158741	3.494524101	Zea mays	117616258.2	beta-glucanase precursor
1331.541159	JGP_1_3.3666.3766.3	2.322075564	13.91194036	78.04082704	2.40E+06	(K)SVDQLPmNYGDK(R)	m:Oxidized methionine	561.4989498	1320.824665	1.771470957	3.494320052	Zea mays	117624698.1	beta-glucanase precursor
1331.594561	JGP_1_4.1989.2071.3	2.322054299	13.91181665	78.04134711	2.41E+06	(K)IGQmSQIER(A)	m:Oxidized methionine	561.4660558	1320.744561	1.771354503	3.494116004	Zea mays	117633138	beta-glucanase precursor
1331.647963	JGP_1_3.7113.7119.4	2.322033035	13.91169294	78.04186718	2.41E+06	(R)ATGIPYTFAPCVAVCR(D)	C:Carbamidomethylation	561.4331619	1320.664458	1.771238049	3.493911955	Zea mays	117641578	beta-glucanase precursor
1331.701365	JGP_1_3.7102.7189.3	2.32201177	13.91156923	78.04238725	2.41E+06	(R)ATGIPYTFAPCVAVCR(D)	C:Carbamidomethylation	561.400268	1320.584354	1.771121595	3.493707906	Zea mays	117650017.9	beta-glucanase precursor
1331.754767	JGP_1_3.2689.2781.3	2.321990506	13.91144552	78.04290732	2.41E+06	(K)ASASVWQK(M)		561.367374	1320.50425	1.771005141	3.493503857	Zea mays	117658457.8	beta-glucanase precursor
1331.808169	JGP_1_4.5664.5674.5	2.321969241	13.91132181	78.04342739	2.41E+06	(K)ILVAGSHAHDLGSQCGGWTIK(W)		C:Carbamidomethylation	561.3344801	1320.424147	1.770888687	3.493299808	Zea mays	117666897.7 beta-glucanase precursor
1331.861571	JGP_1_3.1552.1631.3	2.321947977	13.9111981	78.04394746	2.41E+06	(K)HFVGDGGTTR(G)		561.3015862	1320.344043	1.770772233	3.49309576	Zea mays	117675337.7	beta-glucanase precursor
1331.914972	JGP_1_4.2713.2716.3	2.321926712	13.91107439	78.04446753	2.41E+06	(K)ASASVWQK(M)		561.2686922	1320.26394	1.77065578	3.492891711	Zea mays	117683777.6	beta-glucanase precursor
1331.968374	JGP_1_4.7380.7395.3	2.321905448	13.91095067	78.0449876	2.41E+06	(R)ATGIPYTFAPCVAVCR(D)	C:Carbamidomethylation	561.2357983	1320.183836	1.770539326	3.492687662	Zea mays	117692217.5	beta-glucanase precursor
1332.021776	JGP_1_3.3343.3358.3	2.321884183	13.91082696	78.04550767	2.41E+06	(K)IGQMSQIER(A)		561.2029044	1320.103733	1.770422872	3.492483613	Zea mays	117700657.4	beta-glucanase precursor
1332.075178	JGP_1_4.1492.1567.3	2.321862919	13.91070325	78.04602774	2.41E+06	(K)HFVGDGGTTR(G)		561.1700104	1320.023629	1.770306418	3.492279564	Zea mays	117709097.4	beta-glucanase precursor
1332.12858	JGP_1_5.1463.1471.3	2.321841654	13.91057954	78.04654781	2.41E+06	(K)HFVGDGGTTR(G)		561.1371165	1319.943525	1.770189964	3.492075516	Zea mays	117717537.3	beta-glucanase precursor
1332.181982	JGP_1_5.5437.5443.4	2.32182039	13.91045583	78.04706788	2.41E+06	(K)YGQDATNVGDEGGFAPNIQENK(E)			561.1042225	1319.863422	1.77007351	3.491871467	Arabidopsis thaliana	117725977.2 bifunctional enolase 2/transcriptional activator
1332.235384	JGP_1_5.5123.5123.4	2.321799125	13.91033212	78.04758796	2.41E+06	(K)KYGQDATNVGDEGGFAPNIQENK(E)			561.0713286	1319.783318	1.769957056	3.491667418	Arabidopsis thaliana	117734417.2 bifunctional enolase 2/transcriptional activator

1332.288786	JGP_1_5.5458.5458.3	2.321777861	13.91020841	78.04810803	2.41E+06	(K)YGQDATNVGDEGGFAPNIQENK(E)		561.0384347	1319.703215	1.769840603	3.491463369	Arabidopsis thaliana	117742857.1	bifunctional enolase 2/transcriptional activator
1332.342188	JGP_1_5.5114.5193.3	2.321756596	13.9100847	78.0486281	2.41E+06	(K)TYDLNFK(E)		561.0055407	1319.623111	1.769724149	3.491259321	Arabidopsis thaliana	117751297	bifunctional enolase 2/transcriptional activator
1332.39559	JGP_1_2.5228.5228.3	2.321735332	13.90996099	78.04914817	2.42E+06	(K)EGLELLK(T)		560.9726468	1319.543008	1.769607695	3.491055272	Arabidopsis thaliana	117759736.9	bifunctional enolase 2/transcriptional activator
1332.448991	JGP_1_2.4778.4783.4	2.321714067	13.90983728	78.04966824	2.42E+06	(K)YGQDATNVGDEGGFAPNIQENK(E)		560.9397529	1319.462904	1.769491241	3.490851223	Arabidopsis thaliana	117768176.9	bifunctional enolase 2/transcriptional activator
1332.502393	JGP_1_5.0780.0786.3	2.321692803	13.90971357	78.05018831	2.42E+06	(K)TGAPCR(S)	C:Carbamidomethylation	560.9068589	1319.3828	1.769374787	3.490647174	Arabidopsis thaliana	117776616.8	bifunctional enolase 2/transcriptional activator
1332.555795	JGP_1_8.4129.4228.3	2.321671538	13.90958986	78.05070838	2.42E+06	(R)TFSAGVLK(K)		560.873965	1319.302697	1.769258333	3.490443125	Arabidopsis thaliana	117785056.7	bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein
1332.609197	JGP_1_7.3119.3216.3	2.321650274	13.90946615	78.05122845	2.42E+06	(R)IISSIEQK(E)		560.8410711	1319.222593	1.76914188	3.490239077	Oryza sativa	117793496.6	brain specific protein
1332.662599	JGP_1_8.6904.6909.4	2.321629009	13.90934244	78.05174852	2.42E+06	(K)EAFSLFDKDGDGCITTK(E)	C:Carbamidomethylation	560.8081771	1319.14249	1.769025426	3.490035028	Arabidopsis thaliana	117801936.6	calmodulin 5
1332.716001	JGP_1_1.6169.6203.4	2.321607745	13.90921873	78.05226859	2.42E+06	(R)VFDKDQNGFISAAELR(H)		560.7752832	1319.062386	1.768908972	3.489830979	Arabidopsis thaliana	117810376.5	calmodulin 5
1332.769403	JGP_1_5.1935.2018.3	2.32158648	13.90909502	78.05278866	2.42E+06	(K)AAFDAAEK(K)		560.7423892	1318.982283	1.768792518	3.48962693	Triticum aestivum	117818816.4	calreticulin-like protein
1332.822805	JGP_1_3.5547.5626.3	2.321565216	13.90897131	78.05330873	2.42E+06	(K)EAVNVSLENLK(T)		560.7094953	1318.902179	1.768676064	3.489422882	Zea mays	117827256.3	carbonic anhydrase
1332.876207	JGP_1_6.6211.6219.3	2.321543951	13.9088476	78.0538288	2.42E+06	(K)EAVNVSLENLK(T)		560.6766014	1318.822076	1.76855961	3.489218833	Zea mays	117835696.3	carbonic anhydrase
1332.929609	JGP_1_2.5208.5286.3	2.321522687	13.90872389	78.05434887	2.42E+06	(K)EAVNVSLENLK(T)		560.6437074	1318.741972	1.768443156	3.489014784	Zea mays	117844136.2	carbonic anhydrase
1332.98301	JGP_1_6.4638.4643.3	2.321501422	13.90860018	78.05486894	2.42E+06	(K)TYPFVK(E)		560.6108135	1318.661868	1.768326703	3.488810735	Oryza sativa	117852576.1	carbonic anhydrase
1333.036412	JGP_1_2.5123.5196.4	2.321480158	13.90847647	78.05538901	2.42E+06	(K)KPELFEPLK(A)		560.5779196	1318.581765	1.768210249	3.488606686	Oryza sativa	117861016.1	carbonic anhydrase
1333.089814	JGP_1_1.4144.4225.3	2.321458893	13.90835276	78.05590908	2.42E+06	(K)TYPFVK(E)		560.5450256	1318.501661	1.768093795	3.488402638	Oryza sativa	117869456	carbonic anhydrase
1333.143216	JGP_1_7.4432.4439.3	2.321437628	13.90822905	78.05642915	2.42E+06	(K)TYPFVK(E)		560.5121317	1318.421558	1.767977341	3.488198589	Oryza sativa	117877895.9	carbonic anhydrase
1333.196618	JGP_1_1.5489.5581.3	2.321416364	13.90810534	78.05694922	2.43E+06	(K)EAVNVSLENLK(T)		560.4792377	1318.341454	1.767860887	3.48799454	Zea mays	117886335.8	carbonic anhydrase
1333.25002	JGP_1_8.4404.4407.3	2.321395099	13.90798163	78.05746929	2.43E+06	(K)TYPFVK(E)		560.4463438	1318.261351	1.767744433	3.487790491	Oryza sativa	117894775.8	carbonic anhydrase
1333.303422	JGP_1_5.4383.4393.3	2.321373835	13.90785792	78.05798936	2.43E+06	(K)TYPFVK(E)		560.4134499	1318.181247	1.76762798	3.487586443	Oryza sativa	117903215.7	carbonic anhydrase
1333.356824	JGP_1_2.3962.4047.3	2.32135257	13.90773421	78.05850943	2.43E+06	(K)TYPFVK(E)		560.3805559	1318.101143	1.767511526	3.487382394	Oryza sativa	117911655.6	carbonic anhydrase
1333.410226	JGP_1_3.4234.4317.3	2.321331306	13.9076105	78.0590295	2.43E+06	(K)TYPFVK(E)		560.347662	1318.02104	1.767395072	3.487178345	Oryza sativa	117920095.5	carbonic anhydrase
1333.463628	JGP_1_4.5753.5758.3	2.321310041	13.90748679	78.05954957	2.43E+06	(K)EAVNVSLENLK(T)		560.3147681	1317.940936	1.767278618	3.486974296	Zea mays	117928535.5	carbonic anhydrase
1333.517029	JGP_1_4.4310.4312.3	2.321288777	13.90736308	78.06006964	2.43E+06	(K)TYPFVK(E)		560.2818741	1317.860833	1.767162164	3.486770247	Oryza sativa	117936975.4	carbonic anhydrase
1333.570431	JGP_1_2.3848.3937.3	2.321267512	13.90723937	78.06058971	2.43E+06	(R)NIASmVPPYDK(I)	m:Oxidized methionine	560.2489802	1317.780729	1.76704571	3.486566199	Zea mays	117945415.3	carbonic anhydrase
1333.623833	JGP_1_8.6151.6155.3	2.321246248	13.90711566	78.06110978	2.43E+06	(K)EAVNVSLENLK(T)		560.2160863	1317.700626	1.766929256	3.48636215	Zea mays	117953855.2	carbonic anhydrase
1333.677235	JGP_1_3.5432.5512.4	2.321224983	13.90699195	78.06162985	2.43E+06	(K)KPELFEPLK(A)		560.1831923	1317.620522	1.766812803	3.486158101	Oryza sativa	117962295.2	carbonic anhydrase
1333.730637	JGP_1_8.3166.3287.3	2.321203719	13.90686824	78.06214992	2.43E+06	(K)GPLTIR(V)		560.1502984	1317.540418	1.766696349	3.485954052	Arabidopsis thaliana	117970735.1	CBL-interacting serine/threonine-protein kinase 14
1333.784039	JGP_1_5.9759.9850.3	2.321182454	13.90674453	78.06266999	2.43E+06	(K)LYEVVPPILTELGK(V)		560.1174044	1317.460315	1.766579895	3.485750003	Oryza sativa	117979175	citrate synthase
1333.837441	JGP_1_6.5860.5865.4	2.32116119	13.90662082	78.06319006	2.43E+06	(R)ALGLPLERPK(S)		560.0845105	1317.380211	1.766463441	3.485545955	Nicotiana tabacum	117987615	citrate synthase
1333.890843	JGP_1_5.5604.5609.4	2.321139925	13.90649711	78.06371014	2.43E+06	(R)ALGLPLERPK(S)		560.0516166	1317.300108	1.766346987	3.485341906	Nicotiana tabacum	117996054.9	citrate synthase
1333.944245	JGP_1_1.5267.5273.4	2.321118661	13.90637339	78.06423021	2.43E+06	(R)ALGLPLERPK(S)		560.0187226	1317.220004	1.766230533	3.485137857	Nicotiana tabacum	118004494.8	citrate synthase
1333.997647	JGP_1_1.9221.9290.3	2.321097396	13.90624968	78.06475028	2.43E+06	(K)LYEVVPPILTELGK(V)		559.9858287	1317.139901	1.76611408	3.484933808	Oryza sativa	118012934.7	citrate synthase
1334.051048	JGP_1_5.2165.2168.3	2.321076132	13.90612597	78.06527035	2.44E+06	(K)EQVDALSK(E)		559.9529348	1317.059797	1.765997626	3.48472976	Oryza sativa	118021374.7	citrate synthase
1334.10445	JGP_1_5.9790.9810.4	2.321054867	13.90600226	78.06579042	2.44E+06	(K)LYEVVPPILTELGK(V)		559.9200408	1316.979693	1.765881172	3.484525711	Oryza sativa	118029814.6	citrate synthase
1334.157852	JGP_1_2.8729.8732.3	2.321033603	13.90587855	78.06631049	2.44E+06	(K)LYEVVPPILTELGK(V)		559.8871469	1316.89959	1.765764718	3.484321662	Oryza sativa	118038254.5	citrate synthase
1334.211254	JGP_1_2.5059.5063.4	2.321012338	13.90575484	78.06683056	2.44E+06	(R)ALGLPLERPK(S)		559.8542529	1316.819486	1.765648264	3.484117613	Nicotiana tabacum	118046694.4	citrate synthase
1334.264656	JGP_1_6.6351.6450.3	2.320991074	13.90563113	78.06735063	2.44E+06	(R)CPGVVSCADIVAMAAR(D)	C:Carbamidomethylation	559.821359	1316.739383	1.76553181	3.483913564	Arabidopsis thaliana	118055134.4	class III peroxidase ATP32
1334.318058	JGP_1_7.6190.6198.3	2.320969809	13.90550742	78.0678707	2.44E+06	(R)CPGVVSCADIVAMAAR(D)	C:Carbamidomethylation	559.7884651	1316.659279	1.765415356	3.483709516	Arabidopsis thaliana	118063574.3	class III peroxidase ATP32
1334.37146	JGP_1_4.5970.5985.3	2.320948545	13.90538371	78.06839077	2.44E+06	(K)EVPTSFGFDTACK(V)	C:Carbamidomethylation	559.7555711	1316.579176	1.765298903	3.483505467	Arabidopsis thaliana	118072014.2	contains similarity to phosphofructokinases (Pfam
		" PFK.hmm, score"	36.60)											
1334.424862	JGP_1_3.2837.2921.3	2.32092728	13.90526	78.06891084	2.44E+06	(K)ILYAR(H)		559.7226772	1316.499072	1.765182449	3.483301418	Arabidopsis thaliana	118080454.2	COP9 signalosome complex subunit 1
1334.478264	JGP_1_4.2824.2916.3	2.320906016	13.90513629	78.06943091	2.44E+06	(K)ILYAR(H)		559.6897833	1316.418968	1.765065995	3.483097369	Arabidopsis thaliana	118088894.1	COP9 signalosome complex subunit 1
1334.531666	JGP_1_2.2761.2841.3	2.320884751	13.90501258	78.06995098	2.44E+06	(K)ILYAR(H)		559.6568893	1316.338865	1.764949541	3.482893321	Arabidopsis thaliana	118097334	COP9 signalosome complex subunit 1
1334.585067	JGP_1_1.2793.2888.3	2.320863487	13.90488887	78.07047105	2.44E+06	(K)ILYAR(H)		559.6239954	1316.258761	1.764833087	3.482689272	Arabidopsis thaliana	118105773.9	COP9 signalosome complex subunit 1
1334.638469	JGP_1_8.4283.4283.3	2.320842222	13.90476516	78.07099112	2.44E+06	(R)AVVVHADPDDLGK(G)		559.5911015	1316.178658	1.764716633	3.482485223	Arabidopsis thaliana	118114213.9	copper/zinc superoxide dismutase 3
1334.691871	JGP_1_8.4216.4322.4	2.320820958	13.90464145	78.07151119	2.44E+06	(R)AVVVHADPDDLGK(G)		559.5582075	1316.098554	1.76460018	3.482281174	Arabidopsis thaliana	118122653.8	copper/zinc superoxide dismutase 3
1334.745273	JGP_1_7.4253.4253.4	2.320799693	13.90451774	78.07203126	2.44E+06	(R)AVVVHADPDDLGK(G)		559.5253136	1316.018451	1.764483726	3.482077125	Arabidopsis thaliana	118131093.7	copper/zinc superoxide dismutase 3
1334.798675	JGP_1_8.6924.6924.4	2.320778429	13.90439403	78.07255133	2.44E+06	(R)AFVVHELEDDLGK(G)		559.4924196	1315.938347	1.764367272	3.481873077	Triticum aestivum	118139533.6	Cu/Zn superoxide dismutase
1334.852077	JGP_1_8.7002.7005.3	2.320757164	13.90427032	78.0730714	2.45E+06	(K)VYFDIEIDGKPAGR(V)		559.4595257	1315.858243	1.764250818	3.481669028	Triticum aestivum	118147973.6	cyclophilin

1334.905479	JGP_1_8.9471.9547.3	2.3207359	13.90414661	78.07359147	2.45E+06	(R)IIPSFMIQGGDFTLGDGR(G)			559.4266318	1315.77814	1.764134364	3.481464979	Triticum aestivum	118156413.5	cyclophilin
1334.958881	JGP_1_8.8966.9049.3	2.320714635	13.9040229	78.07411154	2.45E+06	(R)IIPSFmIQGGDFTLGDGR(G)	m:Oxidized methionine		559.3937378	1315.698036	1.76401791	3.48126093	Triticum aestivum	118164853.4	cyclophilin
1335.012283	JGP_1_8.7566.7570.3	2.32069337	13.90389919	78.07463161	2.45E+06	(R)VIPDFMCQGGDFTR(G)	C:Carbamidomethylation		559.3608439	1315.617933	1.763901456	3.481056882	Triticum aestivum	118173293.3	cyclophilin
1335.065685	JGP_1_8.10676.10690.4	2.320672106	13.90377548	78.07515168	2.45E+06	(R)DTNGSQFFITTVTTSWLDGK(H)			559.32795	1315.537829	1.763785003	3.480852833	Triticum aestivum	118181733.3	cyclophilin
1335.119086	JGP_1_8.9477.9545.4	2.320650841	13.90365177	78.07567175	2.45E+06	(R)IIPSFMIQGGDFTLGDGR(G)			559.295056	1315.457726	1.763668549	3.480648784	Triticum aestivum	118190173.2	cyclophilin
1335.172488	JGP_1_8.6425.6508.3	2.320629577	13.90352806	78.07619182	2.45E+06	(R)VIPDFmCQGGDFTR(G)	C:Carbamidomethylation	m:Oxidized methionine	559.2621621	1315.377622	1.763552095	3.480444735	Triticum aestivum	118198613.1	cyclophilin
1335.22589	JGP_1_3.5768.5789.3	2.320608312	13.90340435	78.07671189	2.45E+06	(R)VIPDFmCQGGDFTR(G)	C:Carbamidomethylation	m:Oxidized methionine	559.2292681	1315.297518	1.763435641	3.480240686	Triticum aestivum	118207053.1	cyclophilin
1335.279292	JGP_1_1.5759.5762.3	2.320587048	13.90328064	78.07723196	2.45E+06	(R)VIPDFmCQGGDFTR(G)	C:Carbamidomethylation	m:Oxidized methionine	559.1963742	1315.217415	1.763319187	3.480036638	Triticum aestivum	118215493	cyclophilin
1335.332694	JGP_1_7.7606.7629.3	2.320565783	13.90315693	78.07775203	2.45E+06	(R)VIPDFMCQGGDFTR(G)	C:Carbamidomethylation		559.1634803	1315.137311	1.763202733	3.479832589	Triticum aestivum	118223932.9	cyclophilin
1335.386096	JGP_1_8.7592.7602.4	2.320544519	13.90303322	78.0782721	2.45E+06	(R)VIPDFMCQGGDFTR(G)	C:Carbamidomethylation		559.1305863	1315.057208	1.76308628	3.47962854	Triticum aestivum	118232372.8	cyclophilin
1335.439498	JGP_1_8.8984.9059.4	2.320523254	13.90290951	78.07879217	2.45E+06	(R)IIPSFmIQGGDFTLGDGR(G)	m:Oxidized methionine		559.0976924	1314.977104	1.762969826	3.479424491	Triticum aestivum	118240812.8	cyclophilin
1335.4929	JGP_1_8.5851.5854.3	2.32050199	13.9027858	78.07931224	2.45E+06	(R)VLSGMDVVYK(V)			559.0647985	1314.897001	1.762853372	3.479220442	Triticum aestivum	118249252.7	cyclophilin
1335.546302	JGP_1_2.5444.5454.3	2.320480725	13.90266209	78.07983232	2.45E+06	(R)VIPDFmCQGGDFTR(G)	C:Carbamidomethylation	m:Oxidized methionine	559.0319045	1314.816897	1.762736918	3.479016394	Triticum aestivum	118257692.6	cyclophilin
1335.599704	JGP_1_8.10671.10671.3	2.320459461	13.90253838	78.08035239	2.45E+06	(R)DTNGSQFFITTVTTSWLDGK(H)			558.9990106	1314.736793	1.762620464	3.478812345	Triticum aestivum	118266132.5	cyclophilin
1335.653105	JGP_1_8.4213.4217.3	2.320438196	13.90241467	78.08087246	2.46E+06	(R)VLSGmDVVYK(V)	m:Oxidized methionine		558.9661167	1314.65669	1.76250401	3.478608296	Triticum aestivum	118274572.5	cyclophilin
1335.706507	JGP_1_7.4264.4276.3	2.320416932	13.90229096	78.08139253	2.46E+06	(R)VVEGMDVVK(A)			558.9332227	1314.576586	1.762387556	3.478404247	Oryza sativa	118283012.4	cyclophilin 3
1335.759909	JGP_1_8.8302.8311.3	2.320395667	13.90216725	78.0819126	2.46E+06	(K)VYFDISIGNPVGK(N)			558.9003288	1314.496483	1.762271103	3.478200199	Triticum aestivum	118291452.3	cyclophilin-like protein
1335.813311	JGP_1_8.7251.7385.4	2.320374403	13.90204354	78.08243267	2.46E+06	(R)WVIQNGGLTTEANYPYQAR(R)			558.8674348	1314.416379	1.762154649	3.47799615	Zea mays	118299892.2	cysteine protease precursor
1335.866713	JGP_1_8.7261.7370.3	2.320353138	13.90191983	78.08295274	2.46E+06	(R)WVIQNGGLTTEANYPYQAR(R)			558.8345409	1314.336276	1.762038195	3.477792101	Zea mays	118308332.2	cysteine protease precursor
1335.920115	JGP_1_8.6501.6505.4	2.320331874	13.90179611	78.08347281	2.46E+06	(K)VWEKPWENFK(E)			558.801647	1314.256172	1.761921741	3.477588052	Zea mays	118316772.1	cysteine proteinase inhibitor
1335.973517	JGP_1_7.6370.6370.3	2.320310609	13.9016724	78.08399288	2.46E+06	(K)LVSLSEQELVDCDTK(K)	C:Carbamidomethylation		558.768753	1314.176068	1.761805287	3.477384003	Glycine max	118325212	cysteine proteinase precursor
1336.026919	JGP_1_8.7269.7354.3	2.320289345	13.90154869	78.08451295	2.46E+06	(R)TDLIAYLK(E)			558.7358591	1314.095965	1.761688833	3.477179955	Zea mays	118333652	cytochrome c
1336.080321	JGP_1_8.7434.7442.3	2.32026808	13.90142498	78.08503302	2.46E+06	(R)TDLIAYLK(E)			558.7029652	1314.015861	1.761572379	3.476975906	Zea mays	118342091.9	cytochrome c
1336.133723	JGP_1_8.7716.7737.3	2.320246816	13.90130127	78.08555309	2.46E+06	(R)TDLIAYLK(E)			558.6700712	1313.935758	1.761455926	3.476771857	Zea mays	118350531.8	cytochrome c
1336.187125	JGP_1_8.6510.6593.4	2.320225551	13.90117756	78.08607316	2.46E+06	(K)ERTDLIAYLK(E)			558.6371773	1313.855654	1.761339472	3.476567808	Zea mays	118358971.7	cytochrome c
1336.240526	JGP_1_8.6614.6619.3	2.320204287	13.90105385	78.08659323	2.46E+06	(K)ERTDLIAYLK(E)			558.6042834	1313.775551	1.761223018	3.47636376	Zea mays	118367411.7	cytochrome c
1336.293928	JGP_1_8.1939.1949.3	2.320183022	13.90093014	78.0871133	2.46E+06	(R)FPTTNQTR(H)			558.5713894	1313.695447	1.761106564	3.476159711	Arabidopsis thaliana	118375851.6	cytochrome C oxidase 6B
1336.34733	JGP_1_8.1520.1688.3	2.320161758	13.90080643	78.08763337	2.46E+06	(K)YIPGTK(M)			558.5384955	1313.615344	1.76099011	3.475955662	Arabidopsis thaliana	118384291.5	cytochrome c-2
1336.400732	JGP_1_8.7211.7295.3	2.320140493	13.90068272	78.08815344	2.46E+06	(R)ADLIAYLK(E)			558.5056015	1313.53524	1.760873656	3.475751613	Arabidopsis thaliana	118392731.4	cytochrome c-2
1336.454134	JGP_1_7.7054.7141.3	2.320119229	13.90055901	78.08867351	2.47E+06	(R)ADLIAYLK(E)			558.4727076	1313.455136	1.760757203	3.475547564	Arabidopsis thaliana	118401171.4	cytochrome c-2
1336.507536	JGP_1_8.6504.6520.3	2.320097964	13.9004353	78.08919358	2.47E+06	(K)MVFPGLK(K)			558.4398137	1313.375033	1.760640749	3.475343516	Arabidopsis thaliana	118409611.3	cytochrome c-2
1336.560938	JGP_1_8.3706.3787.3	2.3200767	13.90031159	78.08971365	2.47E+06	(R)LLEVDNR(V)			558.4069197	1313.294929	1.760524295	3.475139467	Triticum aestivum	118418051.2	cytochrome-c oxidase
1336.61434	JGP_1_6.8947.9027.3	2.320055435	13.90018788	78.09023372	2.47E+06	(K)TVIWNGPmGVFEFEK(F)	m:Oxidized methionine		558.3740258	1313.214826	1.760407841	3.474935418	Zea mays	118426491.2	cytosolic 3-phosphoglycerate kinase
1336.667742	JGP_1_6.7862.7940.4	2.320034171	13.90006417	78.09075379	2.47E+06	(K)LASVADLYVNDAFGTAHR(A)			558.3411319	1313.134722	1.760291387	3.474731369	Zea mays	118434931.1	cytosolic 3-phosphoglycerate kinase
1336.721144	JGP_1_6.9483.9557.4	2.320012906	13.89994046	78.09127386	2.47E+06	(K)GVSLLLPTDIVVADK(F)			558.3082379	1313.054619	1.760174933	3.474527321	Zea mays	118443371	cytosolic 3-phosphoglycerate kinase
1336.774545	JGP_1_6.8642.8765.4	2.319991642	13.89981675	78.09179393	2.47E+06	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine		558.275344	1312.974515	1.760058479	3.474323272	Zea mays	118451810.9	cytosolic 3-phosphoglycerate kinase
1336.827947	JGP_1_6.8525.8610.4	2.319970377	13.89969304	78.092314	2.47E+06	(K)SLVEEDKLELATSLIEK(A)			558.24245	1312.894411	1.759942026	3.474119223	Zea mays	118460250.9	cytosolic 3-phosphoglycerate kinase
1336.881349	JGP_1_6.1422.1507.3	2.319949112	13.89956933	78.09283407	2.47E+06	(K)FAADAESK(I)			558.2095561	1312.814308	1.759825572	3.473915174	Zea mays	118468690.8	cytosolic 3-phosphoglycerate kinase
1336.934751	JGP_1_5.9105.9120.4	2.319927848	13.89944562	78.09335414	2.47E+06	(K)GVSLLLPTDIVVADK(F)			558.1766622	1312.734204	1.759709118	3.473711125	Zea mays	118477130.7	cytosolic 3-phosphoglycerate kinase
1336.988153	JGP_1_6.9511.9558.3	2.319906583	13.89932191	78.09387421	2.47E+06	(K)IVPATAIPDDWMGLDVGPDATK(T)			558.1437682	1312.654101	1.759592664	3.473507077	Zea mays	118485570.6	cytosolic 3-phosphoglycerate kinase
1337.041555	JGP_1_6.8265.8345.3	2.319885319	13.8991982	78.09439428	2.47E+06	(K)IGVIESLLAK(V)			558.1108743	1312.573997	1.75947621	3.473303028	Zea mays	118494010.6	cytosolic 3-phosphoglycerate kinase
1337.094957	JGP_1_6.9488.9560.4	2.319864054	13.89907449	78.09491435	2.47E+06	(K)IVPATAIPDDWMGLDVGPDATK(T)			558.0779804	1312.493894	1.759359756	3.473098979	Zea mays	118502450.5	cytosolic 3-phosphoglycerate kinase
1337.148359	JGP_1_5.7468.7548.4	2.31984279	13.89895078	78.09543442	2.47E+06	(K)LASVADLYVNDAFGTAHR(A)			558.0450864	1312.41379	1.759243303	3.47289493	Zea mays	118510890.4	cytosolic 3-phosphoglycerate kinase
1337.201761	JGP_1_5.8050.8155.4	2.319821525	13.89882707	78.0959545	2.47E+06	(K)SLVEEDKLELATSLIEK(A)			558.0121925	1312.333686	1.759126849	3.472690882	Zea mays	118519330.3	cytosolic 3-phosphoglycerate kinase
1337.255163	JGP_1_6.7164.7180.4	2.319800261	13.89870336	78.09647457	2.48E+06	(K)LASVADLYVNDAFGTAHR(A)			557.9792986	1312.253583	1.759010395	3.472486833	Zea mays	118527770.3	cytosolic 3-phosphoglycerate kinase
1337.308564	JGP_1_6.10132.10208.4	2.319778996	13.89857965	78.09699464	2.48E+06	(K)VDILILGGGmIYTFYK(A)	m:Oxidized methionine		557.9464046	1312.173479	1.758893941	3.472282784	Zea mays	118536210.2	cytosolic 3-phosphoglycerate kinase
1337.361966	JGP_1_6.8367.8447.4	2.319757732	13.89845594	78.09751471	2.48E+06	(K)SLVEEDKLELATSLIEK(A)			557.9135107	1312.093376	1.758777487	3.472078735	Zea mays	118544650.1	cytosolic 3-phosphoglycerate kinase
1337.415368	JGP_1_5.1304.1378.3	2.319736467	13.89833223	78.09803478	2.48E+06	(K)FAADAESK(I)			557.8806167	1312.013272	1.758661033	3.471874686	Zea mays	118553090.1	cytosolic 3-phosphoglycerate kinase
1337.46877	JGP_1_6.7427.7511.4	2.319715203	13.89820852	78.09855485	2.48E+06	(K)KLASVADLYVNDAFGTAHR(A)			557.8477228	1311.933169	1.758544579	3.471670638	Zea mays	118561530	cytosolic 3-phosphoglycerate kinase

1337.522172	JGP_1_5.7849.7997.3	2.319693938	13.89808481	78.09907492	2.48E+06	(K)IGVIESLLAK(V)		557.8148289	1311.853065	1.758428126	3.471466589	Zea mays	118569969.9	cytosolic 3-phosphoglycerate kinase
1337.575574	JGP_1_6.8691.8766.3	2.319672674	13.8979611	78.09959499	2.48E+06	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine	557.7819349	1311.772961	1.758311672	3.47126254	Zea mays	118578409.8	cytosolic 3-phosphoglycerate kinase
1337.628976	JGP_1_6.10106.10175.3	2.319651409	13.89783739	78.10011506	2.48E+06	(K)VDILILGGGmIYTFYK(A)	m:Oxidized methionine	557.749041	1311.692858	1.758195218	3.471058491	Zea mays	118586849.8	cytosolic 3-phosphoglycerate kinase
1337.682378	JGP_1_7.8078.8084.3	2.319630145	13.89771368	78.10063513	2.48E+06	(K)IGVIESLLAK(V)		557.7161471	1311.612754	1.758078764	3.470854442	Zea mays	118595289.7	cytosolic 3-phosphoglycerate kinase
1337.73578	JGP_1_5.8319.8400.4	2.31960888	13.89758997	78.1011552	2.48E+06	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine	557.6832531	1311.532651	1.75796231	3.470650394	Zea mays	118603729.6	cytosolic 3-phosphoglycerate kinase
1337.789182	JGP_1_8.8056.8150.3	2.319587616	13.89746626	78.10167527	2.48E+06	(K)IGVIESLLAK(V)		557.6503592	1311.452547	1.757845856	3.470446345	Zea mays	118612169.5	cytosolic 3-phosphoglycerate kinase
1337.842583	JGP_1_5.2869.2973.3	2.319566351	13.89734255	78.10219534	2.48E+06	(K)LAELTTTK(G)		557.6174652	1311.372444	1.757729403	3.470242296	Zea mays	118620609.5	cytosolic 3-phosphoglycerate kinase
1337.895985	JGP_1_2.7107.7184.3	2.319545087	13.89721883	78.10271541	2.48E+06	(K)IGVIESLLAK(V)		557.5845713	1311.29234	1.757612949	3.470038247	Zea mays	118629049.4	cytosolic 3-phosphoglycerate kinase
1337.949387	JGP_1_6.7455.7540.4	2.319523822	13.89709512	78.10323548	2.48E+06	(K)YLKPAVAGFLMQK(E)		557.5516774	1311.212236	1.757496495	3.469834199	Zea mays	118637489.3	cytosolic 3-phosphoglycerate kinase
1338.002789	JGP_1_6.6810.6894.3	2.319502558	13.89697141	78.10375555	2.48E+06	(K)YLKPAVAGFLmQK(E)	m:Oxidized methionine	557.5187834	1311.132133	1.757380041	3.46963015	Zea mays	118645929.2	cytosolic 3-phosphoglycerate kinase
1338.056191	JGP_1_1.7566.7644.3	2.319481293	13.8968477	78.10427562	2.49E+06	(K)IGVIESLLAK(V)		557.4858895	1311.052029	1.757263587	3.469426101	Zea mays	118654369.2	cytosolic 3-phosphoglycerate kinase
1338.109593	JGP_1_6.2713.2819.3	2.319460029	13.89672399	78.10479569	2.49E+06	(K)KLAELTTTK(G)		557.4529956	1310.971926	1.757147133	3.469222052	Zea mays	118662809.1	cytosolic 3-phosphoglycerate kinase
1338.162995	JGP_1_4.7767.7786.3	2.319438764	13.89660028	78.10531576	2.49E+06	(K)IGVIESLLAK(V)		557.4201016	1310.891822	1.757030679	3.469018003	Zea mays	118671249	cytosolic 3-phosphoglycerate kinase
1338.216397	JGP_1_6.8503.8503.3	2.3194175	13.89647657	78.10583583	2.49E+06	(K)SLVEEDKLELATSLIEK(A)		557.3872077	1310.811719	1.756914226	3.468813955	Zea mays	118679689	cytosolic 3-phosphoglycerate kinase
1338.269799	JGP_1_5.9050.9118.3	2.319396235	13.89635286	78.1063559	2.49E+06	(K)GVSLLLPTDIVVADK(F)		557.3543138	1310.731615	1.756797772	3.468609906	Zea mays	118688128.9	cytosolic 3-phosphoglycerate kinase
1338.323201	JGP_1_6.9991.10065.4	2.319374971	13.89622915	78.10687597	2.49E+06	(K)GVSLLLPTDIVVADKFAADAESK(I)		557.3214198	1310.651511	1.756681318	3.468405857	Zea mays	118696568.8	cytosolic 3-phosphoglycerate kinase
1338.376602	JGP_1_6.7918.7922.5	2.319353706	13.89610544	78.10739604	2.49E+06	(K)LASVADLYVNDAFGTAHR(A)		557.2885259	1310.571408	1.756564864	3.468201808	Zea mays	118705008.7	cytosolic 3-phosphoglycerate kinase
1338.430004	JGP_1_6.6781.6868.4	2.319332442	13.89598173	78.10791611	2.49E+06	(K)YLKPAVAGFLmQK(E)	m:Oxidized methionine	557.2556319	1310.491304	1.75644841	3.46799776	Zea mays	118713448.7	cytosolic 3-phosphoglycerate kinase
1338.483406	JGP_1_5.8324.8338.3	2.319311177	13.89585802	78.10843618	2.49E+06	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine	557.222738	1310.411201	1.756331956	3.467793711	Zea mays	118721888.6	cytosolic 3-phosphoglycerate kinase
1338.536808	JGP_1_6.1265.1347.3	2.319289913	13.89573431	78.10895625	2.49E+06	(K)FAADAESK(I)		557.1898441	1310.331097	1.756215503	3.467589662	Zea mays	118730328.5	cytosolic 3-phosphoglycerate kinase
1338.59021	JGP_1_6.3015.3123.3	2.319268648	13.8956106	78.10947632	2.49E+06	(K)LAELTTTK(G)		557.1569501	1310.250994	1.756099049	3.467385613	Zea mays	118738768.4	cytosolic 3-phosphoglycerate kinase
1338.643612	JGP_1_6.9417.9485.3	2.319247383	13.89548689	78.10999639	2.49E+06	(K)GVSLLLPTDIVVADK(F)		557.1240562	1310.17089	1.755982595	3.467181564	Zea mays	118747208.4	cytosolic 3-phosphoglycerate kinase
1338.697014	JGP_1_5.7085.7085.4	2.319226119	13.89536318	78.11051646	2.49E+06	(K)KLASVADLYVNDAFGTAHR(A)		557.0911623	1310.090786	1.755866141	3.466977516	Zea mays	118755648.3	cytosolic 3-phosphoglycerate kinase
1338.750416	JGP_1_6.14482.14586.4	2.319204854	13.89523947	78.11103653	2.49E+06	(K)SLVEEDKLELATSLIEK(A)		557.0582683	1310.010683	1.755749687	3.466773467	Zea mays	118764088.2	cytosolic 3-phosphoglycerate kinase
1338.803818	JGP_1_3.7531.7534.3	2.31918359	13.89511576	78.1115566	2.49E+06	(K)IGVIESLLAK(V)		557.0253744	1309.930579	1.755633233	3.466569418	Zea mays	118772528.2	cytosolic 3-phosphoglycerate kinase
1338.85722	JGP_1_5.2600.2604.3	2.319162325	13.89499205	78.11207668	2.50E+06	(K)KLAELTTTK(G)		556.9924804	1309.850476	1.755516779	3.466365369	Zea mays	118780968.1	cytosolic 3-phosphoglycerate kinase
1338.910621	JGP_1_6.14525.14598.4	2.319141061	13.89486834	78.11259675	2.50E+06	(K)SLVEEDKLELATSLIEK(A)		556.9595865	1309.770372	1.755400326	3.466161321	Zea mays	118789408	cytosolic 3-phosphoglycerate kinase
1338.964023	JGP_1_7.2480.2480.3	2.319119796	13.89474463	78.11311682	2.50E+06	(K)KLAELTTTK(G)		556.9266926	1309.690269	1.755283872	3.465957272	Zea mays	118797847.9	cytosolic 3-phosphoglycerate kinase
1339.017425	JGP_1_6.1394.1513.3	2.319098532	13.89462092	78.11363689	2.50E+06	(K)AQGYSVGK(S)		556.8937986	1309.610165	1.755167418	3.465753223	Zea mays	118806287.9	cytosolic 3-phosphoglycerate kinase
1339.070827	JGP_1_7.7096.7101.4	2.319077267	13.89449721	78.11415696	2.50E+06	(K)YLKPAVAGFLMQK(E)		556.8609047	1309.530061	1.755050964	3.465549174	Zea mays	118814727.8	cytosolic 3-phosphoglycerate kinase
1339.124229	JGP_1_6.9550.9627.3	2.319056003	13.8943735	78.11467703	2.50E+06	(K)GVSLLLPTDIVVADK(F)		556.8280108	1309.449958	1.75493451	3.465345125	Zea mays	118823167.7	cytosolic 3-phosphoglycerate kinase
1339.177631	JGP_1_5.1339.1418.3	2.319034738	13.89424979	78.1151971	2.50E+06	(K)AQGYSVGK(S)		556.7951168	1309.369854	1.754818056	3.465141077	Zea mays	118831607.6	cytosolic 3-phosphoglycerate kinase
1339.231033	JGP_1_5.7074.7147.4	2.319013474	13.89412608	78.11571717	2.50E+06	(K)YLKPAVAGFLMQK(E)		556.7622229	1309.289751	1.754701603	3.464937028	Zea mays	118840047.6	cytosolic 3-phosphoglycerate kinase
1339.284435	JGP_1_6.8693.8698.4	2.318992209	13.89400237	78.11623724	2.50E+06	(K)SLVEEDKLELATSLIEK(A)		556.729329	1309.209647	1.754585149	3.464732979	Zea mays	118848487.5	cytosolic 3-phosphoglycerate kinase
1339.337837	JGP_1_6.7893.7903.3	2.318970945	13.89387866	78.11675731	2.50E+06	(K)LASVADLYVNDAFGTAHR(A)		556.696435	1309.129544	1.754468695	3.46452893	Zea mays	118856927.4	cytosolic 3-phosphoglycerate kinase
1339.391239	JGP_1_5.9189.9194.3	2.31894968	13.89375495	78.11727738	2.50E+06	(K)GVSLLLPTDIVVADK(F)		556.6635411	1309.04944	1.754352241	3.464324881	Zea mays	118865367.3	cytosolic 3-phosphoglycerate kinase
1339.44464	JGP_1_7.6165.6165.4	2.318928416	13.89363124	78.11779745	2.50E+06	(K)LVEIPFKPAR(V)		556.6306471	1308.969337	1.754235787	3.464120833	Nicotiana tabacum	118873807.3	cytosolic aconitase
1339.498042	JGP_1_2.5449.5522.4	2.318907151	13.89350753	78.11831752	2.50E+06	(K)LVEIPFKPAR(V)		556.5977532	1308.889233	1.754119333	3.463916784	Nicotiana tabacum	118882247.2	cytosolic aconitase
1339.551444	JGP_1_7.6756.6759.4	2.318885887	13.89338382	78.11883759	2.50E+06	(K)QmGLSDKDIVALSGGHTLGR(C)	m:Oxidized methionine	556.5648593	1308.809129	1.754002879	3.463712735	Nicotiana tabacum	118890687.1	cytosolic ascorbate peroxidase
1339.604846	JGP_1_6.2850.2855.3	2.318864622	13.89326011	78.11935766	2.50E+06	(K)AQASALEAHAAPNCK(V)	C:Carbamidomethylation	556.5319653	1308.729026	1.753886426	3.463508686	Triticum aestivum	118899127.1	cytosolic malate dehydrogenase
1339.658248	JGP_1_8.9107.9186.4	2.318843358	13.8931364	78.11987773	2.51E+06	(K)LVDLANKPDWLFEINPEGK(V)		556.4990714	1308.648922	1.753769972	3.463304638	Zea mays	118907567	dehydroascorbate reductase
1339.71165	JGP_1_7.9058.9130.4	2.318822093	13.89301269	78.1203978	2.51E+06	(K)LVDLANKPDWLFEINPEGK(V)		556.4661775	1308.568819	1.753653518	3.463100589	Zea mays	118916006.9	dehydroascorbate reductase
1339.765052	JGP_1_7.5654.5660.3	2.318800829	13.89288898	78.12091787	2.51E+06	(R)VLLTIEEK(H)		556.4332835	1308.488715	1.753537064	3.46289654	Zea mays	118924446.8	dehydroascorbate reductase
1339.818454	JGP_1_7.3532.3575.3	2.318779564	13.89276526	78.12143794	2.51E+06	(K)LNVVVK(R)		556.4003896	1308.408612	1.75342061	3.462692491	Zea mays	118932886.8	delta-COP
1339.871856	JGP_1_7.6108.6114.3	2.3187583	13.89264155	78.12195801	2.51E+06	(K)VTGILPLK(E)		556.3674957	1308.328508	1.753304156	3.462488442	Zea mays	118941326.7	delta-COP
1339.925258	JGP_1_3.5711.5796.3	2.318737035	13.89251784	78.12247808	2.51E+06	(K)ILSVFR(L)		556.3346017	1308.248404	1.753187702	3.462284394	Arabidopsis thaliana	118949766.6	dicer-like protein 4
1339.978659	JGP_1_6.6345.6360.3	2.318715771	13.89239413	78.12299815	2.51E+06	(K)ILSVFR(L)		556.3017078	1308.168301	1.753071249	3.462080345	Arabidopsis thaliana	118958206.5	dicer-like protein 4

1340.032061	JGP_1_4.5915.5918.3	2.318694506	13.89227042	78.12351822	2.51E+06	(K)ILSVFR(L)		556.2688138	1308.088197	1.752954795	3.461876296	Arabidopsis thaliana	118966646.5	dicer-like protein 4
1340.085463	JGP_1_3.5868.5873.3	2.318673242	13.89214671	78.12403829	2.51E+06	(K)ILSVFR(L)		556.2359199	1308.008094	1.752838341	3.461672247	Arabidopsis thaliana	118975086.4	dicer-like protein 4
1340.138865	JGP_1_2.5422.5497.3	2.318651977	13.892023	78.12455836	2.51E+06	(K)ILSVFR(L)		556.203026	1307.92799	1.752721887	3.461468199	Arabidopsis thaliana	118983526.3	dicer-like protein 4
1340.192267	JGP_1_6.1435.1517.3	2.318630713	13.89189929	78.12507843	2.51E+06	(R)AVmDAIK(L)	m:Oxidized methionine	556.170132	1307.847887	1.752605433	3.46126415	Arabidopsis thaliana	118991966.2	"disease resistance gene, putative"
1340.245669	JGP_1_6.2918.3032.3	2.318609448	13.89177558	78.1255985	2.51E+06	(K)NVLLDK(S)		556.1372381	1307.767783	1.752488979	3.461060101	Arabidopsis thaliana	119000406.2	disease resistance protein kinase Pto-like protein
1340.299071	JGP_1_7.5497.5597.3	2.318588184	13.89165187	78.12611857	2.51E+06	(K)LIGEMGLHTK(I)		556.1043442	1307.687679	1.752372526	3.460856052	Arabidopsis thaliana	119008846.1	DNA repair protein RAD51-like 3
1340.352473	JGP_1_1.8492.8551.3	2.318566919	13.89152816	78.12663864	2.51E+06	(K)LSISNIPTGSSR(F)		556.0714502	1307.607576	1.752256072	3.460652003	Arabidopsis thaliana	119017286	early-responsive to dehydration stress-related protein
1340.405875	JGP_1_2.4539.4539.3	2.318545655	13.89140445	78.12715871	2.51E+06	(K)IGGIGTVPVGR(V)		556.0385563	1307.527472	1.752139618	3.460447955	Oryza sativa	119025726	EF-1 alpha
1340.459277	JGP_1_1.4717.4726.3	2.31852439	13.89128074	78.12767878	2.52E+06	(K)IGGIGTVPVGR(V)		556.0056623	1307.447369	1.752023164	3.460243906	Oryza sativa	119034165.9	EF-1 alpha
1340.512678	JGP_1_1.10441.10441.4	2.318503125	13.89115703	78.12819886	2.52E+06	(R)LLEPVYLVEIQAPENALGGIYGVLNQK(R)			555.9727684	1307.367265	1.75190671	3.460039857	Triticum aestivum	119042605.8	elongation factor
1340.56608	JGP_1_8.6268.6354.3	2.318481861	13.89103332	78.12871893	2.52E+06	(R)SIAELLR(E)		555.9398745	1307.287162	1.751790256	3.459835808	Arabidopsis thaliana	119051045.7	endonuclease/exonuclease/phosphatase domain-containing protein
1340.619482	JGP_1_8.6091.6183.3	2.318460596	13.89090961	78.129239	2.52E+06	(R)SIAELLR(E)		555.9069805	1307.207058	1.751673802	3.45963176	Arabidopsis thaliana	119059485.7	endonuclease/exonuclease/phosphatase domain-containing protein
1340.672884	JGP_1_2.5813.5894.4	2.318439332	13.8907859	78.12975907	2.52E+06	(K)IPLYKHIANIAGNK(K)		555.8740866	1307.126954	1.751557349	3.459427711	Glycine max	119067925.6	enolase
1340.726286	JGP_1_5.9769.9833.4	2.318418067	13.89066219	78.13027914	2.52E+06	(R)SGETEDTFIADLSVGLATGQIK(T)			555.8411927	1307.046851	1.751440895	3.459223662	Glycine max	119076365.5	enolase
1340.779688	JGP_1_5.10725.10739.4	2.318396803	13.89053848	78.13079921	2.52E+06	(R)SGETEDNFIADLAVGLASGQIK(T)			555.8082987	1306.966747	1.751324441	3.459019613	Zea mays	119084805.4	enolase
1340.83309	JGP_1_5.5536.5637.3	2.318375538	13.89041477	78.13131928	2.52E+06	(R)IEEELGDAAVYAGAK(F)		555.7754048	1306.886644	1.751207987	3.458815564	Zea mays	119093245.4	enolase 1
1340.886492	JGP_1_5.5982.6068.4	2.318354274	13.89029106	78.13183935	2.52E+06	(K)KIPLYQHIANLAGNK(T)		555.7425109	1306.80654	1.751091533	3.458611516	Zea mays	119101685.3	enolase 1
1340.939894	JGP_1_4.5355.5440.3	2.318333009	13.89016735	78.13235942	2.52E+06	(R)IEEELGDAAVYAGAK(F)		555.7096169	1306.726437	1.750975079	3.458407467	Zea mays	119110125.2	enolase 1
1340.993296	JGP_1_2.5842.5911.3	2.318311745	13.89004364	78.13287949	2.52E+06	(K)VNQIGSVTESIEAVR(M)		555.676723	1306.646333	1.750858626	3.458203418	Zea mays	119118565.2	enolase 1
1341.046697	JGP_1_1.6195.6267.3	2.31829048	13.88991993	78.13339956	2.52E+06	(K)VNQIGSVTESIEAVR(M)		555.643829	1306.566229	1.750742172	3.457999369	Zea mays	119127005.1	enolase 1
1341.100099	JGP_1_5.7798.7873.3	2.318269216	13.88979622	78.13391963	2.52E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	555.6109351	1306.486126	1.750625718	3.45779532	Zea mays	119135445	enolase 1
1341.153501	JGP_1_4.5885.5967.4	2.318247951	13.88967251	78.1344397	2.52E+06	(K)KIPLYQHIANLAGNK(T)		555.5780412	1306.406022	1.750509264	3.457591272	Zea mays	119143884.9	enolase 1
1341.206903	JGP_1_1.5684.5773.4	2.318226687	13.8895488	78.13495977	2.52E+06	(K)KIPLYQHIANLAGNK(T)		555.5451472	1306.325919	1.75039281	3.457387223	Zea mays	119152324.9	enolase 1
1341.260305	JGP_1_5.7960.8082.3	2.318205422	13.88942509	78.13547984	2.53E+06	(R)GAVPSGASTGIYEALELR(D)			555.5122533	1306.245815	1.750276356	3.457183174	Zea mays	119160764.8	enolase 1
1341.313707	JGP_1_2.5401.5484.4	2.318184158	13.88930138	78.13599991	2.53E+06	(K)KIPLYQHIANLAGNK(T)		555.4793594	1306.165712	1.750159902	3.456979125	Zea mays	119169204.7	enolase 1
1341.367109	JGP_1_6.9335.9342.4	2.318162893	13.88917767	78.13651998	2.53E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			555.4464654	1306.085608	1.750043449	3.456775077	Zea mays	119177644.6	enolase 1
1341.420511	JGP_1_2.7887.7952.4	2.318141629	13.88905396	78.13704005	2.53E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			555.4135715	1306.005504	1.749926995	3.456571028	Zea mays	119186084.6	enolase 1
1341.473913	JGP_1_5.6506.6513.4	2.318120364	13.88893025	78.13756012	2.53E+06	(K)IPLYQHIANLAGNK(T)		555.3806775	1305.925401	1.749810541	3.456366979	Zea mays	119194524.5	enolase 1
1341.527315	JGP_1_3.8339.8408.4	2.3180991	13.88880654	78.13808019	2.53E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			555.3477836	1305.845297	1.749694087	3.45616293	Zea mays	119202964.4	enolase 1
1341.580716	JGP_1_3.6188.6263.3	2.318077835	13.88868283	78.13860026	2.53E+06	(K)VNQIGSVTESIEAVR(M)		555.3148897	1305.765194	1.749577633	3.455958881	Zea mays	119211404.3	enolase 1
1341.634118	JGP_1_4.5090.5094.4	2.318056571	13.88855912	78.13912033	2.53E+06	(K)ISGDSLKDLYK(S)		555.2819957	1305.68509	1.749461179	3.455754833	Zea mays	119219844.3	enolase 1
1341.68752	JGP_1_5.9020.9144.4	2.318035306	13.88843541	78.1396404	2.53E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			555.2491018	1305.604987	1.749344726	3.455550784	Zea mays	119228284.2	enolase 1
1341.740922	JGP_1_4.2741.2747.3	2.318014042	13.8883117	78.14016047	2.53E+06	(R)AGWGVmASHR(S)	m:Oxidized methionine	555.2162079	1305.524883	1.749228272	3.455346735	Zea mays	119236724.1	enolase 1
1341.794324	JGP_1_5.6584.6677.3	2.317992777	13.88818798	78.14068054	2.53E+06	(K)VNQIGSVTESIEAVR(M)		555.1833139	1305.444779	1.749111818	3.455142686	Zea mays	119245164.1	enolase 1
1341.847726	JGP_1_4.7607.7681.3	2.317971513	13.88806427	78.14120061	2.53E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	555.15042	1305.364676	1.748995364	3.454938638	Zea mays	119253604	enolase 1
1341.901128	JGP_1_4.6413.6498.3	2.317950248	13.88794056	78.14172068	2.53E+06	(K)VNQIGSVTESIEAVR(M)		555.1175261	1305.284572	1.74887891	3.454734589	Zea mays	119262043.9	enolase 1
1341.95453	JGP_1_4.6430.6433.4	2.317928984	13.88781685	78.14224075	2.53E+06	(K)VNQIGSVTESIEAVR(M)		555.0846321	1305.204469	1.748762456	3.45453054	Zea mays	119270483.8	enolase 1
1342.007932	JGP_1_5.4604.4696.3	2.317907719	13.88769314	78.14276082	2.53E+06	(K)TCNALLLK(V)	C:Carbamidomethylation	555.0517382	1305.124365	1.748646002	3.454326491	Zea mays	119278923.8	enolase 1
1342.061334	JGP_1_1.8409.8474.4	2.317886455	13.88756943	78.14328089	2.54E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			555.0188442	1305.044262	1.748529549	3.454122442	Zea mays	119287363.7	enolase 1
1342.114735	JGP_1_4.8607.8674.4	2.31786519	13.88744572	78.14380097	2.54E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			554.9859503	1304.964158	1.748413095	3.453918394	Zea mays	119295803.6	enolase 1
1342.168137	JGP_1_2.6942.7007.3	2.317843926	13.88732201	78.14432104	2.54E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	554.9530564	1304.884054	1.748296641	3.453714345	Zea mays	119304243.5	enolase 1
1342.221539	JGP_1_5.8903.8908.3	2.317822661	13.8871983	78.14484111	2.54E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			554.9201624	1304.803951	1.748180187	3.453510296	Zea mays	119312683.5	enolase 1
1342.274941	JGP_1_2.4934.4942.3	2.317801397	13.88707459	78.14536118	2.54E+06	(R)IEEELGDAAVYAGAK(F)		554.8872685	1304.723847	1.748063733	3.453306247	Zea mays	119321123.4	enolase 1
1342.328343	JGP_1_2.4234.4306.3	2.317780132	13.88695088	78.14588125	2.54E+06	(K)TCNALLLK(V)	C:Carbamidomethylation	554.8543746	1304.643744	1.747947279	3.453102199	Zea mays	119329563.3	enolase 1
1342.381745	JGP_1_5.8887.8957.4	2.317758867	13.88682717	78.14640132	2.54E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			554.8214806	1304.56364	1.747830826	3.45289815	Zea mays	119338003.2	enolase 1
1342.435147	JGP_1_1.8434.8439.3	2.317737603	13.88670346	78.14692139	2.54E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			554.7885867	1304.483537	1.747714372	3.452694101	Zea mays	119346443.2	enolase 1
1342.488549	JGP_1_5.4397.4408.4	2.317716338	13.88657975	78.14744146	2.54E+06	(K)MGVEVYHNLK(S)		554.7556927	1304.403433	1.747597918	3.452490052	Zea mays	119354883.1	enolase 1
1342.541951	JGP_1_1.7397.7402.3	2.317695074	13.88645604	78.14796153	2.54E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	554.7227988	1304.323329	1.747481464	3.452286003	Zea mays	119363323	enolase 1
1342.595353	JGP_1_1.7464.7464.3	2.317673809	13.88633233	78.1484816	2.54E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	554.6899049	1304.243226	1.74736501	3.452081955	Zea mays	119371763	enolase 1
1342.648754	JGP_1_1.4852.4903.4	2.317652545	13.88620862	78.14900167	2.54E+06	(K)ISGDSLKDLYK(S)		554.6570109	1304.163122	1.747248556	3.451877906	Zea mays	119380202.9	enolase 1
1342.702156	JGP_1_1.6162.6239.4	2.31763128	13.88608491	78.14952174	2.54E+06	(K)IPLYQHIANLAGNK(T)		554.624117	1304.083019	1.747132102	3.451673857	Zea mays	119388642.8	enolase 1
1342.755558	JGP_1_5.3444.3448.3	2.317610016	13.8859612	78.15004181	2.54E+06	(K)mGVEVYHNLK(S)	m:Oxidized methionine	554.5912231	1304.002915	1.747015649	3.451469808	Zea mays	119397082.7	enolase 1
1342.80896	JGP_1_5.7799.7872.4	2.317588751	13.88583749	78.15056188	2.54E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	554.5583291	1303.922812	1.746899195	3.451265759	Zea mays	119405522.7	enolase 1
1342.862362	JGP_1_8.4633.4645.3	2.317567487	13.88571378	78.15108195	2.55E+06	(K)TCNALLLK(V)	C:Carbamidomethylation	554.5254352	1303.842708	1.746782741	3.451061711	Zea mays	119413962.6	enolase 1
1342.915764	JGP_1_1.5146.5151.3	2.317546222	13.88559007	78.15160202	2.55E+06	(R)IEEELGDAAVYAGAK(F)		554.4925413	1303.762605	1.746666287	3.450857662	Zea mays	119422402.5	enolase 1
1342.969166	JGP_1_3.5719.5802.4	2.317524958	13.88546636	78.15212209	2.55E+06	(K)KIPLYQHIANLAGNK(T)		554.4596473	1303.682501	1.746549833	3.450653613	Zea mays	119430842.4	enolase 1
1343.022568	JGP_1_5.1705.1878.3	2.317503693	13.88534265	78.15264216	2.55E+06	(K)ISGDSLK(D)		554.4267534	1303.602397	1.746433379	3.450449564	Zea mays	119439282.4	enolase 1
1343.07597	JGP_1_5.7962.8092.4	2.317482429	13.88521894	78.15316223	2.55E+06	(R)GAVPSGASTGIYEALELR(D)			554.3938594	1303.522294	1.746316926	3.450245516	Zea mays	119447722.3	enolase 1
1343.129372	JGP_1_1.6277.6284.4	2.317461164	13.88509523	78.1536823	2.55E+06	(K)VNQIGSVTESIEAVR(M)		554.3609655	1303.44219	1.746200472	3.450041467	Zea mays	119456162.2	enolase 1
1343.182773	JGP_1_5.6589.6592.4	2.3174399	13.88497152	78.15420237	2.55E+06	(K)VNQIGSVTESIEAVR(M)		554.3280716	1303.362087	1.746084018	3.449837418	Zea mays	119464602.2	enolase 1
1343.236175	JGP_1_4.4594.4677.3	2.317418635	13.88484781	78.15472244	2.55E+06	(K)TCNALLLK(V)	C:Carbamidomethylation	554.2951776	1303.281983	1.745967564	3.449633369	Zea mays	119473042.1	enolase 1
1343.289577	JGP_1_1.4421.4490.3	2.317397371	13.8847241	78.15524251	2.55E+06	(K)TCNALLLK(V)	C:Carbamidomethylation	554.2622837	1303.20188	1.74585111	3.44942932	Zea mays	119481482	enolase 1
1343.342979	JGP_1_3.7374.7374.3	2.317376106	13.88460039	78.15576258	2.55E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	554.2293898	1303.121776	1.745734656	3.449225272	Zea mays	119489921.9	enolase 1
1343.396381	JGP_1_2.5916.5921.4	2.317354842	13.88447668	78.15628265	2.55E+06	(K)VNQIGSVTESIEAVR(M)		554.1964958	1303.041672	1.745618202	3.449021223	Zea mays	119498361.9	enolase 1
1343.449783	JGP_1_2.7907.7907.3	2.317333577	13.88435297	78.15680272	2.55E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			554.1636019	1302.961569	1.745501749	3.448817174	Zea mays	119506801.8	enolase 1
1343.503185	JGP_1_6.6990.6994.3	2.317312313	13.88422926	78.15732279	2.55E+06	(K)VNQIGSVTESIEAVR(M)		554.1307079	1302.881465	1.745385295	3.448613125	Zea mays	119515241.7	enolase 1
1343.556587	JGP_1_5.5978.6072.5	2.317291048	13.88410555	78.15784286	2.55E+06	(K)KIPLYQHIANLAGNK(T)		554.097814	1302.801362	1.745268841	3.448409077	Zea mays	119523681.6	enolase 1
1343.609989	JGP_1_3.6199.6207.4	2.317269784	13.88398184	78.15836293	2.55E+06	(K)VNQIGSVTESIEAVR(M)		554.0649201	1302.721258	1.745152387	3.448205028	Zea mays	119532121.6	enolase 1
1343.663391	JGP_1_6.4924.5013.3	2.317248519	13.88385813	78.158883	2.55E+06	(K)TCNALLLK(V)	C:Carbamidomethylation	554.0320261	1302.641155	1.745035933	3.448000979	Zea mays	119540561.5	enolase 1
1343.716793	JGP_1_2.6934.7001.4	2.317227255	13.88373442	78.15940307	2.56E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	553.9991322	1302.561051	1.744919479	3.44779693	Zea mays	119549001.4	enolase 1
1343.770194	JGP_1_5.9505.9505.3	2.31720599	13.8836107	78.15992315	2.56E+06	(K)LAMQEFMILPTGASSFK(E)		553.9662383	1302.480947	1.744803025	3.447592881	Zea mays	119557441.3	enolase 1
1343.823596	JGP_1_3.5224.5224.3	2.317184726	13.88348699	78.16044322	2.56E+06	(R)IEEELGDAAVYAGAK(F)		553.9333443	1302.400844	1.744686572	3.447388833	Zea mays	119565881.3	enolase 1
1343.876998	JGP_1_3.7379.7379.3	2.317163461	13.88336328	78.16096329	2.56E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	553.9004504	1302.32074	1.744570118	3.447184784	Zea mays	119574321.2	enolase 1
1343.9304	JGP_1_3.8375.8375.3	2.317142197	13.88323957	78.16148336	2.56E+06	(K)LTDEIGQKVQIVGDDLLVTNPTR(V)			553.8675565	1302.240637	1.744453664	3.446980735	Zea mays	119582761.1	enolase 1
1343.983802	JGP_1_5.6043.6043.3	2.317120932	13.88311586	78.16200343	2.56E+06	(K)KIPLYQHIANLAGNK(T)		553.8346625	1302.160533	1.74433721	3.446776686	Zea mays	119591201.1	enolase 1
1344.037204	JGP_1_3.7358.7368.4	2.317099668	13.88299215	78.1625235	2.56E+06	(K)LAmQEFmILPTGASSFK(E)	m:Oxidized methionine	553.8017686	1302.08043	1.744220756	3.446572638	Zea mays	119599641	enolase 1
1344.090606	JGP_1_1.5128.5131.4	2.317078403	13.88286844	78.16304357	2.56E+06	(R)ILASGVHVVVGTPGR(V)		553.7688746	1302.000326	1.744104302	3.446368589	Zea mays	119608080.9	eukaryotic initiation factor 4A
1344.144008	JGP_1_4.4915.4993.3	2.317057138	13.88274473	78.16356364	2.56E+06	(R)IAIWTK(N)		553.7359807	1301.920222	1.743987849	3.44616454	Zea mays	119616520.8	eukaryotic translation initiation factor 4E-2
1344.19741	JGP_1_2.5712.5792.3	2.317035874	13.88262102	78.16408371	2.56E+06	(R)LPTDETLVAQIK(E)		553.7030868	1301.840119	1.743871395	3.445960491	Zea mays	119624960.8	eukaryotic translation initiation factor 5A

1344.250812	JGP_1_3.6068.6071.3	2.317014609	13.88249731	78.16460378	2.56E+06	(R)LPTDETLVAQIK(E)		553.6701928	1301.760015	1.743754941	3.445756442	Zea mays	119633400.7	eukaryotic translation initiation factor 5A
1344.304213	JGP_1_2.2203.2274.3	2.316993345	13.8823736	78.16512385	2.56E+06	(K)TYPQQAGTVR(K)		553.6372989	1301.679912	1.743638487	3.445552394	Zea mays	119641840.6	eukaryotic translation initiation factor 5A
1344.357615	JGP_1_3.2257.2263.3	2.31697208	13.88224989	78.16564392	2.56E+06	(K)TYPQQAGTVR(K)		553.604405	1301.599808	1.743522033	3.445348345	Zea mays	119650280.5	eukaryotic translation initiation factor 5A
1344.411017	JGP_1_1.6044.6123.3	2.316950816	13.88212618	78.16616399	2.56E+06	(R)LPTDETLVAQIK(E)		553.571511	1301.519705	1.743405579	3.445144296	Zea mays	119658720.5	eukaryotic translation initiation factor 5A
1344.464419	JGP_1_6.2369.2373.3	2.316929551	13.88200247	78.16668406	2.56E+06	(K)TYPQQAGTVR(K)		553.5386171	1301.439601	1.743289125	3.444940247	Zea mays	119667160.4	eukaryotic translation initiation factor 5A
1344.517821	JGP_1_1.2189.2273.3	2.316908287	13.88187876	78.16720413	2.57E+06	(K)TYPQQAGTVR(K)		553.5057232	1301.359497	1.743172672	3.444736199	Zea mays	119675600.3	eukaryotic translation initiation factor 5A
1344.571223	JGP_1_7.7538.7618.3	2.316887022	13.88175505	78.1677242	2.57E+06	(K)GSNPNYLAVLVK(F)		553.4728292	1301.279394	1.743056218	3.44453215	Triticum aestivum	119684040.2	expansin EXPB5
1344.624625	JGP_1_7.7390.7468.3	2.316865758	13.88163134	78.16824427	2.57E+06	(K)GSNPNYLAVLVK(F)		553.4399353	1301.19929	1.742939764	3.444328101	Triticum aestivum	119692480.2	expansin EXPB5
1344.678027	JGP_1_1.6976.7125.3	2.316844493	13.88150763	78.16876434	2.57E+06	(K)GSNPNYLAVLVK(F)		553.4070413	1301.119187	1.74282331	3.444124052	Triticum aestivum	119700920.1	expansin EXPB5
1344.731429	JGP_1_3.7092.7207.3	2.316823229	13.88138392	78.16928441	2.57E+06	(K)GSNPNYLAVLVK(F)		553.3741474	1301.039083	1.742706856	3.443920003	Triticum aestivum	119709360	expansin EXPB5
1344.784831	JGP_1_3.6943.7021.3	2.316801964	13.88126021	78.16980448	2.57E+06	(K)GSNPNYLAVLVK(F)		553.3412535	1300.95898	1.742590402	3.443715955	Triticum aestivum	119717800	expansin EXPB5
1344.838232	JGP_1_4.7328.7461.3	2.3167807	13.8811365	78.17032455	2.57E+06	(K)GSNPNYLAVLVK(F)		553.3083595	1300.878876	1.742473949	3.443511906	Triticum aestivum	119726239.9	expansin EXPB5
1344.891634	JGP_1_6.7896.7996.3	2.316759435	13.88101279	78.17084462	2.57E+06	(K)GSNPNYLAVLVK(F)		553.2754656	1300.798772	1.742357495	3.443307857	Triticum aestivum	119734679.8	expansin EXPB5
1344.945036	JGP_1_2.6564.6641.3	2.316738171	13.88088908	78.17136469	2.57E+06	(K)GSNPNYLAVLVK(F)		553.2425717	1300.718669	1.742241041	3.443103808	Triticum aestivum	119743119.7	expansin EXPB5
1344.998438	JGP_1_2.6706.6821.3	2.316716906	13.88076537	78.17188476	2.57E+06	(K)GSNPNYLAVLVK(F)		553.2096777	1300.638565	1.742124587	3.442899759	Triticum aestivum	119751559.7	expansin EXPB5
1345.05184	JGP_1_5.7370.7447.3	2.316695642	13.88064166	78.17240483	2.57E+06	(K)GSNPNYLAVLVK(F)		553.1767838	1300.558462	1.742008133	3.442695711	Triticum aestivum	119759999.6	expansin EXPB5
1345.105242	JGP_1_4.7180.7259.3	2.316674377	13.88051795	78.1729249	2.57E+06	(K)GSNPNYLAVLVK(F)		553.1438898	1300.478358	1.741891679	3.442491662	Triticum aestivum	119768439.5	expansin EXPB5
1345.158644	JGP_1_1.7130.7196.3	2.316653113	13.88039424	78.17344497	2.57E+06	(K)GSNPNYLAVLVK(F)		553.1109959	1300.398255	1.741775225	3.442287613	Triticum aestivum	119776879.4	expansin EXPB5
1345.212046	JGP_1_2.6597.6671.4	2.316631848	13.88027053	78.17396504	2.57E+06	(K)GSNPNYLAVLVK(F)		553.078102	1300.318151	1.741658772	3.442083564	Triticum aestivum	119785319.4	expansin EXPB5
1345.265448	JGP_1_6.7737.7820.3	2.316610584	13.88014682	78.17448511	2.57E+06	(K)GSNPNYLAVLVK(F)		553.045208	1300.238047	1.741542318	3.441879516	Triticum aestivum	119793759.3	expansin EXPB5
1345.31885	JGP_1_3.6979.7056.4	2.316589319	13.88002311	78.17500518	2.58E+06	(K)GSNPNYLAVLVK(F)		553.0123141	1300.157944	1.741425864	3.441675467	Triticum aestivum	119802199.2	expansin EXPB5
1345.372251	JGP_1_1.7006.7089.4	2.316568055	13.8798994	78.17552525	2.58E+06	(K)GSNPNYLAVLVK(F)		552.9794202	1300.07784	1.74130941	3.441471418	Triticum aestivum	119810639.2	expansin EXPB5
1345.425653	JGP_1_4.7236.7238.4	2.31654679	13.87977569	78.17604533	2.58E+06	(K)GSNPNYLAVLVK(F)		552.9465262	1299.997737	1.741192956	3.441267369	Triticum aestivum	119819079.1	expansin EXPB5
1345.479055	JGP_1_5.7422.7428.4	2.316525526	13.87965198	78.1765654	2.58E+06	(K)GSNPNYLAVLVK(F)		552.9136323	1299.917633	1.741076502	3.44106332	Triticum aestivum	119827519	expansin EXPB5
1345.532457	JGP_1_5.7555.7559.3	2.316504261	13.87952827	78.17708547	2.58E+06	(K)GSNPNYLAVLVK(F)		552.8807384	1299.83753	1.740960049	3.440859272	Triticum aestivum	119835958.9	expansin EXPB5
1345.585859	JGP_1_7.7408.7489.4	2.316482997	13.87940456	78.17760554	2.58E+06	(K)GSNPNYLAVLVK(F)		552.8478444	1299.757426	1.740843595	3.440655223	Triticum aestivum	119844398.9	expansin EXPB5
1345.639261	JGP_1_1.6590.6673.4	2.316461732	13.87928085	78.17812561	2.58E+06	(R)LSLLHEFDVSNNR(F)		552.8149505	1299.677322	1.740727141	3.440451174	Zea mays	119852838.8	extensin-like protein
1345.692663	JGP_1_1.9309.9371.3	2.316440468	13.87915714	78.17864568	2.58E+06	(R)FVGVFPYVCLEmVSLK(Y)	C:Carbamidomethylation m:Oxidized methionine	552.7820565	1299.597219	1.740610687	3.440247125	Zea mays	119861278.7	extensin-like protein
1345.746065	JGP_1_1.7457.7460.3	2.316419203	13.87903342	78.17916575	2.58E+06	(K)TLDEIIFLNNK(L)		552.7491626	1299.517115	1.740494233	3.440043077	Zea mays	119869718.6	extensin-like protein
1345.799467	JGP_1_1.5838.5842.5	2.316397939	13.87890971	78.17968582	2.58E+06	(K)ALVNLDDRDNCLGALRPAQK(T)	C:Carbamidomethylation	552.7162687	1299.437012	1.740377779	3.439839028	Zea mays	119878158.6	extensin-like protein
1345.852869	JGP_1_8.10625.10702.3	2.316376674	13.878786	78.18020589	2.58E+06	(R)GFIFGPPIALAIGAK(F)		552.6833747	1299.356908	1.740261325	3.439634979	Arabidopsis thaliana	119886598.5	F17L21.25
1345.90627	JGP_1_4.5384.5468.3	2.31635541	13.87866229	78.18072596	2.58E+06	(K)SIVILK(L)		552.6504808	1299.276805	1.740144872	3.43943093	Arabidopsis thaliana	119895038.4	F5I10.18 gene product
1345.959672	JGP_1_3.5249.5336.3	2.316334145	13.87853858	78.18124603	2.58E+06	(K)SIVILK(L)		552.6175869	1299.196701	1.740028418	3.439226881	Arabidopsis thaliana	119903478.3	F5I10.18 gene product
1346.013074	JGP_1_3.2399.2404.3	2.31631288	13.87841487	78.1817661	2.58E+06	(R)TPFPHR(A)		552.5846929	1299.116597	1.739911964	3.439022833	Arabidopsis thaliana	119911918.3	FAD-binding and BBE domain-containing protein
1346.066476	JGP_1_5.2238.2245.3	2.316291616	13.87829116	78.18228617	2.58E+06	(R)TPFPHR(A)		552.551799	1299.036494	1.73979551	3.438818784	Arabidopsis thaliana	119920358.2	FAD-binding and BBE domain-containing protein
1346.119878	JGP_1_4.2363.2367.3	2.316270351	13.87816745	78.18280624	2.59E+06	(R)TPFPHR(A)		552.518905	1298.95639	1.739679056	3.438614735	Arabidopsis thaliana	119928798.1	FAD-binding and BBE domain-containing protein
1346.17328	JGP_1_8.2720.2725.3	2.316249087	13.87804374	78.18332631	2.59E+06	(R)QAYVNYR(D)		552.4860111	1298.876287	1.739562602	3.438410686	Arabidopsis thaliana	119937238.1	FAD-binding and BBE domain-containing protein
1346.226682	JGP_1_6.0950.0953.3	2.316227822	13.87792003	78.18384638	2.59E+06	(K)AAKEAEMEK(T)		552.4531172	1298.796183	1.739446149	3.438206638	Arabidopsis thaliana	119945678	formin-like protein 20
1346.280084	JGP_1_6.3849.3860.3	2.316206558	13.87779632	78.18436645	2.59E+06	(R)FANACGAITTTK(K)	C:Carbamidomethylation	552.4202232	1298.71608	1.739329695	3.438002589	Arabidopsis thaliana	119954117.9	fructokinase
1346.333486	JGP_1_6.5293.5299.3	2.316185293	13.87767261	78.18488652	2.59E+06	(K)APGGAPANVAIAVSR(L)		552.3873293	1298.635976	1.739213241	3.43779854	Arabidopsis thaliana	119962557.8	fructokinase
1346.386888	JGP_1_6.7507.7595.3	2.316164029	13.8775489	78.18540659	2.59E+06	(R)TALAFVTLK(K)		552.3544354	1298.555873	1.739096787	3.437594491	Arabidopsis thaliana	119970997.8	fructokinase
1346.440289	JGP_1_6.8726.8805.4	2.316142764	13.87742519	78.18592666	2.59E+06	(K)FGDDEFGHmLVNILK(K)	m:Oxidized methionine	552.3215414	1298.475769	1.738980333	3.437390442	Arabidopsis thaliana	119979437.7	fructokinase
1346.493691	JGP_1_6.6830.6921.3	2.3161215	13.87730148	78.18644673	2.59E+06	(K)EAGALLSYDPNLR(L)		552.2886475	1298.395665	1.738863879	3.437186394	Nicotiana tabacum	119987877.6	fructokinase
1346.547093	JGP_1_1.6796.6880.3	2.316100235	13.87717777	78.1869668	2.59E+06	(R)TALAFVTLK(K)		552.2557536	1298.315562	1.738747425	3.436982345	Arabidopsis thaliana	119996317.5	fructokinase
1346.600495	JGP_1_6.4799.4804.3	2.316078971	13.87705406	78.18748687	2.59E+06	(R)LGGSSAFIGK(V)		552.2228596	1298.235458	1.738630972	3.436778296	Arabidopsis thaliana	120004757.5	fructokinase
1346.653897	JGP_1_2.6399.6468.3	2.316057706	13.87693035	78.18800694	2.59E+06	(R)TALAFVTLK(K)		552.1899657	1298.155355	1.738514518	3.436574247	Arabidopsis thaliana	120013197.4	fructokinase
1346.707299	JGP_1_6.10073.10150.4	2.316036442	13.87680664	78.18852701	2.59E+06	(K)FGDDEFGHMLVNILK(K)		552.1570717	1298.075251	1.738398064	3.436370198	Arabidopsis thaliana	120021637.3	fructokinase

1346.760701	JGP_1_7.7189.7283.3	2.316015177	13.87668293	78.18904708	2.59E+06	(R)TALAFVTLK(K)		552.1241778	1297.995148	1.73828161	3.43616615	Arabidopsis thaliana	120030077.2	fructokinase
1346.814103	JGP_1_1.6953.6958.3	2.315993913	13.87655922	78.18956715	2.59E+06	(R)TALAFVTLR(G)		552.0912839	1297.915044	1.738165156	3.435962101	Arabidopsis thaliana	120038517.2	fructokinase
1346.867505	JGP_1_6.7658.7745.3	2.315972648	13.87643551	78.19008722	2.59E+06	(R)TALAFVTLR(G)		552.0583899	1297.83494	1.738048702	3.435758052	Arabidopsis thaliana	120046957.1	fructokinase
1346.920907	JGP_1_7.4559.4652.3	2.315951384	13.8763118	78.19060729	2.60E+06	(R)LGGSSAFIGK(V)		552.025496	1297.754837	1.737932248	3.435554003	Arabidopsis thaliana	120055397	fructokinase
1346.974308	JGP_1_6.7673.7673.3	2.315930119	13.87618809	78.19112736	2.60E+06	(R)TALAFVTLK(K)		551.9926021	1297.674733	1.737815795	3.435349955	Arabidopsis thaliana	120063837	fructokinase
1347.02771	JGP_1_6.7438.7523.3	2.315908855	13.87606438	78.19164743	2.60E+06	(K)LLLVTLGDQGCK(Y)	C:Carbamidomethylation	551.9597081	1297.59463	1.737699341	3.435145906	Zea mays	120072276.9	fructokinase-1
1347.081112	JGP_1_6.1625.1634.3	2.31588759	13.87594067	78.19216751	2.60E+06	(K)DPSSLQDEK(K)		551.9268142	1297.514526	1.737582887	3.434941857	Zea mays	120080716.8	fructokinase-1
1347.134514	JGP_1_6.9096.9173.3	2.315866326	13.87581696	78.19268758	2.60E+06	(R)TQILSIWDQADIVK(V)		551.8939202	1297.434423	1.737466433	3.434737808	Zea mays	120089156.7	fructokinase-1
1347.187916	JGP_1_6.10808.10812.4	2.315845061	13.87569325	78.19320765	2.60E+06	(K)GAIPSLPTEAEVLQLIEK(A)			551.8610263	1297.354319	1.737349979	3.434533759	Zea mays	120097596.7	fructokinase-1
1347.241318	JGP_1_6.7518.7518.4	2.315823797	13.87556954	78.19372772	2.60E+06	(K)LLLVTLGDQGCK(Y)	C:Carbamidomethylation	551.8281324	1297.274215	1.737233525	3.434329711	Zea mays	120106036.6	fructokinase-1
1347.29472	JGP_1_6.10800.10867.3	2.315802532	13.87544583	78.19424779	2.60E+06	(K)GAIPSLPTEAEVLQLIEK(A)			551.7952384	1297.194112	1.737117072	3.434125662	Zea mays	120114476.5	fructokinase-1
1347.348122	JGP_1_6.5458.5465.4	2.315781268	13.87532212	78.19476786	2.60E+06	(R)DFHGAVPSFK(V)		551.7623445	1297.114008	1.737000618	3.433921613	Zea mays	120122916.4	fructokinase-1
1347.401524	JGP_1_6.7403.7490.3	2.315760003	13.87519841	78.19528793	2.60E+06	(R)LPLWPSPDAAR(E)		551.7294506	1297.033905	1.736884164	3.433717564	Zea mays	120131356.4	fructokinase-2
1347.454926	JGP_1_6.5095.5192.3	2.315738739	13.8750747	78.195808	2.60E+06	(K)APGGAPANVACAIAK(L)	C:Carbamidomethylation	551.6965566	1296.953801	1.73676771	3.433513516	Zea mays	120139796.3	fructokinase-2
1347.508327	JGP_1_7.7080.7163.3	2.315717474	13.87495099	78.19632807	2.60E+06	(R)LPLWPSPDAAR(E)		551.6636627	1296.873698	1.736651256	3.433309467	Zea mays	120148236.2	fructokinase-2
1347.561729	JGP_1_6.7567.7567.3	2.31569621	13.87482728	78.19684814	2.60E+06	(R)LPLWPSPDAAR(E)		551.6307688	1296.793594	1.736534802	3.433105418	Zea mays	120156676.2	fructokinase-2
1347.615131	JGP_1_6.3597.3602.3	2.315674945	13.87470357	78.19736821	2.60E+06	(K)DDSIFHNEEK(L)		551.5978748	1296.71349	1.736418348	3.432901369	Zea mays	120165116.1	fructokinase-2
1347.668533	JGP_1_6.8246.8325.3	2.315653681	13.87457986	78.19788828	2.60E+06	(R)EGILSIWK(E)		551.5649809	1296.633387	1.736301895	3.43269732	Zea mays	120173556	fructokinase-2
1347.721935	JGP_1_1.6730.6740.3	2.315632416	13.87445614	78.19840835	2.61E+06	(R)LPLWPSPDAAR(E)		551.5320869	1296.553283	1.736185441	3.432493272	Zea mays	120181995.9	fructokinase-2
1347.775337	JGP_1_6.3514.3625.3	2.315611152	13.87433243	78.19892842	2.61E+06	(K)FSNACGAICTTK(K)	C:Carbamidomethylation	551.499193	1296.47318	1.736068987	3.432289223	Zea mays	120190435.9	fructokinase-2
1347.828739	JGP_1_7.5028.5033.3	2.315589887	13.87420872	78.19944849	2.61E+06	(K)APGGAPANVACAIAK(L)	C:Carbamidomethylation	551.4662991	1296.393076	1.735952533	3.432085174	Zea mays	120198875.8	fructokinase-2
1347.882141	JGP_1_6.3472.3479.3	2.315568622	13.87408501	78.19996856	2.61E+06	(K)EADFIK(V)		551.4334051	1296.312973	1.735836079	3.431881125	Zea mays	120207315.7	fructokinase-2
1347.935543	JGP_1_6.9362.9430.3	2.315547358	13.8739613	78.20048863	2.61E+06	(K)GAIPALPTXATAQDLIAK(A)			551.4005112	1296.232869	1.735719625	3.431677077	Zea mays	120215755.6	fructokinase-2
1347.988945	JGP_1_7.3471.3478.4	2.315526093	13.87383759	78.2010087	2.61E+06	(K)DDSIFHNEEK(L)		551.3676173	1296.152765	1.735603172	3.431473028	Zea mays	120224195.6	fructokinase-2
1348.042346	JGP_1_7.8040.8045.3	2.315504829	13.87371388	78.20152877	2.61E+06	(R)EGILSIWK(E)		551.3347233	1296.072662	1.735486718	3.431268979	Zea mays	120232635.5	fructokinase-2
1348.095748	JGP_1_2.8000.8008.3	2.315483564	13.87359017	78.20204884	2.61E+06	(K)GAIPALPTXATAQDLIAK(A)			551.3018294	1295.992558	1.735370264	3.43106493	Zea mays	120241075.4	fructokinase-2
1348.14915	JGP_1_7.3460.3460.3	2.3154623	13.87346646	78.20256891	2.61E+06	(K)FSNACGAICTTK(K)	C:Carbamidomethylation	551.2689355	1295.912455	1.73525381	3.430860881	Zea mays	120249515.3	fructokinase-2
1348.202552	JGP_1_7.3215.3351.3	2.315441035	13.87334275	78.20308898	2.61E+06	(K)EADFIK(V)		551.2360415	1295.832351	1.735137356	3.430656833	Zea mays	120257955.3	fructokinase-2
1348.255954	JGP_1_6.6801.6806.3	2.315419771	13.87321904	78.20360905	2.61E+06	(-)SLSFSFGR(A)		551.2031476	1295.752248	1.735020902	3.430452784	Arabidopsis thaliana	120266395.2	fructose bisphosphate aldolase - like protein
1348.309356	JGP_1_6.9736.9817.4	2.315398506	13.87309533	78.20412912	2.61E+06	(R)TVPAAVPAVVFLSGGQSEEEATLNLNAmNK(L)		m:Oxidized methionine	551.1702536	1295.672144	1.734904448	3.430248735	Zea mays	120274835.1	fructose-bisphosphate aldolase cytoplasmic isozyme
1348.362758	JGP_1_6.10173.10180.4	2.315377242	13.87297162	78.20464919	2.61E+06	(R)YAAIAQDNGLVPIVEPEILLDGDHGIER(T)			551.1373597	1295.59204	1.734787995	3.430044686	Triticum aestivum	120283275.1	"fructose-bisphosphate aldolase, chloroplast precursor, expressed"
1348.41616	JGP_1_6.5069.5168.3	2.315355977	13.87284791	78.20516926	2.61E+06	(K)GILAADESTGTIGK(R)		551.1044658	1295.511937	1.734671541	3.429840637	Arabidopsis thaliana	120291715	"fructose-bisphosphate aldolase, class I"
1348.469562	JGP_1_6.2318.2322.3	2.315334713	13.8727242	78.20568933	2.61E+06	(R)TLEVAEK(V)		551.0715718	1295.431833	1.734555087	3.429636589	Arabidopsis thaliana	120300154.9	"fructose-bisphosphate aldolase, class I"
1348.522964	JGP_1_3.4651.4658.3	2.315313448	13.87260049	78.2062094	2.62E+06	(K)GILAADESTGTIGK(R)		551.0386779	1295.35173	1.734438633	3.42943254	Arabidopsis thaliana	120308594.8	"fructose-bisphosphate aldolase, class I"
1348.576365	JGP_1_1.4534.4609.3	2.315292184	13.87247678	78.20672947	2.62E+06	(K)GILAADESTGTIGK(R)		551.005784	1295.271626	1.734322179	3.429228491	Arabidopsis thaliana	120317034.8	"fructose-bisphosphate aldolase, class I"
1348.629767	JGP_1_6.10100.10190.4	2.315270919	13.87235307	78.20724954	2.62E+06	(R)YAIICQENGLVPIVEPEILVDGPHDIDR(C)	C:Carbamidomethylation	550.97289	1295.191523	1.734205725	3.429024442	Zea mays	120325474.7	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
1348.683169	JGP_1_6.10102.10202.5	2.315249655	13.87222936	78.20776961	2.62E+06	(R)YAIICQENGLVPIVEPEILVDGPHDIDR(C)	C:Carbamidomethylation	550.9399961	1295.111419	1.734089272	3.428820394	Zea mays	120333914.6	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
1348.736571	JGP_1_6.3260.3273.3	2.31522839	13.87210565	78.20828969	2.62E+06	(K)GDAAADTESLHVK(D)		550.9071021	1295.031315	1.733972818	3.428616345	Zea mays	120342354.5	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
1348.789973	JGP_1_6.1029.1029.3	2.315207126	13.87198194	78.20880976	2.62E+06	(K)ETTTQGHDDLGKR(C)		550.8742082	1294.951212	1.733856364	3.428412296	Zea mays	120350794.5	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
1348.843375	JGP_1_6.8051.8136.3	2.315185861	13.87185823	78.20932983	2.62E+06	(K)IGPNEPSQLAIDLNAQGLAR(Y)			550.8413143	1294.871108	1.73373991	3.428208247	Zea mays	120359234.4	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
1348.896777	JGP_1_6.2989.3097.3	2.315164597	13.87173452	78.2098499	2.62E+06	(K)NAAYIGTPGK(G)		550.8084203	1294.791005	1.733623456	3.428004198	Zea mays	120367674.3	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
1348.950179	JGP_1_6.6560.6564.5	2.315143332	13.87161081	78.21036997	2.62E+06	(K)ALNEHHVLLEGTLLKPNmVTPGSDSK(K)	m:Oxidized methionine	550.7755264	1294.710901	1.733507002	3.42780015	Zea mays	120376114.2	"fructose-bisphosphate aldolase, cytoplasmic isozyme"
1349.003581	JGP_1_6.4839.4844.4	2.315122068	13.8714871	78.21089004	2.62E+06	(R)LSSINVENVEENRR(A)		550.7426325	1294.630798	1.733390548	3.427596101	Zea mays	120384554.2	"fructose-bisphosphate aldolase, cytoplasmic isozyme"

Supplementary Table E5. Detection of peptides in the whole JGP proteome matching peptides predicted from the total JGP transcripome[a]

Protein Family	Transcript	Allergen Group	Peptides in Proteome	Number of unique spectra
β-expansins,(B1, B9, B11)	492/493	1	148	13
	CL153		203	20
C terminal of expansin	CL1122.1,	2	112	6
	CL1122.2,		161	16
	UG551		13	6
Berbine bridge family, reticuline oxidases, FAD -containing dehydrogenase	UG808	4	254	34
EF-handed Ca^{2+} binding protein-polcalcin	UG451	7	13	2
Cytochrome C	UG439	10	7	5
Extensin	UG1910	11	5	3
	UG282		23	12
	CL2052.1		33	10
	UG540		35	6
	CL1272.5		8	5
Profilin	UG308	12	40	2
	UG1043		27	3
Polygalacturonase	UG552	13	26	10
	UG332		82	14
	UG248		248	19
	CL986.1		27	13
	CL110.1		18	3
	Cl1737.1		264	17
	CL1737.2		95	8
Enolase	CL70.1	22	86	21
	UG15352		2	2
Isoflavone reductase[b]	CL2295.1	Bet v 6	5	5
Heat shock protein 70[b]	Cl336.1		17	11
Glucanase[b]	UG5255		3	2
	CL535.1		2	2
Chitinase[b]	UG9701		5	4
Pectinesterase (Invertase) inhibitor[b]	UG2181		43	10
	UG3234		29	8
Pathogenesis related protein 1[b]	CL830.1	24	32	9

[a] Raw proteomic data with peptide spectra details available Suppl. Table E6.

[b] Matches with members of the 29 protein families within which pollen allergens have been identified.[43] Proteins for which only one peptide spectra was detected were excluded.

Table E6 Mass spectra data of JGP proteome analysed against the 6 possible reading frames for the JGP transcriptome

score	Local FDR (%)	Global FDR (%)	percent_scored_peak_intensity	totalIntensity	sequence	modifications	accession_number	reading_F_of_match	nr_annotation
22.96	<0.1%	<0.1%	89.5	5.86E+05	(K)IADASGmEWFSIITTPNPIFSHLAGK(T)	m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
21.12	<0.1%	<0.1%	92.2	5.64E+05	(K)VAYVLQGTGTCGIVLPEATK(E)	C:Carbamidomethylation	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
20.43	<0.1%	<0.1%	86.9	2.32E+05	(K)AYGGEGGSYYEWSPADLPmLGVASIGAAK(L)	m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
19.96	<0.1%	<0.1%	96.4	1.53E+06	(R)VVVLNTVNLPLVK(D)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
19.4	<0.1%	<0.1%	87.3	5.86E+05	(K)IADASGmEWFSIITTPNPIFSHLAGK(T)	m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
19.06	<0.1%	<0.1%	82.5	1.57E+05	(K)IADASGmEWFSIITTPNPIFSHLAGK(T)	m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
18.15	<0.1%	<0.1%	77	1.20E+04	(R)KAYGGEGGSYYEWSPADLPmLGVASIGAAK(L)	m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
17.99	<0.1%	<0.1%	89.1	1.65E+06	(R)AEGGVLFIVPR(F)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
17.21	<0.1%	<0.1%	75.3	3.01E+05	(R)IDAHSmCSPGFSCDSAYQVTYIVR(G)	C:Carbamidomethylation m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
17.1	<0.1%	<0.1%	85.2	2.23E+05	(K)AVSAEVLQASFNTTPEMEQLFR(S)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
15.79	0.20%	<0.1%	93.1	3.33E+06	(K)LVSSQPASGIVK(T)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
15.73	0.20%	<0.1%	80.7	3.40E+05	(K)DREGmALNCLEAPLDVDIPGGGR(V)	C:Carbamidomethylation m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
15.7	0.20%	<0.1%	78.5	4.50E+05	(K)GHKPGQFTNFQLTGSTGIFTGLTTEFVSR(A)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
15.14	0.20%	<0.1%	83.9	1.51E+06	(R)VQVVGPDGK(R)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
15.1	0.20%	<0.1%	77.4	6.21E+04	(K)LSLAAGGLALPSYSDSAK(V)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
15.07	0.20%	<0.1%	82.1	1.44E+05	(R)VVVLNTVNLPLVK(D)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
14.87	0.20%	<0.1%	79.4	1.13E+05	(R)AEGGVLFIVPR(F)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
14.81	0.20%	<0.1%	70.3	2.09E+05	(K)IADASGMEWFSIITTPNPIFSHLAGK(T)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
14.71	0.20%	<0.1%	77.3	9.72E+05	(K)VAYVLQGTGTCGIVLPEATK(E)	C:Carbamidomethylation	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
13.82	2%	0.50%	81.3	2.59E+06	(K)LSLAAGGLALPSYSDSAK(V)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
13.8	2%	0.50%	75.9	5.62E+05	(R)VVVLNTVNLPLVK(D)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
13.77	2%	0.50%	74.6	1.44E+06	(R)AWDLPEADAAK(L)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
13.62	2%	0.50%	70.3	2.43E+05	(K)IADASGMEWFSIITTPNPIFSHLAGK(T)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
12.92	2%	0.60%	67.6	1.13E+06	(R)VQVVGPDGKR(V)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
12.69	2%	0.60%	75.7	9.99E+04	(R)VVVLNTVNLPLVK(D)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
12.64	2%	0.70%	78.9	5.31E+05	(K)AVSAEVLQASFNTTPEmEQLFR(S)	m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
12.28	2%	0.70%	76.5	2.24E+06	(K)TSIALPTGSPK(D)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
12.25	3%	0.70%	82.8	1.99E+06	(K)DVGLGADLVR(I)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
12.1	3%	0.70%	64.8	2.51E+05	(K)IADASGMEWFSIITTPNPIFSHLAGK(T)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
11.66	3%	0.90%	64.5	1.11E+05	(R)EGmALNCLEAPLDVDIPGGGR(V)	C:Carbamidomethylation m:Oxidized methionine	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
10.52	3%	1%	77.9	6.99E+05	(K)LVSSQPASGIVK(T)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
10.51	3%	1%	65.5	1.95E+05	(K)IADASGMEWFSIITTPNPIFSHLAGK(T)	CL820.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g001680 [S bicolor] >gi|241945765|gb|EES18910.1| hypothet prot SORBIDRAFT_09g001680 [S bicolor]
13.06	2%	0.60%	79.9	5.58E+04	(R)HIEILGYLLYVAK(V)	UG1779	S.halepenseF1	hypothet prot SORBIDRAFT_01g036830 [S bicolor] >gi|241921794|gb|EER94938.1| hypothet prot SORBIDRAFT_01g036830 [S bicolor]
18.72	<0.1%	<0.1%	78.2	4.22E+05	(K)AAQDIALAELAPTHPIR(L)	UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
18.46	<0.1%	<0.1%	83.7	1.01E+06	(R)IISSIEQKEEGR(G)	UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
16.85	<0.1%	<0.1%	76.2	2.57E+05	(K)AAQDIALAELAPTHPIR(L)	UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]

14.43	2%	<0.1%	75.2	9.84E+04	(R)IISSIEQKEEGR(G)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
13.39	2%	0.50%	85.8	1.68E+06	(R)YLAEFK(T)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
12.57	2%	0.60%	74	1.01E+06	(R)NLLSVAYK(N)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
12.43	2%	0.60%	69.6	1.31E+05	(R)NLLSVAYK(N)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
12.29	2%	0.70%	71.8	1.01E+05	(R)NLLSVAYK(N)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
11.63	3%	0.90%	87.8	1.26E+06	(R)IISSIEQK(E)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
11.26	3%	1%	83	1.36E+05	(K)LAEQAER(Y)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
10.39	3%	1%	62.2	2.78E+05	(R)NLLSVAYK(N)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
10.29	3%	1%	63.9	1.46E+05	(R)IISSIEQKEEGR(G)		UG2107	S.halepenseF1	hypothet prot SORBIDRAFT_06g019100 [S bicolor] >gi|241937809|gb|EES10954.1| hypothet prot SORBIDRAFT_06g019100 [S bicolor]
10.46	3%	1%	65.9	2.46E+05	(K)TVDVEELTVEER(N)		UG1787	S.halepenseF1Rev	LOC100285226 [Zea mays] >gi|195647998|gb|ACG43467.1| 14-3-3-like protein [Zea mays]
10.31	3%	1%	76.7	5.94E+05	(R)IVSSIEQK(E)		UG1787	S.halepenseF1Rev	LOC100285226 [Zea mays] >gi|195647998|gb|ACG43467.1| 14-3-3-like protein [Zea mays]
16.89	<0.1%	<0.1%	87.1	2.00E+05	(R)DNLTLWTSDTNEDGGDEIK(E)		CL2259.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
13.01	2%	0.60%	74.2	7.20E+04	(K)QAFDEAISELDSLGEESYKDSTLImQLLR(D)	m:Oxidized methionine	CL2259.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
21.83	<0.1%	<0.1%	98	2.10E+05	(R)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
21.62	<0.1%	<0.1%	87.7	1.50E+06	(R)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
20.68	<0.1%	<0.1%	90.2	1.21E+06	(R)SAGGAGGGEELSVEER(N)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
20.07	<0.1%	<0.1%	81.1	1.53E+06	(K)AAQDIALADLAPTHPIR(L)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
19.98	<0.1%	<0.1%	81.2	1.81E+06	(R)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
17.97	<0.1%	<0.1%	82.9	1.29E+05	(R)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
17.92	<0.1%	<0.1%	86.3	1.97E+05	(K)AAQDIALADLAPTHPIR(L)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
17.47	<0.1%	<0.1%	80.6	1.46E+05	(K)AAQDIALADLAPTHPIR(L)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
16.74	<0.1%	<0.1%	76.9	1.31E+05	(R)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
15.96	<0.1%	<0.1%	83.3	5.36E+05	(K)DAAESTmNAYK(A)	m:Oxidized methionine	CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
15.82	0.20%	<0.1%	69	1.83E+05	(R)SAGGAGGGEELSVEER(N)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
15.06	0.20%	<0.1%	71	2.07E+05	(R)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
14.06	2%	0.30%	75	1.95E+05	(K)AAQDIALADLAPTHPIR(L)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
12.2	3%	0.70%	83.5	7.07E+05	(K)IEAELAR(I)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
12.1	3%	0.70%	61.3	1.32E+05	(K)AAQDIALADLAPTHPIR(L)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
11.08	3%	1%	70.8	4.37E+05	(R)SKIEAELAR(I)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
10.89	3%	1%	77.9	5.83E+05	(K)IEAELAR(I)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
10.87	3%	1%	61.5	4.38E+05	(K)AAQDIALADLAPTHPIR(L)		CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
10.12	3%	1%	60.8	9.68E+04	(R)ICDGILALLDSHLVPSAGAAESK(V)	C:Carbamidomethylation	CL395.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021020 [S bicolor] >gi|241935499|gb|EES08644.1| hypothet prot SORBIDRAFT_05g021020 [S bicolor]
24.95	<0.1%	<0.1%	100	1.35E+06	(R)SGYFDETKEEYVEVPSDSGITFNVAPK(M)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
22.96	<0.1%	<0.1%	90.1	9.21E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
22.78	<0.1%	<0.1%	86.1	5.62E+06	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
21.87	<0.1%	<0.1%	93.5	2.99E+05	(K)AVGPVLDGDAVVTLNFR(A)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
21.34	<0.1%	<0.1%	81.5	3.20E+06	(K)ALEYADFDKFDR(V)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
21.19	<0.1%	<0.1%	84.4	2.05E+05	(K)ALEYADFDKFDR(V)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
21.18	<0.1%	<0.1%	92.8	4.95E+05	(K)ALEYADFDKFDR(V)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
20.78	<0.1%	<0.1%	92.8	2.13E+05	(K)AVGPVLDGDAVVTLNFR(A)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
20.4	<0.1%	<0.1%	87.3	1.57E+06	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
19.96	<0.1%	<0.1%	89.4	6.85E+03	(K)AVGPVLDGDAVVTLNFR(A)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
19.21	<0.1%	<0.1%	79.8	2.67E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
18.91	<0.1%	<0.1%	89.2	8.33E+05	(K)IILDAVEQVGGIYLVTADHGNAEDmVK(R)	m:Oxidized methionine	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
18.58	<0.1%	<0.1%	84.6	1.10E+06	(R)YAGmLQYDGELK(L)	m:Oxidized methionine	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
18.57	<0.1%	<0.1%	91.2	3.07E+06	(K)IYSGDGFNYIK(E)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]

18.21	<0.1%	<0.1%	95.8	3.27E+06	(K)GIDAQIASGGGR(M)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
18.18	<0.1%	<0.1%	86.8	5.60E+05	(R)AQPNANDQYLPPFVIVDDSGK(A)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
18.05	<0.1%	<0.1%	78.6	1.86E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
17.97	<0.1%	<0.1%	80.1	5.11E+06	(R)LDQLQLLLK(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
17.97	<0.1%	<0.1%	86.4	4.41E+04	(K)GKPVAVVVLDGWGEASPDQYNCIHVAQTPVmDSLK(N)	C:Carbamidomethylation m:Oxidized methionine	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
17.89	<0.1%	<0.1%	73.6	5.91E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
17.67	<0.1%	<0.1%	67	3.60E+05	(R)DVLDGSSVGFVETLENDLSELR(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
17.55	<0.1%	<0.1%	88	2.49E+06	(K)GIDAQIASGGGR(M)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
17.32	<0.1%	<0.1%	90.5	3.80E+06	(R)YLVSPPEIDR(T)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
17.29	<0.1%	<0.1%	79.5	1.25E+05	(R)DVLDGSSVGFVETLENDLSELR(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
17.28	<0.1%	<0.1%	75.5	5.11E+06	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.98	<0.1%	<0.1%	84.3	4.09E+06	(K)AHGTAVGLPSDDDmGNSEVGHNALGAGR(I)	m:Oxidized methionine	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.8	<0.1%	<0.1%	77.2	5.75E+05	(R)SGYFDETK(E)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.6	<0.1%	<0.1%	81.4	3.27E+05	(R)LDQLQLLLK(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.59	<0.1%	<0.1%	75.5	5.19E+05	(R)YAGmLQYDGELKLPSR(Y)	m:Oxidized methionine	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.49	<0.1%	<0.1%	89	3.61E+06	(R)YLVSPPEIDR(T)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.4	<0.1%	<0.1%	66	1.05E+05	(K)ALEYADFDKFDR(V)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.38	<0.1%	<0.1%	80.6	7.64E+05	(R)YAGmLQYDGELK(L)	m:Oxidized methionine	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.36	<0.1%	<0.1%	86.3	3.38E+06	(R)TFACSETVK(F)	C:Carbamidomethylation	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.34	<0.1%	<0.1%	80.3	3.44E+05	(R)SGYFDETKEEYVEVPSDSGITFNVAPK(M)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
16.21	<0.1%	<0.1%	87.5	1.94E+05	(K)RGWDAQVLGEAPYK(F)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
15.67	0.20%	<0.1%	70.3	8.87E+04	(R)DVLDGSSVGFVETLENDLSELR(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
15.55	0.20%	<0.1%	91.1	4.66E+06	(K)LVDSALASGK(I)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
15.55	0.20%	<0.1%	84.8	5.17E+05	(K)LVDSALASGK(I)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
15.49	0.20%	<0.1%	75.5	3.46E+05	(R)YAGMLQYDGELK(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
15.41	0.20%	<0.1%	85	5.72E+05	(K)AGKPLLDK(N)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
15.31	0.20%	<0.1%	72.5	2.48E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
15.01	0.20%	<0.1%	78.2	2.87E+05	(R)LDQLQLLLK(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.99	0.20%	<0.1%	81.7	9.39E+04	(K)AVGPVLDGDAVVTLNFR(A)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.93	0.20%	<0.1%	83	7.95E+05	(K)RGWDAQVLGEAPYK(F)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.89	0.20%	<0.1%	87.4	3.65E+06	(K)SALEAVK(T)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.83	0.20%	<0.1%	77.7	3.26E+04	(K)IILDAVEQVGGIYLVTADHGNAEDmVKR(N)	m:Oxidized methionine	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.78	0.20%	<0.1%	72.8	6.27E+05	(R)YENDWDVVK(R)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.77	0.20%	<0.1%	80.2	1.23E+06	(R)GWDAQVLGEAPYK(F)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.6	2%	<0.1%	81.6	2.55E+05	(R)LDQLQLLLK(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.37	2%	<0.1%	69.6	1.79E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.34	2%	<0.1%	82.7	4.73E+05	(R)YLVSPPEIDR(T)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.32	2%	<0.1%	76.2	2.01E+05	(R)LDQLQLLLK(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.2	2%	<0.1%	61.3	3.16E+05	(K)ALEYADFDKFDR(V)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
14.09	2%	0.30%	85.5	1.91E+05	(K)LVDSALASGK(I)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
13.18	2%	0.50%	81.8	1.90E+05	(K)SALEAVK(T)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
13.18	2%	0.50%	73	1.36E+05	(K)IILDAVEQVGGIYLVTADHGNAEDMVK(R)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
13.08	2%	0.60%	66.4	5.40E+05	(K)FGHVTFFWNGNR(S)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
12.96	2%	0.60%	62.9	6.28E+05	(K)AHGTAVGLPSDDDMGNSEVGHNALGAGR(I)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
12.92	2%	0.60%	68.6	8.51E+04	(R)LDQLQLLLK(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
12.63	2%	0.70%	61.8	1.97E+05	(R)LDQLQLLLK(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
12.41	2%	0.60%	62.9	3.21E+05	(R)AQPNANDQYLPPFVIVDDSGK(A)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
12.3	2%	0.70%	77.8	4.18E+05	(K)NGGIQILTSHTLQPVPVAIGGPGLHSGVK(F)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
12.13	3%	0.80%	66.8	1.98E+05	(K)AHGTAVGLPSDDDmGNSEVGHNALGAGR(I)	m:Oxidized methionine	UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
12	3%	0.80%	65.5	2.25E+05	(K)ESFESGTLHLIGLLSDGGVHSR(L)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.94	3%	0.90%	66.9	2.11E+05	(R)YLVSPPEIDR(T)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.8	3%	0.90%	79.6	1.22E+05	(K)LVDSALASGK(I)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.8	3%	0.90%	72.1	1.85E+05	(R)LDQLQLLLK(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.65	3%	0.90%	78.4	4.06E+05	(K)SALEAVK(T)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.61	3%	0.90%	72	1.84E+05	(R)YLVSPPEIDR(T)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.46	3%	1.00%	73.3	4.18E+05	(K)NGGIQILTSHTLQPVPVAIGGPGLHSGVK(F)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.43	3%	1.00%	61	8.36E+04	(R)DVLDGSSVGFVETLENDLSELR(G)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.31	3%	1.00%	67.6	2.42E+06	(K)NGGIQILTSHTLQPVPVAIGGPGLHSGVK(F)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.14	3%	1%	73.3	2.74E+05	(K)LVDSALASGK(I)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.13	3%	1%	70.7	1.92E+05	(R)GWDAQVLGEAPYK(F)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
11.01	3%	1%	68.1	3.00E+05	(K)GIDAQIASGGGR(M)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
10.92	3%	1%	79.4	1.35E+06	(K)FDQVR(V)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
10.62	3%	1%	81.5	2.76E+06	(R)DALLSGK(F)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
10.41	3%	1%	69.3	2.04E+05	(K)GIDAQIASGGGR(M)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
10.05	5%	1%	64.5	2.46E+05	(K)LVDSALASGK(I)		UG1479	S.halepenseF2	uncharacterized protein LOC100381658 [Zea mays]
10.58	3%	1%	88.2	3.88E+06	(R)GLVAGRR(R)		UG4522	S.halepenseF2Rev	hypothet prot SORBIDRAFT_04g007170 [S bicolor] >gi|241933347|gb|EES06492.1| hypothet prot SORBIDRAFT_04g007170 [S bicolor]
11.9	3%	0.90%	67.8	5.08E+05	(R)VmLILK(H)	m:Oxidized methionine	UG7970	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_07g001490 [S bicolor] >gi|241941271|gb|EES14416.1| hypothet prot SORBIDRAFT_07g001490 [S bicolor]
11.59	3%	0.90%	64.2	3.32E+06	(R)VmLILK(H)	m:Oxidized methionine	UG7970	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_07g001490 [S bicolor] >gi|241941271|gb|EES14416.1| hypothet prot SORBIDRAFT_07g001490 [S bicolor]
13.75	2%	0.50%	82.6	1.02E+05	(R)XGGFLK(S)	CL1702.c1	S.halepenseF3RevF3Rev		hypothet prot SORBIDRAFT_08g015010 [S bicolor] >gi|241942843|gb|EES15988.1| hypothet prot SORBIDRAFT_08g015010 [S bicolor]
13.51	2%	0.50%	81.1	8.57E+04	(R)DAGCTLWQVLPLVPPGR(T)	C:Carbamidomethylation	UG561	S.halepenseF1	hypothet prot SORBIDRAFT_02g040000 [S bicolor] >gi|241924441|gb|EER97585.1| hypothet prot SORBIDRAFT_02g040000 [S bicolor]

12.38	2%	0.60%	75.7	9.16E+04	(R)IDHILGFFR(I)	UG1345	S.halepenseF2	hypothet prot SORBIDRAFT_02g042100 [S bicolor] >gi|241924542|gb|EER97686.1| hypothet prot SORBIDRAFT_02g042100 [S bicolor]
11.73	3%	0.90%	90.2	1.36E+07	(K)XASIPXSR(S)	UG8331	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g042670 [S bicolor] >gi|241928758|gb|EES01903.1| hypothet prot SORBIDRAFT_03g042670 [S bicolor]
10.44	3%	1%	88.7	1.45E+07	(K)XASIPXSR(S)	UG8331	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g042670 [S bicolor] >gi|241928758|gb|EES01903.1| hypothet prot SORBIDRAFT_03g042670 [S bicolor]
21.09	<0.1%	<0.1%	85.2	3.54E+05	(K)SEHAFYLDWAVHSFR(I)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
20.34	<0.1%	<0.1%	90.1	2.07E+06	(K)YGAGIGPGVYDIHSPR(I)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
19.44	<0.1%	<0.1%	83.6	3.31E+05	(R)NIWADDLAASLSTLQSLEAVAGK(D)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
19.33	<0.1%	<0.1%	88.4	1.11E+06	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
19.13	<0.1%	<0.1%	93.2	2.87E+05	(K)KLNLPVLPTTTIGSFPQTPELR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
18.94	<0.1%	<0.1%	90.4	6.71E+05	(K)AAGASWIQFDEPTLVK(D)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
18.77	<0.1%	<0.1%	92	2.01E+05	(K)mLAVLDTNILWVNPDCGLK(T)	C:Carbamidomethylation m:Oxidized methionine	CL1119.c1 S.halepenseF2Rev	methionine synthase protein [S bicolor]
18.37	<0.1%	<0.1%	87.7	2.32E+05	(K)ALAGQKDEAYFAANAAAQASR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
18.18	<0.1%	<0.1%	90.1	5.99E+05	(K)LNLPVLPTTTIGSFPQTPELR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
18.02	<0.1%	<0.1%	86.5	3.39E+05	(K)mLAVLDTNILWVNPDCGLK(T)	C:Carbamidomethylation m:Oxidized methionine	CL1119.c1 S.halepenseF2Rev	methionine synthase protein [S bicolor]
17.76	<0.1%	<0.1%	88.5	1.57E+06	(K)YLFAGVVDGR(N)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
17.52	<0.1%	<0.1%	92.6	2.22E+05	(K)LNLPVLPTTTIGSFPQTPELR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
17.33	<0.1%	<0.1%	82.9	1.08E+06	(K)LVVSTSCSLmHTAVDLVNETK(L)	C:Carbamidomethylation m:Oxidized methionine	CL1119.c1 S.halepenseF2Rev	methionine synthase protein [S bicolor]
17.15	<0.1%	<0.1%	83.7	2.63E+05	(K)ISEEEYISAIK(E)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
16.84	<0.1%	<0.1%	79.6	4.37E+05	(K)KLNLPVLPTTTIGSFPQTPELR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
16.82	<0.1%	<0.1%	80.5	1.79E+05	(K)AAGASWIQFDEPTLVK(D)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
16.69	<0.1%	<0.1%	84.2	2.53E+05	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
16.54	<0.1%	<0.1%	81.5	1.83E+05	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
16.53	<0.1%	<0.1%	78.9	1.00E+06	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
16.16	<0.1%	<0.1%	83.7	2.25E+05	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
16.15	<0.1%	<0.1%	79.8	8.70E+05	(K)ISEEEYISAIKEEISK(V)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
15.95	<0.1%	<0.1%	76	3.00E+05	(K)YGAGIGPGVYDIHSPR(I)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
15.81	0.20%	<0.1%	84.9	1.11E+05	(K)KLNLPVLPTTTIGSFPQTPELR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
15.44	0.20%	<0.1%	76.8	2.21E+04	(K)IQEELDIDVLVHGEPER(N)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
15.33	0.20%	<0.1%	76.7	4.87E+04	(R)NIWADDLAASLSTLQSLEAVAGK(D)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
15.13	0.20%	<0.1%	73	6.42E+05	(K)SWLAFAAQK(V)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
15.1	0.20%	<0.1%	79.6	1.29E+06	(K)KLNLPVLPTTTIGSFPQTPELR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
15.09	0.20%	<0.1%	75.2	1.81E+06	(K)GmLTGPVTILNWSFVR(N)	m:Oxidized methionine	CL1119.c1 S.halepenseF2Rev	methionine synthase protein [S bicolor]
15.01	0.20%	<0.1%	67.9	1.36E+04	(R)CVKPPIIYGDVSRPNPmTVFWSK(T)	C:Carbamidomethylation m:Oxidized methionine	CL1119.c1 S.halepenseF2Rev	methionine synthase protein [S bicolor]
14.95	0.20%	<0.1%	82.3	3.56E+05	(R)IPTTEEIADR(V)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
14.89	0.20%	<0.1%	84.1	3.03E+05	(K)YLFAGVVDGR(N)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
14.68	2%	<0.1%	70.4	1.06E+05	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
14.49	2%	<0.1%	82.1	1.42E+06	(K)YLFAGVVDGR(N)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
14.43	2%	<0.1%	68.7	1.80E+05	(R)FETCYQIALAIK(K) C:Carbamidomethylation	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
14.3	2%	<0.1%	75.8	2.08E+06	(R)IPTTEEIADR(V)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
14.23	2%	<0.1%	62.3	2.09E+05	(R)NIWADDLAASLSTLQSLEAVAGK(D)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
14.19	2%	0.10%	74.3	1.29E+05	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
13.78	2%	0.50%	92.5	1.88E+06	(K)LLSVFR(E)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
13.71	2%	0.50%	89.7	2.41E+05	(K)LLSVFR(E)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
13.55	2%	0.50%	67.8	4.49E+05	(K)EVEDLEAAGIQVIQIDEAALR(E)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
13.49	2%	0.50%	74.2	9.03E+04	(K)DEAYFAANAAAQASR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
13.37	2%	0.50%	87.2	4.96E+05	(K)LDDEIK(S)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
13.35	2%	0.50%	83.1	4.45E+05	(K)EVEDLEAAGIQVIQIDEAALR(E)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
12.94	2%	0.60%	64.7	1.14E+05	(K)GmLTGPVTILNWSFVR(N)	m:Oxidized methionine	CL1119.c1 S.halepenseF2Rev	methionine synthase protein [S bicolor]
12.89	2%	0.60%	72.5	1.07E+05	(K)YLFAGVVDGR(N)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
12.59	2%	0.60%	88.5	1.76E+06	(K)TLDLIR(S)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
12.22	3%	0.70%	68.5	7.31E+04	(K)YLFAGVVDGR(N)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
12.22	3%	0.70%	61.4	1.78E+05	(K)SEHAFYLDWAVHSFR(I)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
12.2	3%	0.70%	70	7.54E+04	(K)LNLPVLPTTTIGSFPQTPELR(R)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
12.2	3%	0.70%	70.6	3.16E+05	(K)YLFAGVVDGR(N)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
11.79	3%	0.90%	83.6	1.67E+05	(K)LLSVFR(E)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
11.57	3%	1.00%	68.7	1.58E+05	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
11.16	3%	1%	64.6	7.05E+04	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
11.04	3%	1%	68.3	1.69E+06	(R)EGLPLR(K)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
10.99	3%	1%	68	1.70E+05	(K)YLFAGVVDGR(N)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
10.95	3%	1%	71.6	1.04E+05	(K)TLTSLSGVTAYGFDLIR(G)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
10.55	3%	1%	71	1.50E+06	(K)VVEVNALAK(A)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
10.45	3%	1%	73.3	7.68E+05	(R)SSFPSGK(Y)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
10.18	3%	1%	81.9	8.98E+05	(K)LLSVFR(E)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
10.03	5%	1%	80.1	1.81E+05	(K)LLSVFR(E)	CL1119.c1	S.halepenseF2Rev	methionine synthase protein [S bicolor]
20.39	<0.1%	<0.1%	91.6	9.02E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	UG7553	S.halepenseF3RevF3Rev unknown [Zea mays]
19.09	<0.1%	<0.1%	75.1	3.05E+04	(K)WFDTNYHFIVPELGPSTK(F)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
17.27	<0.1%	<0.1%	84.4	1.98E+05	(K)ALGIDTVPVLVGPVSYLLLSKPAK(G)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
16.73	<0.1%	<0.1%	67.5	6.62E+05	(K)WFDTNYHFIVPELGPSTK(F)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
16.21	<0.1%	<0.1%	74.9	1.29E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	UG7553	S.halepenseF3RevF3Rev unknown [Zea mays]
14.73	0.20%	<0.1%	77.7	3.24E+05	(K)FALESFWDGK(S)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
14.45	2%	<0.1%	61.7	3.88E+05	(K)WFDTNYHFIVPELGPSTK(F)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
13.8	2%	0.50%	68.1	7.30E+05	(K)FALESFWDGK(S)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
12.83	2%	0.60%	79.1	2.87E+05	(K)ALGIDTVPVLVGPVSYLLLSKPAK(G)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
12.73	2%	0.60%	69.2	2.50E+04	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	UG7553	S.halepenseF3RevF3Rev unknown [Zea mays]

11.91	3%	0.90%	70.5	2.28E+05	(K)SSAEDLEK(V)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]	
11.46	3%	1.00%	76.4	1.33E+06	(K)ALGIDTVPVLVGPVSYLLLSKPAK(G)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]	
11.09	3%	1%	74.3	7.84E+04	(K)ALGIDTVPVLVGPVSYLLLSKPAK(G)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]	
11.01	3%	1%	80.9	1.16E+06	(K)VATDLR(S)	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]	
10.7	3%	1%	62.7	1.76E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
10.52	3%	1%	71.6	1.28E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
10.33	3%	1%	63.8	1.13E+05	(K)YIPSNTFSYYDQVLDTTAmLGAVPER(Y)	m:Oxidized methionine	UG7553	S.halepenseF3RevF3Rev	unknown [Zea mays]
15.54	0.20%	<0.1%	73	4.50E+05	(K)HLPYGVTFGHPTGR(C)	UG13046	S.halepenseF2Rev	GDSL-lipase [S bicolor]	
14.57	2%	<0.1%	71.9	2.95E+05	(K)HLPYGVTFGHPTGR(C)	UG13046	S.halepenseF2Rev	GDSL-lipase [S bicolor]	
13.18	2%	0.50%	61.7	5.36E+05	(K)YTFGTDQEIR(R)	UG13046	S.halepenseF2Rev	GDSL-lipase [S bicolor]	
12.49	2%	0.60%	64.4	2.75E+05	(K)YTFGTDQEIR(R)	UG13046	S.halepenseF2Rev	GDSL-lipase [S bicolor]	
20.57	<0.1%	<0.1%	90.5	2.95E+05	(K)INPLVPVDLVIDHSVQVDVAR(S)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
16.57	<0.1%	<0.1%	74.6	2.38E+05	(K)DAYCLLNFGDSITTDHISPAGNIHPDSPAAK(Y)	C:Carbamidomethylation	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]	
16.55	<0.1%	<0.1%	83.3	9.49E+04	(K)INPLVPVDLVIDHSVQVDVAR(S)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
16.47	<0.1%	<0.1%	84.1	1.07E+05	(K)LVEIPFKPAR(V)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
16.27	<0.1%	<0.1%	80.7	5.22E+05	(K)LVEIPFKPAR(V)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
15.68	0.20%	<0.1%	81.8	1.04E+05	(K)INPLVPVDLVIDHSVQVDVAR(S)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
15.27	0.20%	<0.1%	81.1	1.23E+05	(R)VLLQDFTGVPAVVDLACmR(D)	C:Carbamidomethylation m:Oxidized methionine	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
13.73	2%	0.50%	75.1	3.13E+05	(R)VLLQDFTGVPAVVDLACmR(D)	C:Carbamidomethylation m:Oxidized methionine	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
13.12	2%	0.60%	65.1	1.95E+05	(R)NTYDEILTGLK(R)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
12.98	2%	0.60%	86.1	2.39E+05	(K)TLDYLK(L)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
12.96	2%	0.60%	85.3	4.57E+05	(R)ILLESAIR(N)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
12.86	2%	0.60%	78	4.07E+05	(K)TSLAPGSGVVK(K)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
12.55	2%	0.60%	70.4	9.57E+04	(K)INPLVPVDLVIDHSVQVDVAR(S)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
12.46	2%	0.60%	78.9	1.90E+05	(K)YYSLPALSDPR(I)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
12.15	3%	0.70%	64.2	3.00E+05	(R)SDDTVAmVESYLR(A) m:Oxidized methionine	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
12.07	3%	0.80%	69.7	1.73E+05	(K)LAVFDAAmK(Y) m:Oxidized methionine	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
11.66	3%	0.90%	69.9	4.76E+05	(K)TSLAPGSGVVK(K)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
11.54	3%	0.90%	62.1	1.29E+05	(K)TLDYLK(L)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
11.38	3%	1.00%	72.6	2.29E+04	(K)TLDYLK(L)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
10.61	3%	1%	69.8	8.78E+04	(K)ILDWEK(S)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
10.02	5%	1%	73	1.10E+05	(R)ILLESAIR(N)	CL1895.c1 S.halepenseF3	hypothet prot SORBIDRAFT_01g047850 [S bicolor] >gi|92429669|gb|ABE77202.1| putative aconitate hydratase 1 [S bicolor] >gi|241919755|gb|EER92899.1| hypothet prot SORBIDRAFT_01g047850 [S bicolor]		
11.68	3%	0.90%	70.6	9.67E+03	(R)SNLVGmGIIPLCFK(A)	C:Carbamidomethylation m:Oxidized methionine	UG2501	S.halepenseF1	"aconitase2 [Zea mays] >gi|195611330|gb|ACG27495.1| aconitate hydratase, cytoplasmic [Zea mays]"
10.26	3%	1%	69.4	1.56E+05	(K)TIHVPTGEK(L)	UG5662	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_07g005390 [S bicolor] >gi|241941524|gb|EES14669.1| hypothet prot SORBIDRAFT_07g005390 [S bicolor]	
12.99	2%	0.60%	76.9	1.03E+05	(K)VVAPPER(K)	CL1648.c2 S.halepenseF1Rev	uncharacterized protein LOC100191561 [Zea mays] >gi|53759189|gb|AAU93346.1| actin [Saccharum officinarum] >gi|195622644|gb|ACG33152.1| actin-97 [Zea mays] >gi|195644342|gb|ACG41639.1| actin-97 [Zea mays]		
12.64	2%	0.70%	79.7	1.79E+05	(K)VVAPPER(K)	CL1648.c2 S.halepenseF1Rev	uncharacterized protein LOC100191561 [Zea mays] >gi|53759189|gb|AAU93346.1| actin [Saccharum officinarum] >gi|195622644|gb|ACG33152.1| actin-97 [Zea mays] >gi|195644342|gb|ACG41639.1| actin-97 [Zea mays]		
12.5	2%	0.60%	80.6	1.10E+05	(K)VVAPPER(K)	CL1648.c2 S.halepenseF1Rev	uncharacterized protein LOC100191561 [Zea mays] >gi|53759189|gb|AAU93346.1| actin [Saccharum officinarum] >gi|195622644|gb|ACG33152.1| actin-97 [Zea mays] >gi|195644342|gb|ACG41639.1| actin-97 [Zea mays]		
10.71	3%	1%	68.2	1.65E+05	(K)VVAPPER(K)	CL1648.c2 S.halepenseF1Rev	uncharacterized protein LOC100191561 [Zea mays] >gi|53759189|gb|AAU93346.1| actin [Saccharum officinarum] >gi|195622644|gb|ACG33152.1| actin-97 [Zea mays] >gi|195644342|gb|ACG41639.1| actin-97 [Zea mays]		
10.63	3%	1%	75.4	5.53E+05	(K)VVAPPER(K)	CL1648.c2 S.halepenseF1Rev	uncharacterized protein LOC100191561 [Zea mays] >gi|53759189|gb|AAU93346.1| actin [Saccharum officinarum] >gi|195622644|gb|ACG33152.1| actin-97 [Zea mays] >gi|195644342|gb|ACG41639.1| actin-97 [Zea mays]		
10.42	3%	1%	67.6	2.40E+05	(K)VVAPPER(K)	CL1648.c2 S.halepenseF1Rev	uncharacterized protein LOC100191561 [Zea mays] >gi|53759189|gb|AAU93346.1| actin [Saccharum officinarum] >gi|195622644|gb|ACG33152.1| actin-97 [Zea mays] >gi|195644342|gb|ACG41639.1| actin-97 [Zea mays]		
18.35	<0.1%	<0.1%	75.7	1.57E+05	(K)AEYDESGPSIVHR(K)	CL1648.c5 S.halepenseF2Rev	LOC100284092 [Zea mays] >gi|195639446|gb|ACG39191.1| actin-1 [Zea mays]		
15	0.20%	<0.1%	74.4	9.32E+04	(K)LAYIALDYDQEmETAK(T)	m:Oxidized methionine	CL1648.c5 S.halepenseF2Rev	LOC100284092 [Zea mays] >gi|195639446|gb|ACG39191.1| actin-1 [Zea mays]	
14.79	0.20%	<0.1%	70.4	3.93E+05	(K)AEYDESGPSIVHR(K)	CL1648.c5 S.halepenseF2Rev	LOC100284092 [Zea mays] >gi|195639446|gb|ACG39191.1| actin-1 [Zea mays]		
10.23	3%	1%	76.8	3.76E+05	(R)LDLAGR(D)	CL1648.c1 S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g021660 [S bicolor] >gi|241946458|gb|EES19603.1| hypothet prot SORBIDRAFT_09g021660 [S bicolor]		
13.28	2%	0.50%	70.5	2.67E+05	(K)AGFAGDDAPR(A)	UG12952	S.halepenseF1Rev	unknown [Medicago truncatula]	
12.96	2%	0.60%	78.9	7.69E+04	(K)DAYVGDEAQSK(R)	UG12952	S.halepenseF1Rev	unknown [Medicago truncatula]	

12.23	3%	0.70%	71.8	1.78E+05	(K)DAYVGDEAQSK(R)		UG12952	S.halepenseF1Rev	unknown [Medicago truncatula]
11.58	3%	1.00%	70.1	5.94E+05	(K)AGFAGDDAPR(A)		UG12952	S.halepenseF1Rev	unknown [Medicago truncatula]
10.73	3%	1%	61.4	3.35E+05	(K)AGFAGDDAPR(A)		UG12952	S.halepenseF1Rev	unknown [Medicago truncatula]
21.98	<0.1%	<0.1%	96.8	1.14E+06	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)		UG3530	S.halepenseF2	actin [Pogonatherum paniceum]
19.6	<0.1%	<0.1%	94	5.91E+05	(K)SYELPDGQVITIGAER(F)		UG3530	S.halepenseF2	actin [Pogonatherum paniceum]
17.01	<0.1%	<0.1%	91	1.83E+05	(K)SYELPDGQVITIGAER(F)		UG3530	S.halepenseF2	actin [Pogonatherum paniceum]
15.94	<0.1%	<0.1%	84.9	1.19E+05	(K)SYELPDGQVITIGAER(F)		UG3530	S.halepenseF2	actin [Pogonatherum paniceum]
14.62	2%	<0.1%	81.4	2.10E+04	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)		UG3530	S.halepenseF2	actin [Pogonatherum paniceum]
14.16	2%	0.20%	82.6	1.72E+05	(K)SYELPDGQVITIGAER(F)		UG3530	S.halepenseF2	actin [Pogonatherum paniceum]
12.03	3%	0.80%	68.9	1.22E+05	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)		UG3530	S.halepenseF2	actin [Pogonatherum paniceum]
11.12	3%	1%	64.6	1.52E+05	(R)TTGIVLDSGDGVSHTVPIYEGYALPHAILR(L)		UG3530	S.halepenseF2	actin [Pogonatherum paniceum]
22.38	<0.1%	<0.1%	93.2	1.61E+05	(R)LGEPGESYDAFTACLPADECR(Y)	C:Carbamidomethylation	CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
18.97	<0.1%	<0.1%	86.8	5.05E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
17.05	<0.1%	<0.1%	82.3	1.53E+05	(R)LGEPGESYDAFTACLPADECR(Y)	C:Carbamidomethylation	CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
17.04	<0.1%	<0.1%	80.2	2.56E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
16.9	<0.1%	<0.1%	77.3	2.70E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
15.62	0.20%	<0.1%	65.6	6.80E+04	(R)YAVFDFDFVTDENCQK(S)	C:Carbamidomethylation	CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
14.23	2%	<0.1%	71.1	2.32E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
13.97	2%	0.30%	73.7	1.13E+06	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
13.54	2%	0.50%	68.4	2.96E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
13.53	2%	0.50%	70.3	1.13E+06	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
12.78	2%	0.60%	74.3	2.77E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
12.59	2%	0.60%	72	3.04E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
12.43	2%	0.60%	77.7	1.83E+05	(R)FIVFK(I)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
12.24	3%	0.70%	65.7	2.18E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
11.88	3%	0.90%	73.9	1.16E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
11.53	3%	0.90%	63.3	3.20E+05	(K)INENVQQVVVDR(L)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
11.4	3%	1.00%	83	1.27E+06	(R)FIVFK(I)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
11.26	3%	1%	81.8	3.90E+05	(R)FIVFK(I)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
11.23	3%	1%	79.8	3.75E+05	(R)FIVFK(I)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
11.17	3%	1%	81.1	2.43E+05	(R)FIVFK(I)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
10.46	3%	1%	79.9	3.23E+05	(R)FIVFK(I)		CL939.c1	S.halepenseF3	actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]
22.66	<0.1%	<0.1%	93.6	3.51E+05	(R)YAIYDLDFTTVENCQK(S)	C:Carbamidomethylation	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
19.52	<0.1%	<0.1%	83.7	2.93E+05	(R)LGEPNQGYGDFTDSLPADECR(Y)	C:Carbamidomethylation	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
17.77	<0.1%	<0.1%	89.1	3.38E+05	(K)IFFFSWSPDTAR(T)		UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
17.64	<0.1%	<0.1%	88.5	1.11E+06	(K)IFFFSWSPDTAR(T)		UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
17.4	<0.1%	<0.1%	90.5	9.39E+05	(K)IFFFSWSPDTAR(T)		UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
17.36	<0.1%	<0.1%	90.4	3.05E+05	(K)IFFFSWSPDTAR(T)		UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
17.27	<0.1%	<0.1%	87.7	2.65E+05	(R)LGEPNQGYGDFTDSLPADECR(Y)	C:Carbamidomethylation	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
15.89	0.20%	<0.1%	83.6	1.54E+04	(K)IFFFSWSPDTAR(T)		UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
15.81	0.20%	<0.1%	86.6	2.26E+05	(K)IFFFSWSPDTAR(T)		UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
14.99	0.20%	<0.1%	66.9	4.72E+05	(R)IDDKDmEIKVDR(L)	m:Oxidized methionine	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
14.45	2%	<0.1%	72.5	6.63E+04	(R)YAIYDLDFTTVENCQK(S)	C:Carbamidomethylation	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]

14.12	2%	0.30%	83.2	5.75E+05	(K)IFFFSWSPDTAR(T)	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
13.78	2%	0.50%	79	1.71E+05	(K)IFFFSWSPDTAR(T)	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
13.64	2%	0.50%	81.2	7.36E+04	(K)IFFFSWSPDTAR(T)	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
13.44	2%	0.50%	74.5	1.25E+05	(R)ELDGIQCEIQATDPSEmSLDIVR(S)	C:Carbamidomethylation m:Oxidized methionine	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
12.91	2%	0.60%	67.4	1.58E+05	(R)ELDGIQCEIQATDPSEmSLDIVR(S)	C:Carbamidomethylation m:Oxidized methionine	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
12.87	2%	0.60%	65.2	1.52E+05	(K)IFFFSWSPDTAR(T)	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
12.72	2%	0.60%	71.6	1.33E+06	(R)IDDKDmEIKVDR(L)	m:Oxidized methionine	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
12.61	2%	0.70%	69.1	1.75E+05	(K)IFFFSWSPDTAR(T)	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
12.01	3%	0.80%	71	7.14E+05	(R)IDDKDmEIK(V)	m:Oxidized methionine	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
10.39	3%	1%	76.4	1.70E+05	(K)IFFFSWSPDTAR(T)	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
10.13	3%	1%	64.3	4.92E+04	(K)IFFFSWSPDTAR(T)	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
10.07	5%	1%	65.5	1.45E+05	(K)IFFFSWSPDTAR(T)	UG291	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g033380 [S bicolor] >gi|241924077|gb|EER97221.1| hypothet prot SORBIDRAFT_02g033380 [S bicolor]
17.1	<0.1%	<0.1%	83.3	2.43E+05	(K)INEQTQQVVVDR(L)	CL939.c2	S.halepenseF3	putative actin depolymerizing factor [S bicolor]
16.2	<0.1%	<0.1%	78.7	1.32E+05	(K)INEQTQQVVVDR(L)	CL939.c2	S.halepenseF3	putative actin depolymerizing factor [S bicolor]
16.18	<0.1%	<0.1%	82.8	1.29E+06	(K)INEQTQQVVVDR(L)	CL939.c2	S.halepenseF3	putative actin depolymerizing factor [S bicolor]
15.44	0.20%	<0.1%	76.1	1.14E+05	(K)INEQTQQVVVDR(L)	CL939.c2	S.halepenseF3	putative actin depolymerizing factor [S bicolor]
11.36	3%	1.00%	73.4	2.38E+04	(K)INEQTQQVVVDR(L)	CL939.c2	S.halepenseF3	putative actin depolymerizing factor [S bicolor]
10.64	3%	1%	82.9	8.27E+05	(R)FITFK(I)	CL939.c2	S.halepenseF3	putative actin depolymerizing factor [S bicolor]
13.53	2%	0.50%	83.7	3.49E+06	(K)MIYASSK(E)	UG8872	S.halepenseF3	unknown [Zea mays] >gi|238011688|gb|ACR36879.1| unknown [Zea mays]
12.28	2%	0.70%	82.7	2.14E+05	(K)TLPESTSNENK(L)	UG2942	S.halepenseF1	hypothet prot SORBIDRAFT_07g004260 [S bicolor] >gi|241941460|gb|EES14605.1| hypothet prot SORBIDRAFT_07g004260 [S bicolor]
10.38	3%	1%	63.3	1.21E+05	(R)GFIFGPPIALAIGAK(F)	UG2934	S.halepenseF1Rev	hypothet prot SORBIDRAFT_08g019790 [S bicolor] >gi|241944152|gb|EES17297.1| hypothet prot SORBIDRAFT_08g019790 [S bicolor]
18.5	<0.1%	<0.1%	89.9	2.16E+05	(K)TFPVILLPK(E)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
17.96	<0.1%	<0.1%	90.7	6.31E+05	(K)TFPVILLPK(E)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
17.38	<0.1%	<0.1%	84.7	4.68E+05	(R)IAVITQGADPVVVAEDGK(V)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
17.13	<0.1%	<0.1%	92.2	3.04E+05	(K)TFPVILLPK(E)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
16.07	<0.1%	<0.1%	82.7	1.24E+05	(K)TFPVILLPK(E)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
15.94	<0.1%	<0.1%	87.1	1.23E+06	(K)ISQLPLASGK(Q)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
14.6	2%	<0.1%	81.5	2.83E+05	(K)TFPVILLPK(E)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
13.45	2%	0.50%	76.1	1.44E+05	(K)ISQLPLASGK(Q)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
13.26	2%	0.50%	70.8	9.46E+04	(K)LVDTNGAGDAFVGGFLSQLAQGK(S)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
13.26	2%	0.50%	77.4	5.95E+04	(K)TFPVILLPK(E)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
12.94	2%	0.60%	75.1	5.78E+04	(K)TFPVILLPK(E)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
12.94	2%	0.60%	70.3	2.07E+05	(K)LVDTNGAGDAFVGGFLSQLAQGK(S)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
11.57	3%	1.00%	64	3.06E+04	(K)LVDTNGAGDAFVGGFLSQLAQGK(S)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
11.22	3%	1%	65.1	3.12E+05	(R)IAVITQGADPVVVAEDGK(V)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
11.19	3%	1%	78.6	1.87E+05	(K)ISQLPLASGK(Q)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
10.78	3%	1%	60.5	1.86E+04	(K)LVDTNGAGDAFVGGFLSQLAQGK(S)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
10.68	3%	1%	68.7	1.15E+05	(R)IAVITQGADPVVVAEDGK(V)	UG6226	S.halepenseF3RevF3Rev	adenosine kinase 2 [Zea mays]
14.49	2%	<0.1%	75.7	4.13E+05	(R)SLIANLSAANCYK(S)	C:Carbamidomethylation	UG9724	S.halepenseF1	adenosine kinase 2 [Zea mays]
22.64	<0.1%	<0.1%	77.7	1.75E+05	(R)WCSCNIFSTQDHAAAAIAR(D)	C:Carbamidomethylation	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
16.5	<0.1%	<0.1%	85.1	5.14E+05	(R)LVGVSEETTTGVK(R)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
16.03	<0.1%	<0.1%	83.7	3.26E+05	(K)IPDPESTDNAEFK(I)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
13.38	2%	0.50%	79.9	4.02E+04	(R)LYQmQETGALLFPAINVNDSVTK(S)	m:Oxidized methionine	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
12.62	2%	0.70%	71.6	2.93E+05	(R)DSAAVFAWK(G)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
12.56	2%	0.60%	67.1	1.49E+05	(K)SQADYISVPIEGPYKPAHYR(Y)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
11.99	3%	0.80%	82.6	1.64E+05	(K)IVLTIIR(D)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
11.74	3%	0.90%	87.7	2.90E+05	(K)IVLTIIR(D)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
11.34	3%	1.00%	83.8	4.78E+05	(K)IVLTIIR(D)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
11.22	3%	1%	81.6	1.08E+06	(R)ITIKPQTDR(W)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
11.17	3%	1%	71.7	2.77E+05	(K)NNAIVCNIGHFDNEIDmLGLETYPGVK(R)	C:Carbamidomethylation m:Oxidized methionine	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
11.14	3%	1%	67.6	1.43E+05	(K)IPDPESTDNAEFK(I)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
11.11	3%	1%	69.5	1.89E+05	(R)ITIKPQTDR(W)	UG815	S.halepenseF2Rev	adenosylhomocysteinase [Zea mays] >gi|195620086|gb|ACG31873.1| adenosylhomocysteinase [Zea mays]
15.63	0.20%	<0.1%	77.7	9.55E+04	(K)FGLVHISAGDLLR(A)	UG5144	S.halepenseF2Rev	hypothet prot SORBIDRAFT_07g000980 [S bicolor] >gi|241941242|gb|EES14387.1| hypothet prot SORBIDRAFT_07g000980 [S bicolor]
12.26	3%	0.70%	66.5	5.07E+04	(K)LFSDAGLVCIASLISPYR(R)	C:Carbamidomethylation	CL1817.c1	S.halepenseF3	hypothet prot SORBIDRAFT_02g037100 [S bicolor] >gi|241924275|gb|EER97419.1| hypothet prot SORBIDRAFT_02g037100 [S bicolor]
15.75	0.20%	<0.1%	73.4	1.76E+05	(K)LGEIVTTIPTIGFNVETVEYK(N)	CL563.c1	S.halepenseF1	ADP ribosylation factor [Medicago truncatula] >gi|307135971|gb|ADN33830.1| ADP-ribosylation factor [Cucumis melo subsp. melo] >gi|355480401|gb|AES61604.1| ADP ribosylation factor [Medicago truncatula]

15.52 0.20% <0.1% 74.8 2.13E+05 (K)NISFTVWDVGGQDK(I) CL563.c1 S.halepenseF1 ADP ribosylation factor [Medicago truncatula] >gi|307135971|gb|ADN33830.1| ADP-ribosylation factor [Cucumis melo subsp. melo] >gi|355480401|gb|AES61604.1| ADP ribosylation factor [Medicago truncatula]
11.56 3% 1.00% 65.9 1.03E+05 (K)LGEIVTTIPTIGFNVETVEYK(N) CL563.c1 S.halepenseF1 ADP ribosylation factor [Medicago truncatula] >gi|307135971|gb|ADN33830.1| ADP-ribosylation factor [Cucumis melo subsp. melo] >gi|355480401|gb|AES61604.1| ADP ribosylation factor [Medicago truncatula]
11.7 3% 0.90% 79.3 2.10E+05 (R)ILMVGLDAAGK(T) CL563.c2 S.halepenseF1 hypothet prot OsJ_23579 [Oryza sativa Japonica Group]
11.83 3% 0.90% 75.9 2.97E+05 (R)IIGVDLNPSR(F) CL2435.c1 S.halepenseF3RevF3Rev "alcohol dehydrogenase 1, partial [Miscanthus floridulus x Miscanthus sinensis] >gi|380006503|gb|AFD29642.1| alcohol dehydrogenase 1, partial [Miscanthus floridulus x Miscanthus sinensis]"
14.27 2% <0.1% 77.2 1.67E+05 (K)GSTVAIFGLGAVGLAAAEGAR(I) CL2435.c2 S.halepenseF1 alcohol dehydrogenase 1 [Coix lacryma-jobi]
15.8 0.20% <0.1% 79 6.00E+05 (K)LGTIDPYFVK(L) CL1141.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g015090 [S bicolor] >gi|241918114|gb|EER91258.1| hypothet prot SORBIDRAFT_01g015090 [S bicolor]
15.78 0.20% <0.1% 89.2 2.19E+05 (R)EGTHTAVSHGLWLNIPDYDAPTQLVKPK(E) CL1141.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g015090 [S bicolor] >gi|241918114|gb|EER91258.1| hypothet prot SORBIDRAFT_01g015090 [S bicolor]
14.78 0.20% <0.1% 71.6 6.35E+05 (K)VPEGFDYELYNR(N) CL1141.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g015090 [S bicolor] >gi|241918114|gb|EER91258.1| hypothet prot SORBIDRAFT_01g015090 [S bicolor]
13.44 2% 0.50% 75 2.81E+05 (K)YIYTIDDDCFVAK(D) C:Carbamidomethylation CL1141.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g015090 [S bicolor] >gi|241918114|gb|EER91258.1| hypothet prot SORBIDRAFT_01g015090 [S bicolor]
12.04 3% 0.80% 62.9 6.06E+05 (K)VICDHLSLGVK(T) C:Carbamidomethylation CL1141.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g015090 [S bicolor] >gi|241918114|gb|EER91258.1| hypothet prot SORBIDRAFT_01g015090 [S bicolor]
10.32 3% 1% 65 5.45E+05 (K)TGLPYIWHSK(A) CL1141.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g015090 [S bicolor] >gi|241918114|gb|EER91258.1| hypothet prot SORBIDRAFT_01g015090 [S bicolor]
19.53 <0.1% <0.1% 89.5 2.16E+05 (R)SGAFGSYDYEPLLDSLEGNSGFGR(G) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
17.4 <0.1% <0.1% 80.3 1.73E+04 (R)EEVGEDNFFLFGAK(A) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
15.53 0.20% <0.1% 81.8 1.80E+05 (R)FFGHVEILPDGSR(K) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
15.19 0.20% <0.1% 69.8 4.34E+05 (R)ALTNAVGNLGITGAYAEAVKK(F) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
14.7 0.20% <0.1% 81.3 2.04E+05 (K)VLDSSNPQKPVVR(M) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
14.47 2% <0.1% 81.4 2.01E+05 (R)FFGHVEILPDGSR(K) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
14.34 2% <0.1% 71.7 2.45E+05 (R)ALTNAVGNLGITGAYAEAVK(K) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
13.97 2% 0.30% 67.5 9.42E+04 (R)GDYFLVGYDFPSYIDAQDR(V) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
13.94 2% 0.30% 70.4 2.62E+05 (K)SDQWTSNLDLLTGLR(K) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
13.76 2% 0.50% 77.1 1.85E+05 (R)TISYTNHTVLPEALEK(W) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
13.63 2% 0.50% 80.4 1.43E+05 (R)QLLNILGAVYR(Y) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
13.56 2% 0.50% 80.4 1.53E+05 (K)SDQWTSNLDLLTGLR(K) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
13.56 2% 0.50% 69.6 7.61E+04 (R)SGAFGSYDYEPLLDSLEGNSGFGR(G) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
13.38 2% 0.50% 67.4 2.89E+05 (K)VAVQLNDTHPTLAIPELmR(L) m:Oxidized methionine UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
12.86 2% 0.60% 75.6 7.35E+05 (R)FFGHVEILPDGSR(K) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
12.84 2% 0.60% 75.6 4.83E+05 (R)QLLNILGAVYR(Y) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
12.77 2% 0.60% 71.9 2.15E+05 (K)FGYELEALAGQEK(D) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
12.14 3% 0.70% 64 3.37E+05 (K)mSILNTAGSGK(F) m:Oxidized methionine UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
12.06 3% 0.80% 69 3.66E+05 (K)ALAYDCPIPGYK(T) C:Carbamidomethylation UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
11.55 3% 0.90% 70.2 4.67E+05 (K)AFATYTNAK(R) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
11.55 3% 0.90% 70.6 2.09E+05 (K)VLDSSNPQKPVVR(M) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
11.34 3% 1.00% 63.5 2.48E+03 (K)AFATYTNAK(R) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
11.14 3% 1% 77.7 1.82E+05 (R)HDVVFPVR(F) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
11.08 3% 1% 80.6 3.84E+05 (R)TIAQYAK(E) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
10.84 3% 1% 64.1 1.87E+05 (R)ALTNAVGNLGITGAYAEAVK(K) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
10.81 3% 1% 64.5 1.35E+06 (K)VAVQLNDTHPTLAIPELmR(L) m:Oxidized methionine UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
10.66 3% 1% 71 6.42E+04 (R)SGAFGSYDYEPLLDSLEGNSGFGR(G) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
10.42 3% 1% 67 6.69E+04 (R)HDVVFPVR(F) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]

10.24 3% 1% 69.5 1.17E+05 (R)QLLNILGAVYR(Y) UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
10.15 3% 1% 75.5 2.45E+05 (K)VVFIPNYNVSVAEVLIPGSELSQHISTAGmEASGTSNmK(F) m:Oxidized methionine UG796 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g040060 [S bicolor] >gi|241930748|gb|EES03893.1| hypothet prot SORBIDRAFT_03g040060 [S bicolor]
11.05 3% 1% 65.4 1.50E+05 (K)SAEPLLEGLLEAR(V) UG3315 S.halepenseF3 hypothet prot SORBIDRAFT_10g017820 [S bicolor] >gi|241916642|gb|EER89786.1| hypothet prot SORBIDRAFT_10g017820 [S bicolor]
10.76 3% 1% 71 1.90E+05 (R)GGSAATLSALLNR(F) UG3315 S.halepenseF3 hypothet prot SORBIDRAFT_10g017820 [S bicolor] >gi|241916642|gb|EER89786.1| hypothet prot SORBIDRAFT_10g017820 [S bicolor]
10.2 3% 1% 62 5.96E+03 (K)TPEAPESDER(K) UG13508 S.halepenseF1Rev hypothet prot SORBIDRAFT_10g017820 [S bicolor] >gi|241916642|gb|EER89786.1| hypothet prot SORBIDRAFT_10g017820 [S bicolor]
13.6 2% 0.50% 81.5 8.70E+04 (K)LLGYPSKPIGLFIR(R) UG1484 S.halepenseF1Rev hypothet prot SORBIDRAFT_10g017820 [S bicolor] >gi|241916642|gb|EER89786.1| hypothet prot SORBIDRAFT_10g017820 [S bicolor]
10.51 3% 1% 74.5 9.72E+04 (R)SLLALQGPLAAPTLQLLTK(E) UG8614 S.halepenseF3 hypothet prot SORBIDRAFT_06g029020 [S bicolor] >gi|241938304|gb|EES11449.1| hypothet prot SORBIDRAFT_06g029020 [S bicolor]
19.36 <0.1% <0.1% 82.8 1.51E+05 (R)SLEEDVAAHVTGDFR(K) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
15.63 0.20% <0.1% 85.4 2.79E+05 (R)TVILWTLDPAER(D) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
15.33 0.20% <0.1% 76.1 5.28E+05 (R)LALGGVGTDEDALTR(V) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
14.46 2% <0.1% 63.9 5.35E+05 (R)ALGDEIHGK(F) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
14 2% 0.30% 73.3 3.05E+05 (R)LALGGVGTDEDALTR(V) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
13.55 2% 0.50% 84.3 2.30E+05 (K)LIISILAHR(N) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
12.4 2% 0.60% 81.9 3.83E+05 (K)LLVPLVSAYR(Y) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
12.15 3% 0.70% 71.5 1.77E+05 (R)TVILWTLDPAER(D) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
11.93 3% 0.90% 71.7 1.35E+05 (K)LLVPLVSAYR(Y) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
10.43 3% 1% 69 1.47E+05 (R)TVILWTLDPAER(D) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
10.29 3% 1% 80.2 1.68E+05 (K)LIISILAHR(N) CL1428.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g027590 [S bicolor] >gi|241932368|gb|EES05513.1| hypothet prot SORBIDRAFT_04g027590 [S bicolor]
17.61 <0.1% <0.1% 77.9 4.51E+05 (R)GVQGPESVADHmYR(M) m:Oxidized methionine UG534 S.halepenseF3RevF3Rev LOC100281836 precursor [Zea mays] >gi|195616818|gb|ACG30239.1| HDDC2 protein [Zea mays]
16.51 <0.1% <0.1% 86.4 1.70E+04 (K)mAIVHDIAEAIVGDITPSDGVPKEEK(S) m:Oxidized methionine UG534 S.halepenseF3RevF3Rev LOC100281836 precursor [Zea mays] >gi|195616818|gb|ACG30239.1| HDDC2 protein [Zea mays]
13.35 2% 0.50% 60.1 2.62E+05 (R)GVQGPESVADHMYR(M) UG534 S.halepenseF3RevF3Rev LOC100281836 precursor [Zea mays] >gi|195616818|gb|ACG30239.1| HDDC2 protein [Zea mays]
13.07 2% 0.60% 77.7 7.19E+04 (K)mAIVHDIAEAIVGDITPSDGVPK(E) m:Oxidized methionine UG534 S.halepenseF3RevF3Rev LOC100281836 precursor [Zea mays] >gi|195616818|gb|ACG30239.1| HDDC2 protein [Zea mays]
12.7 2% 0.60% 84 6.10E+04 (K)MAIVHDIAEAIVGDITPSDGVPKEEK(S) UG534 S.halepenseF3RevF3Rev LOC100281836 precursor [Zea mays] >gi|195616818|gb|ACG30239.1| HDDC2 protein [Zea mays]
12.37 2% 0.60% 70.9 1.00E+04 (K)mAIVHDIAEAIVGDITPSDGVPK(E) m:Oxidized methionine UG534 S.halepenseF3RevF3Rev LOC100281836 precursor [Zea mays] >gi|195616818|gb|ACG30239.1| HDDC2 protein [Zea mays]
12.42 2% 0.60% 80.5 2.68E+05 (R)ISLAGLSLAK(C) UG17015 S.halepenseF3 unknown [Zea mays]
22.75 <0.1% <0.1% 89.1 1.41E+05 (K)TSPVmFGAMADLGK(Y) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
21.82 <0.1% <0.1% 92.5 1.43E+06 (K)FSYCLTPFADR(K) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
21.04 <0.1% <0.1% 90.3 1.57E+06 (R)SVDDYPVCFELPR(G) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
21.01 <0.1% <0.1% 89.3 1.36E+06 (R)SVDDYPVCFELPR(G) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
20.56 <0.1% <0.1% 88.6 3.84E+05 (K)VILDLGSDLLWTQCSLVGPTAK(Q) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
19.97 <0.1% <0.1% 92.3 4.24E+05 (R)SVDDYPVCFELPR(G) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
19.56 <0.1% <0.1% 90.6 1.89E+06 (R)SSSFSVLPCDSK(L) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
19.34 <0.1% <0.1% 90.2 1.11E+06 (R)SVDDYPVCFELPR(G) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
19.09 <0.1% <0.1% 87.5 3.14E+05 (R)SVDDYPVCFELPR(G) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
17.93 <0.1% <0.1% 72.6 2.13E+06 (K)TSPVmFGAmADLGK(Y) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
17.22 <0.1% <0.1% 82.3 4.16E+05 (K)VILDLGSDLLWTQCSLVGPTAK(Q) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
16.62 <0.1% <0.1% 90.4 2.72E+05 (K)NPVEDIYYYVPmVGmSVGSK(R) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
16.5 <0.1% <0.1% 86.2 1.92E+06 (K)QLEPVFDAAR(S) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]

16.13 <0.1% <0.1% 80.1 2.96E+05 (R)GmSmEGVQVPPLVLHFDGDAEmSLPR(D) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
16.12 <0.1% <0.1% 75.7 6.38E+05 (K)FSYCLTPFADRK(T) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
16.07 <0.1% <0.1% 80 3.90E+05 (R)LDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
16 <0.1% <0.1% 86.5 1.13E+06 (K)QLEPVFDAAR(S) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
15.95 <0.1% <0.1% 78.8 6.65E+05 (K)VILDLGSDLLWTQCSLVGPTAK(Q) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
15.36 0.20% <0.1% 83.5 2.64E+06 (K)FSYAPTK(C) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
15.28 0.20% <0.1% 74.9 2.35E+06 (K)AVmEGIK(L) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
15.22 0.20% <0.1% 82.6 1.68E+06 (K)FSYAPTK(C) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
14.91 0.20% <0.1% 83 4.92E+05 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
14.86 0.20% <0.1% 88.8 3.28E+06 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
14.27 2% <0.1% 69.2 1.34E+05 (R)LDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
14.13 2% 0.30% 85.5 4.06E+05 (K)NPVEDIYYYVPmVGmSVGSK(R) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
14.08 2% 0.30% 60.2 8.40E+05 (K)FSYCLTPFADR(K) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13.87 2% 0.40% 71.2 9.69E+05 (K)FSYAPTK(C) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13.86 2% 0.40% 63.9 1.19E+05 (K)FSYCLTPFADR(K) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13.67 2% 0.50% 78.6 3.12E+06 (K)VQTIPLLK(N) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13.65 2% 0.50% 67.5 1.40E+05 (K)TSPVmFGAMADLGK(Y) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13.56 2% 0.50% 74.3 4.29E+06 (K)VQTIPLLK(N) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13.17 2% 0.50% 78.3 2.50E+05 (R)KFSYAPTK(C) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13.08 2% 0.60% 73.5 1.46E+06 (R)SSSFSVLPCDSK(L) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13.05 2% 0.60% 73.4 5.25E+05 (R)LDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
13 2% 0.60% 76.8 1.72E+06 (K)AVmEGIK(L) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
12.63 2% 0.70% 81.2 2.94E+05 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
12.57 2% 0.60% 75.3 5.06E+05 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELK(K) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
12.52 2% 0.60% 82.8 2.41E+06 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
12.48 2% 0.60% 67.1 2.88E+05 (K)VILDLGSDLLWTQCSLVGPTAK(Q) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
12.44 2% 0.60% 78.9 7.03E+05 (K)AVMEGIK(L) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
12.03 3% 0.80% 76.8 7.77E+05 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELK(K) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
11.83 3% 0.90% 76 1.72E+05 (K)TSPVMFGAMADLGK(Y) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
11.8 3% 0.90% 81 9.83E+05 (K)AVMEGIK(L) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
11.51 3% 0.90% 69 3.34E+05 (R)KFSYAPTK(C) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
11.33 3% 1.00% 72.1 1.49E+05 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
11.23 3% 1% 74.1 2.43E+05 (K)TSPVMFGAmADLGK(Y) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
10.66 3% 1% 67.9 1.09E+05 (R)LDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
10.52 3% 1% 68.1 1.43E+05 (R)LDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELK(K) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
10.35 3% 1% 60.2 1.30E+05 (K)VILDLGSDLLWTQCSLVGPTAK(Q) C:Carbamidomethylation UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
10.33 3% 1% 60.2 1.27E+05 (K)NPVEDIYYYVPmVGmSVGSK(R) m:Oxidized methionine UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
10.29 3% 1% 70.6 1.12E+06 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELKK(A) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor] >gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]

10.13 3% 1% 68.9 1.52E+05 (K)RLDVPQETLAIKPDGTGGTVLDSATTLAYLVEPAFTELK(K) UG1322 S.halepenseF2 hypothet prot SORBIDRAFT_07g019450 [S bicolor]
>gi|241941802|gb|EES14947.1| hypothet prot SORBIDRAFT_07g019450 [S bicolor]
21.38 <0.1% <0.1% 88.4 9.03E+05 (K)DVVLGCSSSHDGQSFR(S) C:Carbamidomethylation UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor]
>gi|241946780|gb|EES19925.1| hypothet prot SORBIDRAFT_09g028050 [S bicolor]
20.98 <0.1% <0.1% 92.7 2.40E+05 (K)SGGVILDSGNTLTVLAAPAYK(A) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
18.15 <0.1% <0.1% 78.8 7.94E+05 (R)GIVGTESATIALPGGK(V) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
17.9 <0.1% <0.1% 79.2 1.72E+05 (K)SGGVILDSGNTLTVLAAPAYK(A) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
17.83 <0.1% <0.1% 86.4 2.81E+05 (K)VDAIHVAGK(A) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
16.85 <0.1% <0.1% 82 4.11E+05 (K)LFLDPEmPFYGVK(V) m:Oxidized methionine UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1|
hypothet prot SORBIDRAFT_09g028050 [S bicolor]
16.84 <0.1% <0.1% 64.4 6.00E+05 (R)FGGSFSYCLVDHLAPR(N) C:Carbamidomethylation UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor]
>gi|241946780|gb|EES19925.1| hypothet prot SORBIDRAFT_09g028050 [S bicolor]
16.38 <0.1% <0.1% 82 4.87E+05 (K)LFLDPEmPFYGVK(V) m:Oxidized methionine UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1|
hypothet prot SORBIDRAFT_09g028050 [S bicolor]
16.32 <0.1% <0.1% 74 5.24E+05 (K)DVVLGCSSSHDGQSFR(S) C:Carbamidomethylation UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor]
>gi|241946780|gb|EES19925.1| hypothet prot SORBIDRAFT_09g028050 [S bicolor]
15.29 0.20% <0.1% 84.4 1.60E+05 (K)LFLDPEMPFYGVK(V) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
14.86 0.20% <0.1% 72.5 6.56E+05 (K)SYVIDVKPGVK(C) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
14.5 2% <0.1% 80.1 6.35E+05 (R)GIVGTESATIALPGGK(V) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
14.22 2% <0.1% 88.6 4.14E+05 (K)ALDIPAEVWDAK(S) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
13.76 2% 0.50% 84.7 9.63E+05 (K)ISFATQAAAR(F) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
13.66 2% 0.50% 80 1.69E+06 (K)ISFATQAAAR(F) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
12.9 2% 0.60% 70.7 1.90E+06 (K)VDAIHVAGK(A) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
12.48 2% 0.60% 72.5 1.71E+05 (R)VGTPVQEFTLVADTGSDLTWVK(C) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
12.43 2% 0.60% 82.8 1.33E+06 (K)AVVAALSK(H) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
12.32 2% 0.70% 77.5 9.45E+05 (K)AVVAALSK(H) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.85 3% 0.90% 78.1 8.47E+05 (K)LAVQFAGSAR(L) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.81 3% 0.90% 73.6 6.81E+05 (K)ALDIPAEVWDAK(S) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.77 3% 0.90% 68.8 2.32E+05 (R)GIVGTESATIALPGGK(V) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.76 3% 0.90% 70.3 2.43E+05 (K)VDAIHVAGK(A) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.6 3% 0.90% 70.9 1.57E+06 (K)VDAIHVAGK(A) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.23 3% 1% 69.4 2.46E+05 (K)SGGVILDSGNTLTVLAAPAYK(A) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.22 3% 1% 66.2 1.38E+05 (R)VGTPVQEFTLVADTGSDLTWVK(C) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.15 3% 1% 79.8 8.40E+05 (R)LEPPAK(S) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
11.08 3% 1% 65.7 2.46E+05 (K)LFLDPEMPFYGVK(V) UG365 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g028050 [S bicolor] >gi|241946780|gb|EES19925.1| hypothet prot
SORBIDRAFT_09g028050 [S bicolor]
16.57 <0.1% <0.1% 83.2 7.67E+03 (R)VVDALGVPIDGK(G) UG10226 S.halepenseF3RevF3Rev ATPase subunit 1 [Ferrocalamus rimosivaginus] >gi|372861939|gb|AEX98090.1| ATPase subunit 1
(mitochondrion) [Ferrocalamus rimosivaginus]
18.44 <0.1% <0.1% 78.4 1.43E+05 (R)VGLTGLTVAEHFR(D) CL350.c2 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g031470 [S bicolor] >gi|241928137|gb|EES01282.1| hypothet prot
SORBIDRAFT_03g031470 [S bicolor]
13.47 2% 0.50% 62.5 6.79E+04 (R)VGLTGLTVAEHFR(D) CL350.c2 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g031470 [S bicolor] >gi|241928137|gb|EES01282.1| hypothet prot
SORBIDRAFT_03g031470 [S bicolor]
14.91 0.20% <0.1% 81.2 1.41E+05 (R)VLNTGSPITVPVGR(A) UG2436 S.halepenseF2 hypothet prot SORBIDRAFT_03g031470 [S bicolor] >gi|241928137|gb|EES01282.1| hypothet prot
SORBIDRAFT_03g031470 [S bicolor]
10.94 3% 1% 77.2 9.55E+05 (K)YEIVK(R) CL607.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g036040 [S bicolor] >gi|241932814|gb|EES05959.1| hypothet prot
SORBIDRAFT_04g036040 [S bicolor]
10.31 3% 1% 71.3 4.97E+05 (K)YEIVK(R) CL607.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g036040 [S bicolor] >gi|241932814|gb|EES05959.1| hypothet prot
SORBIDRAFT_04g036040 [S bicolor]
10.29 3% 1% 63.4 2.43E+05 (K)YEIVK(R) CL607.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g036040 [S bicolor] >gi|241932814|gb|EES05959.1| hypothet prot
SORBIDRAFT_04g036040 [S bicolor]
21.68 <0.1% <0.1% 87.7 3.19E+05 (R)GALGPFGLLVLADK(H) CL1444.c1 S.halepenseF1 soluble acid invertase [S bicolor]
20.51 <0.1% <0.1% 87.7 3.47E+05 (R)GALGPFGLLVLADK(H) CL1444.c1 S.halepenseF1 soluble acid invertase [S bicolor]
18.77 <0.1% <0.1% 88.4 2.09E+05 (R)YDAATNEWTPLDAEK(D) CL1444.c1 S.halepenseF1 soluble acid invertase [S bicolor]
18.3 <0.1% <0.1% 82.4 1.15E+05 (K)IAWGHAVSR(D) CL1444.c1 S.halepenseF1 soluble acid invertase [S bicolor]

17.67	<0.1%	<0.1%	87.5	5.07E+05	(R)TKDFVSFELLPGLLHR(V)		CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
17.16	<0.1%	<0.1%	83.8	4.44E+05	(K)DFVSFELLPGLLHR(V)		CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
17.13	<0.1%	<0.1%	82.1	1.19E+05	(K)DFVSFELLPGLLHR(V)		CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
16.16	<0.1%	<0.1%	70.6	9.06E+05	(K)IAWGHAVSR(D)	CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]	
15.81	0.20%	<0.1%	75.4	2.27E+05	(R)VLVDHSIVESFAQGGR(S)		CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
15.41	0.20%	<0.1%	84.1	2.95E+05	(K)YEGNPVLYPPPGIGPK(D)		CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
14.5	2%	<0.1%	76.6	1.97E+05	(R)TKDFVSFELLPGLLHR(V)		CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
14.13	2%	0.30%	74	1.12E+05	(R)GALGPFGLLVLADK(H)		CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
13.43	2%	0.50%	77.6	3.74E+05	(K)GWASLQGIPR(T)	CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]	
12.24	3%	0.70%	81.5	9.63E+05	(R)TVLLDTK(T)	CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]	
11.82	3%	0.90%	68.9	1.46E+05	(R)TGmWECIDFYPVATR(G)	C:Carbamidomethylation m:Oxidized methionine	CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
11.61	3%	0.90%	67.5	5.84E+05	(K)TFYDPAK(R)	CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]	
11.45	3%	1.00%	84.1	5.46E+05	(R)IVIGSK(D)	CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]	
10.58	3%	1%	66	5.35E+04	(K)DFVSFELLPGLLHR(V)		CL1444.c1	S.halepenseF1	soluble acid invertase [S bicolor]
17.91	<0.1%	<0.1%	75.6	1.44E+05	(R)EKGEVGPFGLWVLAAGDLTER(T)		CL200.c1	S.halepenseF2	hypothet prot SORBIDRAFT_0067s002010 [S bicolor] >gi|241947385|gb|EES20530.1| hypothet prot SORBIDRAFT_0067s002010 [S bicolor]
14.68	2%	<0.1%	78.3	1.39E+05	(K)GGQYFEVDGFK(S)	CL200.c1	S.halepenseF2	hypothet prot SORBIDRAFT_0067s002010 [S bicolor] >gi|241947385|gb|EES20530.1| hypothet prot SORBIDRAFT_0067s002010 [S bicolor]	
10.25	3%	1%	71.2	7.57E+04	(R)TAVFFR(V)	CL200.c1	S.halepenseF2	hypothet prot SORBIDRAFT_0067s002010 [S bicolor] >gi|241947385|gb|EES20530.1| hypothet prot SORBIDRAFT_0067s002010 [S bicolor]	
13.8	2%	0.50%	76.8	1.00E+05	(R)EIPDIVFR(T)	UG455	S.halepenseF2Rev	hypothet prot SORBIDRAFT_07g024870 [S bicolor] >gi|241942084|gb|EES15229.1| hypothet prot SORBIDRAFT_07g024870 [S bicolor]	
13.61	2%	0.50%	76.7	1.54E+05	(R)SAEDIAFAVAR(F)	UG455	S.halepenseF2Rev	hypothet prot SORBIDRAFT_07g024870 [S bicolor] >gi|241942084|gb|EES15229.1| hypothet prot SORBIDRAFT_07g024870 [S bicolor]	
12.9	2%	0.60%	71.9	1.12E+05	(R)EIPDIVFR(T)	UG455	S.halepenseF2Rev	hypothet prot SORBIDRAFT_07g024870 [S bicolor] >gi|241942084|gb|EES15229.1| hypothet prot SORBIDRAFT_07g024870 [S bicolor]	
12.36	2%	0.70%	69.6	5.50E+04	(R)SAEDIAFAVAR(F)	UG455	S.halepenseF2Rev	hypothet prot SORBIDRAFT_07g024870 [S bicolor] >gi|241942084|gb|EES15229.1| hypothet prot SORBIDRAFT_07g024870 [S bicolor]	
20.68	<0.1%	<0.1%	85.3	8.70E+05	(K)SIEDEFAAHR(A)	UG1913	S.halepenseF1Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]	
16.72	<0.1%	<0.1%	84.6	7.72E+05	(K)YLQELQYAIR(D)	UG2114	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]	
15.67	0.20%	<0.1%	83	7.16E+04	(K)YLQELQYAIR(D)	UG2114	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]	
15.04	0.20%	<0.1%	84.3	1.23E+06	(R)IDYFQK(Y)	UG2114	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]	
13.88	2%	0.40%	77.5	1.79E+06	(R)FGIVHVDR(S)	UG2114	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]	
13.87	2%	0.40%	70.6	1.81E+05	(R)FGIVHVDR(S)	UG2114	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]	
13.83	2%	0.40%	84.4	5.82E+05	(K)ALIWTK(E)	UG2114	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]	
12.24	3%	0.70%	71.2	1.70E+05	(K)YLQELQYAIR(D)	UG2114	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]	
10.99	3%	1%	61.3	9.67E+03	(R)GYSDWLYVVPWGLYK(A)		UG2114	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
21.4	<0.1%	<0.1%	89.8	3.92E+05	(R)IVPDFTAFADFCFK(T)	C:Carbamidomethylation	UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
17.34	<0.1%	<0.1%	85.7	8.06E+05	(R)GPSIWDTFLK(Y)		UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
16.74	<0.1%	<0.1%	83.3	3.45E+05	(R)ETFPPGFVFGTASSAYQVEGNTR(K)		UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
15.37	0.20%	<0.1%	85.1	5.54E+05	(R)GPSIWDTFLK(Y)		UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
15.19	0.20%	<0.1%	83.7	1.14E+06	(R)FSISWSR(I)		UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
14.79	0.20%	<0.1%	74.3	2.24E+05	(K)DGVDYYHR(L)		UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
13.2	2%	0.50%	66.2	2.27E+05	(R)ETFPPGFVFGTASSAYQVEGNTR(K)		UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
11.93	3%	0.90%	75.1	1.63E+06	(R)VGFDAYR(F)		UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
11.9	3%	0.90%	67.5	1.20E+05	(R)GPSIWDTFLK(Y)		UG2752	S.halepenseF3	hypothet prot SORBIDRAFT_10g028060 [S bicolor] >gi|241917135|gb|EER90279.1| hypothet prot SORBIDRAFT_10g028060 [S bicolor]
22.31	<0.1%	<0.1%	94.1	1.00E+06	(K)IGEATAHETR(A)	UG2484	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]	
20.32	<0.1%	<0.1%	90.3	1.30E+06	(K)YFVGSVLSGGGSVPAEK(A)		UG2484	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
19.52	<0.1%	<0.1%	91.8	4.05E+05	(K)LVQLmTSNmVAGLQGDVPK(K)	m:Oxidized methionine	UG2484	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
19.49	<0.1%	<0.1%	80.4	4.00E+05	(K)IGEATAHETR(A)	UG2484	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]	
17.84	<0.1%	<0.1%	82.5	4.39E+05	(K)YFVGSVLSGGGSVPAEK(A)		UG2484	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
17.53	<0.1%	<0.1%	76.8	9.96E+05	(K)IGQmSQIER(A)	m:Oxidized methionine	UG2484	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]

17.06 <0.1% <0.1% 77.4 1.48E+05 (K)LVQLmTSNmVAGLQGDVPK(K) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
16.72 <0.1% <0.1% 91.4 9.29E+05 (K)FTmGLFEDPIPDPR(L) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
16.57 <0.1% <0.1% 87.6 7.98E+05 (K)FLITETLK(N) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
16.53 <0.1% <0.1% 74.1 6.96E+04 (K)IGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.7 0.20% <0.1% 84.7 7.29E+05 (K)SVDQLPmNYGDK(H) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.7 0.20% <0.1% 89.1 1.24E+06 (K)ETIHAGIDmVmIPYDYPEFVADLVK(Q) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.69 0.20% <0.1% 87.8 2.09E+06 (K)FLITETLK(N) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.66 0.20% <0.1% 76.1 4.25E+05 (K)IGQmSQIER(A) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.61 0.20% <0.1% 74.9 5.43E+04 (K)IGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.47 0.20% <0.1% 75.2 1.26E+05 (K)IGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.46 0.20% <0.1% 93.5 9.86E+05 (K)HYDPLFPFGFGLTTK(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.17 0.20% <0.1% 86.1 1.14E+06 (K)DVCGLVK(C) C:Carbamidomethylation UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.08 0.20% <0.1% 65.9 1.97E+05 (K)IGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
15.06 0.20% <0.1% 86.6 6.87E+04 (K)HYDPLFPFGFGLTTK(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.82 0.20% <0.1% 75.1 2.77E+05 (K)SASDYEYAVVAVGEPPYAETAGDSK(N) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.82 0.20% <0.1% 75.8 1.90E+05 (R)ATGIPYTFAPCVAVCR(D) C:Carbamidomethylation UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.77 0.20% <0.1% 75.8 1.60E+05 (K)FTMGLFEDPIPDPR(L) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.54 2% <0.1% 83.2 3.78E+05 (R)ATGIPYTFAPCVAVCR(D) C:Carbamidomethylation UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.48 2% <0.1% 83.7 1.75E+06 (R)VQDLLSR(M) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.48 2% <0.1% 81.6 1.97E+05 (K)FTmGLFEDPIPDPR(L) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.35 2% <0.1% 86 7.16E+05 (K)HYDPLFPFGFGLTTK(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.34 2% <0.1% 79.8 9.11E+05 (K)ASASVWQK(M) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
14.27 2% <0.1% 72.5 2.01E+05 (R)CYESFSEETK(L) C:Carbamidomethylation UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
13.85 2% 0.40% 84 1.37E+06 (K)LVQLmTSNmVAGLQGDVPK(K) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
13.8 2% 0.50% 80.9 2.23E+05 (K)FLITETLK(N) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
13.79 2% 0.50% 68.3 1.31E+05 (K)KIGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
13.62 2% 0.50% 67.4 3.52E+05 (K)ILVAGSHAHDLGSQCGGWTIK(W) C:Carbamidomethylation UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
13.57 2% 0.50% 82.1 9.35E+05 (K)GVPFVGGSK(K) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
13.41 2% 0.50% 79.7 2.00E+05 (K)FTmGLFEDPIPDPR(L) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
13.32 2% 0.50% 82.8 4.78E+05 (K)ETIHAGIDmVmIPYDYPEFVADLVK(Q) m:Oxidized methionine UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
13.06 2% 0.60% 81.6 6.02E+05 (R)VQDLLSR(M) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
12.96 2% 0.60% 83.2 7.99E+05 (K)HFVGDGGTTR(G) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
12.92 2% 0.60% 73.4 3.42E+05 (K)ASASVWQK(M) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
12.85 2% 0.60% 65.5 3.67E+04 (K)KIGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
12.82 2% 0.60% 82.5 1.74E+05 (R)ATGIPYTFAPCVAVCR(D) C:Carbamidomethylation UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
12.59 2% 0.60% 75.3 1.84E+05 (K)FLITETLK(N) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
12.45 2% 0.60% 65.6 1.36E+05 (K)KIGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
12.36 2% 0.70% 70.5 4.48E+04 (R)VQDLLSR(M) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]

11.7 3% 0.90% 68.5 6.11E+04 (K)KIGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
11.66 3% 0.90% 72.4 5.35E+04 (K)IGQMSQIER(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
11.4 3% 1.00% 78.8 3.19E+05 (K)HFVGDGGTTR(G) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
11.12 3% 1% 70.9 3.74E+05 (R)INDAVSR(I) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
10.9 3% 1% 63.3 6.00E+05 (R)INDAVSR(I) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
10.2 3% 1% 71.1 1.00E+05 (K)HFVGDGGTTR(G) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
10.18 3% 1% 74.6 2.40E+05 (K)HYDPLFPFGFGLTTK(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
10.08 4% 1% 64.8 1.22E+05 (K)IGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
10.07 5% 1% 67 5.43E+04 (K)IGEATAHETR(A) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
10.02 5% 1% 63.3 1.46E+05 (R)INDAVSR(I) UG2484 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g008050 [S bicolor] >gi|241920310|gb|EER93454.1| hypothet prot SORBIDRAFT_01g008050 [S bicolor]
18.14 <0.1% <0.1% 86.1 4.76E+05 (K)DLGPLEPTYK(A) CL244.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g026480 [S bicolor] >gi|241925862|gb|EER99006.1| hypothet prot SORBIDRAFT_02g026480 [S bicolor]
14.36 2% <0.1% 72.5 2.04E+05 (K)DLGPLEPTYK(A) CL244.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g026480 [S bicolor] >gi|241925862|gb|EER99006.1| hypothet prot SORBIDRAFT_02g026480 [S bicolor]
13.33 2% 0.50% 78.5 4.47E+05 (K)AVVAVLFSTK(A) CL244.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g026480 [S bicolor] >gi|241925862|gb|EER99006.1| hypothet prot SORBIDRAFT_02g026480 [S bicolor]
12.57 2% 0.60% 62.9 4.55E+05 (K)VEDASKEEVDSIDR(V) CL244.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g026480 [S bicolor] >gi|241925862|gb|EER99006.1| hypothet prot SORBIDRAFT_02g026480 [S bicolor]
11.21 3% 1% 76 2.79E+05 (K)GTVDPSTWIDK(A) CL244.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g026480 [S bicolor] >gi|241925862|gb|EER99006.1| hypothet prot SORBIDRAFT_02g026480 [S bicolor]
10.13 3% 1% 65.6 1.06E+05 (K)EEVDSIDR(V) CL244.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g026480 [S bicolor] >gi|241925862|gb|EER99006.1| hypothet prot SORBIDRAFT_02g026480 [S bicolor]
15.19 0.20% <0.1% 78.8 8.73E+04 (R)FPLELHLVHK(S) UG404 S.halepenseF2 hypothet prot SORBIDRAFT_05g003270 [S bicolor] >gi|241934852|gb|EES07997.1| hypothet prot SORBIDRAFT_05g003270 [S bicolor]
14.83 0.20% <0.1% 74 1.73E+05 (R)YTGSLTVPPCTENVVWSVLGK(V) C:Carbamidomethylation UG404 S.halepenseF2 hypothet prot SORBIDRAFT_05g003270 [S bicolor] >gi|241934852|gb|EES07997.1| hypothet prot SORBIDRAFT_05g003270 [S bicolor]
11.38 3% 1.00% 69.7 5.82E+05 (R)TGSYFR(Y) UG404 S.halepenseF2 hypothet prot SORBIDRAFT_05g003270 [S bicolor] >gi|241934852|gb|EES07997.1| hypothet prot SORBIDRAFT_05g003270 [S bicolor]
10.85 3% 1% 64.1 3.81E+05 (R)TYAAVPATLINDGHDIK(L) UG404 S.halepenseF2 hypothet prot SORBIDRAFT_05g003270 [S bicolor] >gi|241934852|gb|EES07997.1| hypothet prot SORBIDRAFT_05g003270 [S bicolor]
10.63 3% 1% 63.7 3.42E+05 (K)VGTVTVNGK(V) UG404 S.halepenseF2 hypothet prot SORBIDRAFT_05g003270 [S bicolor] >gi|241934852|gb|EES07997.1| hypothet prot SORBIDRAFT_05g003270 [S bicolor]
10.61 3% 1% 70.5 3.62E+05 (K)EQLQLLK(A) UG404 S.halepenseF2 hypothet prot SORBIDRAFT_05g003270 [S bicolor] >gi|241934852|gb|EES07997.1| hypothet prot SORBIDRAFT_05g003270 [S bicolor]
10.08 3% 1% 61.3 5.22E+05 (K)LEFGSK(V) UG404 S.halepenseF2 hypothet prot SORBIDRAFT_05g003270 [S bicolor] >gi|241934852|gb|EES07997.1| hypothet prot SORBIDRAFT_05g003270 [S bicolor]
10.62 3% 1% 70.1 6.83E+04 (K)NIIFLIDGTPIR(V) UG339 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g007020 [S bicolor] >gi|241940432|gb|EES13577.1| hypothet prot SORBIDRAFT_07g007020 [S bicolor]
11.02 3% 1% 81.5 2.40E+05 (R)FIISK(V) UG13158 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g007900 [S bicolor] >gi|241923018|gb|EER96162.1| hypothet prot SORBIDRAFT_02g007900 [S bicolor]
13.48 2% 0.50% 90.7 1.12E+07 (R)DAVTIR(A) CL230.c1 S.halepenseF1 hypothet prot SORBIDRAFT_09g024100 [S bicolor] >gi|241946589|gb|EES19734.1| hypothet prot SORBIDRAFT_09g024100 [S bicolor]
16.02 <0.1% <0.1% 80.2 1.17E+05 (K)EAFSLFDKDGDGCITTK(E) C:Carbamidomethylation CL1715.c1 S.halepenseF1 hypothet prot SORBIDRAFT_02g043510 [S bicolor] >gi|241924624|gb|EER97768.1| hypothet prot SORBIDRAFT_02g043510 [S bicolor]
13.95 2% 0.30% 78.6 6.72E+04 (R)VFDKDQNGFISAAELR(H) CL1715.c1 S.halepenseF1 hypothet prot SORBIDRAFT_02g043510 [S bicolor] >gi|241924624|gb|EER97768.1| hypothet prot SORBIDRAFT_02g043510 [S bicolor]
19.03 <0.1% <0.1% 81.9 8.17E+05 (K)LDCGGGYVK(L) C:Carbamidomethylation CL1082.c1 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
15.36 0.20% <0.1% 85 6.86E+05 (K)GIQTSEDYR(F) CL1082.c1 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
15.02 0.20% <0.1% 82.4 5.23E+05 (R)FYAISAEYPEFSSK(D) CL1082.c1 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
14.91 0.20% <0.1% 86.3 3.70E+05 (K)KPEDWDDKEYIPDPEDKKPEGYDDIPK(E) CL1082.c1 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
14.74 0.20% <0.1% 84.9 3.24E+05 (K)TLVLQFSVK(H) CL1082.c1 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
13.84 2% 0.40% 79.2 1.59E+05 (K)KPEGYDDIPK(E) CL1082.c1 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
12.19 3% 0.70% 76 1.15E+06 (K)EIPDPDAK(K) CL1082.c1 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
23.12 <0.1% <0.1% 89.9 3.61E+05 (K)YIGIELWQVK(S) CL1082.c3 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
21.09 <0.1% <0.1% 92.8 7.04E+05 (K)SGTLFDNFIITDDPALAK(T) CL1082.c3 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
17.33 <0.1% <0.1% 89.4 9.42E+05 (K)AAFDAAEK(K) CL1082.c3 S.halepenseF2 calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin

16.77	<0.1%	<0.1%	82.6	4.57E+05	(K)APmIDNPDFKDDPYIYAFDSLK(Y)	m:Oxidized methionine	CL1082.c3	S.halepenseF2	calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
12.39	2%	0.60%	67.7	3.86E+05	(K)IKNPNYQGK(W)		CL1082.c3	S.halepenseF2	calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
12.22	3%	0.70%	63.6	3.66E+05	(K)APmIDNPDFKDDPYIYAFDSLK(Y)	m:Oxidized methionine	CL1082.c3	S.halepenseF2	calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
11.22	3%	1%	63.7	2.17E+05	(K)SGTLFDNFIITDDPALAK(T)		CL1082.c3	S.halepenseF2	calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
11.21	3%	1%	66.9	5.15E+05	(K)TFAEETWGK(H)		CL1082.c3	S.halepenseF2	calreticulin2 precursor [Zea mays] >gi|577612|emb|CAA86728.1| calcium-binding protein [Zea mays] >gi|927572|emb|CAA61939.1| Calreticulin precursor [Zea mays] >gi|195622592|gb|ACG33126.1| calreticulin precursor [Zea mays] >gi|1587033|prf||2205314A calreticulin
19.15	<0.1%	<0.1%	87.4	1.75E+05	(K)ALLSLEDGAPDKFHFVEEWVR(I)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]
19.12	<0.1%	<0.1%	86.8	1.80E+05	(K)ALLSLEDGAPDKFHFVEEWVR(I)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]
17.68	<0.1%	<0.1%	78.8	2.48E+05	(K)ALLSLEDGAPDKFHFVEEWVR(I)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]
17.14	<0.1%	<0.1%	77.2	1.36E+05	(K)ALLSLEDGAPDKFHFVEEWVR(I)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]
16.19	<0.1%	<0.1%	83	1.57E+05	(K)ALLSLEDGAPDKFHFVEEWVR(I)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]
15.39	0.20%	<0.1%	80.7	9.80E+04	(K)ALLSLEDGAPDKFHFVEEWVR(I)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]
15.04	0.20%	<0.1%	88.5	5.84E+05	(K)EAVNVSLENLK(T)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
13.87	2%	0.40%	78.3	3.43E+05	(K)EAVNVSLENLK(T)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
13.55	2%	0.50%	75.2	4.08E+05	(K)ALLSLEDGAPDK(F)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
13.38	2%	0.50%	77.3	2.13E+04	(K)TDHASVPFEDQCSILEK(E)	C:Carbamidomethylation	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
13.28	2%	0.50%	76.1	7.39E+05	(K)EAVNVSLENLK(T)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
13.19	2%	0.50%	77.3	1.33E+05	(K)ALLSLEDGAPDKFHFVEEWVR(I)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
13.15	2%	0.50%	75.4	1.96E+05	(K)TGFEQFK(A)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
12.47	2%	0.60%	88.5	3.51E+05	(K)KPELFEPLK(A)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
12.35	2%	0.70%	71.3	1.28E+05	(K)ALLSLEDGAPDKFHFVEEWVR(I)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
12.31	2%	0.70%	73.8	3.90E+05	(K)ALLSLEDGAPDK(F)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
11.85	3%	0.90%	77	4.81E+05	(K)TGFEQFK(A)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
11.61	3%	0.90%	83.1	1.14E+06	(K)EAVNVSLENLK(T)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
11.33	3%	1.00%	66.7	2.54E+05	(K)ADVYDKKPELFEPLK(A)		CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
11.01	3%	1%	66.3	3.41E+05	(K)EAVNVSLENLK(T)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
10.65	3%	1%	69.3	6.10E+05	(R)NIASmVPPYDK(T)	m:Oxidized methionine	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
10.37	3%	1%	61.3	1.48E+05	(K)FHFVEEWVR(I)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
10.16	3%	1%	74	2.91E+05	(K)EAVNVSLENLK(T)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
10.01	5%	1%	79.8	2.24E+05	(K)KPELFEPLK(A)	CL859.c2	S.halepenseF2Rev	carbonic anhydrase [Zea mays] >gi|195636930|gb|ACG37933.1| carbonic anhydrase [Zea mays]	
13.04	2%	0.60%	81.3	2.36E+05	(K)TYPFVK(E)	UG6181	S.halepenseF1	unknown [Zea mays] >gi|223948691|gb|ACN28429.1| unknown [Zea mays]	
12.44	2%	0.60%	81.7	4.06E+05	(K)TYPFVK(E)	UG6181	S.halepenseF1	unknown [Zea mays] >gi|223948691|gb|ACN28429.1| unknown [Zea mays]	
12.13	3%	0.80%	82.3	2.88E+05	(K)TYPFVK(E)	UG6181	S.halepenseF1	unknown [Zea mays] >gi|223948691|gb|ACN28429.1| unknown [Zea mays]	
11.43	3%	1.00%	77.9	4.01E+05	(K)TYPFVK(E)	UG6181	S.halepenseF1	unknown [Zea mays] >gi|223948691|gb|ACN28429.1| unknown [Zea mays]	
11.41	3%	1.00%	74.1	1.79E+05	(K)TYPFVK(E)	UG6181	S.halepenseF1	unknown [Zea mays] >gi|223948691|gb|ACN28429.1| unknown [Zea mays]	
11.22	3%	1%	76.1	3.01E+05	(K)TYPFVK(E)	UG6181	S.halepenseF1	unknown [Zea mays] >gi|223948691|gb|ACN28429.1| unknown [Zea mays]	
11.2	3%	1%	73.9	2.63E+05	(K)TYPFVK(E)	UG6181	S.halepenseF1	unknown [Zea mays] >gi|223948691|gb|ACN28429.1| unknown [Zea mays]	
10.8	3%	1%	67.2	1.44E+05	(K)TYPFVK(E)	UG6181	S.halepenseF1	unknown [Zea mays] >gi|223948691|gb|ACN28429.1| unknown [Zea mays]	
10.18	3%	1%	83.6	1.73E+06	(K)XIPDIPK(A)	CL273.c1	S.halepenseF3RevF3Rev	predicted protein [Hordeum vulgare subsp. vulgare] >gi|326514652|dbj|BAJ96313.1| predicted protein [Hordeum vulgare subsp. vulgare]	
12.22	3%	0.70%	79.2	3.94E+05	(R)LAIQAAQR(N)	UG1242	S.halepenseF2	hypothet prot SORBIDRAFT_03g012790 [S bicolor] >gi|241927511|gb|EES00656.1| hypothet prot SORBIDRAFT_03g012790 [S bicolor]	
12.07	3%	0.80%	75.9	1.82E+05	(R)LAIQAAQR(N)	UG1242	S.halepenseF2	hypothet prot SORBIDRAFT_03g012790 [S bicolor] >gi|241927511|gb|EES00656.1| hypothet prot SORBIDRAFT_03g012790 [S bicolor]	
11.66	3%	0.90%	67	3.45E+05	(K)TADTAGLAR(L)	UG1242	S.halepenseF2	hypothet prot SORBIDRAFT_03g012790 [S bicolor] >gi|241927511|gb|EES00656.1| hypothet prot SORBIDRAFT_03g012790 [S bicolor]	
10.57	3%	1%	71.7	1.17E+05	(R)LAIQAAQR(N)	UG1242	S.halepenseF2	hypothet prot SORBIDRAFT_03g012790 [S bicolor] >gi|241927511|gb|EES00656.1| hypothet prot SORBIDRAFT_03g012790 [S bicolor]	
10.46	3%	1%	74.7	9.89E+04	(K)TADTAGLAR(L)	UG1242	S.halepenseF2	hypothet prot SORBIDRAFT_03g012790 [S bicolor] >gi|241927511|gb|EES00656.1| hypothet prot SORBIDRAFT_03g012790 [S bicolor]	
11.86	3%	0.90%	81	6.12E+05	(R)IGFYQR(Y)	UG11756	S.halepenseF3	hypothet prot SORBIDRAFT_03g011710 [S bicolor] >gi|241929664|gb|EES02809.1| hypothet prot SORBIDRAFT_03g011710 [S bicolor]	
15.7	0.20%	<0.1%	85.5	1.02E+06	(K)FAATGDLSTR(K)	UG9701	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g011710 [S bicolor] >gi|241929664|gb|EES02809.1| hypothet prot SORBIDRAFT_03g011710 [S bicolor]	
15.46	0.20%	<0.1%	72.4	1.70E+05	(K)GFYTYAAFIQAAR(T)	UG9701	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g011710 [S bicolor] >gi|241929664|gb|EES02809.1| hypothet prot SORBIDRAFT_03g011710 [S bicolor]	
15.33	0.20%	<0.1%	81	8.28E+04	(R)TALWFWMTPR(R)	UG9701	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g011710 [S bicolor] >gi|241929664|gb|EES02809.1| hypothet prot SORBIDRAFT_03g011710 [S bicolor]	
14.39	2%	<0.1%	82.8	2.74E+05	(K)FAATGDLSTR(K)	UG9701	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g011710 [S bicolor] >gi|241929664|gb|EES02809.1| hypothet prot SORBIDRAFT_03g011710 [S bicolor]	
14.09	2%	0.30%	73.3	1.76E+05	(R)TALWFWmTPR(R)	m:Oxidized methionine	UG9701	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g011710 [S bicolor] >gi|241929664|gb|EES02809.1| hypothet prot SORBIDRAFT_03g011710 [S bicolor]	
13.66	2%	0.50%	82.6	1.30E+05	(K)LYEVVPPILTELGK(V)		UG1768	S.halepenseF1	uncharacterized protein LOC100194338 [Zea mays]	
13.46	2%	0.50%	81.2	8.39E+04	(K)HLPEDPLFQLVSK(L)	UG1768	S.halepenseF1	uncharacterized protein LOC100194338 [Zea mays]		
12.85	2%	0.60%	84.3	1.86E+05	(R)ALGLPLERPK(S)	UG1768	S.halepenseF1	uncharacterized protein LOC100194338 [Zea mays]		
12.35	2%	0.70%	82.8	2.57E+05	(R)ALGLPLERPK(S)	UG1768	S.halepenseF1	uncharacterized protein LOC100194338 [Zea mays]		
12.23	3%	0.70%	78	1.30E+05	(R)ALGLPLERPK(S)	UG1768	S.halepenseF1	uncharacterized protein LOC100194338 [Zea mays]		
12.22	3%	0.70%	83.3	1.50E+05	(K)LYEVVPPILTELGK(V)		UG1768	S.halepenseF1	uncharacterized protein LOC100194338 [Zea mays]	
11.47	3%	1.00%	76.5	1.94E+05	(K)EQVDALSK(E)	UG1768	S.halepenseF1	uncharacterized protein LOC100194338 [Zea mays]		
11.34	3%	1.00%	64.8	7.75E+04	(K)LYEVVPPILTELGK(V)		UG1768	S.halepenseF1	uncharacterized protein LOC100194338 [Zea mays]	

10.79 3% 1% 76.9 8.98E+04 (K)LYEVVPPILTELGK(V) UG1768 S.halepenseF1 uncharacterized protein LOC100194338 [Zea mays]
10.64 3% 1% 74.3 7.33E+04 (R)ALGLPLERPK(S) UG1768 S.halepenseF1 uncharacterized protein LOC100194338 [Zea mays]
10.45 3% 1% 76 2.03E+05 (K)VTGILPLK(E) CL1642.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g006370 [S bicolor] >gi|241943710|gb|EES16855.1| hypothet prot SORBIDRAFT_08g006370 [S bicolor]
12.66 2% 0.60% 81.7 4.19E+05 (K)LNVVVK(R) UG10342 S.halepenseF1Rev hypothet prot SORBIDRAFT_08g006370 [S bicolor] >gi|241943710|gb|EES16855.1| hypothet prot SORBIDRAFT_08g006370 [S bicolor]
13.39 2% 0.50% 94.5 4.72E+06 (K)ILYAR(H) UG3763 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g049510 [S bicolor] >gi|241919837|gb|EER92981.1| hypothet prot SORBIDRAFT_01g049510 [S bicolor]
11.58 3% 1.00% 92.3 8.07E+06 (K)ILYAR(H) UG3763 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g049510 [S bicolor] >gi|241919837|gb|EER92981.1| hypothet prot SORBIDRAFT_01g049510 [S bicolor]
10.74 3% 1% 85.5 6.11E+05 (K)ILYAR(H) UG3763 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g049510 [S bicolor] >gi|241919837|gb|EER92981.1| hypothet prot SORBIDRAFT_01g049510 [S bicolor]
10.41 3% 1% 81.9 1.37E+06 (K)ILYAR(H) UG3763 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g049510 [S bicolor] >gi|241919837|gb|EER92981.1| hypothet prot SORBIDRAFT_01g049510 [S bicolor]
13.11 2% 0.60% 76.3 2.95E+05 (R)LGQQQPDGSYK(V) UG8685 S.halepenseF1 hypothet prot [Zea mays]
14.85 0.20% <0.1% 61.3 1.52E+05 (K)VWEKPWENFK(E) UG1361 S.halepenseF3 unknown [Zea mays]
15.51 0.20% <0.1% 92.1 1.68E+07 (R)ISNFAK(S) CL1208.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g010730 [S bicolor] >gi|241929604|gb|EES02749.1| hypothet prot SORBIDRAFT_03g010730 [S bicolor]
15.39 0.20% <0.1% 87.6 1.35E+07 (R)ISNFAK(S) CL1208.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g010730 [S bicolor] >gi|241929604|gb|EES02749.1| hypothet prot SORBIDRAFT_03g010730 [S bicolor]
15.27 0.20% <0.1% 84.4 4.95E+06 (R)ISNFAK(S) CL1208.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g010730 [S bicolor] >gi|241929604|gb|EES02749.1| hypothet prot SORBIDRAFT_03g010730 [S bicolor]
15.14 0.20% <0.1% 63.4 3.25E+05 (K)DVPANENDLHLQELAR(F) CL1208.c1 S.halepenseF3 hypothet prot SORBIDRAFT_03g010730 [S bicolor] >gi|241929604|gb|EES02749.1| hypothet prot SORBIDRAFT_03g010730 [S bicolor]
15.3 0.20% <0.1% 91.2 1.11E+07 (K)YIPGTK(M) UG15774 S.halepenseF1 RecName: Full=Cytochrome c >gi|440586|emb|CAA79708.1| mitochondrial cytochrome c [Stellaria longipes]
16.08 <0.1% <0.1% 83.8 1.49E+06 (R)TDLIAYLK(E) UG439 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g034230 [S bicolor] >gi|241938573|gb|EES11718.1| hypothet prot SORBIDRAFT_06g034230 [S bicolor]
15.4 0.20% <0.1% 64.7 1.56E+06 (R)QSGTTLGYAYSTANK(N) UG439 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g034230 [S bicolor] >gi|241938573|gb|EES11718.1| hypothet prot SORBIDRAFT_06g034230 [S bicolor]
14.47 2% <0.1% 77.4 2.02E+04 (R)TDLIAYLK(E) UG439 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g034230 [S bicolor] >gi|241938573|gb|EES11718.1| hypothet prot SORBIDRAFT_06g034230 [S bicolor]
14.16 2% 0.20% 80.9 6.89E+04 (R)TDLIAYLK(E) UG439 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g034230 [S bicolor] >gi|241938573|gb|EES11718.1| hypothet prot SORBIDRAFT_06g034230 [S bicolor]
13.16 2% 0.50% 84.5 9.19E+05 (K)ERTDLIAYLK(E) UG439 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g034230 [S bicolor] >gi|241938573|gb|EES11718.1| hypothet prot SORBIDRAFT_06g034230 [S bicolor]
10.6 3% 1% 76 1.08E+05 (K)MVFPGLK(K) UG439 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g034230 [S bicolor] >gi|241938573|gb|EES11718.1| hypothet prot SORBIDRAFT_06g034230 [S bicolor]
10.4 3% 1% 80.1 4.21E+05 (K)ERTDLIAYLK(E) UG439 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g034230 [S bicolor] >gi|241938573|gb|EES11718.1| hypothet prot SORBIDRAFT_06g034230 [S bicolor]
14.01 2% 0.30% 74.5 1.09E+06 (R)ADLIAYLK(E) UG3191 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g020710 [S bicolor] >gi|241945105|gb|EES18250.1| hypothet prot SORBIDRAFT_09g020710 [S bicolor]
12.09 3% 0.80% 63.4 1.13E+05 (R)ADLIAYLK(E) UG3191 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g020710 [S bicolor] >gi|241945105|gb|EES18250.1| hypothet prot SORBIDRAFT_09g020710 [S bicolor]
13.79 2% 0.50% 73.9 4.55E+05 (R)FPTTNQTR(H) UG2269 S.halepenseF1 hypothet prot SORBIDRAFT_04g025700 [S bicolor] >gi|241933989|gb|EES07134.1| hypothet prot SORBIDRAFT_04g025700 [S bicolor]
20.33 <0.1% <0.1% 91.5 7.29E+05 (K)SVLFEGFCFDSDK(C) C:Carbamidomethylation UG501 S.halepenseF1 hypothet prot SORBIDRAFT_04g026680 [S bicolor] >gi|241932316|gb|EES05461.1| hypothet prot SORBIDRAFT_04g026680 [S bicolor]
11.42 3% 1.00% 73.5 2.97E+05 (K)SVLFEGFCFDSDK(C) C:Carbamidomethylation UG501 S.halepenseF1 hypothet prot SORBIDRAFT_04g026680 [S bicolor] >gi|241932316|gb|EES05461.1| hypothet prot SORBIDRAFT_04g026680 [S bicolor]
15.81 0.20% <0.1% 79.1 1.04E+05 (K)VVGCDTSGDGVK(L) C:Carbamidomethylation CL2294.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g013290 [S bicolor] >gi|241929744|gb|EES02889.1| hypothet prot SORBIDRAFT_03g013290 [S bicolor]
14.14 2% 0.20% 73.3 1.65E+05 (R)TPFTSGIGLETLGVETDK(A) CL2294.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g013290 [S bicolor] >gi|241929744|gb|EES02889.1| hypothet prot SORBIDRAFT_03g013290 [S bicolor]
11.2 3% 1% 73.7 2.03E+05 (K)GVYAIGDAIPGPmLAHK(A) m:Oxidized methionine CL2294.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g013290 [S bicolor] >gi|241929744|gb|EES02889.1| hypothet prot SORBIDRAFT_03g013290 [S bicolor]
10.14 3% 1% 66.4 1.74E+05 (R)TPFTSGIGLETLGVETDK(A) CL2294.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g013290 [S bicolor] >gi|241929744|gb|EES02889.1| hypothet prot SORBIDRAFT_03g013290 [S bicolor]
12 3% 0.80% 72.1 1.46E+05 (K)FPLLANSR(A) UG10160 S.halepenseF1 hypothet prot SORBIDRAFT_09g004610 [S bicolor] >gi|241944621|gb|EES17766.1| hypothet prot SORBIDRAFT_09g004610 [S bicolor]
10.93 3% 1% 67.7 1.51E+05 (R)IPIFK(G) UG425 S.halepenseF1 hypothet prot SORBIDRAFT_10g031050 [S bicolor] >gi|241917293|gb|EER90437.1| hypothet prot SORBIDRAFT_10g031050 [S bicolor]
12.76 2% 0.60% 83.5 8.18E+05 (R)LEISEXNR(L) UG1701 S.halepenseF3 hypothet prot SORBIDRAFT_07g003610 [S bicolor] >gi|241940222|gb|EES13367.1| hypothet prot SORBIDRAFT_07g003610 [S bicolor]
12.04 3% 0.80% 68.1 2.28E+05 (R)LEISEXNR(L) UG1701 S.halepenseF3 hypothet prot SORBIDRAFT_07g003610 [S bicolor] >gi|241940222|gb|EES13367.1| hypothet prot SORBIDRAFT_07g003610 [S bicolor]
15.3 0.20% <0.1% 79.5 5.72E+05 (R)VQVGDVLSFK(Y) CL1769.c1 S.halepenseF2Rev uclacyanin-2 precursor [Zea mays] >gi|195647352|gb|ACG43144.1| uclacyanin-2 precursor [Zea mays]
10.28 3% 1% 74.3 7.05E+05 (K)QCSTETPVSR(F) C:Carbamidomethylation CL1769.c1 S.halepenseF2Rev uclacyanin-2 precursor [Zea mays] >gi|195647352|gb|ACG43144.1| uclacyanin-2 precursor [Zea mays]
17.93 <0.1% <0.1% 75.3 2.10E+05 (R)FLVGDIVHFK(Y) UG839 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g032620 [S bicolor] >gi|241939938|gb|EES13083.1| hypothet prot SORBIDRAFT_06g032620 [S bicolor]
16.49 <0.1% <0.1% 75.9 2.83E+05 (R)FLVGDIVHFK(Y) UG839 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g032620 [S bicolor] >gi|241939938|gb|EES13083.1| hypothet prot SORBIDRAFT_06g032620 [S bicolor]
18.79 <0.1% <0.1% 69.1 2.28E+05 (K)GTSPEWNENFIFTVSDR(T) UG883 S.halepenseF2 hypothet prot SORBIDRAFT_04g027270 [S bicolor] >gi|241932345|gb|EES05490.1| hypothet prot SORBIDRAFT_04g027270 [S bicolor]
16.69 <0.1% <0.1% 79 3.38E+04 (R)GLPEDFGGWK(Q) UG883 S.halepenseF2 hypothet prot SORBIDRAFT_04g027270 [S bicolor] >gi|241932345|gb|EES05490.1| hypothet prot SORBIDRAFT_04g027270 [S bicolor]

14.78 0.20% <0.1% 72.7 1.88E+05 (K)LmDSDTGTADDFVGEATIPLEAVYTER(S) m:Oxidized methionine UG883 S.halepenseF2 hypothet prot SORBIDRAFT_04g027270 [S bicolor] >gi|241932345|gb|EES05490.1| hypothet prot SORBIDRAFT_04g027270 [S bicolor]
14.35 2% <0.1% 79.7 1.21E+05 (R)TTDLLIK(L) UG883 S.halepenseF2 hypothet prot SORBIDRAFT_04g027270 [S bicolor] >gi|241932345|gb|EES05490.1| hypothet prot SORBIDRAFT_04g027270 [S bicolor]
14.26 2% <0.1% 86.7 1.20E+06 (R)TTDLLIK(L) UG883 S.halepenseF2 hypothet prot SORBIDRAFT_04g027270 [S bicolor] >gi|241932345|gb|EES05490.1| hypothet prot SORBIDRAFT_04g027270 [S bicolor]
13.24 2% 0.50% 77.4 2.73E+04 (K)LMDSDTGTADDFVGEATIPLEAVYTER(S) UG883 S.halepenseF2 hypothet prot SORBIDRAFT_04g027270 [S bicolor] >gi|241932345|gb|EES05490.1| hypothet prot SORBIDRAFT_04g027270 [S bicolor]
12.5 2% 0.60% 79.7 1.19E+05 (R)TTDLLIK(L) UG883 S.halepenseF2 hypothet prot SORBIDRAFT_04g027270 [S bicolor] >gi|241932345|gb|EES05490.1| hypothet prot SORBIDRAFT_04g027270 [S bicolor]
10.29 3% 1% 67.7 1.87E+05 (R)TTDLLIK(L) UG883 S.halepenseF2 hypothet prot SORBIDRAFT_04g027270 [S bicolor] >gi|241932345|gb|EES05490.1| hypothet prot SORBIDRAFT_04g027270 [S bicolor]
12.41 2% 0.60% 74.8 1.19E+05 (K)IGGIGTVPVGR(V) CL1135.c1 S.halepenseF2Rev predicted protein [Hordeum vulgare subsp. vulgare]
10.21 3% 1% 69.8 3.45E+05 (K)IGGIGTVPVGR(V) CL1135.c1 S.halepenseF2Rev predicted protein [Hordeum vulgare subsp. vulgare]
13.51 2% 0.50% 74.5 2.24E+05 (R)VETGIIKPGmVVTFGPSGLTTEVK(S) m:Oxidized methionine CL79.c3 S.halepenseF2Rev LOC100286309 [Zea mays] >gi|195658719|gb|ACG48827.1| elongation factor 1-alpha [Zea mays]
10.36 3% 1% 62.2 1.11E+05 (R)VETGIIKPGmVVTFGPSGLTTEVK(S) m:Oxidized methionine CL79.c3 S.halepenseF2Rev LOC100286309 [Zea mays] >gi|195658719|gb|ACG48827.1| elongation factor 1-alpha [Zea mays]
14.09 2% 0.30% 74.1 6.73E+04 (R)LLEPVYLVEIQAPENALGGIYGVLNQK(R) UG8760 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034200 [S bicolor] >gi|241928310|gb|EES01455.1| hypothet prot SORBIDRAFT_03g034200 [S bicolor]
12.25 3% 0.70% 68.4 1.06E+05 (K)AYLPVIESFGFSSQLR(A) UG8760 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034200 [S bicolor] >gi|241928310|gb|EES01455.1| hypothet prot SORBIDRAFT_03g034200 [S bicolor]
15.71 0.20% <0.1% 75.3 8.46E+04 (K)AHEIQAAVLLHPSFVTIDDIK(E) UG5255 S.halepenseF2Rev hypothet prot SORBIDRAFT_09g019630 [S bicolor] >gi|241945047|gb|EES18192.1| hypothet prot SORBIDRAFT_09g019630 [S bicolor]
10.73 3% 1% 68.1 1.36E+05 (K)GFEEAKPVIATLK(E) UG5255 S.halepenseF2Rev hypothet prot SORBIDRAFT_09g019630 [S bicolor] >gi|241945047|gb|EES18192.1| hypothet prot SORBIDRAFT_09g019630 [S bicolor]
10.47 3% 1% 60.1 6.70E+04 (K)AHEIQAAVLLHPSFVTIDDIK(E) UG5255 S.halepenseF2Rev hypothet prot SORBIDRAFT_09g019630 [S bicolor] >gi|241945047|gb|EES18192.1| hypothet prot SORBIDRAFT_09g019630 [S bicolor]
19.43 <0.1% <0.1% 85.9 2.08E+05 (K)VQADNFVCAVLPDTPFHQVFITPGGVIHLR(D) C:Carbamidomethylation CL535.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g034920 [S bicolor] >gi|241932745|gb|EES05890.1| hypothet prot SORBIDRAFT_04g034920 [S bicolor]
15 0.20% <0.1% 88.1 1.05E+05 (K)LLFLFAK(A) CL535.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g034920 [S bicolor] >gi|241932745|gb|EES05890.1| hypothet prot SORBIDRAFT_04g034920 [S bicolor]
22.94 <0.1% <0.1% 96.1 9.12E+05 (R)IEEELGDAAVYAGAK(F) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
21.2 <0.1% <0.1% 92.3 1.92E+06 (K)KIPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
20.46 <0.1% <0.1% 85.9 4.45E+05 (R)IEEELGDAAVYAGAK(F) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
20.2 <0.1% <0.1% 94.3 5.69E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
19.7 <0.1% <0.1% 84.3 8.61E+04 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
19.62 <0.1% <0.1% 93.1 7.88E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
19.62 <0.1% <0.1% 90.4 6.39E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
19.56 <0.1% <0.1% 86.7 8.23E+05 (K)KIPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
19.45 <0.1% <0.1% 85.6 7.16E+05 (K)KIPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
19.29 <0.1% <0.1% 85.3 2.84E+05 (K)VVIGmDVAASEFFSEK(D) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
19.09 <0.1% <0.1% 86.4 4.18E+05 (K)YGQDATNVGDEGGFAPNIQENK(E) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
19.05 <0.1% <0.1% 77.3 1.88E+06 (R)GAVPSGASTGIYEALELR(D) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
18.81 <0.1% <0.1% 82.7 1.48E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
18.59 <0.1% <0.1% 88.2 1.14E+05 (K)SFVSEYPIVSIEDPFDQDDWTTYAK(L) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
18.35 <0.1% <0.1% 82.8 3.35E+05 (K)KIPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
18.03 <0.1% <0.1% 82.2 4.92E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
17.95 <0.1% <0.1% 77.7 5.10E+05 (K)IPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
17.82 <0.1% <0.1% 82.4 1.67E+05 (K)SFVSEYPIVSIEDPFDQDDWTTYAK(L) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
17.8 <0.1% <0.1% 81.9 3.37E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
17.65 <0.1% <0.1% 88.7 4.15E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
17.61 <0.1% <0.1% 74.8 5.55E+05 (K)SFVSEYPIVSIEDPFDQDDWTTYAK(L) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
17.56 <0.1% <0.1% 79.7 1.61E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]

17.43 <0.1% <0.1% 88.8 3.89E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
17.31 <0.1% <0.1% 77.6 2.04E+05 (K)ISGDSLKDLYK(S) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
17.16 <0.1% <0.1% 76.3 7.57E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.99 <0.1% <0.1% 82.2 2.01E+05 (R)GNPTVEVDIGLSDGSYAR(G) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.76 <0.1% <0.1% 83.5 1.60E+05 (K)KYGQDATNVGDEGGFAPNIQENK(E) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.74 <0.1% <0.1% 69.7 1.59E+05 (R)AGWGVmASHR(S) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.71 <0.1% <0.1% 84.3 2.51E+06 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.52 <0.1% <0.1% 74.7 3.63E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.39 <0.1% <0.1% 83.5 4.21E+05 (K)AVSNVNTIIGPAIVGK(D) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.37 <0.1% <0.1% 87 9.83E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.36 <0.1% <0.1% 79.7 1.48E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.28 <0.1% <0.1% 78.4 7.32E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
16.08 <0.1% <0.1% 76.4 2.92E+06 (K)TCNALLLK(V) C:Carbamidomethylation CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
15.73 0.20% <0.1% 66.6 6.81E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
15.65 0.20% <0.1% 84.1 2.31E+05 (K)YGQDATNVGDEGGFAPNIQENK(E) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
15.32 0.20% <0.1% 81.3 2.20E+05 (R)GNPTVEVDIGLSDGSYAR(G) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
15.22 0.20% <0.1% 77.6 2.33E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
15.07 0.20% <0.1% 78.7 2.61E+05 (R)SGETEDTFIADLSVGLATGQIK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
14.93 0.20% <0.1% 73.1 2.49E+05 (K)IPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
14.91 0.20% <0.1% 81.1 3.54E+05 (R)IEEELGDAAVYAGAK(F) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
14.88 0.20% <0.1% 71.6 4.28E+05 (K)TCNALLLK(V) C:Carbamidomethylation CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
14.29 2% <0.1% 73.2 3.78E+05 (R)GNPTVEVDIGLSDGSYAR(G) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
14.2 2% <0.1% 71.4 3.01E+05 (K)MGVEVYHNLK(S) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
14.02 2% 0.30% 65.4 2.16E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.99 2% 0.30% 70.4 2.65E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.89 2% 0.40% 71.9 2.64E+04 (K)ISGDSLKDLYK(S) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.8 2% 0.50% 79.5 1.32E+05 (R)GNPTVEVDIGLSDGSYAR(G) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.78 2% 0.50% 66.1 1.09E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.72 2% 0.50% 65.9 2.58E+05 (K)IPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.66 2% 0.50% 78.7 2.05E+05 (K)TYDLNFK(E) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.65 2% 0.50% 67.4 2.20E+05 (K)SFVSEYPIVSIEDPFDQDDWTTYAK(L) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.58 2% 0.50% 74.7 1.68E+05 (K)AVSNVNTIIGPAIVGK(D) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.54 2% 0.50% 60.8 5.00E+05 (K)MGVEVYHNLK(S) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.42 2% 0.50% 84.3 6.43E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.37 2% 0.50% 87.8 4.38E+05 (K)EGLELLK(A) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.36 2% 0.50% 63.9 1.83E+05 (K)TCNALLLK(V) C:Carbamidomethylation CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.34 2% 0.50% 69.5 3.77E+05 (K)AVSNVNTIIGPAIVGK(D) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.31 2% 0.50% 68 3.91E+05 (R)IEEELGDAAVYAGAK(F) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]

13.28 2% 0.50% 60.8 3.61E+05 (K)KIPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
13.18 2% 0.50% 74.4 2.11E+05 (K)AVSNVNTIIGPAIVGK(D) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.89 2% 0.60% 87.7 2.55E+06 (K)ISGDSLK(D) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.63 2% 0.70% 64.7 5.72E+05 (R)GAVPSGASTGIYEALELR(D) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.62 2% 0.70% 66.1 6.44E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.57 2% 0.60% 67.4 1.18E+06 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.56 2% 0.60% 62.2 9.91E+05 (K)TCNALLLK(V) C:Carbamidomethylation CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.46 2% 0.60% 65.8 5.17E+05 (K)TCNALLLK(V) C:Carbamidomethylation CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.3 2% 0.70% 67.3 1.02E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.01 3% 0.80% 61.6 1.69E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.9 3% 0.90% 66.9 4.75E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.85 3% 0.90% 75.4 3.46E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.7 3% 0.90% 79.2 1.11E+06 (K)EGLELLK(A) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.58 3% 1.00% 71.1 1.46E+06 (K)KIPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.55 3% 1.00% 70.4 3.76E+04 (K)YGQDATNVGDEGGFAPNIQENK(E) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.44 3% 1.00% 65.8 3.36E+05 (K)VNQIGSVTESIEAVR(M) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.43 3% 1.00% 72.9 3.73E+05 (R)GNPTVEVDIGLSDGSYAR(G) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.3 3% 1.00% 66.3 1.03E+05 (K)LTDEIGQQVQIVGDDLLVTNPTR(V) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
11.12 3% 1% 68.2 4.87E+05 (K)TCNALLLK(V) C:Carbamidomethylation CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
10.63 3% 1% 77.3 3.06E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
10.58 3% 1% 62.2 1.72E+04 (K)LAMQEFMILPTGASSFK(E) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
10.48 3% 1% 60.4 1.95E+05 (R)IEEELGDAAVYAGAK(F) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
10.39 3% 1% 66.1 1.70E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
10.37 3% 1% 75.5 2.88E+05 (K)SFVSEYPIVSIEDPFDQDDWTTYAK(L) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
10.07 5% 1% 65.6 2.20E+05 (K)KIPLYQHIANLAGNK(T) CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
10.04 5% 1% 69.3 2.19E+05 (K)LAmQEFmILPTGASSFK(E) m:Oxidized methionine CL70.c1 S.halepenseF2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays]
12.74 2% 0.60% 66.7 5.32E+04 (R)SGETEDNFIADLAVGLASGQIK(T) UG15352 S.halepenseF1 hypothet prot SORBIDRAFT_02g023480 [S bicolor] >gi|241925675|gb|EER98819.1| hypothet prot SORBIDRAFT_02g023480 [S bicolor]
10.42 3% 1% 71.5 8.02E+03 (K)TGAPCR(S) C:Carbamidomethylation UG15352 S.halepenseF1 hypothet prot SORBIDRAFT_02g023480 [S bicolor] >gi|241925675|gb|EER98819.1| hypothet prot SORBIDRAFT_02g023480 [S bicolor]
12.51 2% 0.60% 65.2 2.31E+05 (R)ILASGVHVVVGTPGR(V) CL1374.c1 S.halepenseF1 hypothet prot SORBIDRAFT_04g003390 [S bicolor] >gi|241931367|gb|EES04512.1| hypothet prot SORBIDRAFT_04g003390 [S bicolor]
11.44 3% 1.00% 66.7 9.93E+04 (K)ASVTSAEVSQDGR(F) UG1571 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g023300 [S bicolor] >gi|241916858|gb|EER90002.1| hypothet prot SORBIDRAFT_10g023300 [S bicolor]
11.25 3% 1% 73.2 1.59E+05 (K)TYPQQAGTIR(K) UG15677 S.halepenseF1Rev hypothet prot OsJ_24987 [Oryza sativa Japonica Group]
18.65 <0.1% <0.1% 81.8 3.03E+05 (R)LPTDETLVAQIK(E) UG3363 S.halepenseF2Rev eukaryotic translation initiation factor 5A [Zea mays] >gi|162464130|ref|NP_001105550.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|12643437|sp|P80639.2|IF5A_MAIZE RecName: Full=Eukaryotic translation initiation factor 5A; Short=eIF-5A; AltName: Full=eIF-4D >gi|1546919|emb|CAA69225.1| translation initiation factor 5A [Zea mays] >gi|2668738|gb|AAB88614.1| translation initiation factor 5A [Zea mays] >gi|195605740|gb|ACG24700.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618026|gb|ACG30843.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618512|gb|ACG31086.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195619390|gb|ACG31525.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195620274|gb|ACG31967.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195621206|gb|ACG32433.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|334361894|gb|AEG78305.1| eukaryotic translation initiation factor 5A [Zea mays]
18.33 <0.1% <0.1% 85.7 1.81E+05 (R)LPTDETLVAQIK(E) UG3363 S.halepenseF2Rev eukaryotic translation initiation factor 5A [Zea mays] >gi|162464130|ref|NP_001105550.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|12643437|sp|P80639.2|IF5A_MAIZE RecName: Full=Eukaryotic translation initiation factor 5A; Short=eIF-5A; AltName: Full=eIF-4D >gi|1546919|emb|CAA69225.1| translation initiation factor 5A [Zea mays] >gi|2668738|gb|AAB88614.1| translation initiation factor 5A [Zea mays] >gi|195605740|gb|ACG24700.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618026|gb|ACG30843.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618512|gb|ACG31086.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195619390|gb|ACG31525.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195620274|gb|ACG31967.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195621206|gb|ACG32433.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|334361894|gb|AEG78305.1| eukaryotic translation initiation factor 5A [Zea mays]
16.92 <0.1% <0.1% 87 2.28E+05 (K)TYPQQAGTVR(K) UG3363 S.halepenseF2Rev eukaryotic translation initiation factor 5A [Zea mays] >gi|162464130|ref|NP_001105550.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|12643437|sp|P80639.2|IF5A_MAIZE RecName: Full=Eukaryotic translation initiation factor 5A; Short=eIF-5A; AltName: Full=eIF-4D >gi|1546919|emb|CAA69225.1| translation initiation factor 5A [Zea mays] >gi|2668738|gb|AAB88614.1| translation initiation factor 5A [Zea mays] >gi|195605740|gb|ACG24700.1| eukaryotic translation initiation factor 5A [Zea mays]

>gi|195618026|gb|ACG30843.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618512|gb|ACG31086.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195619390|gb|ACG31525.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195620274|gb|ACG31967.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195621206|gb|ACG32433.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|334361894|gb|AEG78305.1| eukaryotic translation initiation factor 5A [Zea mays]
16.53 <0.1% <0.1% 83.2 2.46E+05 (K)TYPQQAGTVR(K) UG3363 S.halepenseF2Rev eukaryotic translation initiation factor 5A [Zea mays] >gi|162464130|ref|NP_001105550.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|12643437|sp|P80639.2|IF5A_MAIZE RecName: Full=Eukaryotic translation initiation factor 5A; Short=eIF-5A; AltName: Full=eIF-4D >gi|1546919|emb|CAA69225.1| translation initiation factor 5A [Zea mays] >gi|2668738|gb|AAB88614.1| translation initiation factor 5A [Zea mays] >gi|195605740|gb|ACG24700.1| eukaryotic translation initiation factor 5A [Zea mays]
>gi|195618026|gb|ACG30843.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618512|gb|ACG31086.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195619390|gb|ACG31525.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195620274|gb|ACG31967.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195621206|gb|ACG32433.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|334361894|gb|AEG78305.1| eukaryotic translation initiation factor 5A [Zea mays]
15.62 0.20% <0.1% 76.6 3.70E+05 (R)LPTDETLVAQIK(E) UG3363 S.halepenseF2Rev eukaryotic translation initiation factor 5A [Zea mays] >gi|162464130|ref|NP_001105550.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|12643437|sp|P80639.2|IF5A_MAIZE RecName: Full=Eukaryotic translation initiation factor 5A; Short=eIF-5A; AltName: Full=eIF-4D >gi|1546919|emb|CAA69225.1| translation initiation factor 5A [Zea mays] >gi|2668738|gb|AAB88614.1| translation initiation factor 5A [Zea mays] >gi|195605740|gb|ACG24700.1| eukaryotic translation initiation factor 5A [Zea mays]
>gi|195618026|gb|ACG30843.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618512|gb|ACG31086.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195619390|gb|ACG31525.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195620274|gb|ACG31967.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195621206|gb|ACG32433.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|334361894|gb|AEG78305.1| eukaryotic translation initiation factor 5A [Zea mays]
15.61 0.20% <0.1% 87.4 3.67E+05 (K)TYPQQAGTVR(K) UG3363 S.halepenseF2Rev eukaryotic translation initiation factor 5A [Zea mays] >gi|162464130|ref|NP_001105550.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|12643437|sp|P80639.2|IF5A_MAIZE RecName: Full=Eukaryotic translation initiation factor 5A; Short=eIF-5A; AltName: Full=eIF-4D >gi|1546919|emb|CAA69225.1| translation initiation factor 5A [Zea mays] >gi|2668738|gb|AAB88614.1| translation initiation factor 5A [Zea mays] >gi|195605740|gb|ACG24700.1| eukaryotic translation initiation factor 5A [Zea mays]
>gi|195618026|gb|ACG30843.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618512|gb|ACG31086.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195619390|gb|ACG31525.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195620274|gb|ACG31967.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195621206|gb|ACG32433.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|334361894|gb|AEG78305.1| eukaryotic translation initiation factor 5A [Zea mays]
11.05 3% 1% 72.5 2.93E+05 (K)TYPQQAGTVR(K) UG3363 S.halepenseF2Rev eukaryotic translation initiation factor 5A [Zea mays] >gi|162464130|ref|NP_001105550.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|12643437|sp|P80639.2|IF5A_MAIZE RecName: Full=Eukaryotic translation initiation factor 5A; Short=eIF-5A; AltName: Full=eIF-4D >gi|1546919|emb|CAA69225.1| translation initiation factor 5A [Zea mays] >gi|2668738|gb|AAB88614.1| translation initiation factor 5A [Zea mays] >gi|195605740|gb|ACG24700.1| eukaryotic translation initiation factor 5A [Zea mays]
>gi|195618026|gb|ACG30843.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195618512|gb|ACG31086.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195619390|gb|ACG31525.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195620274|gb|ACG31967.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|195621206|gb|ACG32433.1| eukaryotic translation initiation factor 5A [Zea mays] >gi|334361894|gb|AEG78305.1| eukaryotic translation initiation factor 5A [Zea mays]
13.59 2% 0.50% 68.9 8.38E+04 (K)LPSDEALQAQIK(S) UG6350 S.halepenseF2 uncharacterized protein LOC100192991 [Zea mays] >gi|195621288|gb|ACG32474.1| eukaryotic translation initiation factor 5A-1/2 [Zea mays]
22.97 <0.1% <0.1% 97 6.39E+05 (K)VLPTSVLFVNNQNTVVR(D) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
18.82 <0.1% <0.1% 88.2 2.25E+06 (K)GTAATQVAVLLR(C) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
18.6 <0.1% <0.1% 83.4 2.93E+06 (K)ISAPSNSPNTDGIHIER(S) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
18.48 <0.1% <0.1% 72.2 2.47E+04 (K)AACGSAGAVTmVVTPGTYYIGPVQFHGPCK(A) C:Carbamidomethylation m:Oxidized methionine CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
18.14 <0.1% <0.1% 71.3 9.18E+05 (K)YCPYYNCEHK(Y) C:Carbamidomethylation CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
17.95 <0.1% <0.1% 88.6 8.95E+05 (K)VLPTSVLFVNNQNTVVR(D) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
17.83 <0.1% <0.1% 86.9 5.21E+05 (R)ISTGDDCISIGQGNDNVQIAR(V) C:Carbamidomethylation CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
17.66 <0.1% <0.1% 73.9 8.56E+05 (R)ISTGDDCISIGQGNDNVQIAR(V) C:Carbamidomethylation CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
16.79 <0.1% <0.1% 76.9 3.74E+04 (K)ISAPSNSPNTDGIHIER(S) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
16.51 <0.1% <0.1% 77.9 3.24E+05 (K)VLPTSVLFVNNQNTVVR(D) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
16.12 <0.1% <0.1% 66.2 2.47E+04 (K)AACGSAGAVTmVVTPGTYYIGPVQFHGPCK(A) C:Carbamidomethylation m:Oxidized methionine CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
15.5 0.20% <0.1% 80.6 1.58E+05 (K)ISAPSNSPNTDGIHIER(S) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
15.34 0.20% <0.1% 81.6 4.14E+04 (R)CGVPCQGLVLQDVDLR(Y) C:Carbamidomethylation CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
14.39 2% <0.1% 76 4.69E+05 (K)FFHMALLTVK(N) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
14.25 2% <0.1% 79.3 1.11E+06 (K)DVQNPIIIDQK(Y) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
13.7 2% 0.50% 70.6 4.45E+04 (R)YASEGDVTR(V) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
13.45 2% 0.50% 85.2 2.39E+06 (R)DVTSVNPK(F) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
13.34 2% 0.50% 72.5 4.68E+05 (R)VQCGPGHGMSVGSLGR(Y) C:Carbamidomethylation CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
12.68 2% 0.60% 80 1.94E+06 (R)YASEGDVTR(V) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
12.63 2% 0.70% 82.5 2.57E+06 (R)SSGIQITDTR(I) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
12.6 2% 0.70% 67.6 7.05E+03 (R)YASEGDVTR(V) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
12.51 2% 0.60% 71.4 8.35E+04 (K)FFHMALLTVK(N) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
12.25 3% 0.70% 67.8 7.68E+03 (K)FFHMALLTVK(N) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]

11.52 3% 0.90% 66.8 1.96E+06 (K)FFHmALLTVK(N) m:Oxidized methionine CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor]
>gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
11.31 3% 1.00% 75.1 2.89E+05 (K)GTAATQVAVLLR(C) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot
SORBIDRAFT_07g016970 [S bicolor]
10.63 3% 1% 60.1 2.17E+05 (K)FFHmALLTVK(N) m:Oxidized methionine CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor]
>gi|241940587|gb|EES13732.1| hypothet prot SORBIDRAFT_07g016970 [S bicolor]
10.44 3% 1% 64.9 3.76E+05 (R)SSGIQITDTR(I) CL986.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_07g016970 [S bicolor] >gi|241940587|gb|EES13732.1| hypothet prot
SORBIDRAFT_07g016970 [S bicolor]
21.3 <0.1% <0.1% 87.4 1.27E+06 (K)IPCTGVTmDNVK(V) C:Carbamidomethylation m:Oxidized methionine CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor]
>gi|241916892|gb|EER90036.1| hypothet prot SORBIDRAFT_10g024000 [S bicolor]
20.02 <0.1% <0.1% 84.9 2.29E+06 (K)IPCTGVTmDNVK(V) C:Carbamidomethylation m:Oxidized methionine CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor]
>gi|241916892|gb|EER90036.1| hypothet prot SORBIDRAFT_10g024000 [S bicolor]
19 <0.1% <0.1% 79 2.49E+06 (K)IPCTGVTmDNVK(V) C:Carbamidomethylation m:Oxidized methionine CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor]
>gi|241916892|gb|EER90036.1| hypothet prot SORBIDRAFT_10g024000 [S bicolor]
18.44 <0.1% <0.1% 83.8 1.37E+06 (K)IPCTGVTmDNVK(V) C:Carbamidomethylation m:Oxidized methionine CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor]
>gi|241916892|gb|EER90036.1| hypothet prot SORBIDRAFT_10g024000 [S bicolor]
17.3 <0.1% <0.1% 62.8 3.23E+06 (K)IPCTGVTMDNVK(V) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
17.17 <0.1% <0.1% 75.2 9.16E+06 (K)TMAVCQNAK(G) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
17.01 <0.1% <0.1% 76 1.06E+07 (K)IPCTGVTmDNVK(V) C:Carbamidomethylation m:Oxidized methionine CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor]
>gi|241916892|gb|EER90036.1| hypothet prot SORBIDRAFT_10g024000 [S bicolor]
15.92 <0.1% <0.1% 66.9 5.63E+05 (K)TmAVCQNAK(G) C:Carbamidomethylation m:Oxidized methionine CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor]
>gi|241916892|gb|EER90036.1| hypothet prot SORBIDRAFT_10g024000 [S bicolor]
14.99 0.20% <0.1% 79 1.09E+06 (K)GSATGCLK(E) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
14.25 2% <0.1% 82 1.73E+06 (K)GSATGCLK(E) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
13.18 2% 0.50% 78.2 1.77E+05 (K)IPCTGVTMDNVK(V) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
12.14 3% 0.70% 74.7 2.91E+06 (K)TMAVCQNAK(G) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
11.57 3% 1.00% 68 5.50E+06 (K)TMAVCQNAK(G) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
11.36 3% 1.00% 67.9 7.90E+05 (K)TMAVCQNAK(G) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
11.18 3% 1% 71.7 2.73E+04 (K)IPCTGVTMDNVK(V) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
10.7 3% 1% 62.1 1.97E+05 (K)IPCTGVTMDNVK(V) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
10.65 3% 1% 73.5 3.57E+05 (K)TMAVCQNAK(G) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
10.61 3% 1% 61.5 3.50E+05 (K)TMAVCQNAK(G) C:Carbamidomethylation CL110.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g024000 [S bicolor] >gi|241916892|gb|EER90036.1|
hypothet prot SORBIDRAFT_10g024000 [S bicolor]
27 <0.1% <0.1% 100 1.17E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
26.42 <0.1% <0.1% 100 2.93E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1|
hypothet prot SORBIDRAFT_10g021590 [S bicolor]
25.5 <0.1% <0.1% 100 8.52E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
25.13 <0.1% <0.1% 98.1 2.01E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
24.42 <0.1% <0.1% 93.8 4.78E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1|
hypothet prot SORBIDRAFT_10g021590 [S bicolor]
22.9 <0.1% <0.1% 97.3 4.10E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1|
hypothet prot SORBIDRAFT_10g021590 [S bicolor]
22.66 <0.1% <0.1% 94.4 4.73E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1|
hypothet prot SORBIDRAFT_10g021590 [S bicolor]
22.58 <0.1% <0.1% 98.1 2.63E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
22.35 <0.1% <0.1% 92 2.51E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1|
hypothet prot SORBIDRAFT_10g021590 [S bicolor]
22.25 <0.1% <0.1% 90.2 2.62E+04 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1|
hypothet prot SORBIDRAFT_10g021590 [S bicolor]
22.18 <0.1% <0.1% 94.8 1.18E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
22.15 <0.1% <0.1% 89.9 1.14E+07 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1|
hypothet prot SORBIDRAFT_10g021590 [S bicolor]
22.04 <0.1% <0.1% 84.4 4.31E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.87 <0.1% <0.1% 94.7 7.89E+06 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.67 <0.1% <0.1% 98 1.39E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.64 <0.1% <0.1% 97.7 1.23E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor]
>gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]

21.5 <0.1% <0.1% 79.6 3.43E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.45 <0.1% <0.1% 100 4.21E+06 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.43 <0.1% <0.1% 89.1 1.05E+06 (K)LHYENIAmDDVANPIIIDMK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.37 <0.1% <0.1% 95.3 1.66E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.29 <0.1% <0.1% 94.7 4.30E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.2 <0.1% <0.1% 100 7.18E+06 (K)LHYENIAmDDVANPIIIDMK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.15 <0.1% <0.1% 93 2.54E+06 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.14 <0.1% <0.1% 95 1.24E+07 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
21.02 <0.1% <0.1% 93.8 4.65E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.99 <0.1% <0.1% 93.5 1.41E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.98 <0.1% <0.1% 97.5 9.03E+05 (K)LHYENIAmDDVANPIIIDMK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.93 <0.1% <0.1% 86.7 8.04E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.92 <0.1% <0.1% 97.8 1.75E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.82 <0.1% <0.1% 91.3 1.41E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.78 <0.1% <0.1% 86.7 3.10E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.78 <0.1% <0.1% 100 2.96E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.73 <0.1% <0.1% 93.1 1.08E+07 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.73 <0.1% <0.1% 93.6 9.93E+06 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.73 <0.1% <0.1% 93.5 4.08E+07 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.71 <0.1% <0.1% 83.2 8.84E+06 (K)IPCSGVTmDNIK(V) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.71 <0.1% <0.1% 97.6 1.43E+07 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.62 <0.1% <0.1% 93.2 1.47E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.6 <0.1% <0.1% 91 3.99E+06 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.57 <0.1% <0.1% 91.6 8.94E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.55 <0.1% <0.1% 92.1 2.35E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.55 <0.1% <0.1% 91.2 1.02E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.44 <0.1% <0.1% 82.9 2.10E+06 (K)IPCSGVTmDNIK(V) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.44 <0.1% <0.1% 76 4.67E+06 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.35 <0.1% <0.1% 93.8 1.66E+06 (K)LHYENIAmDDVANPIIIDMK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.23 <0.1% <0.1% 91 4.41E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.23 <0.1% <0.1% 91.2 1.60E+06 (K)LHYENIAMDDVANPIIIDMK(Y) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.15 <0.1% <0.1% 92.8 1.00E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.14 <0.1% <0.1% 91.6 2.04E+07 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20.04 <0.1% <0.1% 89.2 1.02E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
20 <0.1% <0.1% 83.7 1.57E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.98 <0.1% <0.1% 88.9 4.32E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.96 <0.1% <0.1% 93.1 8.08E+05 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.94 <0.1% <0.1% 85.5 3.73E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]

19.94 <0.1% <0.1% 89.9 2.85E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.75 <0.1% <0.1% 81.5 3.00E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.67 <0.1% <0.1% 91.8 4.98E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.65 <0.1% <0.1% 84.4 1.03E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.64 <0.1% <0.1% 82.5 3.43E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.63 <0.1% <0.1% 85.5 9.18E+05 (K)SYEDAACVITASK(L) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.61 <0.1% <0.1% 91.2 7.21E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.46 <0.1% <0.1% 90.7 1.05E+06 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.45 <0.1% <0.1% 88.8 2.89E+05 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.44 <0.1% <0.1% 93.1 3.85E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.43 <0.1% <0.1% 83.5 3.16E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.21 <0.1% <0.1% 91.3 1.44E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.15 <0.1% <0.1% 85 4.11E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.13 <0.1% <0.1% 92.7 8.29E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
19.04 <0.1% <0.1% 88.5 1.22E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.96 <0.1% <0.1% 90.7 2.99E+06 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.93 <0.1% <0.1% 95.2 2.21E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.89 <0.1% <0.1% 86.7 3.43E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.85 <0.1% <0.1% 86.2 5.10E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.79 <0.1% <0.1% 91.4 2.87E+06 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.69 <0.1% <0.1% 87.8 1.12E+06 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.56 <0.1% <0.1% 85.8 2.75E+06 (R)YKDEKDVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.43 <0.1% <0.1% 79.9 1.12E+06 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.4 <0.1% <0.1% 84.9 4.04E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.38 <0.1% <0.1% 82.5 7.71E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.33 <0.1% <0.1% 76 1.09E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.32 <0.1% <0.1% 87.7 2.46E+06 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.31 <0.1% <0.1% 76 8.39E+03 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.24 <0.1% <0.1% 93.4 1.69E+06 (K)LHYENIAmDDVANPIIIDMK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.22 <0.1% <0.1% 88.4 4.71E+05 (K)LHYENIAMDDVANPIIIDMK(Y) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.21 <0.1% <0.1% 65.3 5.25E+05 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.16 <0.1% <0.1% 94.1 1.68E+06 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.13 <0.1% <0.1% 81.5 3.10E+05 (K)SYEDAACVITASK(L) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.13 <0.1% <0.1% 85.6 1.01E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.08 <0.1% <0.1% 63.2 8.72E+06 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.05 <0.1% <0.1% 90.4 7.19E+05 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.03 <0.1% <0.1% 87.3 1.18E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
18.01 <0.1% <0.1% 84.2 5.00E+05 (K)LHYENIAMDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]

17.98 <0.1% <0.1% 82.7 4.37E+06 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.94 <0.1% <0.1% 84.5 2.76E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.91 <0.1% <0.1% 81.5 1.87E+04 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.91 <0.1% <0.1% 81.1 1.68E+06 (K)FFHMNVFQCK(G) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.86 <0.1% <0.1% 87.3 3.90E+06 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.77 <0.1% <0.1% 74.8 7.45E+04 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.74 <0.1% <0.1% 86.7 5.67E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.71 <0.1% <0.1% 90.4 1.62E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.64 <0.1% <0.1% 84.5 1.03E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.59 <0.1% <0.1% 85 9.86E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.55 <0.1% <0.1% 84.9 6.35E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.53 <0.1% <0.1% 80.2 7.10E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.5 <0.1% <0.1% 86.9 9.63E+05 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.48 <0.1% <0.1% 82.7 8.52E+05 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.46 <0.1% <0.1% 80.9 1.20E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.43 <0.1% <0.1% 71.3 1.18E+06 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.32 <0.1% <0.1% 80.8 1.82E+06 (K)IPCSGVTmDNIK(V) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.27 <0.1% <0.1% 85 5.51E+05 (K)LHYENIAmDDVANPIIIDMK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.26 <0.1% <0.1% 85.6 3.92E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.19 <0.1% <0.1% 87.1 6.84E+06 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.14 <0.1% <0.1% 78 1.86E+05 (R)YKDEKDVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.14 <0.1% <0.1% 82.9 9.16E+05 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.03 <0.1% <0.1% 71.7 5.74E+05 (K)SYEDAACVITASK(L) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.01 <0.1% <0.1% 71.2 2.72E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17.01 <0.1% <0.1% 80.7 4.18E+06 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
17 <0.1% <0.1% 86.5 1.46E+07 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.91 <0.1% <0.1% 76.4 2.41E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.78 <0.1% <0.1% 82.1 4.14E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.66 <0.1% <0.1% 67.2 3.08E+06 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.54 <0.1% <0.1% 74.9 7.84E+05 (K)IPCSGVTmDNIK(V) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.51 <0.1% <0.1% 87 2.52E+06 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.49 <0.1% <0.1% 75.7 1.83E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.48 <0.1% <0.1% 82.1 3.20E+04 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.39 <0.1% <0.1% 82 3.85E+06 (K)EGPQTLmIPK(G) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.37 <0.1% <0.1% 73.1 5.30E+05 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.34 <0.1% <0.1% 86.6 2.90E+05 (K)GSVTIQLDGNLLGTTDLSAYK(T) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.29 <0.1% <0.1% 77.2 1.01E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.25 <0.1% <0.1% 85.6 2.13E+06 (R)YKDEKDVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]

16.16 <0.1% <0.1% 71.7 2.81E+05 (K)FFHMNVFQCK(G) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.15 <0.1% <0.1% 86.5 1.90E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.12 <0.1% <0.1% 72.6 7.93E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.1 <0.1% <0.1% 85.2 7.17E+05 (K)IPCSGVTMDNIK(V) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.08 <0.1% <0.1% 71.9 1.33E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
16.06 <0.1% <0.1% 75.8 8.51E+05 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.96 <0.1% <0.1% 90.5 4.10E+06 (K)DVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.95 <0.1% <0.1% 89.8 1.54E+07 (K)DVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.91 0.20% <0.1% 85.7 1.78E+06 (K)IPCSGVTMDNIK(V) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.91 0.20% <0.1% 88.9 1.62E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.88 0.20% <0.1% 84.7 1.15E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.86 0.20% <0.1% 84.9 2.86E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.84 0.20% <0.1% 80 1.07E+07 (K)EGPQTLmIPK(G) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.78 0.20% <0.1% 75.8 1.33E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.68 0.20% <0.1% 89.3 1.48E+07 (K)DVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.63 0.20% <0.1% 72.9 4.12E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.61 0.20% <0.1% 81.1 4.86E+06 (K)LHYENIAMDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.6 0.20% <0.1% 82.9 9.48E+04 (K)LHYENIAMDDVANPIIIDMK(Y) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.59 0.20% <0.1% 75.1 7.67E+06 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.57 0.20% <0.1% 80.9 8.65E+05 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.57 0.20% <0.1% 81.9 8.02E+05 (R)YKDEKDVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.35 0.20% <0.1% 87 2.74E+06 (K)DVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.33 0.20% <0.1% 73.7 1.40E+07 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.32 0.20% <0.1% 74.1 5.04E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.32 0.20% <0.1% 66.8 7.35E+05 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.24 0.20% <0.1% 75.9 6.15E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.23 0.20% <0.1% 67.6 4.50E+05 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.22 0.20% <0.1% 76 4.30E+05 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.1 0.20% <0.1% 60.2 6.33E+05 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
15.03 0.20% <0.1% 66.8 1.04E+07 (K)FFHMNVFQCK(G) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.93 0.20% <0.1% 82.8 1.64E+06 (K)IPCSGVTMDNIK(V) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.93 0.20% <0.1% 72.3 2.79E+05 (R)YKDEKDVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.92 0.20% <0.1% 81.3 5.15E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.92 0.20% <0.1% 74.6 1.45E+06 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.88 0.20% <0.1% 87.8 3.52E+06 (K)DVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.82 0.20% <0.1% 77.6 1.46E+07 (K)EGPQTLmIPK(G) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.81 0.20% <0.1% 82.2 4.71E+05 (K)LHYENIAMDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.69 0.20% <0.1% 79.5 6.39E+06 (K)EGPQTLMIPK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]

14.53 2% <0.1% 79.7 2.71E+05 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.53 2% <0.1% 71.9 2.72E+05 (K)GSVTIQLDGNLLGTTDLSAYK(T) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.5 2% <0.1% 71.6 5.68E+05 (R)YKDEKDVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.5 2% <0.1% 62 3.54E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.44 2% <0.1% 73.7 2.32E+06 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.41 2% <0.1% 60.3 2.02E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.39 2% <0.1% 72.1 5.07E+05 (R)YKDEKDVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.39 2% <0.1% 75.7 3.13E+05 (K)DVTVTAPGDSPNTDGIHIGDSSK(V) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.38 2% <0.1% 73.7 7.68E+04 (K)EGPQTLmIPK(G) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.33 2% <0.1% 73.1 2.13E+05 (K)EGPQTLMIPK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.31 2% <0.1% 74.4 1.61E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.21 2% <0.1% 76.9 2.82E+05 (K)LHYENIAMDDVANPIIIDMK(Y) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.15 2% 0.20% 82.3 2.14E+06 (K)DVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.13 2% 0.30% 72.9 1.53E+06 (K)EGPQTLMIPK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14.07 2% 0.30% 72.6 3.36E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
14 2% 0.30% 84.3 1.83E+06 (K)DVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.88 2% 0.40% 74.9 1.19E+06 (K)ALNEAWAAACGK(E) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.83 2% 0.50% 74.2 1.62E+05 (K)LHYENIAMDDVANPIIIDMK(Y) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.81 2% 0.50% 68.5 9.87E+06 (K)FFHMNVFQCK(G) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.69 2% 0.50% 66.6 6.91E+06 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.61 2% 0.50% 61.6 4.30E+05 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.55 2% 0.50% 65.1 2.08E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.54 2% 0.50% 75 1.30E+05 (K)GSVTIQLDGNLLGTTDLSAYK(T) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.51 2% 0.50% 68.2 1.34E+05 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.48 2% 0.50% 74 3.36E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.43 2% 0.50% 73 5.06E+06 (K)EGPQTLmIPK(G) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.41 2% 0.50% 69.4 2.82E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.41 2% 0.50% 70.1 1.20E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.3 2% 0.50% 75.6 2.59E+05 (K)GSVTIQLDGNLLGTTDLSAYK(T) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.02 2% 0.60% 60.6 1.12E+06 (K)FFHMNVFQCK(G) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
13.01 2% 0.60% 65.1 5.87E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.97 2% 0.60% 64 5.63E+05 (R)YKDEKDVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.96 2% 0.60% 72.7 1.07E+05 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.95 2% 0.60% 75.8 1.05E+06 (K)LHYENIAmDDVANPIIIDMK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.94 2% 0.60% 67.8 2.90E+05 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.93 2% 0.60% 64.5 1.11E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.92 2% 0.60% 66.7 1.03E+05 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.91 2% 0.60% 66.3 8.62E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]

12.85 2% 0.60% 72.7 6.34E+06 (K)EGPQTLmIPK(G) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.85 2% 0.60% 64.4 3.00E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.72 2% 0.60% 81.2 1.74E+06 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.69 2% 0.60% 83.9 1.09E+05 (K)SGGAPAEAPSGSAGGSDISK(L) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.66 2% 0.60% 62.3 3.36E+06 (K)QVWDNNK(C) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.6 2% 0.70% 68.1 2.37E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.48 2% 0.60% 76.3 8.82E+06 (K)LHYENIAMDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.46 2% 0.60% 64.1 3.09E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.44 2% 0.60% 75.4 1.47E+04 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.27 2% 0.70% 77.5 6.57E+06 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.26 2% 0.70% 62.6 2.37E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.23 3% 0.70% 68.9 7.10E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.18 3% 0.70% 69.8 2.99E+05 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.12 3% 0.80% 62.3 3.78E+04 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.06 3% 0.80% 82.1 5.11E+05 (K)GTLDGQGK(Q) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.05 3% 0.80% 74.5 1.04E+06 (K)LHYENIAMDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
12.04 3% 0.80% 73.3 9.10E+05 (K)DVTDINVK(D) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.87 3% 0.90% 70.3 2.04E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.68 3% 0.90% 67.1 2.85E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.59 3% 1.00% 87.3 1.13E+07 (K)DVTFK(N) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.59 3% 1.00% 63.8 3.53E+06 (K)FFHMNVFQCK(G) C:Carbamidomethylation CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.56 3% 1.00% 63.8 2.82E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.55 3% 1.00% 86.5 6.28E+06 (K)DVTFK(N) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.54 3% 0.90% 64.6 5.15E+06 (K)EGPQTLmIPK(G) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.43 3% 1.00% 62.9 3.35E+06 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.41 3% 1.00% 72.3 3.07E+05 (K)LHYENIAmDDVANPIIIDmK(Y) m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.39 3% 1.00% 62.6 6.30E+06 (K)QVWDNNK(C) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.37 3% 1.00% 63 4.17E+06 (K)EGPQTLMIPK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.34 3% 1.00% 65.5 6.95E+05 (K)QVWDNNK(C) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.28 3% 1% 68.4 2.85E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.24 3% 1% 73.3 3.01E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.21 3% 1% 62.5 6.89E+03 (K)LHYENIAMDDVANPIIIDMK(Y) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.15 3% 1% 68.7 1.16E+06 (K)FFHmNVFQCK(G) C:Carbamidomethylation m:Oxidized methionine CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.09 3% 1% 87 2.40E+07 (K)DVTFK(N) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.07 3% 1% 63.1 2.51E+05 (K)TNWIEIEHVDNLVISGK(G) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.05 3% 1% 85.9 3.37E+06 (K)DVTFK(N) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.05 3% 1% 85.9 4.05E+06 (K)DVTFK(N) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
11.04 3% 1% 63 4.22E+03 (K)ILPNSLVLDYVNNGEVSGITLLNAK(F) CL1737.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]

10.99	3%	1%	63.9	2.81E+03	(K)ILPNSLVLDYVNNGEVSGITLLNAK(F)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.91	3%	1%	73.7	3.93E+05	(K)GSVTIQLDGNLLGTTDLSAYK(T)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.9	3%	1%	76.9	1.45E+06	(K)DVTVTAPGDSPNTDGIHIGDSSK(V)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.88	3%	1%	62.1	3.39E+06	(K)LHYENIAmDDVANPIIIDmK(Y)	m:Oxidized methionine	CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.88	3%	1%	68.6	3.27E+05	(K)TNWIEIEHVDNLVISGK(G)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.86	3%	1%	66.3	5.40E+05	(K)DVTDINVK(D)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.85	3%	1%	65.5	3.12E+03	(K)ILPNSLVLDYVNNGEVSGITLLNAK(F)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.8	3%	1%	64.4	1.88E+05	(K)TNWIEIEHVDNLVISGK(G)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.8	3%	1%	67.9	2.62E+07	(R)YKDEKDVTDINVK(D)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.77	3%	1%	74.2	2.22E+05	(K)FFHMNVFQCK(G)	C:Carbamidomethylation	CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.76	3%	1%	72	7.39E+04	(K)GTLDGQGK(Q)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.62	3%	1%	64	1.60E+05	(K)TNWIEIEHVDNLVISGK(G)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.57	3%	1%	63.4	3.62E+06	(K)FFHmNVFQCK(G)	C:Carbamidomethylation m:Oxidized methionine	CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.51	3%	1%	75.6	1.63E+06	(K)DVTDINVK(D)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.45	3%	1%	61.4	8.51E+03	(K)ILPNSLVLDYVNNGEVSGITLLNAK(F)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.33	3%	1%	61.3	5.24E+05	(K)QVWDNNK(C)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.32	3%	1%	72.2	5.06E+05	(K)LHYENIAmDDVANPIIIDmK(Y)	m:Oxidized methionine	CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.3	3%	1%	62.2	6.45E+05	(K)EGPQTLMIPK(G)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.23	3%	1%	62.9	3.35E+03	(K)ILPNSLVLDYVNNGEVSGITLLNAK(F)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
10.13	3%	1%	61.3	6.36E+04	(K)TNWIEIEHVDNLVISGK(G)		CL1737.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021590 [S bicolor] >gi|241916751|gb|EER89895.1| hypothet prot SORBIDRAFT_10g021590 [S bicolor]
26.33	<0.1%	<0.1%	98.1	1.71E+07	(K)AASGPGGSFDISK(L)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
26.15	<0.1%	<0.1%	100	1.08E+07	(K)AASGPGGSFDISK(L)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
23.47	<0.1%	<0.1%	95.3	3.43E+07	(K)AASGPGGSFDISK(L)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
23.15	<0.1%	<0.1%	95.9	8.95E+06	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
22.37	<0.1%	<0.1%	91.6	7.67E+06	(K)AASGPGGSFDISK(L)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
21.85	<0.1%	<0.1%	93.3	1.19E+06	(K)AASGPGGSFDISK(L)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
21.71	<0.1%	<0.1%	96.5	1.36E+07	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
21.58	<0.1%	<0.1%	93	4.34E+06	(K)AASGPGGSFDISK(L)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
21.42	<0.1%	<0.1%	94.7	8.79E+06	(K)AASGPGGSFDISK(L)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
21.19	<0.1%	<0.1%	95	1.72E+05	(K)GDVTIQVDGNLLATTDLSQYK(G)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
21.04	<0.1%	<0.1%	89.9	5.49E+06	(K)GKLDGQGPAVWSK(N)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
20.81	<0.1%	<0.1%	88.4	2.60E+05	(K)AASGPGGSFDISK(L)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
20.57	<0.1%	<0.1%	92	1.82E+06	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
20.47	<0.1%	<0.1%	93.8	2.11E+06	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
19.82	<0.1%	<0.1%	89.7	1.11E+06	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
19.72	<0.1%	<0.1%	94.1	2.98E+06	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
19.36	<0.1%	<0.1%	72.6	1.66E+07	(K)GKLDGQGPAVWSK(N)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
19.13	<0.1%	<0.1%	88.8	2.05E+06	(K)GKLDGQGPAVWSK(N)		CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]

19.1	<0.1%	<0.1%	83	5.41E+06	(K)AASGPGGSFDISK(L)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
19.08	<0.1%	<0.1%	87.2	3.14E+05	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
18.64	<0.1%	<0.1%	91.1	9.88E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
18.31	<0.1%	<0.1%	91.6	8.40E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
18.3	<0.1%	<0.1%	90.9	3.63E+07	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
17.72	<0.1%	<0.1%	85.7	2.00E+05	(K)AASGPGGSFDISK(L)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
17.68	<0.1%	<0.1%	93.1	8.31E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
17.62	<0.1%	<0.1%	82.8	1.60E+06	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
17.22	<0.1%	<0.1%	91.2	1.09E+07	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
17.08	<0.1%	<0.1%	79.2	2.16E+05	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
17.05	<0.1%	<0.1%	81.6	1.04E+06	(K)AASGPGGSFDISK(L)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
16.6	<0.1%	<0.1%	84.2	6.29E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
16.3	<0.1%	<0.1%	88.9	2.37E+07	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
16.19	<0.1%	<0.1%	86.9	1.03E+07	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
16.13	<0.1%	<0.1%	87.1	7.71E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
16.09	<0.1%	<0.1%	77.6	1.46E+06	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
15.96	<0.1%	<0.1%	82.7	1.20E+07	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
15.91	0.20%	<0.1%	82.5	2.70E+06	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
15.64	0.20%	<0.1%	60.6	2.00E+06	(K)GKLDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
15.64	0.20%	<0.1%	81.8	3.78E+05	(K)AVQEAWTSACGGTGK(Q)	C:Carbamidomethylation	CL1737.c2 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
15.47	0.20%	<0.1%	80.4	8.06E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
15.35	0.20%	<0.1%	81.2	3.48E+05	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
15.26	0.20%	<0.1%	64.8	1.33E+06	(K)GKLDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
15.02	0.20%	<0.1%	76.2	2.89E+06	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
14.74	0.20%	<0.1%	69.9	1.53E+05	(K)AASGPGGSFDISK(L)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
14.63	2%	<0.1%	76.6	3.90E+05	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
14.5	2%	<0.1%	75.1	5.44E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
14.34	2%	<0.1%	74.8	9.50E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
14.33	2%	<0.1%	77.2	1.21E+06	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
14.25	2%	<0.1%	79	4.15E+05	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.92	2%	0.40%	64.3	8.22E+05	(K)GKLDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.91	2%	0.40%	77.8	5.38E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.89	2%	0.40%	66.8	6.42E+05	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.88	2%	0.40%	67.6	2.00E+05	(K)AASGPGGSFDISK(L)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.84	2%	0.40%	80.6	4.38E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.55	2%	0.50%	77.7	1.32E+07	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.43	2%	0.50%	75.5	8.20E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.42	2%	0.50%	74.2	1.30E+06	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]

13.36	2%	0.50%	73.7	4.32E+06	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.29	2%	0.50%	72.5	1.33E+06	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.12	2%	0.60%	73.6	4.96E+06	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
13.04	2%	0.60%	68.8	3.94E+05	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.97	2%	0.60%	74.3	1.42E+06	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.85	2%	0.60%	78.3	1.47E+07	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.8	2%	0.60%	66.1	7.30E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.79	2%	0.60%	75.5	7.37E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.67	2%	0.60%	71	1.62E+06	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.66	2%	0.60%	75.3	5.78E+06	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.59	2%	0.70%	74.2	5.30E+06	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.53	2%	0.60%	73.7	1.73E+05	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.53	2%	0.60%	67.3	9.66E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.47	2%	0.60%	72.1	4.34E+06	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.41	2%	0.60%	75	2.97E+06	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.28	2%	0.70%	70.1	5.27E+05	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.27	2%	0.70%	75.8	8.56E+05	(K)GKLDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
12.14	3%	0.70%	70.2	2.78E+06	(K)GNWIEILR(V)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.8	3%	0.90%	62.7	3.16E+05	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.68	3%	0.90%	66.1	6.42E+05	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.63	3%	0.90%	64.9	7.29E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.52	3%	0.90%	73.2	4.75E+05	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.4	3%	1.00%	70.5	9.45E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.37	3%	1.00%	62.4	8.80E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.33	3%	1.00%	73.4	8.58E+03	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.25	3%	1%	72.2	1.59E+05	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.15	3%	1%	66.7	8.56E+05	(K)GKLDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
11.03	3%	1%	74.7	1.94E+06	(K)QTILIPK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.95	3%	1%	77	3.81E+06	(K)QTILIPK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.82	3%	1%	79.5	1.82E+07	(K)QTILIPK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.67	3%	1%	73.8	8.76E+04	(K)LGASGDGK(K)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.64	3%	1%	61.2	8.00E+05	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.63	3%	1%	68.5	1.51E+06	(K)LDGQGPAVWSK(N)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.53	3%	1%	73	2.53E+06	(K)QTILIPK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.52	3%	1%	79.3	1.23E+06	(K)QTILIPK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.46	3%	1%	66	7.81E+04	(K)GDVTIQVDGNLLATTDLSQYK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.4	3%	1%	60.1	6.84E+06	(R)VDNLVITGK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
10.07	5%	1%	73.8	2.68E+06	(K)QTILIPK(G)	CL1737.c2 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]

10.06	5%	1%	74	1.30E+07	(K)QTILIPK(G)	CL1737.c2	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g024010 [S bicolor] >gi|241915498|gb|EER88642.1| hypothet prot SORBIDRAFT_10g024010 [S bicolor]
22.57	<0.1%	<0.1%	97.8	1.46E+06	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
21.81	<0.1%	<0.1%	97.6	2.14E+06	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
21.66	<0.1%	<0.1%	95.2	3.24E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
21.26	<0.1%	<0.1%	97.9	4.20E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
20.72	<0.1%	<0.1%	92	8.11E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
20.15	<0.1%	<0.1%	94.7	1.34E+06	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
20.11	<0.1%	<0.1%	93.7	2.75E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
19.81	<0.1%	<0.1%	95.5	6.05E+05	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
19.71	<0.1%	<0.1%	95.8	7.59E+06	(K)VAVTDVVFK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
19.53	<0.1%	<0.1%	97.2	5.04E+05	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
19.49	<0.1%	<0.1%	92.9	6.64E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
19.33	<0.1%	<0.1%	94	7.11E+05	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
19.02	<0.1%	<0.1%	92.1	2.20E+06	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.79	<0.1%	<0.1%	93.8	3.74E+05	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.69	<0.1%	<0.1%	94	2.53E+06	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.66	<0.1%	<0.1%	89.7	1.13E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.61	<0.1%	<0.1%	84.5	4.62E+06	(K)VAVTDVVFK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.54	<0.1%	<0.1%	94.5	3.40E+06	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.53	<0.1%	<0.1%	84.9	5.85E+05	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.51	<0.1%	<0.1%	86	9.02E+05	(K)FFHLNIFASK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.5	<0.1%	<0.1%	90	1.73E+06	(K)VAVTDVVFK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.38	<0.1%	<0.1%	81.3	9.48E+04	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.34	<0.1%	<0.1%	78.9	2.14E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.11	<0.1%	<0.1%	87.9	8.91E+04	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
18.06	<0.1%	<0.1%	85.8	2.61E+06	(R)LDGNLLGTGDLNAYK(R)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.99	<0.1%	<0.1%	87.3	6.82E+05	(K)VAVTDVVFK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.93	<0.1%	<0.1%	93.3	3.16E+05	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.65	<0.1%	<0.1%	62.5	3.90E+06	(K)YCPNNICVR(S)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.54	<0.1%	<0.1%	77	9.65E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.5	<0.1%	<0.1%	80.9	8.81E+04	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.5	<0.1%	<0.1%	90.1	6.95E+05	(K)IVIPPGNYLTGGLELK(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.39	<0.1%	<0.1%	87.2	1.16E+06	(K)VAVTDVVFK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.34	<0.1%	<0.1%	85.3	1.64E+06	(R)LDGNLLGTGDLNAYK(R)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.32	<0.1%	<0.1%	80.3	4.23E+05	(K)VLPNSLVLDFVTNAQIR(G)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.24	<0.1%	<0.1%	67.7	5.53E+04	(K)YCPNNICVR(S)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.18	<0.1%	<0.1%	88.5	8.20E+05	(K)VAVTDVVFK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
17.07	<0.1%	<0.1%	84.8	2.71E+05	(K)FFHLNIFASK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]

17.02	<0.1%	<0.1%	61	1.28E+06	(K)YCPNNICVR(S)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
17.01	<0.1%	<0.1%	87.2	1.66E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.99	<0.1%	<0.1%	92.4	9.45E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.73	<0.1%	<0.1%	88.7	6.75E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.64	<0.1%	<0.1%	75.3	2.74E+05	(R)LDGNLLGTGDLNAYKR(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.49	<0.1%	<0.1%	92.7	1.70E+06	(K)NIHGTSNTPEAITLNCADNLPCQGVQLHNVDIK(Y)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.46	<0.1%	<0.1%	90.9	4.91E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.45	<0.1%	<0.1%	87.4	3.43E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.45	<0.1%	<0.1%	87.3	1.56E+05	(K)VLPNSLVLDFVTNAQIR(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.38	<0.1%	<0.1%	77.6	1.16E+06	(R)LDGNLLGTGDLNAYK(R)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.09	<0.1%	<0.1%	86.9	1.63E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
16.03	<0.1%	<0.1%	69.1	5.68E+04	(K)NACDATGVQK(I)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.97	<0.1%	<0.1%	69.7	2.79E+05	(K)YCPNNICVR(S)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.93	<0.1%	<0.1%	84.5	5.41E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.92	0.20%	<0.1%	77.1	2.47E+05	(K)VLPNSLVLDFVTNAQIR(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.91	0.20%	<0.1%	73.5	1.71E+05	(R)LDGNLLGTGDLNAYK(R)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.76	0.20%	<0.1%	72.8	4.51E+05	(K)YCPNNICVR(S)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.76	0.20%	<0.1%	79.4	3.03E+04	(K)NIHGTSNTPEAITLNCADNLPCQGVQLHNVDIK(Y)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.68	0.20%	<0.1%	90.5	1.11E+06	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.68	0.20%	<0.1%	89.5	1.55E+05	(K)VLPNSLVLDFVTNAQIR(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.44	0.20%	<0.1%	89.4	3.23E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.41	0.20%	<0.1%	84.3	1.20E+06	(K)FFHLNIFASK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.34	0.20%	<0.1%	80.5	6.97E+05	(K)VAVTDVVFK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.29	0.20%	<0.1%	80.1	3.54E+05	(R)YKDEKDVEDVK(V)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.23	0.20%	<0.1%	89.9	8.94E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.2	0.20%	<0.1%	81.5	4.36E+06	(K)FFHLNIFASK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.05	0.20%	<0.1%	80.4	1.25E+06	(K)FFHLNIFASK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
15.05	0.20%	<0.1%	83.8	2.90E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
14.89	0.20%	<0.1%	81.8	1.05E+06	(K)VAVTDVVFK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
14.7	0.20%	<0.1%	87.7	8.89E+05	(K)SFGLSK(E)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
14.41	2%	<0.1%	81.5	2.54E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
14.35	2%	<0.1%	89.6	5.93E+06	(R)GITLANSK(F)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
14.1	2%	0.30%	89.9	6.07E+06	(R)GITLANSK(F)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
14	2%	0.30%	78	1.34E+06	(K)FFHLNIFASK(N)	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
13.93	2%	0.40%	70.5	9.27E+05	(R)LDGNLLGTGDLNAYKR(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
13.88	2%	0.40%	77.5	1.09E+06	(R)LDGNLLGTGDLNAYK(R)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
13.69	2%	0.50%	74.7	1.64E+06	(K)CGPGHGISVGSLGR(Y)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	
13.63	2%	0.50%	66.4	2.44E+05	(K)NACDATGVQK(I)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]	

13.58	2%	0.50%	74.4	6.68E+04	(K)FFHLNIFASK(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
13.4	2%	0.50%	83.7	5.83E+05	(K)SFGLSK(E)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
13.4	2%	0.50%	75.9	6.99E+05	(K)FFHLNIFASK(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
13.32	2%	0.50%	82.5	3.96E+05	(K)SFGLSK(E)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
13.22	2%	0.50%	85.6	8.70E+04	(K)NIHGTSNTPEAITLNCADNLPCQGVQLHNVDIK(Y)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
13.09	2%	0.60%	77.9	6.13E+05	(K)FFHLNIFASK(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
13.07	2%	0.60%	83.1	5.54E+05	(R)GITLANSK(F)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
13.01	2%	0.60%	68.9	3.52E+05	(R)LDGNLLGTGDLNAYKR(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.99	2%	0.60%	78.4	9.69E+05	(K)SFGLSK(E)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.94	2%	0.60%	82.3	6.84E+05	(R)GITLANSK(F)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.83	2%	0.60%	67	9.37E+05	(K)SDSTPmILK(A)	m:Oxidized methionine	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.74	2%	0.60%	81.9	2.22E+06	(R)GITLANSK(F)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.55	2%	0.60%	87.5	5.76E+06	(K)SFGLSK(E)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.5	2%	0.60%	77.3	7.32E+05	(K)FFHLNIFASK(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.35	2%	0.70%	63.9	3.79E+05	(K)VAVTDVVFK(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.28	2%	0.70%	70.8	4.62E+05	(K)TMAVCK(N)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.28	2%	0.70%	87.5	7.67E+06	(K)SSIIIR(L)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.27	2%	0.70%	71.5	7.96E+05	(R)LDGNLLGTGDLNAYK(R)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.19	3%	0.70%	71.2	5.98E+05	(R)LDGNLLGTGDLNAYK(R)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.18	3%	0.70%	74.3	5.84E+05	(R)GITLANSK(F)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.07	3%	0.80%	75.5	9.08E+05	(R)GITLANSK(F)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
12.02	3%	0.80%	72.8	3.13E+06	(K)FFHLNIFASK(N)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.74	3%	0.90%	85.4	6.12E+04	(K)NIHGTSNTPEAITLNCADNLPCQGVQLHNVDIK(Y)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.6	3%	0.90%	81.7	8.76E+05	(K)SSIIIR(L)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.44	3%	1.00%	64.8	1.20E+05	(K)VLPNSLVLDFVTNAQIR(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.41	3%	1.00%	71	2.69E+05	(R)LDGNLLGTGDLNAYK(R)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.39	3%	1.00%	82.2	5.10E+05	(K)NIHGTSNTPEAITLNCADNLPCQGVQLHNVDIK(Y)	C:Carbamidomethylation	CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.2	3%	1%	66.1	5.59E+04	(K)VLPNSLVLDFVTNAQIR(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.19	3%	1%	73.6	2.76E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.18	3%	1%	64.9	2.38E+06	(R)YKDEKDVEDVK(V)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
11.06	3%	1%	82.4	5.08E+05	(K)SFGLSK(E)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
10.19	3%	1%	71.6	1.63E+05	(K)IVIPPGNYLTGGLELK(G)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
10.13	3%	1%	71.6	2.60E+06	(K)NVLIDK(V)		CL248.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g006610 [S bicolor] >gi|241931553|gb|EES04698.1| hypothet prot SORBIDRAFT_04g006610 [S bicolor]
23.31	<0.1%	<0.1%	94.6	3.60E+06	(K)AVQDAWTSACR(A)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
23.18	<0.1%	<0.1%	92.8	3.32E+05	(K)TGDSAADSAASGASGTFDISK(L)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
22.74	<0.1%	<0.1%	85.5	1.95E+06	(K)SYEDAESVLTASHLTFENIR(M)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
22.72	<0.1%	<0.1%	92.2	2.54E+06	(K)TGDSAADSAASGASGTFDISK(L)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
22.22	<0.1%	<0.1%	94.6	4.56E+05	(K)GAITIQLDGNLLGSNDLAK(Y)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]

22.15	<0.1%	<0.1%	87.5	4.10E+05	(K)TGDSAADSAASGASGTFDISK(L)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
22.15	<0.1%	<0.1%	90.5	1.02E+06	(K)TGDSAADSAASGASGTFDISK(L)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
21.91	<0.1%	<0.1%	88.5	5.31E+05	(K)ASWIELSHVDNIVmTGSGTLDGQGTAVYK(K)	m:Oxidized methionine	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
21.09	<0.1%	<0.1%	87.9	9.22E+05	(K)ASWIELSHVDNIVmTGSGTLDGQGTAVYK(K)	m:Oxidized methionine	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
20.45	<0.1%	<0.1%	85.8	4.13E+05	(K)TGDSAADSAASGASGTFDISK(L)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
20.07	<0.1%	<0.1%	91.5	6.02E+06	(K)SDSSHVIVK(D)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
19.89	<0.1%	<0.1%	97.4	9.54E+05	(K)SDSSHVIVK(D)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
19.67	<0.1%	<0.1%	87.1	1.48E+06	(K)AVQDAWTSACR(A)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
19.58	<0.1%	<0.1%	86.2	2.45E+05	(K)TGDSAADSAASGASGTFDISK(L)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
19.18	<0.1%	<0.1%	85.1	1.53E+06	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
19.14	<0.1%	<0.1%	90.1	2.38E+05	(K)GAITIQLDGNLLGSNDLAK(Y)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
19.12	<0.1%	<0.1%	83.5	2.62E+05	(K)TGDSAADSAASGASGTFDISK(L)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
19.08	<0.1%	<0.1%	90	5.62E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
19.05	<0.1%	<0.1%	92	6.58E+06	(K)FFHINIDASK(N)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
18.99	<0.1%	<0.1%	88.2	6.27E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
18.65	<0.1%	<0.1%	84.4	1.77E+05	(K)GAITIQLDGNLLGSNDLAK(Y)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
18.49	<0.1%	<0.1%	87.6	6.63E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
18.47	<0.1%	<0.1%	81.5	1.87E+05	(K)ASWIELSHVDNIVmTGSGTLDGQGTAVYK(K)	m:Oxidized methionine	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
18.18	<0.1%	<0.1%	85.2	4.09E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
18.1	<0.1%	<0.1%	84.9	1.92E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
17.67	<0.1%	<0.1%	74.5	2.11E+05	(K)ASWIELSHVDNIVmTGSGTLDGQGTAVYK(K)	m:Oxidized methionine	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
17.62	<0.1%	<0.1%	84.7	6.15E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
17.34	<0.1%	<0.1%	86.7	8.19E+05	(K)SDSSHVIVK(D)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
17.07	<0.1%	<0.1%	76.2	2.54E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.73	<0.1%	<0.1%	85.1	7.17E+05	(K)SDSSHVIVK(D)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.69	<0.1%	<0.1%	80.9	2.54E+05	(R)mEEVANPIIIDQYFCPEK(V)	C:Carbamidomethylation m:Oxidized methionine	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.68	<0.1%	<0.1%	75	3.15E+05	(R)mEEVANPIIIDQYFCPEK(V)	C:Carbamidomethylation m:Oxidized methionine	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.65	<0.1%	<0.1%	85.7	3.43E+06	(K)FFHINIDASK(N)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.52	<0.1%	<0.1%	71.8	2.89E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.5	<0.1%	<0.1%	89.8	4.96E+05	(R)mEEVANPIIIDQYFCPEK(V)	C:Carbamidomethylation m:Oxidized methionine	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.27	<0.1%	<0.1%	84.7	2.20E+06	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.15	<0.1%	<0.1%	77.9	2.72E+05	(K)GDYLVGPLNFVGPCK(G)	C:Carbamidomethylation	UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.08	<0.1%	<0.1%	79.2	1.30E+06	(K)FFHINIDASK(N)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
16.05	<0.1%	<0.1%	87.2	2.48E+05	(K)SDSSHVIVK(D)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
15.4	0.20%	<0.1%	85.2	5.98E+05	(K)SDSSHVIVK(D)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
15.38	0.20%	<0.1%	82.1	1.62E+05	(K)GAITIQLDGNLLGSNDLAK(Y)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
15.34	0.20%	<0.1%	68.6	1.27E+05	(K)SYEDAESVLTASHLTFENIR(M)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
15.22	0.20%	<0.1%	78.7	1.30E+06	(K)FFHINIDASK(N)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]

15.2 0.20% <0.1% 76.6 5.79E+05 (K)ASWIELSHVDNIVmTGSGTLDGQGTAVYK(K) m:Oxidized methionine UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
15.1 0.20% <0.1% 81.8 4.07E+05 (R)mEEVANPIIIDQYFCPEK(V) C:Carbamidomethylation m:Oxidized methionine UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
15.03 0.20% <0.1% 77.4 1.25E+05 (K)GDYLVGPLNFVGPCK(G) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
14.98 0.20% <0.1% 79 8.81E+05 (K)FFHINIDASK(N) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
14.79 0.20% <0.1% 80.3 3.30E+05 (K)GDYLVGPLNFVGPCK(G) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
14.67 2% <0.1% 73.6 5.77E+04 (R)mEEVANPIIIDQYFCPEK(V) C:Carbamidomethylation m:Oxidized methionine UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
14.3 2% <0.1% 75.4 3.32E+06 (R)ATGSATVLIPK(G) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
14.19 2% 0.10% 86 1.57E+05 (K)SDSSHVIVK(D) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
14.11 2% 0.30% 73.6 1.11E+06 (K)GDYLVGPLNFVGPCK(G) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.98 2% 0.30% 71.5 4.21E+05 (K)ASWIELSHVDNIVmTGSGTLDGQGTAVYK(K) m:Oxidized methionine UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.93 2% 0.30% 70.5 7.51E+04 (K)GDYLVGPLNFVGPCK(G) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.87 2% 0.40% 79.1 5.74E+05 (K)AVQDAWTSACR(A) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.85 2% 0.40% 80.8 8.05E+04 (K)LGATGDGK(T) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.55 2% 0.50% 70.9 1.36E+06 (R)ATGSATVLIPK(G) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.46 2% 0.50% 62.7 1.42E+06 (R)YKDEKDVTDVTVR(D) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.25 2% 0.50% 74.5 3.40E+05 (K)GDYLVGPLNFVGPCK(G) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.22 2% 0.50% 69.7 4.42E+05 (K)AVQDAWTSACR(A) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.2 2% 0.50% 71.6 6.63E+06 (R)ATGSATVLIPK(G) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
13.16 2% 0.50% 73.4 7.33E+05 (R)mEEVANPIIIDQYFCPEK(V) C:Carbamidomethylation m:Oxidized methionine UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
12.67 2% 0.60% 68.6 2.68E+05 (R)MEEVANPIIIDQYFCPEK(V) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
12.52 2% 0.60% 69.7 3.49E+05 (K)FFHINIDASK(N) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
12.07 3% 0.80% 70.5 6.63E+06 (R)ATGSATVLIPK(G) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
11.9 3% 0.90% 69.5 1.37E+06 (K)FFHINIDASK(N) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
11.9 3% 0.90% 63.5 9.77E+05 (R)ATGSATVLIPK(G) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
11.75 3% 0.90% 73.6 3.32E+06 (R)ATGSATVLIPK(G) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
11.72 3% 0.90% 71 2.41E+05 (K)DVTDVTVR(D) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
11.72 3% 0.90% 68.5 1.55E+05 (K)GAITIQLDGNLLGSNDLAK(Y) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
11.56 3% 1.00% 64.8 3.20E+05 (K)TGDSAADSAASGASGTFDISK(L) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
11.28 3% 1% 76.7 1.44E+05 (K)SDSSHVIVK(D) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
11.17 3% 1% 71.1 2.38E+05 (K)GDYLVGPLNFVGPCK(G) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
10.64 3% 1% 76.7 1.61E+06 (K)SDSSHVIVK(D) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
10.62 3% 1% 60.4 1.12E+04 (K)TGDSAADSAASGASGTFDISK(L) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
10.61 3% 1% 67.8 5.16E+04 (R)mEEVANPIIIDQYFCPEK(V) C:Carbamidomethylation m:Oxidized methionine UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
10.44 3% 1% 69.5 1.25E+05 (K)SDSSHVIVK(D) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
10.41 3% 1% 68.5 2.00E+04 (R)mEEVANPIIIDQYFCPEK(V) C:Carbamidomethylation m:Oxidized methionine UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
10.32 3% 1% 67.9 3.20E+05 (K)GDYLVGPLNFVGPCK(G) C:Carbamidomethylation UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
10.25 3% 1% 65.7 1.29E+05 (K)SDSSHVIVK(D) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
10.17 3% 1% 63.7 7.58E+05 (K)KSDSSHVIVK(D) UG332 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]

10.1	3%	1%	61.2	2.46E+05	(K)TGDSAADSAASGASGTFDISK(L)		UG332	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g021050 [S bicolor] >gi|241927668|gb|EES00813.1| hypothet prot SORBIDRAFT_03g021050 [S bicolor]
14.19	2%	0.10%	77.7	2.46E+05	(K)AGIVPITYR(K)		UG335	S.halepenseF2Rev	unknown [Zea mays]
24.2	<0.1%	<0.1%	93.2	6.86E+06	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
23.24	<0.1%	<0.1%	88.5	4.38E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
22.17	<0.1%	<0.1%	83.9	4.67E+06	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
21.6	<0.1%	<0.1%	85.4	6.55E+06	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
20.81	<0.1%	<0.1%	86.9	7.03E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
20.78	<0.1%	<0.1%	88.1	1.23E+07	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
20.78	<0.1%	<0.1%	88.4	4.71E+06	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
20.28	<0.1%	<0.1%	89.1	9.50E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
20.22	<0.1%	<0.1%	88	5.14E+06	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
20.13	<0.1%	<0.1%	87.3	5.62E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
19.73	<0.1%	<0.1%	85.6	5.81E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
19.39	<0.1%	<0.1%	83.9	2.23E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
19.34	<0.1%	<0.1%	84.5	4.11E+06	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
19.15	<0.1%	<0.1%	84.3	3.82E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
19.1	<0.1%	<0.1%	77.3	9.58E+05	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
19.03	<0.1%	<0.1%	78.2	1.15E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
18.92	<0.1%	<0.1%	83.4	2.07E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
18.52	<0.1%	<0.1%	83.6	3.80E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
18.47	<0.1%	<0.1%	80.9	3.83E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
18.45	<0.1%	<0.1%	82.4	2.42E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
18.17	<0.1%	<0.1%	76	2.24E+06	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.89	<0.1%	<0.1%	79.1	1.59E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.66	<0.1%	<0.1%	85	1.69E+07	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.61	<0.1%	<0.1%	81.2	1.72E+05	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.51	<0.1%	<0.1%	82	5.32E+05	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.49	<0.1%	<0.1%	77	4.46E+06	(K)ImFHVEK(G)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.27	<0.1%	<0.1%	89.8	7.77E+06	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.24	<0.1%	<0.1%	82.9	2.97E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.24	<0.1%	<0.1%	78.1	3.12E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
17.21	<0.1%	<0.1%	82.9	2.80E+05	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
16.9	<0.1%	<0.1%	78.5	3.30E+05	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
16.73	<0.1%	<0.1%	75.9	1.86E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
16.39	<0.1%	<0.1%	85.6	7.24E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
16.14	<0.1%	<0.1%	78.5	5.07E+05	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
16.1	<0.1%	<0.1%	73.7	4.08E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.81	0.20%	<0.1%	82.6	4.00E+07	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]

15.79	0.20%	<0.1%	82.7	5.03E+06	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.71	0.20%	<0.1%	83.2	2.78E+06	(K)ASPGFKPMK(Q)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.63	0.20%	<0.1%	74.8	4.20E+05	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.57	0.20%	<0.1%	77.7	1.81E+06	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.55	0.20%	<0.1%	73.6	6.24E+05	(K)ImFHVEK(G)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.4	0.20%	<0.1%	74.4	6.67E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.34	0.20%	<0.1%	68.5	3.15E+06	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.01	0.20%	<0.1%	63.7	6.56E+05	(K)ImFHVEK(G)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15	0.20%	<0.1%	76.8	2.63E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.94	0.20%	<0.1%	83.7	4.61E+06	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.92	0.20%	<0.1%	75.1	6.70E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.9	0.20%	<0.1%	82.2	1.56E+06	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.82	0.20%	<0.1%	80.4	3.23E+06	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.8	0.20%	<0.1%	71.9	4.63E+05	(K)NVADDGNIVLMELEDK(A)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.68	2%	<0.1%	77.5	6.13E+06	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.65	2%	<0.1%	78.9	4.18E+06	(K)QSWGAVWR(F)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.44	2%	<0.1%	73.5	6.43E+04	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.39	2%	<0.1%	73.2	4.13E+06	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.38	2%	<0.1%	78.5	8.82E+05	(K)QSWGAVWR(F)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.04	2%	0.30%	74.3	5.90E+06	(K)ASPGFKPmK(Q)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
14.01	2%	0.30%	80.5	3.88E+05	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.75	2%	0.50%	73.3	5.27E+06	(K)ImFHVEK(G)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.75	2%	0.50%	72.7	4.70E+06	(K)ImFHVEK(G)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.75	2%	0.50%	79.6	4.32E+06	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.7	2%	0.50%	75.8	6.00E+05	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.66	2%	0.50%	93.9	1.90E+07	(K)GPFSIR(L)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.6	2%	0.50%	75.6	4.14E+06	(K)ImFHVEK(G)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.59	2%	0.50%	69.2	1.63E+05	(K)GSNPNYLAVLVK(N)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.5	2%	0.50%	66.9	3.23E+06	(K)ASPGFKPmK(Q)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.5	2%	0.50%	71.4	9.90E+06	(K)ImFHVEK(G)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.45	2%	0.50%	71.4	3.16E+06	(K)IMFHVEK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.45	2%	0.50%	71.4	1.71E+06	(K)QSWGAVWR(F)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.35	2%	0.50%	71.1	2.22E+05	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.33	2%	0.50%	78.7	9.76E+05	(R)FDTPKPVK(G)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.33	2%	0.50%	77.3	2.10E+06	(K)ImFHVEK(G)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.31	2%	0.50%	90.5	1.30E+07	(K)GPFSIR(L)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.28	2%	0.50%	64.8	1.65E+06	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine	UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.12	2%	0.60%	64.5	7.53E+05	(K)QSWGAVWR(F)		UG492	S.halepenseF2	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]

13.11 2% 0.60% 83 1.32E+05 (R)LTSESGK(K) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13 2% 0.60% 64.1 7.05E+05 (K)ImFHVEK(G) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.97 2% 0.60% 73.7 3.94E+06 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.93 2% 0.60% 69.3 3.30E+05 (K)ASPGFKPMK(Q) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.92 2% 0.60% 68.5 4.04E+05 (K)ImFHVEK(G) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.87 2% 0.60% 72.7 1.50E+07 (K)ASPGFKPMK(Q) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.84 2% 0.60% 73.4 4.07E+05 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.75 2% 0.60% 65.1 7.56E+05 (K)ImFHVEK(G) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.73 2% 0.60% 65 5.45E+05 (K)QSWGAVWR(F) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.64 2% 0.70% 65 7.04E+05 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.48 2% 0.60% 68.1 4.28E+04 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.46 2% 0.60% 73.5 1.02E+06 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.43 2% 0.60% 72.6 9.63E+05 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.39 2% 0.60% 63.7 8.87E+05 (K)QSWGAVWR(F) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.19 3% 0.70% 66.2 1.33E+05 (K)GSNPNYLAVLVK(N) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.16 3% 0.70% 71.8 2.85E+06 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.06 3% 0.80% 69.2 3.70E+06 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.89 3% 0.90% 66.1 5.89E+05 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.83 3% 0.90% 64 4.64E+06 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.59 3% 1.00% 61.9 2.26E+05 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.56 3% 1.00% 61.8 1.89E+05 (K)GSNPNYLAVLVK(N) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.52 3% 0.90% 77.3 2.63E+06 (K)GPFSIR(L) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.51 3% 0.90% 69.2 8.16E+04 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.46 3% 1.00% 69 9.22E+04 (K)NVADDGNIVLMELEDK(A) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.45 3% 1.00% 66.8 1.03E+06 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.42 3% 1.00% 62.2 6.61E+04 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.28 3% 1% 68.8 1.47E+05 (K)NVADDGNIVLMELEDK(A) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.21 3% 1% 67.8 2.14E+06 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.2 3% 1% 70.7 4.79E+06 (K)ImFHVEK(G) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.12 3% 1% 64.6 3.94E+05 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.01 3% 1% 75.7 3.13E+05 (K)NVADDGNIVLMELEDK(A) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.01 3% 1% 71.9 2.59E+06 (K)ImFHVEK(G) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.92 3% 1% 61.7 5.43E+05 (K)QSWGAVWR(F) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.78 3% 1% 71.2 1.32E+06 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.75 3% 1% 67.8 3.50E+06 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.74 3% 1% 70.3 4.09E+05 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.67 3% 1% 60.6 5.78E+05 (K)IMFHVEK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.66 3% 1% 70.2 1.83E+05 (K)NVADDGNIVLMELEDK(A) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]

10.6 3% 1% 62.5 2.09E+06 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.56 3% 1% 66.3 7.42E+05 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.37 3% 1% 61.9 9.04E+05 (K)GSNPNYLAVLVK(N) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.35 3% 1% 65 1.33E+06 (K)GPFSIR(L) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.25 3% 1% 70.6 2.70E+05 (R)FDTPKPVK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.17 3% 1% 68.9 2.18E+05 (K)IMFHVEK(G) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.15 3% 1% 68 9.33E+04 (K)NVADDGNIVLMELEDK(A) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.06 5% 1% 65 1.59E+06 (K)GPFSIR(L) UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.02 5% 1% 66.9 2.12E+05 (K)NVADDGNIVLmELEDK(A) m:Oxidized methionine UG492 S.halepenseF2 hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
24.84 <0.1% <0.1% 98.1 3.93E+06 (K)ATWYGKPTGAGPDDNGGACGYK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
24.36 <0.1% <0.1% 90.8 2.07E+07 (K)ATWYGKPTGAGPDDNGGACGYK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
23.45 <0.1% <0.1% 100 1.22E+05 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
23.31 <0.1% <0.1% 96 7.72E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
23.15 <0.1% <0.1% 100 8.67E+05 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.95 <0.1% <0.1% 100 1.10E+07 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.88 <0.1% <0.1% 93 1.19E+07 (K)DGLGCGSCFEIK(C) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.86 <0.1% <0.1% 95.2 2.49E+07 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.76 <0.1% <0.1% 97.8 8.08E+05 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.65 <0.1% <0.1% 100 5.84E+06 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.64 <0.1% <0.1% 98.1 1.70E+07 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.59 <0.1% <0.1% 93.1 9.29E+06 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.54 <0.1% <0.1% 98 1.40E+07 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.5 <0.1% <0.1% 89.4 3.06E+05 (K)ATWYGKPTGAGPDDNGGACGYK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.29 <0.1% <0.1% 92.7 4.16E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.1 <0.1% <0.1% 94.9 3.44E+07 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
22.05 <0.1% <0.1% 94.1 3.77E+06 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.96 <0.1% <0.1% 91.4 6.89E+06 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.96 <0.1% <0.1% 97.7 6.92E+06 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.9 <0.1% <0.1% 100 8.60E+05 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.59 <0.1% <0.1% 88.3 4.25E+05 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.57 <0.1% <0.1% 96.1 5.75E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.55 <0.1% <0.1% 96.7 3.14E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.35 <0.1% <0.1% 95.4 3.10E+07 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.26 <0.1% <0.1% 88.9 1.32E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.25 <0.1% <0.1% 95.5 2.03E+06 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.22 <0.1% <0.1% 90.4 2.89E+07 (K)DGLGCGSCFEIK(C) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.13 <0.1% <0.1% 86.3 3.41E+06 (K)DGLGCGSCFEIK(C) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.12 <0.1% <0.1% 89.2 5.18E+06 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]

21.12 <0.1% <0.1% 89.1 1.83E+06 (K)DGLGCGSCFEIK(C) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
21.03 <0.1% <0.1% 97.9 1.74E+07 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.91 <0.1% <0.1% 94.7 1.82E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.71 <0.1% <0.1% 85.8 2.93E+06 (K)ATWYGKPTGAGPDDNGGACGYK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.7 <0.1% <0.1% 97.4 1.09E+06 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.68 <0.1% <0.1% 97.1 4.84E+06 (R)KDSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.63 <0.1% <0.1% 97.4 2.10E+06 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.47 <0.1% <0.1% 92.7 1.21E+07 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.46 <0.1% <0.1% 86.7 2.89E+06 (K)DGLGCGSCFEIK(C) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.36 <0.1% <0.1% 92.6 1.45E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.27 <0.1% <0.1% 95.4 2.26E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.25 <0.1% <0.1% 90 3.80E+07 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.23 <0.1% <0.1% 90.3 3.06E+07 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.21 <0.1% <0.1% 80.9 8.07E+05 (K)ATWYGKPTGAGPDDNGGACGYK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20.01 <0.1% <0.1% 91.5 1.68E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
20 <0.1% <0.1% 97.4 7.16E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.87 <0.1% <0.1% 94.6 5.37E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.85 <0.1% <0.1% 90.1 8.95E+06 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.8 <0.1% <0.1% 88 3.84E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.69 <0.1% <0.1% 93.3 1.78E+07 (K)VTFHVEK(G) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.66 <0.1% <0.1% 93.5 2.06E+07 (K)VTFHVEK(G) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.66 <0.1% <0.1% 92.7 1.56E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.59 <0.1% <0.1% 85.7 1.23E+07 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.58 <0.1% <0.1% 78.7 5.00E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.44 <0.1% <0.1% 89.8 3.87E+06 (K)VTFHVEK(G) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.38 <0.1% <0.1% 88.2 2.71E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.31 <0.1% <0.1% 89.6 4.24E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.3 <0.1% <0.1% 85.3 2.19E+06 (K)DGLGCGSCFEIK(C) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.29 <0.1% <0.1% 87.7 1.29E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.27 <0.1% <0.1% 92.9 1.08E+04 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.22 <0.1% <0.1% 92 1.24E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.21 <0.1% <0.1% 89.7 6.27E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
19.15 <0.1% <0.1% 90.4 3.54E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.87 <0.1% <0.1% 82.4 2.62E+06 (K)DGLGCGSCFEIK(C) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.86 <0.1% <0.1% 79.4 2.85E+06 (K)ATWYGKPTGAGPDDNGGACGYKDVNK(A) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.69 <0.1% <0.1% 88.7 1.18E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.63 <0.1% <0.1% 84.8 1.80E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.6 <0.1% <0.1% 82.9 2.29E+06 (K)DGLGCGSCFEIK(C) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]

18.56	<0.1%	<0.1%	81.8	3.61E+06	(K)YVDGDGDVVGVDIK(E)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.49	<0.1%	<0.1%	85	2.13E+06	(K)GSNPNYLALLVK(Y)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.17	<0.1%	<0.1%	82	2.65E+06	(K)VTFHVEK(G)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.1	<0.1%	<0.1%	82.1	4.99E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.06	<0.1%	<0.1%	90.5	7.21E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18.02	<0.1%	<0.1%	80.2	4.82E+06	(K)YVDGDGDVVGVDIK(E)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
18	<0.1%	<0.1%	91.8	1.89E+06	(K)TAYEDVIPEGWK(A)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.98	<0.1%	<0.1%	76.2	2.42E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.94	<0.1%	<0.1%	72.5	3.80E+06	(K)GSNPNYLALLVK(Y)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.94	<0.1%	<0.1%	91.4	2.66E+05	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.77	<0.1%	<0.1%	84.7	1.10E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.69	<0.1%	<0.1%	93.2	2.65E+06	(K)GSNPNYLALLVK(Y)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.5	<0.1%	<0.1%	73.3	1.59E+06	(K)ATWYGKPTGAGPDDNGGACGYK(D)	C:Carbamidomethylation	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.39	<0.1%	<0.1%	89.4	1.74E+06	(K)GGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.25	<0.1%	<0.1%	77.5	7.34E+05	(K)ATWYGKPTGAGPDDNGGACGYKDVNK(A)	C:Carbamidomethylation	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.13	<0.1%	<0.1%	75.7	2.17E+06	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.12	<0.1%	<0.1%	85.6	6.68E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.09	<0.1%	<0.1%	89.6	3.91E+06	(K)GGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.05	<0.1%	<0.1%	87.6	7.66E+05	(K)VTFHVEK(G)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.03	<0.1%	<0.1%	83.1	6.21E+05	(K)YVDGDGDVVGVDIK(E)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
17.02	<0.1%	<0.1%	66.2	2.13E+07	(K)GSNPNYLALLVK(Y)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.89	<0.1%	<0.1%	86.4	9.64E+05	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.89	<0.1%	<0.1%	78.9	2.89E+06	(K)GSNPNYLALLVK(Y)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.81	<0.1%	<0.1%	87.2	2.05E+07	(K)GGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.79	<0.1%	<0.1%	81.1	1.73E+06	(K)VTFHVEK(G)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.78	<0.1%	<0.1%	87.5	8.23E+06	(K)GGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.64	<0.1%	<0.1%	82	2.33E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.62	<0.1%	<0.1%	86.1	1.43E+06	(K)GGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.6	<0.1%	<0.1%	86.6	6.53E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.49	<0.1%	<0.1%	81.8	3.27E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.48	<0.1%	<0.1%	83.5	3.86E+06	(K)VTFHVEK(G)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.47	<0.1%	<0.1%	78.5	9.74E+05	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.45	<0.1%	<0.1%	86.6	3.72E+06	(K)GGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.41	<0.1%	<0.1%	78.6	1.06E+06	(K)FPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.35	<0.1%	<0.1%	89.1	1.89E+05	(K)TAYEDVIPEGWK(A)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.3	<0.1%	<0.1%	82.3	9.88E+05	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.28	<0.1%	<0.1%	89.2	3.35E+06	(K)GSNPNYLALLVK(Y)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.23	<0.1%	<0.1%	76.3	2.72E+06	(K)GSNPNYLALLVK(Y)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]

16.18 <0.1% <0.1% 77.8 6.53E+05 (K)VTFHVEK(G) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.05 <0.1% <0.1% 82.2 6.66E+05 (K)VTFHVEK(G) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.04 <0.1% <0.1% 81.1 1.32E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16.03 <0.1% <0.1% 60.1 1.77E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
16 <0.1% <0.1% 77.5 2.84E+06 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.96 <0.1% <0.1% 81.5 2.02E+06 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.94 <0.1% <0.1% 90.9 1.08E+07 (K)AGIIDMK(F) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.89 0.20% <0.1% 87.4 2.52E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.81 0.20% <0.1% 83.4 9.99E+05 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.76 0.20% <0.1% 77.1 4.65E+06 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.69 0.20% <0.1% 81.6 7.45E+04 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.61 0.20% <0.1% 89 1.02E+07 (K)GGDAYQPLK(H) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.58 0.20% <0.1% 80.2 1.71E+06 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.57 0.20% <0.1% 84.4 5.75E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.48 0.20% <0.1% 81.4 9.19E+05 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.31 0.20% <0.1% 87.6 3.94E+07 (K)GGDAYQPLK(H) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.29 0.20% <0.1% 88.2 9.19E+06 (R)KDSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.21 0.20% <0.1% 65.1 1.49E+06 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
15.03 0.20% <0.1% 77.4 4.32E+05 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.94 0.20% <0.1% 68.7 7.21E+05 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.92 0.20% <0.1% 85.4 6.91E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.91 0.20% <0.1% 66 5.55E+05 (K)ATWYGKPTGAGPDDNGGACGYK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.89 0.20% <0.1% 78.3 1.75E+06 (K)GGDAYQPLK(H) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.86 0.20% <0.1% 78.4 4.35E+05 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.8 0.20% <0.1% 67.7 4.87E+05 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.76 0.20% <0.1% 79 1.94E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.69 0.20% <0.1% 79.4 3.91E+05 (R)KDSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.57 2% <0.1% 68.2 4.21E+06 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.55 2% <0.1% 65.9 3.73E+05 (K)ATWYGKPTGAGPDDNGGACGYKDVNK(A) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.51 2% <0.1% 69.6 7.37E+05 (K)CDKPAECSGEAVVVHITDMNYEQIAAYHFDLAGTAFGAmAK(K) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.48 2% <0.1% 82.5 3.83E+05 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.46 2% <0.1% 73.2 1.13E+05 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.25 2% <0.1% 73 1.53E+06 (R)KDSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.13 2% 0.30% 69.5 7.75E+05 (K)ATWYGKPTGAGPDDNGGACGYK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.03 2% 0.30% 78.7 1.29E+06 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14.01 2% 0.30% 81.5 1.80E+05 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
14 2% 0.30% 81.7 8.77E+05 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.99 2% 0.30% 78.1 2.79E+05 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]

13.98 2% 0.30% 79.7 1.59E+07 (K)HSWGAIWR(K) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.94 2% 0.30% 69.4 9.52E+05 (K)VTFHVEK(G) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.89 2% 0.40% 75.8 4.81E+05 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.85 2% 0.40% 60.4 2.64E+04 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.79 2% 0.50% 65.1 2.94E+05 (K)CDKPAECSGEAVVVHITDmNYEQIAAYHFDLAGTAFGAmAK(K) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.79 2% 0.50% 75.4 4.30E+05 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.55 2% 0.50% 81 8.40E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.53 2% 0.50% 78.4 4.18E+05 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.53 2% 0.50% 79.1 2.83E+05 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.51 2% 0.50% 76.7 1.30E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.25 2% 0.50% 75.9 2.67E+05 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.16 2% 0.50% 80.6 2.08E+05 (K)TAYEDVIPEGWK(A) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.15 2% 0.50% 70.9 1.63E+06 (K)VTFHVEK(G) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.11 2% 0.60% 63.7 4.43E+04 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.09 2% 0.60% 73.1 1.02E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.08 2% 0.60% 77.1 2.40E+06 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
13.04 2% 0.60% 65.3 1.65E+04 (K)APFNSMGACGNLPIFK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.98 2% 0.60% 62.8 6.28E+04 (K)CDKPAECSGEAVVVHITDmNYEQIAAYHFDLAGTAFGAmAK(K) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.98 2% 0.60% 80.4 2.60E+06 (R)KAGIIDMK(F) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.97 2% 0.60% 76.7 5.37E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.88 2% 0.60% 64.2 6.52E+05 (K)ATWYGKPTGAGPDDNGGACGYK(D) C:Carbamidomethylation CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.86 2% 0.60% 64.8 2.62E+06 (K)APFNSmGACGNLPIFK(D) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.85 2% 0.60% 71.8 5.95E+05 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.8 2% 0.60% 75.4 1.45E+06 (K)HSWGAIWR(K) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.79 2% 0.60% 70.3 3.94E+06 (R)KDSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.63 2% 0.70% 72.8 1.71E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.49 2% 0.60% 67.8 7.81E+05 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.28 2% 0.70% 73.1 1.44E+06 (K)YVDGDGDVVGVDIK(E) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.03 3% 0.80% 65.2 6.32E+04 (K)KGEEEKLR(K) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
12.02 3% 0.80% 75.7 3.66E+05 (K)GSNPNYLALLVK(Y) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
11.99 3% 0.80% 70.2 7.36E+05 (K)FPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
11.75 3% 0.90% 62 9.44E+05 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
11.74 3% 0.90% 77 2.10E+07 (K)HSWGAIWR(K) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
11.67 3% 0.90% 69.4 7.43E+05 (K)HSWGAIWR(K) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
11.58 3% 1.00% 60.4 2.77E+06 (K)AGIIDmK(F) m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
11.51 3% 0.90% 62 4.17E+04 (K)CDKPAECSGEAVVVHITDMNYEQIAAYHFDLAGTAFGAmAK(K) C:Carbamidomethylation m:Oxidized methionine CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
11.45 3% 1.00% 74.5 2.93E+06 (K)DSDKPIKFPVTVQITTEGGTK(T) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]
11.45 3% 1.00% 77.6 7.44E+05 (K)AGIIDMK(F) CL153.c1 S.halepenseF3 hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]

11.35	3%	1.00%	66.6	4.58E+05	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
11.32	3%	1.00%	74.3	1.83E+06	(R)KAGIIDMK(F)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
11.28	3%	1%	66.5	4.37E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
11.23	3%	1%	60.3	3.98E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
11.12	3%	1%	72.9	6.68E+05	(K)TAYEDVIPEGWK(A)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
11.11	3%	1%	68.8	1.17E+05	(K)TAYEDVIPEGWK(A)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.99	3%	1%	68.8	6.72E+05	(K)HSWGAIWR(K)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.9	3%	1%	69	5.17E+05	(K)YVDGDGDVVGVDIK(E)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.86	3%	1%	82.8	7.00E+05	(K)HSWGAIWR(K)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.78	3%	1%	64.7	2.24E+05	(K)ADTTYTAK(X)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.75	3%	1%	62.2	6.02E+06	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.73	3%	1%	79.5	1.61E+06	(K)HSWGAIWR(K)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.69	3%	1%	71	1.84E+06	(K)EKGGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.62	3%	1%	64.1	5.46E+05	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.52	3%	1%	65.3	8.30E+04	(K)GGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.36	3%	1%	84.5	9.69E+06	(K)HSWGAIWR(K)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.31	3%	1%	60.2	9.19E+05	(K)VTFHVEK(G)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.11	3%	1%	64.7	5.43E+05	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.1	3%	1%	63.2	1.86E+06	(K)GGDAYQPLK(H)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.07	5%	1%	64.9	1.57E+05	(K)GSNPNYLALLVK(Y)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.03	5%	1%	64.6	6.82E+05	(K)YVDGDGDVVGVDIK(E)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
10.01	5%	1%	83.5	1.50E+07	(K)HSWGAIWR(K)		CL153.c1	S.halepenseF3	hypothet prot SORBIDRAFT_01g050210 [S bicolor] >gi|241919875|gb|EER93019.1| hypothet prot SORBIDRAFT_01g050210 [S bicolor]	
21.04	<0.1%	<0.1%	92.5	8.93E+06	(K)AFGSLAKPGLNDK(L)		UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
19.24	<0.1%	<0.1%	86.1	4.90E+05	(K)EmPECSGNPITVFITDmNYEPIAPYHFDFSGK(A)	C:Carbamidomethylation m:Oxidized methionine	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
19.23	<0.1%	<0.1%	75.9	8.68E+05	(R)ATWYGQPNGAGPDDNGGACGIK(N)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
19.13	<0.1%	<0.1%	81.9	1.27E+06	(R)ATWYGQPNGAGPDDNGGACGIK(N)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
18.71	<0.1%	<0.1%	90.4	9.51E+05	(K)NVNLPPYNGFTACGNVPIFK(D)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
18.22	<0.1%	<0.1%	68	1.19E+06	(K)EMPECSGNPITVFITDmNYEPIAPYHFDFSGK(A)	C:Carbamidomethylation m:Oxidized methionine	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
16.34	<0.1%	<0.1%	89.3	7.06E+05	(K)NVNLPPYNGFTACGNVPIFK(D)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
16.19	<0.1%	<0.1%	62.9	1.85E+07	(K)GCGSCYEVR(C)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
16.16	<0.1%	<0.1%	62.9	8.74E+05	(K)GCGSCYEVR(C)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
15.98	<0.1%	<0.1%	80.4	5.18E+06	(K)AFGSLAKPGLNDK(L)		UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
15.87	0.20%	<0.1%	63.2	1.26E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
15.68	0.20%	<0.1%	71.4	2.45E+05	(K)EmPECSGNPITVFITDmNYEPIAPYHFDFSGK(A)	C:Carbamidomethylation m:Oxidized methionine	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
15.6	0.20%	<0.1%	74.1	2.70E+05	(K)EmPECSGNPITVFITDmNYEPIAPYHFDFSGK(A)	C:Carbamidomethylation m:Oxidized methionine	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
15.54	0.20%	<0.1%	61.2	1.05E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
15.16	0.20%	<0.1%	83.7	1.97E+05	(K)EmPECSGNPITVFITDMNYEPIAPYHFDFSGK(A)	C:Carbamidomethylation m:Oxidized methionine	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	
14.9	0.20%	<0.1%	60.7	1.20E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	UG493	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]	

14.65 2% <0.1% 67.7 5.47E+05 (K)AFGSLAKPGLNDK(L) UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.71 2% 0.50% 60.7 1.98E+06 (K)GCGSCYEVR(C) C:Carbamidomethylation UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
13.2 2% 0.50% 66.9 3.60E+05 (K)AFGSLAKPGLNDK(L) UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.94 2% 0.60% 73 4.26E+05 (K)EmPECSGNPITVFITDMNYEPIAPYHFDFSGK(A) C:Carbamidomethylation m:Oxidized methionine UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.46 2% 0.60% 75.4 4.41E+04 (K)NVNLPPYNGFTACGNVPIFK(D) C:Carbamidomethylation UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
12.44 2% 0.60% 70.4 3.49E+06 (K)AFGSLAKPGLNDK(L) UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.25 3% 1% 61.3 1.23E+06 (K)AFGSLAKPGLNDK(L) UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
11.01 3% 1% 63.4 4.13E+05 (K)EmPECSGNPITVFITDmNYEPIAPYHFDFSGK(A) C:Carbamidomethylation m:Oxidized methionine UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.88 3% 1% 63.2 5.76E+04 (K)EMPECSGNPITVFITDMNYEPIAPYHFDFSGK(A) C:Carbamidomethylation UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.87 3% 1% 66.1 4.13E+05 (K)EmPECSGNPITVFITDmNYEPIAPYHFDFSGK(A) C:Carbamidomethylation m:Oxidized methionine UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
10.08 5% 1% 65.1 1.18E+04 (R)ATWYGQPNGAGPDDNGGACGIK(N) C:Carbamidomethylation UG493 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g029840 [S bicolor] >gi|241921393|gb|EER94537.1| hypothet prot SORBIDRAFT_01g029840 [S bicolor]
15.63 0.20% <0.1% 80.9 4.78E+04 (K)NVAVLTPDAVSTQTGAFLHR(F) UG688 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g003910 [S bicolor] >gi|241917520|gb|EER90664.1| hypothet prot SORBIDRAFT_01g003910 [S bicolor]
11.14 3% 1% 75.9 9.23E+04 (R)SSIPLDVRPIR(Q) UG688 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g003910 [S bicolor] >gi|241917520|gb|EER90664.1| hypothet prot SORBIDRAFT_01g003910 [S bicolor]
24.2 <0.1% <0.1% 100 1.05E+06 (R)GGQPTVVTTLFQTTGTAR(N) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
20.01 <0.1% <0.1% 93.7 1.07E+06 (K)LFSFLLSNTGVAR(K) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
19.58 <0.1% <0.1% 84.5 7.46E+05 (R)GGQPTVVTTLFQTTGTAR(N) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
18.35 <0.1% <0.1% 93.8 3.08E+05 (K)LFSFLLSNTGVAR(K) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
15.92 <0.1% <0.1% 79 6.96E+05 (K)LFSFLLSNTGVAR(K) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
15.3 0.20% <0.1% 83.4 3.05E+05 (K)LFSFLLSNTGVAR(K) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
14.86 0.20% <0.1% 84.9 1.08E+06 (K)LFSFLLSNTGVAR(K) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
14.58 2% <0.1% 76.5 1.18E+05 (R)NSVTVLIPDNSAVDWLLR(R) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
14.51 2% <0.1% 82.7 6.97E+05 (K)LFSFLLSNTGVAR(K) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
12.83 2% 0.60% 64.2 2.26E+05 (R)NSVTVLIPDNSAVDWLLR(R) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
12.22 3% 0.70% 81.1 4.56E+05 (R)NSVTVLIPDNSAVDWLLR(R) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
11.72 3% 0.90% 79.2 8.79E+05 (R)NSVTVLIPDNSAVDWLLR(R) UG3982 S.halepenseF2 hypothet prot SORBIDRAFT_10g026140 [S bicolor] >gi|241917007|gb|EER90151.1| hypothet prot SORBIDRAFT_10g026140 [S bicolor]
14.17 2% 0.20% 75.1 1.16E+05 (R)LLGEFSDFTTFNNLLSQTK(L) UG1005 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g015850 [S bicolor] >gi|241931849|gb|EES04994.1| hypothet prot SORBIDRAFT_04g015850 [S bicolor]
11.72 3% 0.90% 66 1.15E+05 (R)LLGEFSDFTTFNNLLSQTK(L) UG1005 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g015850 [S bicolor] >gi|241931849|gb|EES04994.1| hypothet prot SORBIDRAFT_04g015850 [S bicolor]
20.03 <0.1% <0.1% 95.7 3.86E+06 (K)VAGEANQLR(A) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
18.63 <0.1% <0.1% 96.5 1.90E+06 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
18.55 <0.1% <0.1% 92 3.53E+06 (R)AATLLVVPDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
18.36 <0.1% <0.1% 83.6 2.52E+05 (R)ADDGQmYFGAPGASCVAK(L) C:Carbamidomethylation m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
18.22 <0.1% <0.1% 89.3 1.90E+06 (R)AATLLVVPDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
18.02 <0.1% <0.1% 94.4 9.11E+06 (K)VAGEANQLR(A) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
18.01 <0.1% <0.1% 93 2.40E+05 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
17.6 <0.1% <0.1% 80.9 6.43E+05 (K)LQPAVANHVLLSYFDPIK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
17.21 <0.1% <0.1% 77.7 6.91E+05 (K)LQPAVANHVLLSYFDPIKLDEMK(T) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
17.18 <0.1% <0.1% 89.7 5.13E+05 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
16.99 <0.1% <0.1% 91.2 4.83E+05 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]

16.3 <0.1% <0.1% 87.1 1.90E+06 (R)AATLLVVPDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
16.21 <0.1% <0.1% 82.6 3.91E+04 (K)SLASLPNDKLQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
16.06 <0.1% <0.1% 83.7 9.46E+05 (R)AATLLVVPDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
16 <0.1% <0.1% 81.7 8.81E+05 (K)LQPAVANHVLLSYFDPIK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
15.6 0.20% <0.1% 85.5 8.10E+05 (R)MPGEGVSGK(V) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
15.24 0.20% <0.1% 82.8 2.42E+05 (R)AATLLVVPDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
15.24 0.20% <0.1% 76.4 2.17E+05 (R)ADDGQmYFGAPGASCVAK(L) C:Carbamidomethylation m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.93 0.20% <0.1% 83.7 2.92E+04 (K)SLASLPNDKLQPAVANHVLLSYFDPIKLDEMK(T) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.83 0.20% <0.1% 71.6 4.83E+05 (K)IKPSAAGLEDSK(M) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.72 0.20% <0.1% 76 1.04E+06 (K)LQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.49 2% <0.1% 82.2 2.23E+05 (K)VAGEANQLR(A) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.31 2% <0.1% 84.2 5.87E+06 (R)YATFSK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.3 2% <0.1% 76.7 8.60E+05 (K)LQPAVANHVLLSYFDPIKLDEMK(T) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.28 2% <0.1% 69.8 4.19E+05 (K)LQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.28 2% <0.1% 90.5 2.88E+06 (K)SLASLPNDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.14 2% 0.20% 85.4 8.50E+05 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.13 2% 0.30% 77.4 2.10E+05 (K)VAGEANQLR(A) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.86 2% 0.40% 69 1.55E+05 (K)LQPAVANHVLLSYFDPIKLDEMK(T) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.83 2% 0.50% 70.9 1.45E+06 (K)LQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.8 2% 0.50% 79.7 9.25E+04 (K)LQPAVANHVLLSYFDPIK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.75 2% 0.50% 73.4 3.00E+06 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.73 2% 0.50% 82.8 3.81E+06 (R)YATFSK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.61 2% 0.50% 79.9 2.98E+05 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.54 2% 0.50% 70.6 8.46E+04 (K)LQPAVANHVLLSYFDPIK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.46 2% 0.50% 76.2 3.08E+04 (K)SLASLPNDKLQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.09 2% 0.60% 72.8 2.72E+05 (R)AATLLVVPDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
13.05 2% 0.60% 75.4 3.66E+05 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
12.85 2% 0.60% 78.3 2.52E+05 (K)SLASLPNDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
12.48 2% 0.60% 68.4 7.86E+04 (K)LQPAVANHVLLSYFDPIK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
12.44 2% 0.60% 81.3 1.22E+05 (K)VAGEANQLR(A) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
12.07 3% 0.80% 66.8 1.00E+06 (K)LQPAVANHVLLSYFDPIKLDEMK(T) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.93 3% 0.90% 79.3 6.05E+05 (K)SLASLPNDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.89 3% 0.90% 69.1 1.45E+05 (K)LQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.89 3% 0.90% 65.8 2.14E+05 (K)LQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.79 3% 0.90% 68.3 1.66E+05 (K)LQPAVANHVLLSYFDPIK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.72 3% 0.90% 70.6 2.46E+05 (K)LQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.68 3% 0.90% 81.3 8.86E+05 (K)VAGEANQLR(A) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.66 3% 0.90% 68.9 8.81E+05 (K)LQPAVANHVLLSYFDPIK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]

11.61 3% 0.90% 71.7 1.75E+04 (K)LQPAVANHVLLSYFDPIKLDEmK(T) m:Oxidized methionine UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.32 3% 1.00% 68.7 9.49E+04 (K)LQPAVANHVLLSYFDPIK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.31 3% 1.00% 62.5 2.91E+05 (R)TAILPTLLSNTDKK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.19 3% 1% 72.9 2.57E+05 (R)ADDGQMYFGAPGASCVAK(L) C:Carbamidomethylation UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.12 3% 1% 71.5 2.34E+06 (K)IKPSAAGLEDSK(M) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
11.05 3% 1% 72.2 1.68E+05 (K)VAGEANQLR(A) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
10.99 3% 1% 69.7 8.53E+05 (R)TAILPTLLSNTDK(K) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
10.98 3% 1% 67.4 3.87E+05 (R)AATLLVVPDK(L) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
10.69 3% 1% 66.6 2.37E+05 (R)TAILPTLLSNTDK(K) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
10.17 3% 1% 71.3 1.35E+05 (K)VAGEANQLR(A) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
10.17 3% 1% 65.3 1.88E+06 (K)IKPSAAGLEDSK(M) UG384 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g013580 [S bicolor] >gi|241931829|gb|EES04974.1| hypothet prot SORBIDRAFT_04g013580 [S bicolor]
14.07 2% 0.30% 95.8 6.91E+06 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
12.91 2% 0.60% 85.5 1.68E+05 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
12.78 2% 0.60% 86.4 5.18E+05 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
12.72 2% 0.60% 92.8 2.45E+06 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
12.65 2% 0.70% 90.6 3.92E+06 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
12.63 2% 0.70% 89.6 3.00E+05 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
12.49 2% 0.60% 84.5 5.71E+05 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
12.07 3% 0.80% 88.2 7.04E+05 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
11.99 3% 0.80% 79.2 1.45E+05 (R)IVLLLK(T) UG2569 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g002930 [S bicolor] >gi|241922722|gb|EER95866.1| hypothet prot SORBIDRAFT_02g002930 [S bicolor]
11.51 3% 1.00% 71.9 5.29E+05 (K)IIHISQR(S) CL1015.c1 S.halepenseF3 conserved hypothet prot [Ricinus communis] >gi|223546320|gb|EEF47822.1| conserved hypothet prot [Ricinus communis]
22.22 <0.1% <0.1% 100 4.23E+05 (R)VVAAEPYSLAVLQVSGFVVPPGVR(V) UG4038 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g005190 [S bicolor] >gi|241931477|gb|EES04622.1| hypothet prot SORBIDRAFT_04g005190 [S bicolor]
22.22 <0.1% <0.1% 100 6.99E+05 (R)VVAAEPYSLAVLQVSGFVVPPGVR(V) UG4038 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g005190 [S bicolor] >gi|241931477|gb|EES04622.1| hypothet prot SORBIDRAFT_04g005190 [S bicolor]
17.87 <0.1% <0.1% 86.4 1.45E+05 (R)VVAAEPYSLAVLQVSGFVVPPGVR(V) UG4038 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g005190 [S bicolor] >gi|241931477|gb|EES04622.1| hypothet prot SORBIDRAFT_04g005190 [S bicolor]
16.37 <0.1% <0.1% 75.1 9.99E+04 (R)VVAAEPYSLAVLQVSGFVVPPGVR(V) UG4038 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g005190 [S bicolor] >gi|241931477|gb|EES04622.1| hypothet prot SORBIDRAFT_04g005190 [S bicolor]
13.46 2% 0.50% 72.1 2.60E+05 (R)VVAAEPYSLAVLQVSGFVVPPGVR(V) UG4038 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g005190 [S bicolor] >gi|241931477|gb|EES04622.1| hypothet prot SORBIDRAFT_04g005190 [S bicolor]
11.96 3% 0.80% 63.8 9.82E+04 (R)VVAAEPYSLAVLQVSGFVVPPGVR(V) UG4038 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g005190 [S bicolor] >gi|241931477|gb|EES04622.1| hypothet prot SORBIDRAFT_04g005190 [S bicolor]
11.83 3% 0.90% 66.3 7.99E+04 (R)VVAAEPYSLAVLQVSGFVVPPGVR(V) UG4038 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g005190 [S bicolor] >gi|241931477|gb|EES04622.1| hypothet prot SORBIDRAFT_04g005190 [S bicolor]
11.57 3% 1.00% 78.3 1.11E+06 (R)ATISSAAPAGQR(N) UG4038 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g005190 [S bicolor] >gi|241931477|gb|EES04622.1| hypothet prot SORBIDRAFT_04g005190 [S bicolor]
18.65 <0.1% <0.1% 89.3 4.14E+06 (R)AAATAGGAVGDYAR(D) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
17.74 <0.1% <0.1% 85.8 2.94E+06 (R)AAATAGGAVGDYAR(D) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
17.25 <0.1% <0.1% 78.1 1.44E+06 (K)ASCAATPHPDVCLR(A) C:Carbamidomethylation UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
16.17 <0.1% <0.1% 81.5 4.64E+05 (R)AAATAGGAVGDYAR(D) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
15.35 0.20% <0.1% 85.9 1.57E+06 (R)VANALIK(R) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
14.9 0.20% <0.1% 62.9 1.53E+05 (K)DNLmWQCLNECAEDIEEALDHLDDSEGGLDDDKLR(D) C:Carbamidomethylation m:Oxidized methionine UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
14.8 0.20% <0.1% 70.9 2.11E+06 (K)ASCAATPHPDVCLR(A) C:Carbamidomethylation UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
14.43 2% <0.1% 80.4 9.28E+05 (R)ALQDDHSIK(G) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
14.33 2% <0.1% 66.6 2.70E+05 (K)ASCAATPHPDVCLR(A) C:Carbamidomethylation UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]

13.33 2% 0.50% 84 2.74E+06 (R)VANALIK(R) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
13.29 2% 0.50% 89 3.16E+06 (R)DLASAAIR(A) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
12.66 2% 0.60% 80.2 2.84E+06 (K)HAPNTPIK(T) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
12.33 2% 0.70% 81.6 3.43E+06 (K)HAPNTPIK(T) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
12.12 3% 0.80% 77.2 1.10E+06 (R)VANALIK(R) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
11.61 3% 0.90% 83.9 1.93E+06 (K)TTLLAK(N) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
11.59 3% 1.00% 79.7 3.68E+06 (K)TTLLAK(N) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
11.35 3% 1.00% 64.4 2.70E+05 (K)ASCAATPHPDVCLR(A) C:Carbamidomethylation UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
10.12 3% 1% 76.8 1.94E+06 (R)DLASAAIR(A) UG428 S.halepenseF1 hypothet prot SORBIDRAFT_01g002330 [S bicolor] >gi|241917427|gb|EER90571.1| hypothet prot SORBIDRAFT_01g002330 [S bicolor]
10.09 3% 1% 64.1 6.83E+05 (R)SGSYPTWLmXAETRDCSSSHLLFVQNHXSRVSGG(-) C:Carbamidomethylation m:Oxidized methionine UG6608 S.halepenseF2 hypothet prot SORBIDRAFT_02g026100 [S bicolor] >gi|241925844|gb|EER98988.1| hypothet prot SORBIDRAFT_02g026100 [S bicolor]
11.12 3% 1% 72.3 1.66E+05 (R)TYLVVVCR(A) C:Carbamidomethylation UG5170 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
11.31 3% 1.00% 78.8 7.42E+03 (R)LLIGGRDAVQQALDR(L) UG1558 S.halepenseF1 "hypothet prot SORBIDRAFT_01g047880 [S bicolor] >gi|92429672|gb|ABE77205.1| putative complex 1 protein, LYR family [S bicolor] >gi|241922407|gb|EER95551.1| hypothet prot SORBIDRAFT_01g047880 [S bicolor]"
18.55 <0.1% <0.1% 94.4 8.55E+03 (K)ARPEAVTSGATAAmVSSLQALATVVPGLAYIHAGPVLR(L) UG17074 S.halepenseF3RevF3Rev unknown [Zea mays]
16.82 <0.1% <0.1% 87.3 3.18E+05 (K)ARPEAVTSGATAAmVSSLQALATVVPGLAYIHAGPVLR(L) m:Oxidized methionine UG17074 S.halepenseF3RevF3Rev unknown [Zea mays]
15.46 0.20% <0.1% 73.7 6.43E+05 (R)SPAAEALGPTHLLHSR(Y) UG17074 S.halepenseF3RevF3Rev unknown [Zea mays]
13.13 2% 0.60% 76.3 1.22E+05 (K)ARPEAVTSGATAAmVSSLQALATVVPGLAYIHAGPVLR(L) m:Oxidized methionine UG17074 S.halepenseF3RevF3Rev unknown [Zea mays]
11.77 3% 0.90% 68 8.55E+03 (K)ARPEAVTSGATAAMVSSLQALATVVPGLAYIHAGPVLR(L) UG17074 S.halepenseF3RevF3Rev unknown [Zea mays]
20.39 <0.1% <0.1% 82.3 7.28E+05 (K)VEGGGEmQVVDK(I) m:Oxidized methionine UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
19.22 <0.1% <0.1% 90.2 6.88E+05 (K)DVGAVNTWLSAAK(I) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
17.61 <0.1% <0.1% 81.7 3.50E+05 (K)VEGGGEmQVVDK(I) m:Oxidized methionine UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
16.92 <0.1% <0.1% 86.5 3.23E+05 (K)IDGDTCMNDCQK(V) C:Carbamidomethylation UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
16.22 <0.1% <0.1% 81.2 2.87E+05 (K)DVGAVNTWLSAAK(I) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
16.13 <0.1% <0.1% 75.9 4.54E+05 (K)FQGALADLQR(S) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
15.51 0.20% <0.1% 77.6 8.52E+05 (K)AAAEQGGLTGLAELSLAQAAQVGTETVAFVK(G) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
14.13 2% 0.30% 63.1 1.28E+05 (K)VEGGGEmQVVDK(I) m:Oxidized methionine UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
14.03 2% 0.30% 72.8 7.86E+05 (K)FQGALADLQR(S) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
13.89 2% 0.40% 75.7 4.74E+05 (K)VEGGGEMQVVDK(I) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
13.79 2% 0.50% 79 2.72E+05 (K)SLSSAKPEAK(A) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
13.71 2% 0.50% 74.1 2.27E+05 (R)MCSIAMSLTDASR(N) C:Carbamidomethylation UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
13.09 2% 0.60% 66.6 2.55E+05 (K)FQGALADLQR(S) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
12.97 2% 0.60% 70.8 4.60E+05 (K)FQGALADLQR(S) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
12.32 2% 0.70% 61.4 1.06E+06 (K)YPELCVK(S) C:Carbamidomethylation UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
11.3 3% 1.00% 60.4 1.41E+05 (R)mCSIAmSLTDASR(N) C:Carbamidomethylation m:Oxidized methionine UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
11.25 3% 1% 65.2 2.08E+05 (K)FQGALADLQR(S) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
10.53 3% 1% 72.1 2.29E+05 (K)AAAEQGGLTGLAELSLAQAAQVGTETVAFVK(G) UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
10.16 3% 1% 64.4 3.01E+05 (R)MCSIAmSLTDASR(N) C:Carbamidomethylation m:Oxidized methionine UG403 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g002320 [S bicolor] >gi|241917426|gb|EER90570.1| hypothet prot SORBIDRAFT_01g002320 [S bicolor]
10.81 3% 1% 71.3 1.81E+05 (K)TDTIAYCTGR(S) C:Carbamidomethylation UG2389 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g007500 [S bicolor] >gi|241929424|gb|EES02569.1| hypothet prot SORBIDRAFT_03g007500 [S bicolor]
10.07 5% 1% 66.9 6.09E+04 (R)RLDAPLDAWAYQDHAYPTTVAR(F) UG2389 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g007500 [S bicolor] >gi|241929424|gb|EES02569.1| hypothet prot SORBIDRAFT_03g007500 [S bicolor]
17.47 <0.1% <0.1% 84.6 5.03E+05 (K)FANACGAITTTK(K) C:Carbamidomethylation UG4279 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g042460 [S bicolor] >gi|241930884|gb|EES04029.1| hypothet prot SORBIDRAFT_03g042460 [S bicolor]
15.03 0.20% <0.1% 83.5 1.54E+05 (K)DPSSLQDEK(K) UG4279 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g042460 [S bicolor] >gi|241930884|gb|EES04029.1| hypothet prot SORBIDRAFT_03g042460 [S bicolor]

11.16 3% 1% 62.3 9.50E+04 (K)GAIPSLPTEAEVLQLIEK(A) UG4279 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g042460 [S bicolor] >gi|241930884|gb|EES04029.1| hypothet prot SORBIDRAFT_03g042460 [S bicolor]
10.47 3% 1% 77.5 1.78E+05 (K)GAIPSLPTEAEVLQLIEK(A) UG4279 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g042460 [S bicolor] >gi|241930884|gb|EES04029.1| hypothet prot SORBIDRAFT_03g042460 [S bicolor]
10.13 3% 1% 66.6 2.91E+05 (R)DFHGAVPSFK(V) UG4279 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g042460 [S bicolor] >gi|241930884|gb|EES04029.1| hypothet prot SORBIDRAFT_03g042460 [S bicolor]
14.41 2% <0.1% 83.3 4.55E+05 (K)EAGALLSYDPNLR(E) UG8947 S.halepenseF2 hypothet prot SORBIDRAFT_03g042460 [S bicolor] >gi|241930884|gb|EES04029.1| hypothet prot SORBIDRAFT_03g042460 [S bicolor]
21.2 <0.1% <0.1% 93.6 1.26E+06 (R)LPLWPSPDAAR(E) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
19.67 <0.1% <0.1% 83.6 5.80E+05 (K)VDTIDTTGAGDAFVGSLLVNVAK(D) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
19.48 <0.1% <0.1% 83.8 3.90E+05 (R)NPSADmLLTEAELNLDLIR(R) m:Oxidized methionine CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
19.44 <0.1% <0.1% 92.9 1.94E+06 (K)APGGAPANVACAIAK(L) C:Carbamidomethylation CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
19.09 <0.1% <0.1% 90.2 3.84E+05 (R)LPLWPSPDAAR(E) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
18.41 <0.1% <0.1% 90.1 4.08E+05 (R)NPSADmLLTEAELNLDLIR(R) m:Oxidized methionine CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
18.17 <0.1% <0.1% 85.6 1.98E+05 (K)NVLSLWFEGLK(L) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
17.99 <0.1% <0.1% 86.4 2.97E+05 (K)GAIPALPTVATAQELIAK(A) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
17.65 <0.1% <0.1% 87 5.37E+05 (K)VSDDEVAFLTK(G) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
16.75 <0.1% <0.1% 83.3 5.69E+05 (K)NVLSLWFEGLK(L) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
16.72 <0.1% <0.1% 87.8 4.78E+05 (K)KGAIPALPTVATAQELIAK(A) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
16.27 <0.1% <0.1% 81.6 5.14E+05 (R)NPSADmLLTEAELNLDLIR(R) m:Oxidized methionine CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
16.07 <0.1% <0.1% 80.3 5.32E+05 (K)VDTIDTTGAGDAFVGSLLVNVAK(D) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
16.06 <0.1% <0.1% 83.7 6.29E+05 (R)LPLWPSPDAAR(E) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
15.81 0.20% <0.1% 80.6 1.65E+05 (K)IFHYGSISLIADPVR(S) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
15.79 0.20% <0.1% 90.2 1.64E+06 (R)TALAFVTLK(H) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
15.73 0.20% <0.1% 77.3 1.44E+06 (K)VSDDEVAFLTK(G) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
15.68 0.20% <0.1% 78.5 7.36E+05 (K)FGDDEFGHmLVNILK(Q) m:Oxidized methionine CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
15.54 0.20% <0.1% 85.3 1.29E+06 (K)AAGILCSYDPNVR(L) C:Carbamidomethylation CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
15.3 0.20% <0.1% 77.2 8.85E+04 (K)GAIPALPTVATAQELIAK(A) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
15.1 0.20% <0.1% 89.1 5.85E+05 (K)GAIPALPTVATAQELIAK(A) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
14.93 0.20% <0.1% 76.2 4.46E+05 (K)DDSIFHNEEK(L) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
14.77 0.20% <0.1% 76.2 5.79E+05 (R)EGILSIWK(E) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
14.74 0.20% <0.1% 81.6 1.51E+05 (K)AAGILCSYDPNVR(L) C:Carbamidomethylation CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
14.65 2% <0.1% 84.6 1.98E+06 (K)LLIVTDGDK(G) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
14.52 2% <0.1% 81.5 9.33E+05 (K)NVLSLWFEGLK(L) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
14.18 2% 0.10% 90.5 1.39E+06 (K)IFHYGSISLIADPVR(S) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13.98 2% 0.30% 87.3 3.15E+05 (R)TALAFVTLK(H) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13.94 2% 0.30% 83.2 1.84E+05 (K)IFHYGSISLIADPVR(S) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13.81 2% 0.50% 69.9 1.83E+05 (K)VSDDEVAFLTK(G) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13.79 2% 0.50% 82.6 1.89E+06 (K)LGGSSAFLGK(F) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13.7 2% 0.50% 70.3 8.41E+04 (K)VDTIDTTGAGDAFVGSLLVNVAK(D) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13.45 2% 0.50% 80.6 1.20E+05 (R)TALAFVTLK(H) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13.34 2% 0.50% 70.7 1.35E+05 (K)VDTIDTTGAGDAFVGSLLVNVAK(D) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]

13.24 2% 0.50% 75.5 9.83E+04 (K)NVLSLWFEGLK(L) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13.23 2% 0.50% 84.9 4.18E+05 (K)IFHYGSISLIADPVR(S) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
13 2% 0.60% 73.7 1.83E+05 (R)LPLWPSPDAAR(E) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.97 2% 0.60% 77.9 8.90E+05 (K)FSNACGAICTTK(K) C:Carbamidomethylation CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.96 2% 0.60% 62.6 3.58E+05 (K)FGDDEFGHMLVNILK(Q) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.54 2% 0.60% 75.2 8.40E+04 (K)NVLSLWFEGLK(L) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.49 2% 0.60% 79.6 2.03E+05 (K)GAIPALPTVATAQELIAK(A) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.47 2% 0.60% 66.9 4.03E+05 (K)VDTIDTTGAGDAFVGSLLVNVAK(D) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.44 2% 0.60% 72.9 7.76E+05 (K)APGGAPANVACAIAK(L) C:Carbamidomethylation CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.43 2% 0.60% 84.1 3.27E+05 (R)TALAFVTLK(H) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.24 3% 0.70% 85.6 4.23E+05 (K)IFHYGSISLIADPVR(S) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.18 3% 0.70% 68.1 8.18E+04 (R)NPSADMLLTEAELNLDLIR(R) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.09 3% 0.70% 73.2 1.29E+06 (K)EADFIK(V) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
11.95 3% 0.90% 68.4 4.56E+05 (K)VDTIDTTGAGDAFVGSLLVNVAK(D) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
11.76 3% 0.90% 74.6 7.80E+05 (K)LGGSSAFLGK(F) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
11.5 3% 1.00% 65.5 4.17E+05 (K)DDSIFHNEEK(L) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
11.14 3% 1% 78.7 8.11E+04 (K)GAIPALPTVATAQELIAK(A) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
11.13 3% 1% 65.7 2.07E+05 (R)EGILSIWK(E) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
10.97 3% 1% 65.1 1.79E+05 (K)AAGILCSYDPNVR(L) C:Carbamidomethylation CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
10.78 3% 1% 68.5 1.74E+04 (R)TALAFVTLK(H) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
10.41 3% 1% 63.9 9.05E+04 (R)NPSADmLLTEAELNLDLIR(R) m:Oxidized methionine CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
10.36 3% 1% 83.3 1.87E+04 (K)GAIPALPTVATAQELIAK(A) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
10.23 3% 1% 67.1 3.47E+05 (K)FSNACGAICTTK(K) C:Carbamidomethylation CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
10.08 5% 1% 63.1 5.47E+05 (K)EADFIK(V) CL1536.c1 S.halepenseF2 fructokinase-2 [Zea mays] >gi|75293603|sp|Q6XZ78.1|SCRK2_MAIZE RecName: Full=Fructokinase-2; AltName: Full=ZmFRK2 >gi|31652276|gb|AAP42806.1| fructokinase 2 [Zea mays]
12.26 3% 0.70% 69.2 2.81E+05 (K)GDAAAGEGVSESLHVK(D) UG2147 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g019020 [S bicolor] >gi|241933653|gb|EES06798.1| hypothet prot SORBIDRAFT_04g019020 [S bicolor]
22.76 <0.1% <0.1% 94.8 4.26E+05 (R)YAIICQENGLVPIVEPEILVDGPHDIDR(C) C:Carbamidomethylation CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
20.15 <0.1% <0.1% 88.3 2.64E+06 (K)GILAADESTGTIGK(R) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
19.91 <0.1% <0.1% 92.8 8.73E+05 (K)VTPELIAEYTVR(T) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
19.78 <0.1% <0.1% 93.9 8.46E+04 (R)YAIICQENGLVPIVEPEILVDGPHDIDR(C) C:Carbamidomethylation CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
19.13 <0.1% <0.1% 89 1.34E+05 (K)GDAAADTESLHVK(D) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
18.04 <0.1% <0.1% 91.4 1.60E+04 (R)TVPAAVPAVVFLSGGQSEEEATLNLNAmNK(L) m:Oxidized methionine CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
16.83 <0.1% <0.1% 72 5.22E+04 (K)ETTTQGHDDLGKR(C) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
16.68 <0.1% <0.1% 84.3 2.46E+05 (K)VTPELIAEYTVR(T) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
16.38 <0.1% <0.1% 73.3 1.47E+06 (K)IGPNEPSQLAIDLNAQGLAR(Y) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
15.91 0.20% <0.1% 80.8 6.61E+05 (K)KVTPELIAEYTVR(T) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
15.26 0.20% <0.1% 77.2 2.92E+06 (K)NAAYIGTPGK(G) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
15.1 0.20% <0.1% 87.3 7.68E+05 (K)ALNEHHVLLEGTLLKPNmVTPGSDSK(K) m:Oxidized methionine CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
15.01 0.20% <0.1% 74.8 1.51E+06 (R)LSSINVENVEENRR(A) CL1434.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]

14	2%	0.30%	75.8	1.42E+06	(K)ANSEATLGTYK(G)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
13.95	2%	0.30%	63.4	1.12E+06	(K)IGPNEPSQLAIDLNAQGLAR(Y)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
13.57	2%	0.50%	72.4	2.09E+05	(K)NAAYIGTPGK(G)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
13.34	2%	0.50%	88.2	1.25E+06	(K)DGKPFVDVLK(E)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
13.19	2%	0.50%	81	1.86E+05	(R)LSSINVENVEENRR(A)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
13.16	2%	0.50%	66.9	4.88E+05	(K)GTIEVAGTDK(E)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
12.33	2%	0.70%	74.8	1.17E+05	(K)GTIEVAGTDKETTTQGHDDLGKR(C)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
12.18	3%	0.70%	74.2	1.60E+05	(K)NAAYIGTPGK(G)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
12.17	3%	0.70%	76	4.15E+05	(K)KPWSLSFSFGR(A)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
12.12	3%	0.80%	70.8	5.17E+04	(K)GILAADESTGTIGK(R)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
11.77	3%	0.90%	61.2	1.63E+05	(K)VTPELIAEYTVR(T)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
11.73	3%	0.90%	72.6	2.27E+05	(R)LSSINVENVEENRR(A)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
11.5	3%	1.00%	76.9	2.14E+05	(K)GILAADESTGTIGK(R)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
11.45	3%	1.00%	73.7	1.08E+05	(K)VTPELIAEYTVR(T)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
10.77	3%	1%	75.2	2.06E+05	(R)LSSINVENVEENRR(A)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
10.68	3%	1%	67	3.06E+05	(K)NAAYIGTPGK(G)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
10.05	5%	1%	72.2	1.77E+05	(K)NAAYIGTPGK(G)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
10.04	5%	1%	77.8	1.24E+05	(K)DGKPFVDVLK(E)		CL1434.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g043140 [S bicolor] >gi|241930919|gb|EES04064.1| hypothet prot SORBIDRAFT_03g043140 [S bicolor]
12.81	2%	0.60%	75	4.00E+05	(R)LSSINVENIEENRR(A)		CL1434.c2	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g019020 [S bicolor] >gi|241933653|gb|EES06798.1| hypothet prot SORBIDRAFT_04g019020 [S bicolor]
13.62	2%	0.50%	72.6	4.86E+04	(K)VVIQGVLGGYAKPPLSETCR(G)	C:Carbamidomethylation	UG994	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g027770 [S bicolor] >gi|241927922|gb|EES01067.1| hypothet prot SORBIDRAFT_03g027770 [S bicolor]
19.97	<0.1%	<0.1%	92.5	3.91E+05	(K)SEPADYDSAGCLR(E)	C:Carbamidomethylation	UG7020	S.halepenseF1	GDSL-lipase [S bicolor]
15.73	0.20%	<0.1%	72.1	4.74E+05	(K)EVLDmGASR(V)	m:Oxidized methionine	UG7020	S.halepenseF1	GDSL-lipase [S bicolor]
13.58	2%	0.50%	78.3	2.60E+05	(K)YLHPQILSFPEK(Y)		UG7020	S.halepenseF1	GDSL-lipase [S bicolor]
12.82	2%	0.60%	66.1	3.09E+05	(K)EVLDmGASR(V)	m:Oxidized methionine	UG7020	S.halepenseF1	GDSL-lipase [S bicolor]
12.52	2%	0.60%	72.9	1.05E+05	(R)VIVPGNFPIGCVPGYLAmNAAK(S)	C:Carbamidomethylation m:Oxidized methionine	UG7020	S.halepenseF1	GDSL-lipase [S bicolor]
11.27	3%	1%	61.7	1.08E+05	(R)LIYHGK(Y)		UG7020	S.halepenseF1	GDSL-lipase [S bicolor]
10.41	3%	1%	62.6	6.10E+05	(K)YLHPQILSFPEK(Y)		UG7020	S.halepenseF1	GDSL-lipase [S bicolor]
19.63	<0.1%	<0.1%	95.1	3.55E+05	(K)ITVDFLASAFGLK(E)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
18.03	<0.1%	<0.1%	76.5	3.87E+05	(K)YVFWDSYHPTER(A)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
17.94	<0.1%	<0.1%	85	1.99E+05	(R)AIGLVEALIGQGAR(Q)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
17.69	<0.1%	<0.1%	87	2.00E+05	(R)AIGLVEALIGQGAR(Q)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
17.17	<0.1%	<0.1%	79.5	4.05E+05	(R)AIGLVEALIGQGAR(Q)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
17.03	<0.1%	<0.1%	81.2	4.82E+05	(K)ITVDFLASAFGLK(E)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
16.59	<0.1%	<0.1%	86.2	8.80E+05	(R)AIGLVEALIGQGAR(Q)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
16.52	<0.1%	<0.1%	81	5.16E+05	(R)AIGLVEALIGQGAR(Q)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
16.25	<0.1%	<0.1%	62.3	1.01E+05	(K)YVFWDSYHPTER(A)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
16.15	<0.1%	<0.1%	76.7	3.51E+05	(R)AIGLVEALIGQGAR(Q)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
16.08	<0.1%	<0.1%	88.6	4.64E+05	(K)ITVDFLASAFGLK(E)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
15.99	<0.1%	<0.1%	83.9	3.02E+05	(K)ITVDFLASAFGLK(E)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
15.87	0.20%	<0.1%	79.1	5.07E+05	(R)AIGLVEALIGQGAR(Q)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
15.38	0.20%	<0.1%	82.8	9.46E+05	(R)AIGLVEALIGQGAR(Q)		UG2188	S.halepenseF1	hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]

15.26 0.20% <0.1% 83.8 5.82E+05 (K)ITVDFLASAFGLK(E) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
15.03 0.20% <0.1% 79.4 1.74E+05 (K)ITVDFLASAFGLK(E) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
14.7 0.20% <0.1% 82.9 9.97E+04 (K)VPALIAFGDSIVDTGNNNYLmTVVK(A) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
14.66 2% <0.1% 79.4 4.56E+05 (R)AIGLVEALIGQGAR(Q) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
13.99 2% 0.30% 78.9 4.69E+05 (R)NQLALLFNR(K) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
13.92 2% 0.40% 76.8 9.59E+04 (R)AIGLVEALIGQGAR(Q) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
13.82 2% 0.50% 81 5.63E+05 (R)AIGLVEALIGQGAR(Q) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
13.71 2% 0.50% 83.5 8.93E+04 (K)VPALIAFGDSIVDTGNNNYLmTVVK(A) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
13.68 2% 0.50% 64.3 6.67E+05 (K)ImIDDFLR(R) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
13.57 2% 0.50% 63.8 4.91E+05 (K)ImIDDFLR(R) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
13.02 2% 0.50% 67.5 3.17E+05 (R)AIGLVEALIGQGAR(Q) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
12.97 2% 0.60% 76 2.53E+05 (K)VSLEVAK(L) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
12.94 2% 0.60% 76.6 2.07E+05 (K)VSLEVAK(L) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
12.73 2% 0.60% 73.8 5.98E+05 (R)AIGLVEALIGQGAR(Q) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
12.72 2% 0.60% 77.6 4.91E+05 (R)NQLALLFNR(K) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
12.49 2% 0.60% 67.2 1.96E+05 (K)VSLEVAK(L) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
12.36 2% 0.70% 62.9 5.21E+05 (K)ImIDDFLR(R) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
12.12 3% 0.80% 74.7 1.20E+05 (K)IMIDDFLR(R) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
12.03 3% 0.80% 71.3 1.07E+05 (K)ITVDFLASAFGLK(E) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
11.83 3% 0.90% 72.3 1.02E+05 (K)ITVDFLASAFGLK(E) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
11.75 3% 0.90% 64 2.35E+05 (R)TSSTmTIER(Q) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
11.66 3% 0.90% 66.4 9.20E+04 (R)AIGLVEALIGQGAR(Q) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
11.58 3% 1.00% 67.7 2.39E+05 (R)TSSTmTIER(Q) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
11.47 3% 1.00% 65.7 2.18E+05 (R)AIGLVEALIGQGAR(Q) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
11.18 3% 1% 72.3 3.90E+05 (R)NQLALLFNR(K) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
11.08 3% 1% 76.5 1.56E+05 (K)IMIDDFLR(R) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
10.82 3% 1% 73 2.72E+05 (K)VSLEVAK(L) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
10.75 3% 1% 75.9 6.97E+05 (R)NQLALLFNR(K) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
10.73 3% 1% 66.6 1.47E+05 (K)VPALIAFGDSIVDTGNNNYLmTVVK(A) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
10.56 3% 1% 63.3 3.37E+04 (R)QLQLFSEYK(A) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
10.51 3% 1% 65.1 1.86E+05 (R)AIGLVEALIGQGAR(Q) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
10.47 3% 1% 71.4 8.15E+04 (K)ITVDFLASAFGLK(E) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
10.31 3% 1% 64.3 1.96E+05 (R)TSSTmTIER(Q) m:Oxidized methionine UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
10.26 3% 1% 73 3.80E+05 (K)ETLPPYLNK(N) UG2188 S.halepenseF1 hypothet prot SORBIDRAFT_01g026440 [S bicolor] >gi|241918611|gb|EER91755.1| hypothet prot SORBIDRAFT_01g026440 [S bicolor]
17.92 <0.1% <0.1% 88.4 5.97E+05 (K)RPGVPVEVFLFDLYDEDGKPGPEFER(H) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
17.24 <0.1% <0.1% 79 4.88E+05 (R)SAVLAHAPADR(V) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
16.88 <0.1% <0.1% 74.9 3.53E+05 (K)IGICHGR(V) C:Carbamidomethylation CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
15.05 0.20% <0.1% 80 2.74E+06 (R)SAVLAHAPADR(V) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]

14.98 0.20% <0.1% 73 4.75E+04 (R)YLAVGNEVLYNNQFYAPHLVPAmR(N) m:Oxidized methionine CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
14.14 2% 0.30% 76 8.59E+05 (R)SAVLAHAPADR(V) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
13.56 2% 0.50% 80.9 4.14E+05 (R)NLHAALAALGLGGR(V) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
12.81 2% 0.60% 80.4 6.32E+05 (R)NLHAALAALGLGGR(V) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
12.44 2% 0.60% 77.4 6.53E+04 (R)NLHAALAALGLGGR(V) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
11.78 3% 0.90% 75.8 4.09E+05 (R)SAVLAHAPADR(V) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
11.24 3% 1% 63.2 3.23E+05 (K)RPGVPVEVFLFDLYDEDGKPGPEFER(H) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
11.1 3% 1% 72.8 3.19E+05 (R)VGSNLPPPSAAAALLK(Q) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
10.64 3% 1% 72.6 5.98E+05 (R)VGSNLPPPSAAAALLK(Q) CL369.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g030930 [S bicolor] >gi|241926101|gb|EER99245.1| hypothet prot SORBIDRAFT_02g030930 [S bicolor]
19.27 <0.1% <0.1% 90.7 2.58E+05 (K)ALDEAGVGDK(V) CL546.c1 S.halepenseF1 hypothet prot SORBIDRAFT_10g022940 [S bicolor] >gi|241916843|gb|EER89987.1| hypothet prot SORBIDRAFT_10g022940 [S bicolor]
16.86 <0.1% <0.1% 86.9 3.12E+05 (K)LLSPVTDVK(Y) CL546.c1 S.halepenseF1 hypothet prot SORBIDRAFT_10g022940 [S bicolor] >gi|241916843|gb|EER89987.1| hypothet prot SORBIDRAFT_10g022940 [S bicolor]
16.39 <0.1% <0.1% 80.8 1.31E+05 (-)DISLGYATFQPGTTVR(D) UG4158 S.halepenseF2 hypothet prot SORBIDRAFT_03g045490 [S bicolor] >gi|241931052|gb|EES04197.1| hypothet prot SORBIDRAFT_03g045490 [S bicolor]
18.62 <0.1% <0.1% 84.7 3.72E+05 (R)VIPCDFIGVVK(S) C:Carbamidomethylation CL2264.c2 S.halepenseF1 hypothet prot SORBIDRAFT_01g006470 [S bicolor] >gi|241917659|gb|EER90803.1| hypothet prot SORBIDRAFT_01g006470 [S bicolor]
15.71 0.20% <0.1% 70.1 4.84E+05 (K)FLEGASSIDNHFNSSSFEK(N) CL2264.c2 S.halepenseF1 hypothet prot SORBIDRAFT_01g006470 [S bicolor] >gi|241917659|gb|EER90803.1| hypothet prot SORBIDRAFT_01g006470 [S bicolor]
14.91 0.20% <0.1% 76 6.63E+05 (R)YLAVKPPTPYDTTVLPK(V) CL2264.c2 S.halepenseF1 hypothet prot SORBIDRAFT_01g006470 [S bicolor] >gi|241917659|gb|EER90803.1| hypothet prot SORBIDRAFT_01g006470 [S bicolor]
13.71 2% 0.50% 73 2.49E+05 (R)YSVCSAVGVLPLSLQYGFPIVQK(F) C:Carbamidomethylation CL2264.c2 S.halepenseF1 hypothet prot SORBIDRAFT_01g006470 [S bicolor] >gi|241917659|gb|EER90803.1| hypothet prot SORBIDRAFT_01g006470 [S bicolor]
13.11 2% 0.60% 67.5 2.49E+05 (R)YSVCSAVGVLPLSLQYGFPIVQK(F) C:Carbamidomethylation CL2264.c2 S.halepenseF1 hypothet prot SORBIDRAFT_01g006470 [S bicolor] >gi|241917659|gb|EER90803.1| hypothet prot SORBIDRAFT_01g006470 [S bicolor]
12.62 2% 0.70% 81.2 3.23E+05 (K)TPEQLHSEK(V) CL2264.c2 S.halepenseF1 hypothet prot SORBIDRAFT_01g006470 [S bicolor] >gi|241917659|gb|EER90803.1| hypothet prot SORBIDRAFT_01g006470 [S bicolor]
10.72 3% 1% 65 6.01E+05 (R)AILPYSQALEK(L) CL2264.c2 S.halepenseF1 hypothet prot SORBIDRAFT_01g006470 [S bicolor] >gi|241917659|gb|EER90803.1| hypothet prot SORBIDRAFT_01g006470 [S bicolor]
17.73 <0.1% <0.1% 84.8 1.30E+05 (R)DAVINSDGVNVVPEVWSVK(D) UG4129 S.halepenseF2 glucose-6-phosphate isomerase [Miscanthus sinensis]
12.89 2% 0.60% 70.8 2.03E+05 (K)DLDPETTLVVVVSK(T) UG4129 S.halepenseF2 glucose-6-phosphate isomerase [Miscanthus sinensis]
12.72 2% 0.60% 77.9 1.43E+05 (R)DAVINSDGVNVVPEVWSVK(D) UG4129 S.halepenseF2 glucose-6-phosphate isomerase [Miscanthus sinensis]
12.49 2% 0.60% 76.3 6.99E+05 (R)FLANVDPVDVAR(S) UG4129 S.halepenseF2 glucose-6-phosphate isomerase [Miscanthus sinensis]
10.5 3% 1% 69.3 2.22E+05 (K)EWIVSSLGPQAVAK(H) UG4129 S.halepenseF2 glucose-6-phosphate isomerase [Miscanthus sinensis]
10.42 3% 1% 63.2 7.94E+04 (R)FLANVDPVDVAR(S) UG4129 S.halepenseF2 glucose-6-phosphate isomerase [Miscanthus sinensis]
11.75 3% 0.90% 76.7 4.33E+05 (R)LIADLGK(T) UG1544 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018050 [S bicolor] >gi|241939103|gb|EES12248.1| hypothet prot SORBIDRAFT_06g018050 [S bicolor]
10.6 3% 1% 73.2 8.22E+04 (K)LIQSSINK(N) UG1544 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018050 [S bicolor] >gi|241939103|gb|EES12248.1| hypothet prot SORBIDRAFT_06g018050 [S bicolor]
16.39 <0.1% <0.1% 85.5 4.36E+05 (R)TLSGPVTDPSK(L) UG1774 S.halepenseF2Rev glutamine synthetase [Saccharum officinarum]
12.32 2% 0.70% 75.4 1.27E+05 (K)LVPLLTEAGAIAGSTSK(T) CL2302.c2 S.halepenseF2Rev hypothet prot SORBIDRAFT_06g022060 [S bicolor] >gi|241937949|gb|EES11094.1| hypothet prot SORBIDRAFT_06g022060 [S bicolor]
17.77 <0.1% <0.1% 90.7 1.46E+05 (K)LYGAVMSWNVTR(C) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
15.85 0.20% <0.1% 76.4 5.39E+05 (R)NPFGQVPALQDGDLYLFESR(A) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
14.05 2% 0.30% 67.9 2.59E+05 (K)LYGAVmSWNVTR(C) m:Oxidized methionine UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
12.96 2% 0.60% 68.3 5.68E+05 (R)NPFGQVPALQDGDLYLFESR(A) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
12.46 2% 0.60% 72.2 1.45E+06 (K)VLEVYEAR(L) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
12.24 3% 0.70% 76.2 2.08E+06 (K)VVDENLEK(L) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
11.25 3% 1% 60.3 7.68E+04 (K)SPEHLAR(N) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
11.02 3% 1% 62.6 7.94E+05 (K)VLEVYEAR(L) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
10.39 3% 1% 71.1 5.04E+05 (R)NPFGQVPALQDGDLYLFESR(A) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
10.07 5% 1% 66.2 7.84E+04 (R)NPFGQVPALQDGDLYLFESR(A) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
10.05 5% 1% 73.5 1.99E+05 (R)NPFGQVPALQDGDLYLFESR(A) UG3644 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035420 [S bicolor] >gi|241930516|gb|EES03661.1| hypothet prot SORBIDRAFT_03g035420 [S bicolor]
20.93 <0.1% <0.1% 91 3.80E+05 (K)LVDLGNKPEWFLEINPEGK(V) UG4080 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]

18.29	<0.1%	<0.1%	81.8	3.66E+05	(K)LVDLGNKPEWFLEINPEGK(V)		UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]
16.92	<0.1%	<0.1%	84	6.23E+03	(K)FPTPSLVTPPEYASVGSK(I)		UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]
16.16	<0.1%	<0.1%	84.6	4.65E+05	(K)ALLDELQALDEHLK(A)		UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]
15.75	0.20%	<0.1%	89.9	4.45E+05	(K)ALLDELQALDEHLK(A)		UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]
14.88	0.20%	<0.1%	80.1	2.91E+05	(K)FPTPSLVTPPEYASVGSK(I)		UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]
14.39	2%	<0.1%	70.6	5.80E+05	(K)IFPAFVK(F)	UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]	
14.29	2%	<0.1%	73.4	9.46E+04	(K)ALLDELQALDEHLK(A)		UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]
13.8	2%	0.50%	69.8	1.32E+05	(K)LFHLQVALEHFK(G)	UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]	
12.54	2%	0.60%	69.5	8.17E+04	(K)ALLDELQALDEHLK(A)		UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]
11.72	3%	0.90%	79.3	3.27E+05	(R)VLLTLEEK(K)	UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]	
11.24	3%	1%	70.2	2.65E+05	(K)FPTPSLVTPPEYASVGSK(I)		UG4080	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g001700 [S bicolor] >gi|241945767|gb|EES18912.1| hypothet prot SORBIDRAFT_09g001700 [S bicolor]
11.34	3%	1.00%	70.8	4.64E+05	(K)AGIALNDNFIK(L)	UG2498	S.halepenseF3	"RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 1 >gi|295853|emb|CAA33620.1| GAPDH [Zea mays] >gi|195606702|gb|ACG25181.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays]"	
13.84	2%	0.40%	78.2	7.46E+05	(K)VIHDNFGIIEGLmTTVHAITATQK(T)	m:Oxidized methionine	CL367.c1	S.halepenseF1	hypothet prot [Zea mays]
12.93	2%	0.60%	69.4	1.27E+05	(K)VIHDNFGIIEGLMTTVHAITATQK(T)		CL367.c1	S.halepenseF1	hypothet prot [Zea mays]
24.18	<0.1%	<0.1%	91.3	2.13E+05	(K)GILGYVDEDLVSTDFQGDSR(S)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
20.44	<0.1%	<0.1%	94.5	4.14E+05	(R)VPTVDVSVVDLTVR(L)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
20.16	<0.1%	<0.1%	88.7	1.16E+06	(R)VPTVDVSVVDLTVR(L)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
19.05	<0.1%	<0.1%	82.4	4.01E+05	(K)FGIVEGLMTTVHAITATQK(T)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
18.19	<0.1%	<0.1%	91.8	1.60E+05	(K)SDINIVSNASCTTNCLAPLAK(V)	C:Carbamidomethylation	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
18.12	<0.1%	<0.1%	88.9	3.05E+05	(R)VPTVDVSVVDLTVR(L)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
17.29	<0.1%	<0.1%	89.1	1.80E+05	(R)VPTVDVSVVDLTVR(L)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
17.26	<0.1%	<0.1%	74.4	9.85E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
17.24	<0.1%	<0.1%	76.3	1.43E+05	(K)GILGYVDEDLVSTDFQGDSR(S)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
16.8	<0.1%	<0.1%	77.5	1.22E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
16.46	<0.1%	<0.1%	78.2	8.60E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
16.19	<0.1%	<0.1%	84.8	9.49E+05	(K)TLLFGEK(E)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
15.69	0.20%	<0.1%	68.5	1.79E+04	(K)YDTVHGQWK(H)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
15.46	0.20%	<0.1%	73.6	7.38E+05	(K)DAPmFVVGVNEK(E)	m:Oxidized methionine	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
15.31	0.20%	<0.1%	75	2.09E+05	(R)VPTVDVSVVDLTVR(L)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
14.9	0.20%	<0.1%	77.4	3.33E+05	(K)LVSWYDNEWGYSTR(V)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
14.24	2%	<0.1%	63.3	2.89E+05	(K)GILGYVDEDLVSTDFQGDSR(S)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
14.2	2%	<0.1%	69	3.67E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
13.96	2%	0.30%	71.9	7.91E+04	(K)FGIVEGLMTTVHAITATQK(T)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
13.43	2%	0.50%	66.6	1.46E+05	(K)GILGYVDEDLVSTDFQGDSR(S)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
13.38	2%	0.50%	88.9	1.29E+06	(K)VVISAPSK(D)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
13.02	2%	0.50%	67.8	1.30E+06	(K)SATYDEIK(A)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
12.85	2%	0.60%	73.6	3.60E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
12.73	2%	0.60%	72.3	1.53E+06	(K)EVAVFGSR(N)		CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
12.47	2%	0.60%	69.9	5.81E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]

12.41	2%	0.60%	76.4	2.09E+05	(K)TLLFGEK(E)	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
12.2	3%	0.70%	81.6	1.94E+06	(R)SSIFDAK(A)	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
12.17	3%	0.70%	69.4	2.12E+05	(K)SATYDEIK(A)	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
11.14	3%	1%	68.6	1.22E+06	(K)KVVISAPSK(D)	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
11.05	3%	1%	75.2	1.09E+06	(K)TLLFGEK(E)	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
10.97	3%	1%	69.8	2.06E+05	(K)KVVISAPSK(D)	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
10.66	3%	1%	80	1.11E+05	(K)TLLFGEK(E)	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
10.64	3%	1%	76.6	4.09E+05	(K)TLLFGEK(E)	CL367.c2	S.halepenseF2	hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
10.33	3%	1%	62.9	1.69E+05	(K)FGIVEGLmTTVHAITATQK(T)	m:Oxidized methionine	CL367.c2	S.halepenseF2 hypothet prot SORBIDRAFT_04g025120 [S bicolor] >gi|241932232|gb|EES05377.1| hypothet prot SORBIDRAFT_04g025120 [S bicolor]
18.18	<0.1%	<0.1%	86.5	2.34E+05	(K)LSEEPGLVNASPYEK(G)	UG3149	S.halepenseF2Rev	hypothet prot SORBIDRAFT_04g004720 [S bicolor] >gi|241931449|gb|EES04594.1| hypothet prot SORBIDRAFT_04g004720 [S bicolor]
25.25	<0.1%	<0.1%	97.5	3.33E+05	(K)AYTGADAGGGVSGGGSGGAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
23.19	<0.1%	<0.1%	88.8	1.81E+05	(K)AYTGADAGGGVSGGGSGGAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
22.78	<0.1%	<0.1%	90.8	6.57E+05	(K)AYTGADAGGGVSGGGSGGAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
22.14	<0.1%	<0.1%	94.9	4.54E+05	(K)VDAGVGGDASVSGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
21.53	<0.1%	<0.1%	86.8	2.26E+05	(K)AYTGADAGGGVSGGGSGGAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
21.29	<0.1%	<0.1%	87.3	1.24E+05	(K)AYTGADAGGGVSGGGSGGAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
20.23	<0.1%	<0.1%	88.3	7.79E+05	(K)VDAGVGGDASVSGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
20.09	<0.1%	<0.1%	92.6	7.67E+05	(K)AEDEVVAAAAAK(T)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
19.95	<0.1%	<0.1%	91.6	4.88E+05	(K)SAAAVGGETAGNVDASGK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
19.83	<0.1%	<0.1%	85.3	4.86E+05	(K)AYTGADAGGGVSGGGSGGAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
19.8	<0.1%	<0.1%	90	5.24E+05	(K)AEDEVVAAAAAK(T)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
19.52	<0.1%	<0.1%	87.5	1.83E+05	(K)VEAEAVADAQAmDK(A)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
19.29	<0.1%	<0.1%	87	1.42E+05	(K)SAAAVGGETAGNVDASGK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
19.16	<0.1%	<0.1%	87.9	1.03E+06	(K)AEDEVVAAAAAK(T)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
18.91	<0.1%	<0.1%	81.5	3.45E+05	(K)AEDEVVAAAAAK(T)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
18.91	<0.1%	<0.1%	82.8	2.41E+05	(K)SAAAVGGETAGNVDASGK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
18.81	<0.1%	<0.1%	78.1	2.07E+05	(K)IGGDASAGADASAGAGGNAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
18.71	<0.1%	<0.1%	80	3.25E+05	(K)AYTGADAGGGVSGGGSGGAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
18.64	<0.1%	<0.1%	90.2	1.09E+06	(K)SAAAVGGETAGNVDASGK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
18.61	<0.1%	<0.1%	83.2	1.37E+06	(K)ADIGGTVGGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
18.3	<0.1%	<0.1%	83.6	4.08E+05	(K)VDAGVGGDASVSGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
18.17	<0.1%	<0.1%	78.9	2.34E+05	(K)VEAEAVADAQAmDK(A)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
17.65	<0.1%	<0.1%	83.9	7.12E+05	(K)SAAAVGGETAGNVDASGK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
17.62	<0.1%	<0.1%	88.2	3.82E+06	(K)AAGEATLLLK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
17.58	<0.1%	<0.1%	80.5	7.83E+05	(K)VEAEAVADAQAmDKAEDEVVAAAAAK(T)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
17.43	<0.1%	<0.1%	81	3.04E+05	(K)VEAEAVADAQAmDK(A)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
17.38	<0.1%	<0.1%	83	7.67E+05	(K)ADIGGTVGGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
17.24	<0.1%	<0.1%	77.2	1.08E+05	(K)IGGDASAGADASAGAGGNAK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
17.24	<0.1%	<0.1%	87	3.02E+06	(K)AAGEATLLLK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
17.14	<0.1%	<0.1%	77.8	2.09E+05	(K)VDAGVGGDASVSGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.96	<0.1%	<0.1%	86.5	4.14E+05	(K)AGGDATVGGGVSGGAK(V)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.92	<0.1%	<0.1%	79.8	6.06E+05	(K)VEAEAVADAQAmDKAEDEVVAAAAAK(T)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.83	<0.1%	<0.1%	83.7	7.31E+05	(K)AAGEATLLLK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.77	<0.1%	<0.1%	87.6	2.59E+06	(K)AAGEATLLLK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.76	<0.1%	<0.1%	79.5	5.74E+05	(K)ASTTPENKPSAPTKPDPEFVK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.76	<0.1%	<0.1%	86.6	2.37E+06	(K)AAGEATLLLK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.61	<0.1%	<0.1%	88.1	1.11E+06	(K)ADIGGTVGGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.51	<0.1%	<0.1%	83.2	3.45E+06	(K)ASTTPENKPSAPTKPDPEFVK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.4	<0.1%	<0.1%	74.8	2.33E+05	(K)GGAGGYVGGK(T)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.4	<0.1%	<0.1%	73.4	5.82E+05	(K)ISGGIHFSAGAR(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.39	<0.1%	<0.1%	82.1	1.34E+06	(K)ADIGGTVGGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.37	<0.1%	<0.1%	76.1	8.79E+05	(K)VEAEAVADAQAmDKAEDEVVAAAAAK(T)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.36	<0.1%	<0.1%	79.5	2.03E+05	(K)GGAGGYVGGK(T)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.32	<0.1%	<0.1%	81.2	3.88E+06	(K)ADIGGTVGGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.17	<0.1%	<0.1%	82.2	3.53E+05	(K)SAAAVGGETAGNVDASGK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.13	<0.1%	<0.1%	77.1	1.66E+05	(K)VDAGVGGDASVSGGVSGGAK(I)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.04	<0.1%	<0.1%	83.4	1.75E+05	(K)VEAEAVADAQAmDK(A)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
16.02	<0.1%	<0.1%	85.3	3.05E+06	(R)VVVGVDIK(V)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.88	0.20%	<0.1%	81.7	3.34E+05	(K)VEAEAVADAQAmDK(A)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.81	0.20%	<0.1%	80.9	1.04E+06	(R)VVVGVDIK(V)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.77	0.20%	<0.1%	74.7	4.51E+05	(K)GGAGGYVGGK(T)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.71	0.20%	<0.1%	79	1.18E+06	(K)AAGEATLLLK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.69	0.20%	<0.1%	82.6	9.30E+05	(K)AGGDATVGGGVSGGAK(V)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.62	0.20%	<0.1%	86.8	5.66E+05	(R)VVVGVDIK(V)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.56	0.20%	<0.1%	90.2	3.03E+06	(R)VVVGVDIK(V)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.46	0.20%	<0.1%	82.2	6.92E+05	(K)AAGEATLLLK(A)	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]

15.41	0.20%	<0.1%	76	1.24E+06	(R)VVVGVDIK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
15.14	0.20%	<0.1%	82.7	2.56E+05	(K)SAAAVGGETAGNVDASGK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.97	0.20%	<0.1%	71.8	1.00E+06	(K)ADIGGTVGGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.92	0.20%	<0.1%	69.8	1.56E+05	(K)AAATDAAMAQK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.84	0.20%	<0.1%	67.4	1.34E+05	(K)IGGDASAGADASAGAGAGGNAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.65	2%	<0.1%	85.7	1.51E+06	(K)AAGEATLLLK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.61	2%	<0.1%	79.7	2.50E+05	(K)AGGDATVGGGVSGGAK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.32	2%	<0.1%	80.6	2.57E+05	(R)LQQDVLKK(T)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.29	2%	<0.1%	82	3.08E+05	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.2	2%	<0.1%	83.5	1.87E+06	(R)LQQDVLK(K)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14.06	2%	0.30%	77.6	5.45E+05	(K)ADIGGTVGGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
14	2%	0.30%	69.9	4.46E+05	(K)AYTGADAGGGVSGGGSGGAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.94	2%	0.30%	88.2	6.41E+05	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.9	2%	0.40%	71	1.07E+05	(K)GGAGGYVGGK(T)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.88	2%	0.40%	81.4	2.43E+06	(R)LQQDVLK(K)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.84	2%	0.40%	81.3	6.24E+05	(K)AAATDAAMAQK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.82	2%	0.50%	72.5	2.03E+05	(K)AYTGADAGGGVSGGGSGGAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.78	2%	0.50%	72.6	2.68E+06	(K)HHPTVAAEDTIK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.78	2%	0.50%	72.3	3.23E+04	(K)DLCAVAGDIAISmSALAEGAAGISGR(V)		C:Carbamidomethylation m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.77	2%	0.50%	72.9	9.78E+04	(K)VDAGVGGDASVSGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.72	2%	0.50%	83.6	1.28E+06	(R)LQQDVLK(K)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.72	2%	0.50%	85.2	3.52E+05	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.68	2%	0.50%	63.2	1.39E+05	(K)IGGDASAGADASAGAGAGGNAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.65	2%	0.50%	78.8	6.56E+05	(K)ADIGGTVGGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.47	2%	0.50%	76.1	1.14E+06	(K)HHPTVAAEDTIK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.45	2%	0.50%	66.2	2.29E+05	(K)IGGDASAGADASAGAGAGGNAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.37	2%	0.50%	64.8	1.06E+06	(K)ISGGIHFSAGAR(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.26	2%	0.50%	75.3	2.84E+06	(K)ADIGGTVGGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.26	2%	0.50%	72.8	8.29E+05	(K)ASTTPENKPSAPTKPDPEFVK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.22	2%	0.50%	70.4	3.03E+04	(K)DLCAVAGDIAISmSALAEGAAGISGR(V)		C:Carbamidomethylation m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.11	2%	0.60%	86.9	1.91E+06	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.03	2%	0.60%	79.8	7.13E+05	(K)AGGDATVGGGVSGGAK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
13.02	2%	0.50%	69.7	4.19E+05	(K)AAATDAAMAQK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.98	2%	0.60%	76.1	7.44E+05	(R)LQQDVLK(K)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.98	2%	0.60%	66.9	9.09E+04	(K)ISGGIHFSAGAR(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.94	2%	0.60%	83.3	1.30E+06	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.91	2%	0.60%	73.8	1.72E+05	(K)VDAGVGGDASVSGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.89	2%	0.60%	70.7	2.08E+05	(K)AEDEVVAAAAAK(T)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.79	2%	0.60%	67.7	2.84E+05	(K)GGAGGYVGGK(T)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.77	2%	0.60%	85.8	1.76E+05	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.75	2%	0.60%	70.8	7.17E+05	(K)FAFHLK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.69	2%	0.60%	77.4	5.21E+05	(R)LQQDVLK(K)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.69	2%	0.60%	64.7	2.37E+05	(K)GGAGGYVGGK(T)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.64	2%	0.70%	69.8	1.57E+05	(K)IGGDASAGADASAGAGAGGNAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.64	2%	0.70%	68.2	1.13E+05	(K)IGGDASAGADASAGAGAGGNAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.55	2%	0.60%	72.7	4.15E+04	(K)DLCAVAGDIAISmSALAEGAAGISGR(V)		C:Carbamidomethylation m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.55	2%	0.60%	78	4.30E+05	(K)AGGDATVGGGVSGGAK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.54	2%	0.60%	88.2	2.57E+05	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.42	2%	0.60%	67.9	9.29E+05	(K)ISGGIHFSAGAR(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.41	2%	0.60%	73.3	2.64E+05	(K)IEmLNGVAK(D)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.28	2%	0.70%	70.6	1.09E+05	(K)AAATDAAmAQK(A)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.24	3%	0.70%	69.1	6.51E+04	(K)AAGEATLLLK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.07	3%	0.80%	67.6	2.29E+05	(K)AEDEVVAAAAAK(T)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
12.05	3%	0.80%	75.9	1.82E+05	(K)FAFHLK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.93	3%	0.90%	81.3	3.25E+05	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.91	3%	0.90%	80.6	9.16E+05	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.87	3%	0.90%	60.1	1.01E+06	(K)ISGGIHFSAGAR(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.85	3%	0.90%	79.1	1.05E+06	(K)SAAAVGGETAGNVDASGK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.78	3%	0.90%	66.8	1.92E+05	(K)AYTGADAGGGVSGGGSGGAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.74	3%	0.90%	72.9	2.03E+05	(K)AGGDATVGGGVSGGAK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.72	3%	0.90%	70.3	6.80E+05	(K)ADIGGTVGGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.64	3%	0.90%	65.7	7.75E+05	(K)ASTTPENKPSAPTKPDPEFVK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.54	3%	0.90%	63.7	4.80E+05	(K)FAFHLK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.38	3%	1.00%	74.9	5.34E+05	(R)LQQDVLK(K)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.37	3%	1.00%	74.5	4.33E+05	(K)AGGDATVGGGVSGGAK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.34	3%	1.00%	66.8	2.92E+05	(K)SAAAVGGETAGNVDASGK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.29	3%	1.00%	60.7	6.19E+05	(K)ASTTPENKPSAPTKPDPEFVK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.27	3%	1%	68	2.59E+05	(K)ASTTPENKPSAPTKPDPEFVK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.09	3%	1%	64.4	1.43E+05	(K)GGAGGYVGGK(T)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.07	3%	1%	68.5	1.73E+06	(K)HIEGIVANVK(F)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
11.06	3%	1%	67.4	4.51E+05	(R)VVVGVDIK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
10.92	3%	1%	65.3	6.47E+05	(R)LQQDVLK(K)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]
10.85	3%	1%	66.2	2.11E+04	(K)IEmLNGVAK(D)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]

10.81	3%	1%	63.8	3.13E+04	(K)IEmLNGVAK(D)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.77	3%	1%	68.8	1.64E+05	(K)FAFHLK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.69	3%	1%	66.1	1.73E+05	(K)IGGDASAGADASAGAGGNAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.68	3%	1%	65.9	4.66E+05	(K)IEmLNGVAK(D)	m:Oxidized methionine	CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.67	3%	1%	62.5	1.15E+05	(K)IGGDASAGADASAGAGGNAK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.62	3%	1%	62.7	3.75E+05	(K)ADIGGTVGGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.47	3%	1%	64.7	2.17E+05	(K)HHPTVAAEDTIK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.47	3%	1%	69.3	2.51E+05	(R)VVVGVDIK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.44	3%	1%	65.1	1.87E+05	(K)AAGEATLLLK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.42	3%	1%	64	2.57E+06	(K)HHPTVAAEDTIK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.4	3%	1%	65.7	1.56E+05	(K)FAFHLK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.39	3%	1%	66.5	2.14E+06	(K)ADIGGTVGGGVSGGAK(I)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.38	3%	1%	64	2.59E+05	(K)ASTTPENKPSAPTKPDPEFVK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.3	3%	1%	70.7	3.49E+05	(K)FAFHLK(V)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.29	3%	1%	64	3.43E+05	(K)ASTTPENKPSAPTKPDPEFVK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
10.07	5%	1%	64.7	1.27E+04	(K)VSGGAAEK(A)		CL2521.c2	S.halepenseF1Rev	hypothet prot OsJ_10582 [Oryza sativa Japonica Group]	
11.93	3%	0.90%	68.3	1.30E+04	(R)GFGFVTFSTEEAMR(S)		CL255.c1	S.halepenseF3	hypothet prot SORBIDRAFT_08g022740 [S bicolor] >gi|241943293|gb|EES16438.1| hypothet prot SORBIDRAFT_08g022740 [S bicolor]	
11.91	3%	0.90%	80.2	1.20E+06	(R)NITVNEAQSR(G)		CL255.c1	S.halepenseF3	hypothet prot SORBIDRAFT_08g022740 [S bicolor] >gi|241943293|gb|EES16438.1| hypothet prot SORBIDRAFT_08g022740 [S bicolor]	
11.22	3%	1%	74.2	2.06E+05	(R)NITVNEAQSR(G)		CL255.c1	S.halepenseF3	hypothet prot SORBIDRAFT_08g022740 [S bicolor] >gi|241943293|gb|EES16438.1| hypothet prot SORBIDRAFT_08g022740 [S bicolor]	
11.6	3%	0.90%	72	4.37E+05	(R)VNIANDRPAGNR(G)		UG4701	S.halepenseF2	hypothet prot SORBIDRAFT_03g043760 [S bicolor] >gi|241928809|gb|EES01954.1| hypothet prot SORBIDRAFT_03g043760 [S bicolor]	
14.39	2%	<0.1%	79.1	3.20E+05	(K)STVVPEETPK(S)		CL1424.c1	S.halepenseF2	hypothet prot SORBIDRAFT_06g021630 [S bicolor] >gi|241937927|gb|EES11072.1| hypothet prot SORBIDRAFT_06g021630 [S bicolor]	
13.76	2%	0.50%	75.1	2.07E+05	(K)FNVVSEENPK(A)		CL1424.c1	S.halepenseF2	hypothet prot SORBIDRAFT_06g021630 [S bicolor] >gi|241937927|gb|EES11072.1| hypothet prot SORBIDRAFT_06g021630 [S bicolor]	
11.82	3%	0.90%	68.7	3.76E+03	(K)FNVVSEENPK(A)		CL1424.c1	S.halepenseF2	hypothet prot SORBIDRAFT_06g021630 [S bicolor] >gi|241937927|gb|EES11072.1| hypothet prot SORBIDRAFT_06g021630 [S bicolor]	
11.58	3%	1.00%	65.2	5.47E+05	(K)STTTLEENPK(S)		CL1424.c1	S.halepenseF2	hypothet prot SORBIDRAFT_06g021630 [S bicolor] >gi|241937927|gb|EES11072.1| hypothet prot SORBIDRAFT_06g021630 [S bicolor]	
11.18	3%	1%	67.9	3.80E+05	(R)GISAVAGSCR(D)	C:Carbamidomethylation	CL1424.c1	S.halepenseF2	hypothet prot SORBIDRAFT_06g021630 [S bicolor] >gi|241937927|gb|EES11072.1| hypothet prot SORBIDRAFT_06g021630 [S bicolor]	
11.01	3%	1%	73	1.44E+05	(K)STVVPEETPK(S)		CL1424.c1	S.halepenseF2	hypothet prot SORBIDRAFT_06g021630 [S bicolor] >gi|241937927|gb|EES11072.1| hypothet prot SORBIDRAFT_06g021630 [S bicolor]	
12.07	3%	0.80%	73.9	1.39E+05	(R)HLTGEFEK(K)		UG13418	S.halepenseF1Rev	unnamed protein product [Vitis vinifera]	
11.17	3%	1%	71.8	6.51E+05	(R)HLTGEFEK(K)		UG13418	S.halepenseF1Rev	unnamed protein product [Vitis vinifera]	
11.11	3%	1%	76.6	1.37E+05	(R)HLTGEFEK(K)		UG13418	S.halepenseF1Rev	unnamed protein product [Vitis vinifera]	
13.6	2%	0.50%	66.1	3.37E+05	(K)SNYNFEKPFLYLAR(K)		CL684.c2	S.halepenseF2Rev	uncharacterized protein LOC100193260 [Zea mays] >gi|195616826|gb|ACG30243.1| GTP-binding nuclear protein Ran-A1 [Zea mays]	
12.97	2%	0.60%	77.4	2.59E+05	(K)NLQYYEISAK(S)		CL684.c2	S.halepenseF2Rev	uncharacterized protein LOC100193260 [Zea mays] >gi|195616826|gb|ACG30243.1| GTP-binding nuclear protein Ran-A1 [Zea mays]	
12.35	2%	0.70%	66.1	9.08E+04	(R)FADDSYLDSYISTIGVDFK(I)		UG993	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g033160 [S bicolor] >gi|194691170|gb|ACF79669.1| unknown [Zea mays] >gi|219887101|gb|ACL53925.1| unknown [Zea mays] >gi|241934384|gb|EES07529.1| hypothet prot SORBIDRAFT_04g033160 [S bicolor]	
10.65	3%	1%	70.3	1.24E+05	(R)LYLDELQK(I)		UG9651	S.halepenseF3RevF3Rev	uncharacterized protein LOC100279899 precursor [Zea mays]	
20.76	<0.1%	<0.1%	86	1.52E+05	(R)TTPSYVAFTDSER(L)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
20.62	<0.1%	<0.1%	87.8	2.76E+05	(R)TTPSYVAFTDSER(L)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
16.51	<0.1%	<0.1%	85.5	4.47E+05	(R)IINEPTAAAIAYGLDK(K)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
14.42	2%	<0.1%	77.5	3.84E+05	(R)IINEPTAAAIAYGLDK(K)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
14.01	2%	0.30%	68.8	1.85E+05	(R)FSDASVQSDVK(L)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
13.24	2%	0.50%	74	1.76E+05	(K)NQVAmNPINTVFDAK(R)	m:Oxidized methionine	CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
12.32	2%	0.70%	68	1.88E+05	(K)VIPGSGDKPmIGVQFR(G)	m:Oxidized methionine	CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
12.28	2%	0.70%	82.5	1.88E+05	(K)NAVVTVPAYFNDSQR(Q)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
12.23	3%	0.70%	62.2	1.25E+05	(K)ATAGDTHLGGEDFDNR(L)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
12.07	3%	0.80%	63.4	3.14E+05	(K)ATAGDTHLGGEDFDNR(L)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
12	3%	0.80%	65.7	1.95E+05	(R)LVNHFVQEFK(R)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
11.29	3%	1.00%	65.9	7.28E+04	(K)NAVVTVPAYFNDSQR(Q)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
11.11	3%	1%	79.1	2.44E+05	(R)LIGDAAK(N)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
10.7	3%	1%	74.9	3.37E+05	(R)VEIIANDQGNR(T)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	
10.48	3%	1%	77.1	1.45E+05	(R)LIGDAAK(N)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]	

10.11	3%	1%	69.4	1.80E+05	(R)VEIIANDQGNR(T)		CL336.c1	S.halepenseF2	hypothet prot SORBIDRAFT_01g039530 [S bicolor] >gi|241921951|gb|EER95095.1| hypothet prot SORBIDRAFT_01g039530 [S bicolor]
11.81	3%	0.90%	63.9	3.57E+05	(-)ITITNDK(G)		CL1539.c1	S.halepenseF2	heat shock protein 70 [Ulva prolifera]
10.18	3%	1%	76.5	1.50E+05	(K)IAELLR(Y)		CL102.c1	S.halepenseF3	hypothet prot SORBIDRAFT_07g028270 [S bicolor] >gi|241941154|gb|EES14299.1| hypothet prot SORBIDRAFT_07g028270 [S bicolor]
11.74	3%	0.90%	69.5	1.17E+05	(K)GIVDSEDLPLNISR(E)		UG11069	S.halepenseF1Rev	heat shock protein 90 [Triticum dicoccoides]
10.31	3%	1%	62	1.04E+05	(K)AVLFVPK(R)		UG11069	S.halepenseF1Rev	heat shock protein 90 [Triticum dicoccoides]
10.04	5%	1%	63.5	5.54E+04	(R)NLXPYVSSLQEVMRmRmMTQMCWCTVVK(G)	C:Carbamidomethylation m:Oxidized methionine	UG9528	S.halepenseF1	hypothet prot SORBIDRAFT_09g024010 [S bicolor] >gi|241946580|gb|EES19725.1| hypothet prot SORBIDRAFT_09g024010 [S bicolor]
17.85	<0.1%	<0.1%	70.8	3.98E+05	(K)LWAALDEIDREEAK(L)		UG5969	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g000890 [S bicolor] >gi|241915914|gb|EER89058.1| hypothet prot SORBIDRAFT_10g000890 [S bicolor]
17.43	<0.1%	<0.1%	80.2	7.84E+05	(R)AGVAAGmPVVGLVTR(N)	m:Oxidized methionine	UG5969	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g000890 [S bicolor] >gi|241915914|gb|EER89058.1| hypothet prot SORBIDRAFT_10g000890 [S bicolor]
15.71	0.20%	<0.1%	67.5	9.15E+04	(K)LWAALDEIDREEAK(L)		UG5969	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g000890 [S bicolor] >gi|241915914|gb|EER89058.1| hypothet prot SORBIDRAFT_10g000890 [S bicolor]
15.23	0.20%	<0.1%	83.3	2.19E+05	(R)NPENSLLEAGAALLIK(D)		UG5969	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g000890 [S bicolor] >gi|241915914|gb|EER89058.1| hypothet prot SORBIDRAFT_10g000890 [S bicolor]
13.02	2%	0.50%	76.3	1.15E+05	(R)AGVAAGMPVVGLVTR(N)		UG5969	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g000890 [S bicolor] >gi|241915914|gb|EER89058.1| hypothet prot SORBIDRAFT_10g000890 [S bicolor]
12.46	2%	0.60%	72.7	2.67E+05	(R)NPENSLLEAGAALLIK(D)		UG5969	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g000890 [S bicolor] >gi|241915914|gb|EER89058.1| hypothet prot SORBIDRAFT_10g000890 [S bicolor]
11.76	3%	0.90%	73	3.27E+05	(R)AGVAAGMPVVGLVTR(N)		UG5969	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g000890 [S bicolor] >gi|241915914|gb|EER89058.1| hypothet prot SORBIDRAFT_10g000890 [S bicolor]
10.74	3%	1%	61.4	1.48E+05	(R)SDVEAAQNLFPDWPLEK(G)		UG5969	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g000890 [S bicolor] >gi|241915914|gb|EER89058.1| hypothet prot SORBIDRAFT_10g000890 [S bicolor]
13.35	2%	0.50%	81.6	3.88E+05	(R)TIEAVEK(L)		CL2411.c1	S.halepenseF1Rev	PREDICTED: inactive poly [ADP-ribose] polymerase RCD1-like [Brachypodium distachyon]
17.9	<0.1%	<0.1%	65	1.86E+05	(K)ACEDLVFDHLR(K)	C:Carbamidomethylation	UG5021	S.halepenseF2	inositol monophosphatase 3 [Zea mays] >gi|195627646|gb|ACG35653.1| inositol monophosphatase 3 [Zea mays]
17.71	<0.1%	<0.1%	87.9	3.04E+05	(K)IPTVGVVFNPImNELFTAVR(G)	m:Oxidized methionine	UG5021	S.halepenseF2	inositol monophosphatase 3 [Zea mays] >gi|195627646|gb|ACG35653.1| inositol monophosphatase 3 [Zea mays]
17.33	<0.1%	<0.1%	92.6	2.19E+05	(K)IPTVGVVFNPIMNELFTAVR(G)		UG5021	S.halepenseF2	inositol monophosphatase 3 [Zea mays] >gi|195627646|gb|ACG35653.1| inositol monophosphatase 3 [Zea mays]
14.17	2%	0.20%	80.9	1.08E+05	(K)IPTVGVVFNPIMNELFTAVR(G)		UG5021	S.halepenseF2	inositol monophosphatase 3 [Zea mays] >gi|195627646|gb|ACG35653.1| inositol monophosphatase 3 [Zea mays]
11.15	3%	1%	73.5	7.77E+04	(K)IPTVGVVFNPIMNELFTAVR(G)		UG5021	S.halepenseF2	inositol monophosphatase 3 [Zea mays] >gi|195627646|gb|ACG35653.1| inositol monophosphatase 3 [Zea mays]
11.03	3%	1%	73.2	8.43E+04	(K)IPTVGVVFNPIMNELFTAVR(G)		UG5021	S.halepenseF2	inositol monophosphatase 3 [Zea mays] >gi|195627646|gb|ACG35653.1| inositol monophosphatase 3 [Zea mays]
10.6	3%	1%	73.2	3.96E+05	(K)ATLDDTTNR(I)		UG5021	S.halepenseF2	inositol monophosphatase 3 [Zea mays] >gi|195627646|gb|ACG35653.1| inositol monophosphatase 3 [Zea mays]
10.23	3%	1%	63.9	2.02E+05	(K)GQVDLVTETDK(A)		UG5021	S.halepenseF2	inositol monophosphatase 3 [Zea mays] >gi|195627646|gb|ACG35653.1| inositol monophosphatase 3 [Zea mays]
14.33	2%	<0.1%	76.3	3.19E+05	(R)FDLASVLCR(G)	C:Carbamidomethylation	CL1437.c1	S.halepenseF1Rev	isoamylase-type starch debranching enzyme ISO3 [Zea mays] >gi|29126649|gb|AAO17049.2| isoamylase-type starch debranching enzyme ISO3 [Zea mays]
13.03	2%	0.60%	70.3	2.48E+05	(R)VVDTNLESPK(D)		CL1437.c1	S.halepenseF1Rev	isoamylase-type starch debranching enzyme ISO3 [Zea mays] >gi|29126649|gb|AAO17049.2| isoamylase-type starch debranching enzyme ISO3 [Zea mays]
13.36	2%	0.50%	75.6	1.55E+05	(R)YASAGGGPVAASK(E)		UG11377	S.halepenseF3RevF3Rev	isoamylase-type starch debranching enzyme ISO3 [Zea mays] >gi|29126649|gb|AAO17049.2| isoamylase-type starch debranching enzyme ISO3 [Zea mays]
13.23	2%	0.50%	72.7	6.50E+03	(R)YASAGGGPVAASK(E)		UG11377	S.halepenseF3RevF3Rev	isoamylase-type starch debranching enzyme ISO3 [Zea mays] >gi|29126649|gb|AAO17049.2| isoamylase-type starch debranching enzyme ISO3 [Zea mays]
18.63	<0.1%	<0.1%	90.9	1.63E+05	(K)TGDIWHVSVEGLPASGVLYGYR(I)		UG8391	S.halepenseF3RevF3Rev	isoamylase-type starch debranching enzyme ISO3 [Zea mays] >gi|29126649|gb|AAO17049.2| isoamylase-type starch debranching enzyme ISO3 [Zea mays]
16.53	<0.1%	<0.1%	83.9	1.48E+05	(R)FDDSVILLDPYAK(L)		UG8391	S.halepenseF3RevF3Rev	isoamylase-type starch debranching enzyme ISO3 [Zea mays] >gi|29126649|gb|AAO17049.2| isoamylase-type starch debranching enzyme ISO3 [Zea mays]
19.87	<0.1%	<0.1%	89.5	1.48E+05	(K)LIFPFLDLDIK(Y)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
17.61	<0.1%	<0.1%	86.6	1.34E+05	(K)TIEAEAAHGTVTR(H)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
17.43	<0.1%	<0.1%	87.5	2.47E+05	(R)SHYLNTEEFIDAVATELR(S)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
17.22	<0.1%	<0.1%	72.1	2.41E+05	(R)LVPGWTKPICIGR(H)	C:Carbamidomethylation	CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
16.68	<0.1%	<0.1%	91	2.45E+05	(R)LLDFALK(L)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
16.21	<0.1%	<0.1%	73.4	7.29E+05	(K)TIEAEAAHGTVTR(H)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
14.75	0.20%	<0.1%	83.1	1.26E+05	(R)SHYLNTEEFIDAVATELR(S)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
14.34	2%	<0.1%	72.1	3.28E+04	(K)LIFPFLDLDIK(Y)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
14.24	2%	<0.1%	71.5	1.20E+05	(R)LVPGWTKPICIGR(H)	C:Carbamidomethylation	CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
12.97	2%	0.60%	75.1	3.10E+05	(K)TIEAEAAHGTVTR(H)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
11.73	3%	0.90%	76.7	1.02E+05	(R)LLDFALK(L)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
11.59	3%	1.00%	71.8	3.01E+05	(R)HAFGDQYR(A)		CL191.c1	S.halepenseF1Rev	uncharacterized protein LOC100217128 [Zea mays]
15.04	0.20%	<0.1%	75.5	1.21E+05	(K)AALLQSFQDAGVTLVK(G)		CL2295.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g008760 [S bicolor] >gi|241927313|gb|EES00458.1| hypothet prot SORBIDRAFT_03g008760 [S bicolor]
12.61	2%	0.70%	66.8	1.06E+05	(K)GDLYDQASLVSAVK(G)		CL2295.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g008760 [S bicolor] >gi|241927313|gb|EES00458.1| hypothet prot SORBIDRAFT_03g008760 [S bicolor]
12.28	2%	0.70%	74.7	4.86E+05	(R)LGHPTVALVR(D)		CL2295.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g008760 [S bicolor] >gi|241927313|gb|EES00458.1| hypothet prot SORBIDRAFT_03g008760 [S bicolor]
11.55	3%	0.90%	80.5	2.04E+05	(K)ILVVGGTGYLGR(H)		CL2295.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g008760 [S bicolor] >gi|241927313|gb|EES00458.1| hypothet prot SORBIDRAFT_03g008760 [S bicolor]
11.38	3%	1.00%	70.5	4.54E+05	(K)AVVLGDGDTK(V)		CL2295.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g008760 [S bicolor] >gi|241927313|gb|EES00458.1| hypothet prot SORBIDRAFT_03g008760 [S bicolor]

13.29	2%	0.50%	72.5	1.14E+05	(-)AFSVFLFNSK(Y)		UG6589	S.halepenseF3	hypothet prot SORBIDRAFT_02g035700 [S bicolor] >gi|241924204|gb|EER97348.1| hypothet prot SORBIDRAFT_02g035700 [S bicolor]
11.98	3%	0.80%	68.6	9.90E+04	(K)ISPWFR(L)		UG6589	S.halepenseF3	hypothet prot SORBIDRAFT_02g035700 [S bicolor] >gi|241924204|gb|EER97348.1| hypothet prot SORBIDRAFT_02g035700 [S bicolor]
10.86	3%	1%	77.8	8.78E+05	(K)IVGALGAQSRR(W)		UG7136	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_09g029170 [S bicolor] >gi|241946836|gb|EES19981.1| hypothet prot SORBIDRAFT_09g029170 [S bicolor]
10.41	3%	1%	64.7	9.69E+04	(K)EGIHINK(G)		UG2772	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g028210 [S bicolor] >gi|241932396|gb|EES05541.1| hypothet prot SORBIDRAFT_04g028210 [S bicolor]
16.89	<0.1%	<0.1%	80.1	3.38E+05	(K)SAEAVELATK(E)		UG10459	S.halepenseF1	hypothet prot [Sporobolus stapfianus]
12.12	3%	0.80%	69.1	4.02E+05	(K)SAEAVELATK(E)		UG10459	S.halepenseF1	hypothet prot [Sporobolus stapfianus]
20.25	<0.1%	<0.1%	96.1	9.62E+05	(R)TFIEVVFENPEK(S)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
18.26	<0.1%	<0.1%	85.1	2.47E+05	(R)TFIEVVFENPEK(S)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
18.04	<0.1%	<0.1%	90.8	6.87E+05	(R)TFIEVVFENPEK(S)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
17.49	<0.1%	<0.1%	87.8	4.69E+05	(R)TFIEVVFENPEK(S)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
16.96	<0.1%	<0.1%	82.7	6.00E+05	(R)STYNLLDTVSR(H)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
16.86	<0.1%	<0.1%	81.4	2.55E+05	(R)STYNLLDTVSR(H)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
16.62	<0.1%	<0.1%	82.3	2.01E+06	(R)STYNLLDTVSR(H)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
14.84	0.20%	<0.1%	79.6	7.49E+05	(R)STYNLLDTVSR(H)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
13.71	2%	0.50%	69.6	8.42E+05	(R)STYNLLDTVSR(H)		CL505.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
17.27	<0.1%	<0.1%	85.2	4.07E+05	(R)AVGGYGGISVYSR(L)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
16.74	<0.1%	<0.1%	81.1	2.93E+05	(R)LLIPVPFDQPPPENDHVVLIGDWYTK(D)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
15.52	0.20%	<0.1%	77.9	2.17E+05	(R)LLIPVPFDQPPPENDHVVLIGDWYTK(D)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
13.94	2%	0.30%	76	5.61E+05	(R)VTYNLLDAVSR(H)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
12.83	2%	0.60%	68.5	3.01E+05	(R)VTYNLLDAVSR(H)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
12.59	2%	0.60%	78	2.22E+05	(K)DLESAPLFTFDAGK(T)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
12.54	2%	0.60%	73.2	9.33E+03	(R)LLIPVPFDQPPPENDHVVLIGDWYTK(D)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
12.02	3%	0.80%	70	2.49E+05	(R)TFIEIVFENPEK(S)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
11.93	3%	0.90%	72.7	5.51E+04	(R)FIHDAK(S)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
10.91	3%	1%	69.9	1.62E+04	(R)LLIPVPFDQPPPENDHVVLIGDWYTK(D)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
10.39	3%	1%	66.1	1.69E+05	(K)VILINGEFPGPR(I)		CL505.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g023770 [S bicolor] >gi|241946566|gb|EES19711.1| hypothet prot SORBIDRAFT_09g023770 [S bicolor]
14.43	2%	<0.1%	79.1	7.86E+05	(K)TImGTPQK(V)	m:Oxidized methionine	UG305	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
14.23	2%	<0.1%	75.1	2.55E+05	(K)TImGTPQK(V)	m:Oxidized methionine	UG305	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
16.14	<0.1%	<0.1%	83	4.50E+05	(K)LPESPSGWAWSINQAR(S)		UG329	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
13.26	2%	0.50%	76.5	7.88E+05	(K)EVSTTTAVIR(Y)		UG329	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
12.68	2%	0.60%	71.3	2.51E+06	(K)EVSTTTAVIR(Y)		UG329	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
11.9	3%	0.90%	71.4	4.78E+04	(K)GASAPPPAK(L)		UG329	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
11.89	3%	0.90%	62.9	1.61E+05	(K)LPESPSGWAWSINQAR(S)		UG329	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
11.38	3%	1.00%	63.7	2.05E+05	(K)LPESPSGWAWSINQAR(S)		UG329	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
10.98	3%	1%	68.9	3.31E+05	(K)EVSTTTAVIR(Y)		UG329	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
16.58	<0.1%	<0.1%	73.1	2.38E+05	(K)DAANPPmYNVEAGK(T)	m:Oxidized methionine	CL2505.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
16.2	<0.1%	<0.1%	83.6	9.58E+05	(K)DAANPPmYNVEAGK(T)	m:Oxidized methionine	CL2505.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
14.54	2%	<0.1%	79	1.11E+05	(K)DAANPPmYNVEAGK(T)	m:Oxidized methionine	CL2505.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
13.81	2%	0.50%	81.7	2.54E+05	(K)DAANPPmYNVEAGK(T)	m:Oxidized methionine	CL2505.c1	S.halepenseF3	hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]

12.64 2% 0.70% 84 2.49E+05 (K)DHAVLAK(N) CL2505.c1 S.halepenseF3 hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
12.14 3% 0.70% 77 3.80E+03 (K)DAANPPMYNVEAGK(T) CL2505.c1 S.halepenseF3 hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
11.14 3% 1% 72.9 2.82E+05 (K)DAANPPmYNVEAGK(T) m:Oxidized methionine CL2505.c1 S.halepenseF3 hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
10.87 3% 1% 75.3 8.44E+04 (K)DHAVLAK(N) CL2505.c1 S.halepenseF3 hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
12.38 2% 0.60% 64.8 2.30E+05 (R)NYLGEQLYISVTSPER(S) UG284 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g037970 [S bicolor] >gi|241928507|gb|EES01652.1| hypothet prot SORBIDRAFT_03g037970 [S bicolor]
22.88 <0.1% <0.1% 93 5.80E+05 (K)SYPTVSAEYSEAVEK(A) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
21.2 <0.1% <0.1% 94.2 6.07E+05 (K)SYPTVSAEYSEAVEK(A) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
17.8 <0.1% <0.1% 82 2.17E+05 (K)NPAELAHGANAGLDIAVR(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
17.55 <0.1% <0.1% 78.3 1.87E+05 (K)ALLSDPAFRPLVDK(Y) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
16.72 <0.1% <0.1% 84.4 3.16E+05 (K)QmGLSDQDIVALSGGHTLGR(C) m:Oxidized methionine UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
15.52 0.20% <0.1% 80.6 2.34E+05 (K)ALLSDPAFRPLVDK(Y) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
15.26 0.20% <0.1% 82.2 5.71E+05 (K)ELLSGDKEGLLQLPSDK(A) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
15.21 0.20% <0.1% 82.1 8.80E+05 (K)EGLLQLPSDK(A) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
15.07 0.20% <0.1% 72.8 5.12E+06 (R)EDKPQPPPEGR(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
15.06 0.20% <0.1% 69.7 4.54E+05 (R)SGFEGAWTSNPLVFDNSYFK(E) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
15.03 0.20% <0.1% 81.1 1.67E+05 (K)ELLSGDKEGLLQLPSDK(A) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
14.89 0.20% <0.1% 71.6 1.96E+05 (K)QMGLSDQDIVALSGGHTLGR(C) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
14.19 2% 0.10% 80.2 1.07E+06 (K)ALLSDPAFRPLVDK(Y) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
14.15 2% 0.20% 65.1 5.79E+06 (R)EDKPQPPPEGR(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
13.8 2% 0.50% 79.9 1.30E+06 (K)ALLSDPAFRPLVDK(Y) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
13.45 2% 0.50% 69.6 2.22E+05 (K)NPAELAHGANAGLDIAVR(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
13.41 2% 0.50% 70.8 2.23E+05 (K)NPAELAHGANAGLDIAVR(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
12.74 2% 0.60% 72.1 1.09E+06 (R)TGGPFGTmK(N) m:Oxidized methionine UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
12.65 2% 0.60% 62.1 4.76E+06 (R)EDKPQPPPEGR(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
12.54 2% 0.60% 69.7 1.44E+05 (K)ALLSDPAFRPLVDK(Y) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
12.32 2% 0.70% 69.7 1.58E+05 (K)ALLSDPAFRPLVDK(Y) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
12.24 3% 0.70% 68.9 7.42E+05 (R)EDKPQPPPEGR(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
11.92 3% 0.90% 72.5 4.83E+05 (K)ELLSGDKEGLLQLPSDK(A) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
11.83 3% 0.90% 74.5 3.32E+05 (K)QmGLSDQDIVALSGGHTLGR(C) m:Oxidized methionine UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
11.82 3% 0.90% 66.4 2.64E+05 (K)ALLSDPAFRPLVDK(Y) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
11.5 3% 1.00% 73.5 2.31E+05 (K)ALLSDPAFRPLVDK(Y) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
11.45 3% 1.00% 68.8 2.67E+05 (K)AFFEDYKEAHLK(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
11.44 3% 1.00% 64.4 1.65E+06 (R)TGGPFGTmK(N) m:Oxidized methionine UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
10.74 3% 1% 72.6 4.17E+05 (K)EGLLQLPSDK(A) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
10.43 3% 1% 67.2 3.96E+05 (R)EDKPQPPPEGR(L) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
10.16 3% 1% 78.5 2.61E+06 (R)ALIAEK(S) UG173 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g038760 [S bicolor] >gi|241921907|gb|EER95051.1| hypothet prot SORBIDRAFT_01g038760 [S bicolor]
17.86 <0.1% <0.1% 87.7 3.65E+05 (R)LPDATQGSDHLR(Q) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
17.42 <0.1% <0.1% 73.2 2.57E+06 (R)LPDATQGSDHLR(Q) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]

16.58 <0.1% <0.1% 86.4 8.48E+05 (K)AYPTVSEDYLK(A) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
16.58 <0.1% <0.1% 83.7 8.20E+05 (K)ALLSDPSFRPLVDK(Y) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
15.61 0.20% <0.1% 83.7 5.70E+05 (K)ALLSDPSFRPLVDK(Y) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
15.22 0.20% <0.1% 72.3 9.76E+05 (K)NPAEQAHGANAGLEIAVR(L) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
14.68 2% <0.1% 82.7 6.47E+05 (K)ALLSDPSFRPLVDK(Y) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
13.87 2% 0.40% 72.9 1.16E+05 (K)ALLSDPSFRPLVDK(Y) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
13.74 2% 0.50% 65.8 1.49E+05 (R)LAWHSAGTFDVATK(T) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
12.63 2% 0.70% 75.2 4.95E+05 (K)AYPTVSEDYLK(A) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
10.89 3% 1% 66.1 3.88E+05 (K)NPAEQAHGANAGLEIAVR(L) UG779 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g044060 [S bicolor] >gi|241926828|gb|EER99972.1| hypothet prot SORBIDRAFT_02g044060 [S bicolor]
22.36 <0.1% <0.1% 91.4 5.46E+05 (R)NYPASGmSALLPLDLR(R) m:Oxidized methionine CL1272.c5 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
19.92 <0.1% <0.1% 86.7 4.79E+05 (K)LGEANTFNAALK(D) CL1272.c5 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
14.62 2% <0.1% 80.9 5.86E+05 (R)ELPVLPGGGR(N) CL1272.c5 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
12.54 2% 0.60% 73.3 1.33E+05 (K)LGEANTFNAALK(D) CL1272.c5 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
12.36 2% 0.70% 78.4 9.89E+05 (R)ALAPTTIPR(M) CL1272.c5 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
10.63 3% 1% 66.6 2.71E+05 (R)NYPASGmSALLPLDLR(R) m:Oxidized methionine CL1272.c5 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
10.47 3% 1% 64.9 2.77E+04 (R)NYPASGmSALLPLDLR(R) m:Oxidized methionine CL1272.c5 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
10.12 3% 1% 60.1 8.54E+04 (R)NYPASGMSALLPLDLR(R) CL1272.c5 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
17.7 <0.1% <0.1% 87.2 2.50E+05 (R)AATDVSSCTISCR(E) C:Carbamidomethylation UG1910 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g002380 [S bicolor] >gi|241917433|gb|EER90577.1| hypothet prot SORBIDRAFT_01g002380 [S bicolor]
16.17 <0.1% <0.1% 84.1 2.16E+05 (R)VIVAQSLTEFAK(M) UG1910 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g002380 [S bicolor] >gi|241917433|gb|EER90577.1| hypothet prot SORBIDRAFT_01g002380 [S bicolor]
15.62 0.20% <0.1% 82.3 3.51E+05 (R)AATDVSSCTISCR(E) C:Carbamidomethylation UG1910 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g002380 [S bicolor] >gi|241917433|gb|EER90577.1| hypothet prot SORBIDRAFT_01g002380 [S bicolor]
15.07 0.20% <0.1% 78.4 3.98E+04 (K)IAGAPGQVDVK(A) UG1910 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g002380 [S bicolor] >gi|241917433|gb|EER90577.1| hypothet prot SORBIDRAFT_01g002380 [S bicolor]
14.4 2% <0.1% 80.8 2.38E+05 (R)VIVAQSLTEFAK(M) UG1910 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g002380 [S bicolor] >gi|241917433|gb|EER90577.1| hypothet prot SORBIDRAFT_01g002380 [S bicolor]
18.43 <0.1% <0.1% 80.1 2.60E+05 (K)EILDmPEYEEWFTKR(F) m:Oxidized methionine UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
18.11 <0.1% <0.1% 87.7 3.29E+05 (K)EILDmPEYEEWFTK(R) m:Oxidized methionine UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
16.45 <0.1% <0.1% 79.1 9.86E+05 (K)SECWTLLK(G) C:Carbamidomethylation UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
16.28 <0.1% <0.1% 86.9 1.76E+05 (K)SSGTVPYDYSANIECIK(E) C:Carbamidomethylation UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
15.7 0.20% <0.1% 77.5 4.24E+05 (K)SECWTLLK(G) C:Carbamidomethylation UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
15.3 0.20% <0.1% 71 3.91E+05 (K)SECWTLLK(G) C:Carbamidomethylation UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
14.97 0.20% <0.1% 71.3 3.92E+05 (K)SECWTLLK(G) C:Carbamidomethylation UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
14.05 2% 0.30% 77.3 1.88E+05 (K)EILDmPEYEEWFTK(R) m:Oxidized methionine UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
14 2% 0.30% 76.7 1.69E+05 (K)ITVESGGKPLPDAELSVVWVAK(G) UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
13.34 2% 0.50% 63.4 4.34E+05 (R)GHNVFWDDQSHQmPWVSK(L) m:Oxidized methionine UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
13 2% 0.60% 79.3 6.10E+05 (K)GTGDITAIIVTPDGK(F) UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
12.51 2% 0.60% 67.3 1.23E+04 (K)GFPLGNAMTK(E) UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
12.37 2% 0.60% 69.2 1.39E+06 (K)GTGDITAIIVTPDGK(F) UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
12.1 3% 0.70% 74 5.72E+04 (K)GYSSEQPTK(T) UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.96 3% 0.80% 60.3 1.38E+05 (K)SECWTLLK(G) C:Carbamidomethylation UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.74 3% 0.90% 67.5 5.14E+05 (K)GGATSYAEGK(S) UG282 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]

11.64	3%	0.90%	69.2	2.33E+05	(K)GGATSYAEGK(S)		UG282	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.3	3%	1.00%	76.4	2.15E+05	(K)SSGTVPYDYSANIECIKEPEKPLYGGGIISAADSSGK(K)	C:Carbamidomethylation	UG282	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.15	3%	1%	60.2	9.02E+05	(K)mLALAEK(H)	m:Oxidized methionine	UG282	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
10.79	3%	1%	73.9	1.15E+05	(K)MLALAEK(H)		UG282	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
10.38	3%	1%	65.9	6.52E+05	(K)GTGDITAIIVTPDGK(F)		UG282	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
10.33	3%	1%	62.4	6.63E+04	(K)EILDmPEYEEWFTK(R)	m:Oxidized methionine	UG282	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
10.12	3%	1%	69.2	4.10E+05	(K)GFPLGNAmTK(E)	m:Oxidized methionine	UG282	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
13.72	2%	0.50%	74.8	9.68E+04	(K)ESYASLVDSINTSR(D)		UG621	S.halepenseF1Rev	hypothet prot SORBIDRAFT_03g032300 [S bicolor] >gi|241930346|gb|EES03491.1| hypothet prot SORBIDRAFT_03g032300 [S bicolor]
19.25	<0.1%	<0.1%	84.1	3.24E+05	(R)VEIESLFDGTDFSEPLTR(A)		CL1078.c1	S.halepenseF3	"polypeptide chain-binding protein, partial [Zea mays]"
16.05	<0.1%	<0.1%	88.8	4.15E+05	(R)LSQEEIDR(M)		CL1078.c1	S.halepenseF3	"polypeptide chain-binding protein, partial [Zea mays]"
12.34	2%	0.70%	67.1	1.54E+05	(R)ARFEELNNDLFR(K)		CL1078.c1	S.halepenseF3	"polypeptide chain-binding protein, partial [Zea mays]"
12.12	3%	0.80%	79.6	3.33E+05	(K)SQIHEIVLVGGSTR(I)		CL1078.c1	S.halepenseF3	"polypeptide chain-binding protein, partial [Zea mays]"
11.24	3%	1%	71.8	7.34E+04	(K)LADKLEAEEK(E)		CL1078.c1	S.halepenseF3	"polypeptide chain-binding protein, partial [Zea mays]"
10.44	3%	1%	72.3	3.20E+05	(K)ITITNEK(G)		CL1078.c1	S.halepenseF3	"polypeptide chain-binding protein, partial [Zea mays]"
10.09	3%	1%	67	1.66E+05	(R)VEIESLFDGTDFSEPLTR(A)		CL1078.c1	S.halepenseF3	"polypeptide chain-binding protein, partial [Zea mays]"
20.83	<0.1%	<0.1%	85.7	3.54E+05	(K)VFSPEEISAmILGK(M)	m:Oxidized methionine	UG4490	S.halepenseF1	unknown [Zea mays]
20.67	<0.1%	<0.1%	92.1	1.91E+05	(R)ITPSWVAFTDSER(L)		UG4490	S.halepenseF1	unknown [Zea mays]
15.72	0.20%	<0.1%	73.8	1.39E+05	(K)VFSPEEISAmILGK(M)	m:Oxidized methionine	UG4490	S.halepenseF1	unknown [Zea mays]
12	3%	0.80%	75.3	4.14E+05	(R)LIGEAAK(N)		UG4490	S.halepenseF1	unknown [Zea mays]
11.94	3%	0.90%	64.6	9.31E+04	(K)VFSPEEISAmILGK(M)	m:Oxidized methionine	UG4490	S.halepenseF1	unknown [Zea mays]
14.03	2%	0.30%	77.4	1.29E+05	(K)NGVEEVLGLGELSDFEK(E)		UG14307	S.halepenseF1	hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
19.09	<0.1%	<0.1%	93.1	5.12E+05	(K)LIDVDVPVVGGHAGITILPLLSK(T)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
18.44	<0.1%	<0.1%	85.4	4.04E+05	(K)VAVLGAAGGIGQPLGLLIK(M)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
15.78	0.20%	<0.1%	84.8	3.12E+05	(K)VAVLGAAGGIGQPLGLLIK(M)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
15.67	0.20%	<0.1%	83.1	1.62E+05	(K)SLVEAVADNCPEAFIHIISNPVNSTVPIAAEVLK(Q)		C:Carbamidomethylation	CL617.c1	S.halepenseF2Rev malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
15.25	0.20%	<0.1%	77.7	7.34E+04	(K)VAVLGAAGGIGQPLGLLIK(M)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
14.14	2%	0.20%	88.6	3.75E+05	(K)GVDVVVIPAGVPR(K)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
13.72	2%	0.50%	85.3	2.17E+05	(K)SGSQISPQASYK(V)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
13.54	2%	0.50%	77.5	4.58E+05	(R)IQNAGTEVVEAK(A)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
13.13	2%	0.60%	80.3	6.55E+04	(K)LIDVDVPVVGGHAGITILPLLSK(T)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
12.85	2%	0.60%	73.5	1.59E+05	(R)DDLFNINASIVK(S)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
11.89	3%	0.90%	70.8	5.56E+04	(K)VAVLGAAGGIGQPLGLLIK(M)		CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
11.88	3%	0.90%	66.5	1.12E+05	(K)SLVEAVADNCPEAFIHIISNPVNSTVPIAAEVLK(Q)		C:Carbamidomethylation	CL617.c1	S.halepenseF2Rev malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
11.62	3%	0.90%	63.7	2.28E+05	(K)mSPLVSELHLYDIANVK(G)	m:Oxidized methionine	CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
10.51	3%	1%	68.8	1.45E+05	(K)mSPLVSELHLYDIANVK(G)	m:Oxidized methionine	CL617.c1	S.halepenseF2Rev	malate dehydrogenase [Zea mays] >gi|195626292|gb|ACG34976.1| malate dehydrogenase [Zea mays]
21.02	<0.1%	<0.1%	89	1.44E+05	(K)AQASALEAHAAPNCK(V)	C:Carbamidomethylation	UG11429	S.halepenseF2	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
18.92	<0.1%	<0.1%	86.3	3.65E+05	(K)mELVDAAFPLLK(G)	m:Oxidized methionine	UG11429	S.halepenseF2	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
14.06	2%	0.30%	83.9	1.32E+06	(K)VLVVANPANTNALILK(E)		UG11429	S.halepenseF2	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
12.24	3%	0.70%	68.4	1.96E+05	(K)MELVDAAFPLLK(G)		UG11429	S.halepenseF2	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
11.97	3%	0.80%	76.9	7.44E+04	(K)VLVVANPANTNALILK(E)		UG11429	S.halepenseF2	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
11.55	3%	1.00%	61.9	1.08E+05	(K)mELVDAAFPLLK(G)	m:Oxidized methionine	UG11429	S.halepenseF2	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
11.19	3%	1%	75.1	4.00E+05	(K)EFAPSIPEK(N)		UG11429	S.halepenseF2	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
11.03	3%	1%	76.7	5.76E+05	(K)VLVVANPANTNALILK(E)		UG11429	S.halepenseF2	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
18.73	<0.1%	<0.1%	93.8	7.15E+05	(K)IVQGLPIDEFSR(K)		UG5385	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
18.36	<0.1%	<0.1%	88.4	5.05E+05	(K)LDATAQELSEEK(T)		UG5385	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
17.14	<0.1%	<0.1%	70.4	4.99E+05	(K)LSSALSAASSACDHIR(D)	C:Carbamidomethylation	UG5385	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g019280 [S bicolor] >gi|241920933|gb|EER94077.1| hypothet prot SORBIDRAFT_01g019280 [S bicolor]
26.7	<0.1%	<0.1%	100	2.93E+06	(K)LNPLVSSLSLYDIAGTPGVAADVSHINSPALVK(G)		CL2460.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
18.33	<0.1%	<0.1%	83	7.81E+04	(K)GLNGVPDVVECSFVQSTVTELPFFASK(V)	C:Carbamidomethylation	CL2460.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
16.59	<0.1%	<0.1%	80.5	1.27E+06	(K)GLCTAIAK(H)	C:Carbamidomethylation	CL2460.c1	S.halepenseF3	hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]

16.47 <0.1% <0.1% 88.6 1.36E+06 (K)LNPLVSSLSLYDIAGTPGVAADVSHINSPALVK(G) CL2460.c1 S.halepenseF3 hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
15.25 0.20% <0.1% 82.9 2.13E+05 (K)HCPNALVNmISNPVNSTVPIAAEVFK(K) C:Carbamidomethylation m:Oxidized methionine CL2460.c1 S.halepenseF3 hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
14.92 0.20% <0.1% 75.9 8.64E+05 (K)GELmSSIEK(G) m:Oxidized methionine CL2460.c1 S.halepenseF3 hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
14.67 2% <0.1% 79.9 9.53E+05 (R)DDLFNINAGIVK(G) CL2460.c1 S.halepenseF3 hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
12.66 2% 0.60% 68.4 1.06E+05 (K)LNPLVSSLSLYDIAGTPGVAADVSHINSPALVK(G) CL2460.c1 S.halepenseF3 hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
11.71 3% 0.90% 70.1 1.39E+06 (K)LNPLVSSLSLYDIAGTPGVAADVSHINSPALVK(G) CL2460.c1 S.halepenseF3 hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
10.17 3% 1% 63 4.74E+04 (K)LNPLVSSLSLYDIAGTPGVAADVSHINSPALVK(G) CL2460.c1 S.halepenseF3 hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
10.01 5% 1% 69.7 1.06E+05 (K)LNPLVSSLSLYDIAGTPGVAADVSHINSPALVK(G) CL2460.c1 S.halepenseF3 hypothet prot SORBIDRAFT_09g029240 [S bicolor] >gi|241946840|gb|EES19985.1| hypothet prot SORBIDRAFT_09g029240 [S bicolor]
18.75 <0.1% <0.1% 93.4 1.60E+06 (K)LFGVTTLDVVR(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
17.09 <0.1% <0.1% 76.4 4.22E+05 (K)ANLPVTDVNVPVVGGHAGITILPLFSQATPATNSLSDEDIK(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
16.93 <0.1% <0.1% 88.6 7.83E+05 (K)LFGVTTLDVVR(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
14.12 2% 0.30% 79.4 1.64E+05 (K)LFGVTTLDVVR(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
13.97 2% 0.30% 70.5 8.18E+05 (K)KLFGVTTLDVVR(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
13.36 2% 0.50% 68 1.58E+06 (R)TQDGGTEVVEAK(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
12.72 2% 0.60% 80.2 1.77E+05 (K)LFGVTTLDVVR(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
12.52 2% 0.60% 85.4 2.42E+05 (K)RTQDGGTEVVEAK(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
12.45 2% 0.60% 77.1 1.83E+06 (K)TFYAGK(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
12.29 2% 0.70% 70.7 1.81E+05 (K)KLFGVTTLDVVR(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
10.48 3% 1% 74.5 8.60E+04 (K)LFGVTTLDVVR(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
10.43 3% 1% 67.1 7.14E+05 (K)RTQDGGTEVVEAK(A) CL2460.c2 S.halepenseF1 hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
17.2 <0.1% <0.1% 84.2 1.23E+06 (K)VAILGAAGGIGQPLSLLmK(L) m:Oxidized methionine UG10626 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
15.25 0.20% <0.1% 83.7 6.88E+05 (K)VAILGAAGGIGQPLSLLMK(L) UG10626 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
15.13 0.20% <0.1% 74.6 6.88E+05 (K)VAILGAAGGIGQPLSLLMK(L) UG10626 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
12.15 3% 0.70% 70.8 1.19E+06 (K)VAILGAAGGIGQPLSLLmK(L) m:Oxidized methionine UG10626 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
11.46 3% 1.00% 74 2.51E+05 (R)KVAILGAAGGIGQPLSLLmK(L) m:Oxidized methionine UG10626 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
10.91 3% 1% 67 2.23E+05 (K)VAILGAAGGIGQPLSLLMK(L) UG10626 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g029570 [S bicolor] >gi|241928026|gb|EES01171.1| hypothet prot SORBIDRAFT_03g029570 [S bicolor]
10.68 3% 1% 75.7 7.89E+05 (R)LPSXSAWSGGR(L) UG888 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g017210 [S bicolor] >gi|241944911|gb|EES18056.1| hypothet prot SORBIDRAFT_09g017210 [S bicolor]
13.06 2% 0.60% 86 4.89E+06 (K)ICISK(N) C:Carbamidomethylation UG1755 S.halepenseF3 hypothet prot SORBIDRAFT_10g031010 [S bicolor] >gi|241917292|gb|EER90436.1| hypothet prot SORBIDRAFT_10g031010 [S bicolor]
11.31 3% 1.00% 72.3 1.10E+05 (R)LLIIHLPK(L) UG3797 S.halepenseF3 hypothet prot SORBIDRAFT_02g037730 [S bicolor] >gi|241924310|gb|EER97454.1| hypothet prot SORBIDRAFT_02g037730 [S bicolor]
23.91 <0.1% <0.1% 93.1 4.19E+05 (K)VVGVFLEGGSAEENQAIAK(V) CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
21.27 <0.1% <0.1% 93.5 2.75E+05 (K)VVGVFLEGGSAEENQAIAK(V) CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
19.49 <0.1% <0.1% 86 2.49E+05 (K)LTDFGVQGAESNNILYLR(D) CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
18.6 <0.1% <0.1% 82.3 7.52E+05 (R)LPGFHTCVGSGGER(L) C:Carbamidomethylation CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
18.18 <0.1% <0.1% 90.2 3.13E+05 (K)TLTSAAGDTFTYETLLIATGSSVIK(L) CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
18.06 <0.1% <0.1% 80.5 3.54E+05 (K)LTDFGVQGAESNNILYLR(D) CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
16.87 <0.1% <0.1% 85.4 3.99E+05 (K)TLTSAAGDTFTYETLLIATGSSVIK(L) CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
16.31 <0.1% <0.1% 80.2 1.67E+05 (K)ESGESVAEYDYLPYFYSR(S) CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
16.15 <0.1% <0.1% 77.2 1.78E+05 (K)ESGESVAEYDYLPYFYSR(S) CL584.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]

16.04	<0.1%	<0.1%	84.6	1.12E+06	(R)VQPPVADVQALK(E)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
15.9	0.20%	<0.1%	78.4	1.58E+06	(K)EPVAPYERPALSK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
15.88	0.20%	<0.1%	83	8.18E+05	(K)YVILGGGVAAGYAAR(E)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
15.36	0.20%	<0.1%	84.6	6.18E+05	(K)GYLFPQNAAR(L)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
15.22	0.20%	<0.1%	86.6	2.48E+05	(K)TLTSAAGDTFTYETLLIATGSSVIK(L)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
14.71	0.20%	<0.1%	81.7	2.76E+05	(R)VQPPVADVQALK(E)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
14.19	2%	0.10%	74.3	1.03E+05	(K)TLTSAAGDTFTYETLLIATGSSVIK(L)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
13.85	2%	0.40%	72.2	1.18E+05	(K)ESGESVAEYDYLPYFYSR(S)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
13.62	2%	0.50%	84.6	3.58E+05	(K)GIELVLSTEIVK(A)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
13.5	2%	0.50%	75.8	1.06E+05	(K)TLTSAAGDTFTYETLLIATGSSVIK(L)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
13.36	2%	0.50%	80.8	9.50E+05	(R)LLPEWYSEK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
13.08	2%	0.60%	78.8	9.28E+05	(R)VQPPVADVQALK(E)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
13.07	2%	0.60%	66.9	3.76E+05	(R)LFTAGIAHFYEGYYTNK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
12.99	2%	0.60%	72.4	1.37E+06	(K)GYLFPQNAAR(L)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
12.82	2%	0.60%	61.9	1.28E+05	(K)TLTSAAGDTFTYETLLIATGSSVIK(L)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
12.51	2%	0.60%	65.2	1.40E+05	(R)LPGFHTCVGSGGER(L)	C:Carbamidomethylation	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
12.42	2%	0.60%	72.5	3.26E+04	(R)VQPPVADVQALK(E)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
12.39	2%	0.60%	76.5	1.96E+05	(R)LLPEWYSEK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
12.25	3%	0.70%	66.7	2.92E+05	(R)LPGFHTCVGSGGER(L)	C:Carbamidomethylation	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
12.15	3%	0.70%	63.7	1.15E+06	(R)LPGFHTCVGSGGER(L)	C:Carbamidomethylation	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11.81	3%	0.90%	70.5	4.64E+05	(K)YVILGGGVAAGYAAR(E)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11.81	3%	0.90%	70	3.23E+05	(K)VVGVFLEGGSAEENQAIAK(V)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11.73	3%	0.90%	77	8.43E+04	(R)LLPEWYSEK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11.71	3%	0.90%	67.7	6.80E+05	(R)LFTAGIAHFYEGYYTNK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11.7	3%	0.90%	78.5	6.64E+04	(K)LYNEQR(R)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11.59	3%	1.00%	66.1	5.35E+05	(R)LFTAGIAHFYEGYYTNK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11.55	3%	1.00%	71	5.25E+05	(R)LLPEWYSEK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11.28	3%	1%	70.4	1.57E+05	(K)LTDFGVQGAESNNILYLR(D)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
11	3%	1%	62.1	2.03E+04	(K)LTDFGVQGAESNNILYLR(D)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
10.9	3%	1%	63	4.19E+05	(K)YVILGGGVAAGYAAR(E)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
10.89	3%	1%	65.2	1.34E+05	(K)TLTSAAGDTFTYETLLIATGSSVIK(L)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
10.75	3%	1%	69.1	1.48E+05	(R)LFTAGIAHFYEGYYTNK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
10.64	3%	1%	65.9	3.11E+05	(R)LLPEWYSEK(G)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
10.32	3%	1%	67.8	9.21E+05	(K)EQGIEFAAK(I)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
10.3	3%	1%	73.5	1.02E+05	(K)LYNEQR(R)	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
10.19	3%	1%	70	1.44E+05	(R)DIADADKLVAAmQAK(K)	m:Oxidized methionine	CL584.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g024320 [S bicolor] >gi|241942045|gb|EES15190.1| hypothet prot SORBIDRAFT_07g024320 [S bicolor]
17.24	<0.1%	<0.1%	88.9	4.42E+05	(K)VLGAFLEGGSPDENK(A)		UG2763	S.halepenseF2	uncharacterized protein LOC100501585 [Zea mays]
14.52	2%	<0.1%	78.5	1.61E+05	(K)VLGAFLEGGSPDENK(A)		UG2763	S.halepenseF2	uncharacterized protein LOC100501585 [Zea mays]
10.12	3%	1%	65.3	5.96E+04	(K)TDAFFETSVPGVYAIGDVATFPLK(M)		UG2763	S.halepenseF2	uncharacterized protein LOC100501585 [Zea mays]
12.7	2%	0.60%	67.8	8.18E+04	(R)TSVPGIFAIGDVAAFPLK(M)		UG5283	S.halepenseF2Rev	uncharacterized protein LOC100272772 [Zea mays]

12.43	2%	0.60%	68.8	8.39E+04	(R)TSVPGIFAIGDVAAFPLK(M)		UG5283	S.halepenseF2Rev	uncharacterized protein LOC100272772 [Zea mays]
14.61	2%	<0.1%	80.1	1.68E+05	(R)LTGQTTVPNVFIGGK(H)		UG3790	S.halepenseF1	hypothet prot SORBIDRAFT_07g023540 [S bicolor] >gi|241942008|gb|EES15153.1| hypothet prot SORBIDRAFT_07g023540 [S bicolor]
10.54	3%	1%	66.8	1.52E+05	(K)GYPDAPR(C)		CL1747.c1	S.halepenseF3	unknown [Zea mays]
19.5	<0.1%	<0.1%	93.9	5.25E+05	(R)SIQVIVVTDGER(I)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
18.63	<0.1%	<0.1%	95.5	6.88E+05	(R)AVFASGSPFPTVELDGK(T)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
17.97	<0.1%	<0.1%	91.1	4.26E+05	(R)GLLPPSLASQELQEK(K)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
16.32	<0.1%	<0.1%	60.3	1.69E+04	(R)YIAmmDLQER(N)	m:Oxidized methionine	CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
16.26	<0.1%	<0.1%	77.1	6.24E+05	(K)VLTQFEDFANHNAFDLLEK(Y)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
15.89	0.20%	<0.1%	80.7	2.12E+04	(R)VRDDmLLAASEALAEQVTEEHFAK(G)	m:Oxidized methionine	CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
15.06	0.20%	<0.1%	67.3	7.75E+04	(R)ATEEQLITPWAFSVASGYTLLR(D)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
14.91	0.20%	<0.1%	75.5	1.37E+05	(K)YAESCmYTPTYR(C)	C:Carbamidomethylation m:Oxidized methionine	CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
14.65	2%	<0.1%	90.7	2.99E+05	(K)KPWAHEHEPVETLLEAVQSLKPTVLIGTSGK(G)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
13.1	2%	0.60%	75.7	1.02E+05	(R)RPQGLYISLK(D)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
12.75	2%	0.60%	82.3	5.74E+05	(R)RPQGLYISLK(D)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
12.71	2%	0.60%	81.3	3.92E+05	(K)GLIFPPFTNIR(A)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
12	3%	0.80%	79.5	1.89E+05	(R)GLLPPSLASQELQEK(K)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
11.88	3%	0.90%	71.2	3.13E+05	(R)IDSLQAFK(K)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
11.78	3%	0.90%	61.6	2.67E+05	(R)ATGEEYHELLEEFmNAVK(Q)	m:Oxidized methionine	CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
11.72	3%	0.90%	70	8.72E+05	(R)VRDDmLLAASEALAEQVTEEHFAK(G)	m:Oxidized methionine	CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
11.27	3%	1%	78.4	4.99E+05	(K)GLIFPPFTNIR(A)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
10.33	3%	1%	62	4.15E+04	(K)LLIDNVEELLPVVYTPTVGEACQK(Y)	C:Carbamidomethylation	CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
10.22	3%	1%	76.4	1.93E+05	(K)HAGSPIEECR(S)	C:Carbamidomethylation	CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
10.17	3%	1%	80.5	6.92E+05	(K)ILEVLK(N)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
10.09	3%	1%	80.4	2.21E+05	(K)KPWAHEHEPVETLLEAVQSLKPTVLIGTSGK(G)		CL2075.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g005810 [S bicolor] >gi|241946019|gb|EES19164.1| hypothet prot SORBIDRAFT_09g005810 [S bicolor]
13.29	2%	0.50%	67.3	4.32E+05	(K)FSQAFHLLPAAGSFFVQNDmFR(L)	m:Oxidized methionine	UG1148	S.halepenseF1	hypothet prot SORBIDRAFT_07g026170 [S bicolor] >gi|241941046|gb|EES14191.1| hypothet prot SORBIDRAFT_07g026170 [S bicolor]
11.96	3%	0.80%	72.6	9.39E+03	(K)AFVDHYYQTFDTNRPALVGLYQETSmLTFEGHK(F)	m:Oxidized methionine	UG1148	S.halepenseF1	hypothet prot SORBIDRAFT_07g026170 [S bicolor] >gi|241941046|gb|EES14191.1| hypothet prot SORBIDRAFT_07g026170 [S bicolor]
11.13	3%	1%	63.4	5.20E+04	(R)TGPEDHPLK(F)		UG1148	S.halepenseF1	hypothet prot SORBIDRAFT_07g026170 [S bicolor] >gi|241941046|gb|EES14191.1| hypothet prot SORBIDRAFT_07g026170 [S bicolor]
10.78	3%	1%	74	2.31E+06	(R)TGPEDHPLK(F)		UG1148	S.halepenseF1	hypothet prot SORBIDRAFT_07g026170 [S bicolor] >gi|241941046|gb|EES14191.1| hypothet prot SORBIDRAFT_07g026170 [S bicolor]
16.51	<0.1%	<0.1%	79.6	1.48E+05	(K)LASNLLSIGAAIHR(X)		CL2370.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g026520 [S bicolor] >gi|241937095|gb|EES10240.1| hypothet prot SORBIDRAFT_05g026520 [S bicolor]
14.4	2%	<0.1%	78.3	7.12E+04	(K)TSLDSVDDALK(R)		CL2370.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g026520 [S bicolor] >gi|241937095|gb|EES10240.1| hypothet prot SORBIDRAFT_05g026520 [S bicolor]
11.88	3%	0.90%	63.8	1.21E+05	(K)VIVAmNAATDR(M)	m:Oxidized methionine	CL2370.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g026520 [S bicolor] >gi|241937095|gb|EES10240.1| hypothet prot SORBIDRAFT_05g026520 [S bicolor]
19.29	<0.1%	<0.1%	92.9	5.63E+05	(K)EIALWFPEGVAEWK(S)		UG1587	S.halepenseF3	hypothet prot SORBIDRAFT_02g033710 [S bicolor] >gi|241926255|gb|EER99399.1| hypothet prot SORBIDRAFT_02g033710 [S bicolor]
15.57	0.20%	<0.1%	85.3	1.55E+06	(R)GDYAVEVGR(N)		UG1587	S.halepenseF3	hypothet prot SORBIDRAFT_02g033710 [S bicolor] >gi|241926255|gb|EER99399.1| hypothet prot SORBIDRAFT_02g033710 [S bicolor]
14.49	2%	<0.1%	87.9	1.10E+06	(R)GLIGDIISR(F)		UG1587	S.halepenseF3	hypothet prot SORBIDRAFT_02g033710 [S bicolor] >gi|241926255|gb|EER99399.1| hypothet prot SORBIDRAFT_02g033710 [S bicolor]
13.24	2%	0.50%	85.1	1.69E+06	(R)IIGATRPWEAAPGTIR(G)		UG1587	S.halepenseF3	hypothet prot SORBIDRAFT_02g033710 [S bicolor] >gi|241926255|gb|EER99399.1| hypothet prot SORBIDRAFT_02g033710 [S bicolor]
10.79	3%	1%	63.9	8.99E+04	(K)EIALWFPEGVAEWK(S)		UG1587	S.halepenseF3	hypothet prot SORBIDRAFT_02g033710 [S bicolor] >gi|241926255|gb|EER99399.1| hypothet prot SORBIDRAFT_02g033710 [S bicolor]
19.04	<0.1%	<0.1%	89.7	1.45E+05	(R)TFIAIKPDGVQR(G)		UG2074	S.halepenseF2Rev	unknown [Zea mays]
21.62	<0.1%	<0.1%	85	3.74E+05	(K)NYHFDSDTCDAGK(M)	C:Carbamidomethylation	CL830.c1	S.halepenseF2Rev	hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
21.1	<0.1%	<0.1%	67.8	2.39E+06	(K)LDPDGDPEVGLNEK(A)		CL830.c1	S.halepenseF2Rev	hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]

21.08 <0.1% <0.1% 90.6 4.68E+06 (K)LDPDGDPEVGLNEK(A) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
21.06 <0.1% <0.1% 94 9.51E+05 (K)GNCQQIHSTSPYGENLmEGTPGLTWK(I) C:Carbamidomethylation m:Oxidized methionine CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
20.33 <0.1% <0.1% 87.4 9.09E+05 (K)EIVDEHNMFR(A) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
19.98 <0.1% <0.1% 89.6 2.82E+05 (K)LDPDGDPEVGLNEK(A) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
19.91 <0.1% <0.1% 89.9 1.07E+06 (K)ITVDGWSEEKK(N) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
19.34 <0.1% <0.1% 87.1 5.57E+05 (K)GNCQQIHSTSPYGENLMEGTPGLTWK(I) C:Carbamidomethylation CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
18.25 <0.1% <0.1% 65.1 1.08E+06 (K)NYHFDSDTCDAGK(M) C:Carbamidomethylation CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
18.25 <0.1% <0.1% 89 2.89E+06 (K)ITVDGWSEEK(K) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
17.25 <0.1% <0.1% 81 5.35E+05 (K)GNCQQIHSTSPYGENLmEGTPGLTWK(I) C:Carbamidomethylation m:Oxidized methionine CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
16.91 <0.1% <0.1% 82 1.31E+06 (K)ITVDGWSEEKK(N) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
16.86 <0.1% <0.1% 84.7 3.39E+05 (K)KNYHFDSDTCDAGK(M) C:Carbamidomethylation CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
16.76 <0.1% <0.1% 84.4 3.30E+06 (K)ITVDGWSEEKK(N) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
16.22 <0.1% <0.1% 85.3 5.48E+05 (K)ITVDGWSEEK(K) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
15.86 0.20% <0.1% 74.1 1.68E+05 (K)GNCQQIHSTSPYGENLmEGTPGLTWK(I) C:Carbamidomethylation m:Oxidized methionine CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
15.75 0.20% <0.1% 71.3 2.71E+05 (K)EIVDEHNMFR(A) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
15.46 0.20% <0.1% 67.3 1.83E+06 (K)KNYHFDSDTCDAGK(M) C:Carbamidomethylation CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
15.34 0.20% <0.1% 73.4 4.83E+05 (K)EIVDEHNMFR(A) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
14.07 2% 0.30% 66.1 4.42E+05 (K)ITVDGWSEEKK(N) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
12.84 2% 0.60% 60.2 2.55E+05 (K)KNYHFDSDTCDAGK(M) C:Carbamidomethylation CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
12.62 2% 0.70% 63.5 3.14E+05 (K)EIVDEHNMFR(A) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
12.43 2% 0.60% 69.5 3.76E+05 (K)ITVDGWSEEKK(N) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
12.29 2% 0.70% 60.2 6.34E+05 (K)NYHFDSDTCDAGK(M) C:Carbamidomethylation CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
12.05 3% 0.80% 68.6 1.14E+05 (K)LDPDGDPEVGLNEK(A) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
11.96 3% 0.80% 71.8 1.07E+06 (K)GNCQQIHSTSPYGENLmEGTPGLTWK(I) C:Carbamidomethylation m:Oxidized methionine CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
11.6 3% 0.90% 65.6 2.11E+06 (K)EIVDEHNMFR(A) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
11.5 3% 1.00% 81.5 4.38E+06 (K)YAETLK(G) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
11.3 3% 1.00% 71.5 4.72E+05 (K)TTTSVGCGR(I) C:Carbamidomethylation CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
11.12 3% 1% 73.9 1.17E+07 (K)YAETLK(G) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
10.3 3% 1% 60.7 6.89E+04 (K)GNCQQIHSTSPYGENLmEGTPGLTWK(I) C:Carbamidomethylation m:Oxidized methionine CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
10.22 3% 1% 72.5 1.18E+06 (K)ITVDGWSEEK(K) CL830.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_08g022830 [S bicolor] >gi|241944341|gb|EES17486.1| hypothet prot SORBIDRAFT_08g022830 [S bicolor]
15.38 0.20% <0.1% 80.4 2.01E+05 (K)WGVPFIPGLLPQEQQGR(T) UG379 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g043780 [S bicolor] >gi|241924637|gb|EER97781.1| hypothet prot SORBIDRAFT_02g043780 [S bicolor]
14.75 0.20% <0.1% 83 5.14E+05 (K)TVTYEEAQK(E) UG379 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g043780 [S bicolor] >gi|241924637|gb|EER97781.1| hypothet prot SORBIDRAFT_02g043780 [S bicolor]
11.44 3% 1.00% 73.7 9.96E+04 (K)WGVPFIPGLLPQEQQGR(T) UG379 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g043780 [S bicolor] >gi|241924637|gb|EER97781.1| hypothet prot SORBIDRAFT_02g043780 [S bicolor]
11 3% 1% 75.1 1.26E+05 (K)WGVPFIPGLLPQEQQGR(T) UG379 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g043780 [S bicolor] >gi|241924637|gb|EER97781.1| hypothet prot SORBIDRAFT_02g043780 [S bicolor]
23.75 <0.1% <0.1% 100 1.95E+06 (K)IGEVTSATMAPALR(V) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
23.3 <0.1% <0.1% 96.3 3.54E+06 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
22.95 <0.1% <0.1% 97.9 8.42E+06 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
22.92 <0.1% <0.1% 100 5.13E+05 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]

22.41 <0.1% <0.1% 94.6 5.73E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
22.37 <0.1% <0.1% 92.3 4.54E+06 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
22.21 <0.1% <0.1% 97.7 6.99E+06 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
22.15 <0.1% <0.1% 100 5.73E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
22.01 <0.1% <0.1% 89.2 8.62E+06 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
21.01 <0.1% <0.1% 95.1 4.89E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
20.98 <0.1% <0.1% 90.5 5.59E+06 (R)SFYEDCNIVSK(S) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
20.59 <0.1% <0.1% 79.3 1.05E+06 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
20.5 <0.1% <0.1% 92.7 2.83E+05 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
20.15 <0.1% <0.1% 94.5 3.22E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
19.73 <0.1% <0.1% 83.4 3.03E+06 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
19.73 <0.1% <0.1% 95.1 3.08E+06 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
19.24 <0.1% <0.1% 91.7 2.50E+05 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
19.18 <0.1% <0.1% 89.4 7.49E+06 (K)IGEVTSATmAPALR(V) m:Oxidized methionine CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
19.04 <0.1% <0.1% 84.9 2.20E+06 (K)TCTITGQSFIFLGR(A) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.96 <0.1% <0.1% 90.9 1.36E+05 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.92 <0.1% <0.1% 85.3 2.85E+06 (K)TCTITGQSFIFLGR(A) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.92 <0.1% <0.1% 89.4 1.05E+06 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.72 <0.1% <0.1% 84.8 3.03E+05 (K)IGEVTSATMAPALR(V) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.66 <0.1% <0.1% 89.4 2.32E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.49 <0.1% <0.1% 89.3 2.93E+06 (K)IGEVTSATmAPALR(V) m:Oxidized methionine CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.3 <0.1% <0.1% 88.8 2.51E+05 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.28 <0.1% <0.1% 87.2 2.27E+06 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.15 <0.1% <0.1% 76.8 4.25E+05 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
18.1 <0.1% <0.1% 88.2 1.93E+06 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
17.97 <0.1% <0.1% 88.8 2.50E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
17.88 <0.1% <0.1% 89.2 9.75E+05 (R)NDAPEPELKR(D) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
17.73 <0.1% <0.1% 90 8.20E+06 (K)DAALSAAEANR(V) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
17.63 <0.1% <0.1% 79 2.28E+05 (K)IGEVTSATmAPALR(V) m:Oxidized methionine CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
17.61 <0.1% <0.1% 84.2 4.60E+04 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
17.28 <0.1% <0.1% 84.7 5.36E+05 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
17.2 <0.1% <0.1% 88.6 5.32E+05 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
16.8 <0.1% <0.1% 86.2 2.21E+06 (R)SFYEDCNIVSK(S) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
16.71 <0.1% <0.1% 90.9 5.14E+06 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
16.57 <0.1% <0.1% 76.3 1.69E+05 (R)NDAPEPELKR(D) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
16.45 <0.1% <0.1% 83.3 2.55E+05 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
16.37 <0.1% <0.1% 84.9 2.44E+06 (K)DAALSAAEANR(V) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
16.13 <0.1% <0.1% 82 2.05E+05 (R)SFYEDCNIVSK(S) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]

16.05 <0.1% <0.1% 87 2.59E+05 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
15.99 <0.1% <0.1% 81 2.20E+05 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
15.85 0.20% <0.1% 87.4 1.81E+05 (K)DAALSAAEANR(V) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
15.68 0.20% <0.1% 73.8 6.45E+05 (R)SFYEDCNIVSK(S) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
15.6 0.20% <0.1% 72.9 5.27E+05 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
15.47 0.20% <0.1% 86.2 2.42E+06 (K)GLHYYK(S) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
15.4 0.20% <0.1% 81 1.93E+06 (K)IGEVTSATmAPALR(V) m:Oxidized methionine CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
15.32 0.20% <0.1% 73 3.26E+05 (K)TCTITGQSFIFLGR(A) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
15.27 0.20% <0.1% 77.6 1.12E+06 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.95 0.20% <0.1% 77 9.26E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.94 0.20% <0.1% 79.1 9.48E+05 (K)TCTITGQSFIFLGR(A) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.74 0.20% <0.1% 86.8 3.83E+05 (R)NDAPEPELKR(D) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.63 2% <0.1% 83.9 3.39E+05 (K)DAALSAAEANR(V) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.56 2% <0.1% 82.8 8.25E+05 (K)IGEVTSATmAPALR(V) m:Oxidized methionine CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.26 2% <0.1% 81.5 2.74E+05 (R)SFYEDCNIVSK(S) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.2 2% <0.1% 76 3.84E+04 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.12 2% 0.30% 66.8 5.12E+05 (K)CTVDGGHGALYDHK(G) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
14.03 2% 0.30% 77 1.01E+05 (R)SFYEDCNIVSK(S) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13.97 2% 0.30% 76.4 7.68E+06 (R)NDAPEPELKR(D) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13.88 2% 0.40% 75 1.04E+06 (K)TCTITGQSFIFLGR(A) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13.83 2% 0.50% 80.3 3.07E+05 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13.77 2% 0.50% 76.1 2.55E+05 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13.77 2% 0.50% 85.7 2.37E+06 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13.34 2% 0.50% 74.2 5.00E+04 (R)SFYEDCNIVSK(S) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13.26 2% 0.50% 70.7 3.33E+05 (K)IGEVTSATmAPALR(V) m:Oxidized methionine CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13.04 2% 0.60% 75.2 8.47E+05 (K)IGEVTSATMAPALR(V) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
13 2% 0.60% 83 2.68E+05 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.95 2% 0.60% 78.5 3.36E+05 (K)DAALSAAEANR(V) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.82 2% 0.60% 76.2 1.66E+04 (K)TCTITGQSFIFLGR(A) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.69 2% 0.60% 61.5 1.33E+05 (R)SFYEDCNIVSK(S) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.62 2% 0.70% 64.7 5.61E+05 (K)TCTITGQSFIFLGR(A) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.37 2% 0.60% 70.7 1.75E+05 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.23 3% 0.70% 70.9 2.82E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.18 3% 0.70% 70.6 4.79E+05 (K)TCTITGQSFIFLGR(A) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.13 3% 0.80% 81.2 2.81E+05 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
12.03 3% 0.80% 62.3 1.71E+05 (R)VVLHVEPADDSSTSDPAIYLNSIGEAIAK(I) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
11.97 3% 0.80% 67.3 3.04E+06 (R)NDAPEPELKR(D) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
11.63 3% 0.90% 76.9 1.06E+06 (R)NDAPEPELK(R) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]

11.56 3% 1.00% 81.6 2.28E+06 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
11.36 3% 1.00% 68.8 1.33E+05 (K)IGEVTSATmAPALR(V) m:Oxidized methionine CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
11.17 3% 1% 73.5 2.29E+05 (R)YIISIQPGAVYR(E) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
11.17 3% 1% 69.1 1.02E+06 (R)NDAPEPELKR(D) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
11.15 3% 1% 76.7 1.87E+05 (K)IPDGNTK(R) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
11.15 3% 1% 66.5 8.15E+05 (K)GLHYYK(S) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
10.85 3% 1% 74.1 3.04E+06 (R)NDAPEPELK(R) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
10.73 3% 1% 66 2.17E+05 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
10.54 3% 1% 72.4 1.57E+04 (K)DAAAGCTCGK(K) C:Carbamidomethylation CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
10.38 3% 1% 61.7 9.59E+03 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
10.32 3% 1% 70.2 1.75E+05 (R)EFAPFLFISYK(N) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
10.21 3% 1% 66.1 3.03E+05 (R)NDAPEPELK(R) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
10.11 3% 1% 60.3 4.01E+04 (K)SATDYLGDLPVAKPPLTLSPAAADGGFSFK(T) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
10.08 5% 1% 61 3.79E+05 (K)GLHYYK(S) CL1256.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g037730 [S bicolor] >gi|241934634|gb|EES07779.1| hypothet prot SORBIDRAFT_04g037730 [S bicolor]
19.52 <0.1% <0.1% 83.3 6.01E+05 (R)TDPNmPTGIVLQGCR(I) C:Carbamidomethylation m:Oxidized methionine UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
19.24 <0.1% <0.1% 92.1 1.68E+06 (R)IVPEQALFPVR(L) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
18.55 <0.1% <0.1% 90.5 9.00E+05 (R)IVPEQALFPVR(L) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
18.47 <0.1% <0.1% 92.8 6.87E+05 (R)IVPEQALFPVR(L) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
17.67 <0.1% <0.1% 86.7 1.32E+06 (R)LQVPSYLGRPWK(E) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
16.91 <0.1% <0.1% 84.3 1.08E+06 (R)IVPEQALFPVR(L) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
15.95 <0.1% <0.1% 79 1.41E+05 (R)IVPEQALFPVR(L) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
15.41 0.20% <0.1% 88.2 1.75E+05 (R)IVPEQALFPVR(L) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
14.87 0.20% <0.1% 76.4 6.82E+05 (R)LQVPSYLGRPWK(E) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
14.71 0.20% <0.1% 77.8 1.61E+05 (R)IVPEQALFPVR(L) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
14.51 2% <0.1% 60.5 4.97E+05 (R)LQVPSYLGRPWK(E) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
13.71 2% 0.50% 79 2.03E+05 (R)LQVPSYLGRPWK(E) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
13.11 2% 0.60% 75.8 6.68E+05 (R)IVPEQALFPVR(L) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.76 2% 0.60% 73.8 1.22E+05 (R)LQVPSYLGRPWK(E) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.65 2% 0.70% 67.8 2.40E+05 (R)TDPNmPTGIVLQGCR(I) C:Carbamidomethylation m:Oxidized methionine UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.28 2% 0.70% 75.2 5.74E+05 (R)LQVPSYLGRPWK(E) UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.09 3% 0.80% 72.7 4.44E+05 (R)TDPNmPTGIVLQGCR(I) C:Carbamidomethylation m:Oxidized methionine UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
10.63 3% 1% 66 2.84E+05 (R)TDPNmPTGIVLQGCR(I) C:Carbamidomethylation m:Oxidized methionine UG2974 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
17.97 <0.1% <0.1% 82.1 1.72E+06 (K)KLDGVHVVFGK(V) UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
15.8 0.20% <0.1% 79.1 1.89E+05 (K)DTNGCQFAITTVEGSK(L) C:Carbamidomethylation UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
14.97 0.20% <0.1% 87.4 3.05E+06 (K)IEAQGQPSGVPK(A) UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
13.64 2% 0.50% 83.5 1.82E+06 (K)IEAQGQPSGVPK(A) UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
12.6 2% 0.70% 70 2.37E+05 (K)LNHAEPGTISmANYGK(D) m:Oxidized methionine UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
11.7 3% 0.90% 73.3 5.59E+05 (K)KLDGVHVVFGK(V) UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]

11 3% 1% 62.3 1.86E+05 (K)VVSGMDVVHK(I) UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
10.8 3% 1% 67.3 4.14E+05 (K)KLDGVHVVFGK(V) UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
10.65 3% 1% 66.9 1.10E+06 (K)LNHAEPGTISmANYGK(D) m:Oxidized methionine UG1094 S.halepenseF1 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
11.84 3% 0.90% 70.4 3.30E+05 (R)ALCTGEK(G) C:Carbamidomethylation UG2815 S.halepenseF1 hypothet prot SORBIDRAFT_02g031150 [S bicolor] >gi|241923955|gb|EER97099.1| hypothet prot SORBIDRAFT_02g031150 [S bicolor]
11.44 3% 1.00% 63.2 5.68E+05 (R)ALCTGEK(G) C:Carbamidomethylation UG2815 S.halepenseF1 hypothet prot SORBIDRAFT_02g031150 [S bicolor] >gi|241923955|gb|EER97099.1| hypothet prot SORBIDRAFT_02g031150 [S bicolor]
17.38 <0.1% <0.1% 86.1 9.17E+05 (R)IVLGLFGDTVPK(T) CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
14.46 2% <0.1% 85 1.18E+06 (R)IVLGLFGDTVPK(T) CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
14.08 2% 0.30% 79.6 1.79E+05 (K)IEAEGQATGVPK(A) CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
13.91 2% 0.40% 82 5.49E+05 (R)IVLGLFGDTVPK(T) CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
13.03 2% 0.60% 68 1.93E+05 (K)TFFDIEIDGKPAGR(I) CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
12.53 2% 0.60% 69.2 5.23E+05 (K)VVEGMDVVK(K) CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
11.84 3% 0.90% 64.2 2.53E+05 (K)TFFDIEIDGKPAGR(I) CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
10.33 3% 1% 79.5 3.03E+05 (K)KIEAEGQATGVPK(A) CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
10.01 5% 1% 67 8.04E+05 (K)HVVFGKVVEGmDVVK(K) m:Oxidized methionine CL1764.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g029470 [S bicolor] >gi|241915789|gb|EER88933.1| hypothet prot SORBIDRAFT_10g029470 [S bicolor]
18.27 <0.1% <0.1% 85.4 1.86E+05 (K)VFFDIQIDGKPEGR(I) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
17.67 <0.1% <0.1% 82.3 7.29E+05 (K)VFFDIQIDGKPEGR(I) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
17.12 <0.1% <0.1% 82.4 1.38E+06 (K)VFFDIQIDGKPEGR(I) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
17.02 <0.1% <0.1% 84 3.28E+05 (K)VFFDIQIDGKPEGR(I) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
16.4 <0.1% <0.1% 90.5 1.43E+06 (R)IVIGLFGK(T) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
16.11 <0.1% <0.1% 81.9 6.60E+05 (R)IVIGLFGK(T) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
16.1 <0.1% <0.1% 83.9 1.18E+05 (K)VFFDIQIDGKPEGR(I) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
15.83 0.20% <0.1% 70.3 5.35E+05 (K)GmGAYGEPLWYK(G) m:Oxidized methionine CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
13.71 2% 0.50% 76.6 9.32E+05 (R)IVIGLFGK(T) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
13.06 2% 0.60% 63 2.24E+05 (K)GMGAYGEPLWYK(G) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
11.56 3% 1.00% 74.9 1.10E+05 (R)ALSTGEK(G) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
11.39 3% 1.00% 80.7 3.76E+05 (K)TAENFR(A) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
10.84 3% 1% 81.1 1.79E+05 (K)TAENFR(A) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
10.77 3% 1% 73 1.17E+05 (K)TAENFR(A) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
10.64 3% 1% 75.8 1.47E+06 (K)TAENFR(A) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
10.15 3% 1% 71.1 2.84E+05 (K)TAENFR(A) CL1807.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g029450 [S bicolor] >gi|241915787|gb|EER88931.1| hypothet prot SORBIDRAFT_10g029450 [S bicolor]
22.92 <0.1% <0.1% 94.2 2.80E+05 (K)VYFDIEIDGKPAGR(I) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
21.56 <0.1% <0.1% 92.8 3.62E+05 (R)IIPSFMLQGGDFTLGDGR(G) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
21.38 <0.1% <0.1% 88.7 4.62E+05 (R)IIPSFmLQGGDFTLGDGR(G) m:Oxidized methionine UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
18.48 <0.1% <0.1% 77 1.47E+05 (R)DTNGSQFFITTVTTSWLDGK(H) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
17.98 <0.1% <0.1% 89.9 4.89E+05 (R)IIPSFMLQGGDFTLGDGR(G) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
15.46 0.20% <0.1% 80.2 4.23E+05 (R)IIPSFmLQGGDFTLGDGR(G) m:Oxidized methionine UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
15.4 0.20% <0.1% 81.4 6.11E+05 (K)VLSGMDVVYK(V) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
13.86 2% 0.40% 70.7 4.85E+05 (R)IVMGLFGK(T) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]

13.58 2% 0.50% 72.6 5.57E+05 (R)IVmGLFGK(T) m:Oxidized methionine UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
11.87 3% 0.90% 66.5 1.36E+05 (R)DTNGSQFFITTVTTSWLDGK(H) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
10.7 3% 1% 63.1 3.62E+06 (K)HVVFGK(V) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
10.32 3% 1% 62.6 1.15E+06 (R)GGESIYGLK(F) UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
10.21 3% 1% 65 1.07E+06 (K)VLSGmDVVYK(V) m:Oxidized methionine UG2985 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g029480 [S bicolor] >gi|241915790|gb|EER88934.1| hypothet prot SORBIDRAFT_10g029480 [S bicolor]
21.18 <0.1% <0.1% 88.8 1.22E+05 (K)GWDEGVmTmQVGEVAR(I) m:Oxidized methionine UG2564 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g033900 [S bicolor] >gi|241934417|gb|EES07562.1| hypothet prot SORBIDRAFT_04g033900 [S bicolor]
17.62 <0.1% <0.1% 84.5 1.92E+05 (K)DPGQQPFSFNIGLGSVIK(G) UG2564 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g033900 [S bicolor] >gi|241934417|gb|EES07562.1| hypothet prot SORBIDRAFT_04g033900 [S bicolor]
13.32 2% 0.50% 78.7 3.24E+05 (R)GDPIEFDLGTGQVIK(G) UG2580 S.halepenseF1 hypothet prot SORBIDRAFT_02g029060 [S bicolor] >gi|241925993|gb|EER99137.1| hypothet prot SORBIDRAFT_02g029060 [S bicolor]
21.36 <0.1% <0.1% 91 7.58E+05 (R)VIPDFMCQGGDFTR(G) C:Carbamidomethylation CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
19.35 <0.1% <0.1% 87.9 3.23E+05 (R)VFFDmTVGGAPAGR(I) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
18.97 <0.1% <0.1% 84.5 4.10E+05 (R)VFFDmTVGGAPAGR(I) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
18.79 <0.1% <0.1% 85.5 8.17E+05 (R)VFFDmTVGGAPAGR(I) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
18.2 <0.1% <0.1% 89.3 1.05E+06 (R)IVMELYANEVPR(T) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
18.14 <0.1% <0.1% 84.2 1.37E+06 (R)VFFDmTVGGAPAGR(I) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
17.57 <0.1% <0.1% 77.3 1.05E+06 (R)VIPDFmCQGGDFTR(G) C:Carbamidomethylation m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
17.28 <0.1% <0.1% 75.6 1.11E+05 (R)VIPDFmCQGGDFTR(G) C:Carbamidomethylation m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
17.07 <0.1% <0.1% 80.7 2.06E+05 (R)IVMELYANEVPR(T) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
17.06 <0.1% <0.1% 76.7 4.79E+04 (R)VIPDFmCQGGDFTR(G) C:Carbamidomethylation m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
16.82 <0.1% <0.1% 87 5.48E+03 (R)VIPDFMCQGGDFTR(G) C:Carbamidomethylation CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
16.17 <0.1% <0.1% 74.9 2.71E+05 (R)VFFDmTVGGAPAGR(I) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
16.17 <0.1% <0.1% 83.3 1.31E+06 (K)HVVFGQVVEGMDVVK(A) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
15.72 0.20% <0.1% 77.9 8.59E+04 (R)VIPDFMCQGGDFTR(G) C:Carbamidomethylation CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
15.45 0.20% <0.1% 75.6 3.57E+05 (K)SGKPLHYK(G) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
15.22 0.20% <0.1% 69 3.34E+05 (K)HVVFGQVVEGmDVVK(A) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
15.17 0.20% <0.1% 85.5 2.55E+05 (K)SGKPLHYK(G) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
14.91 0.20% <0.1% 83.9 3.64E+05 (R)VFFDmTVGGAPAGR(I) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
14.21 2% <0.1% 71.3 8.52E+05 (K)SGKPLHYK(G) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
14.12 2% 0.30% 69 2.83E+05 (R)VFFDmTVGGAPAGR(I) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
14 2% 0.30% 70.3 1.30E+06 (R)VFFDMTVGGAPAGR(I) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
13.68 2% 0.50% 76.4 2.02E+05 (K)SGKPLHYK(G) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
13.35 2% 0.50% 75.6 2.19E+04 (R)VIPDFmCQGGDFTR(G) C:Carbamidomethylation m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
13.16 2% 0.50% 70.8 1.60E+05 (K)HVVFGQVVEGmDVVK(A) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
13.09 2% 0.60% 63.5 2.20E+05 (R)VFFDMTVGGAPAGR(I) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
12.83 2% 0.60% 75.8 2.12E+06 (K)HVVFGQVVEGmDVVK(A) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
12.83 2% 0.60% 77.1 6.04E+05 (K)HVVFGQVVEGMDVVK(A) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
12.8 2% 0.60% 73.2 3.11E+05 (R)VFFDmTVGGAPAGR(I) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
12.51 2% 0.60% 67.1 2.82E+04 (K)HVVFGQVVEGmDVVK(A) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
11.66 3% 0.90% 69.8 2.39E+05 (R)VFFDMTVGGAPAGR(I) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
11.34 3% 1.00% 72 6.02E+04 (K)HVVFGQVVEGMDVVK(A) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
11.27 3% 1% 67.6 1.51E+05 (K)HVVFGQVVEGMDVVK(A) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
11 3% 1% 68.3 2.61E+05 (K)SGKPLHYK(G) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
10.65 3% 1% 65.9 1.36E+05 (K)HVVFGQVVEGmDVVK(A) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
10.55 3% 1% 67.8 3.76E+05 (K)SGKPLHYK(G) CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
10.25 3% 1% 63.8 6.58E+05 (K)HVVFGQVVEGmDVVK(A) m:Oxidized methionine CL1204.c1 S.halepenseF2Rev cyclophilin [S bicolor]
22.02 <0.1% <0.1% 95.8 7.50E+05 (K)GYDVIEEIKTELEK(K) UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
21.67 <0.1% <0.1% 100 5.39E+05 (K)DSGSVDmDSTSPNTFDGSYFGLVLEK(K) m:Oxidized methionine UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
21.35 <0.1% <0.1% 92.2 8.49E+05 (K)CPGVVSCADIVSVSAR(D) C:Carbamidomethylation UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
21.15 <0.1% <0.1% 90.1 5.63E+06 (K)LTGGPEYSVPLGR(R) UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
21.08 <0.1% <0.1% 89.9 3.04E+05 (K)KCPGVVSCADIVSVSAR(D) C:Carbamidomethylation UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
19.67 <0.1% <0.1% 86.1 2.87E+05 (K)GYDVIEEIKTELEK(K) UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
19.31 <0.1% <0.1% 95.2 5.50E+06 (K)IIFGVVEK(R) UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
19.08 <0.1% <0.1% 81.6 1.48E+06 (K)GYDVIEEIKTELEK(K) UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
18.84 <0.1% <0.1% 86.3 1.71E+06 (K)KCPGVVSCADIVSVSAR(D) C:Carbamidomethylation UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
18.14 <0.1% <0.1% 83.7 3.94E+05 (K)GYDVIEEIKTELEK(K) UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
18.12 <0.1% <0.1% 87.4 6.27E+04 (K)GYDVIEEIKTELEK(K) UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
17.83 <0.1% <0.1% 94.4 1.44E+06 (K)TDFVPIFAK(A) UG342 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]

17.8	<0.1%	<0.1%	89.7	2.61E+05	(K)GYDVIEEIKTELEK(K)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
17.5	<0.1%	<0.1%	90.7	5.47E+06	(K)EAGPNISVK(G)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
17.26	<0.1%	<0.1%	89.5	1.43E+06	(K)GYDVIEEIK(T)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
17.26	<0.1%	<0.1%	83	5.85E+05	(K)LTGGPEYSVPLGR(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
17.21	<0.1%	<0.1%	81	2.18E+05	(K)GYDVIEEIKTELEK(K)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.99	<0.1%	<0.1%	75.6	1.85E+06	(K)LTGGPEYSVPLGR(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.87	<0.1%	<0.1%	92.3	2.83E+05	(K)KTDFVPIFAK(A)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.74	<0.1%	<0.1%	84.8	5.69E+05	(K)KCPGVVSCADIVSVSAR(D)	C:Carbamidomethylation	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.7	<0.1%	<0.1%	83.1	2.21E+05	(K)GYDVIEEIKTELEK(K)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.63	<0.1%	<0.1%	78	3.72E+06	(K)LTGGPEYSVPLGR(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.58	<0.1%	<0.1%	79.5	1.12E+05	(R)CFFIETDAAPIDPGYK(K)	C:Carbamidomethylation	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.57	<0.1%	<0.1%	87.8	3.79E+05	(K)IIFGVVEK(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.52	<0.1%	<0.1%	84.3	3.75E+06	(K)ADPGTAAGLLR(L)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.35	<0.1%	<0.1%	71.9	3.58E+05	(K)GYDVIEEIKTELEK(K)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.26	<0.1%	<0.1%	78	4.33E+05	(K)CPGVVSCADIVSVSAR(D)	C:Carbamidomethylation	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.25	<0.1%	<0.1%	86.9	2.71E+05	(K)IIFGVVEK(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
16.17	<0.1%	<0.1%	90	2.97E+05	(K)IIFGVVEK(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
15.99	<0.1%	<0.1%	88.5	5.68E+05	(K)GYDVIEEIK(T)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
15.73	0.20%	<0.1%	86.3	1.06E+06	(K)KTDFVPIFAK(A)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
15.69	0.20%	<0.1%	86.8	6.08E+05	(K)TDFVPIFAK(A)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
15.32	0.20%	<0.1%	82.1	1.96E+05	(K)ADPGTAAGLLR(L)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
15.31	0.20%	<0.1%	87.6	5.49E+05	(K)IIFGVVEK(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
15.21	0.20%	<0.1%	91.2	1.89E+06	(K)IIFGVVEK(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
15.09	0.20%	<0.1%	81.4	5.20E+05	(K)TEPVVQAmADKK(T)	m:Oxidized methionine	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
15.02	0.20%	<0.1%	77	2.46E+06	(K)IIFGVVEK(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.93	0.20%	<0.1%	83.6	3.12E+05	(K)LTGGPEYSVPLGR(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.77	0.20%	<0.1%	73.4	2.98E+05	(K)KCPGVVSCADIVSVSAR(D)	C:Carbamidomethylation	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.43	2%	<0.1%	73.6	7.63E+05	(K)GYDVIEEIKTELEK(K)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.42	2%	<0.1%	82.9	2.34E+05	(K)EAGPNISVK(G)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.38	2%	<0.1%	88.4	6.49E+05	(K)LIDEFSK(Q)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.37	2%	<0.1%	87	4.68E+06	(K)LIDEFSK(Q)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.28	2%	<0.1%	76	2.62E+05	(K)EAGPNISVK(G)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.19	2%	0.10%	78.9	2.46E+05	(K)EAGPNISVK(G)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.18	2%	0.10%	82.7	2.58E+05	(K)IIFGVVEK(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.11	2%	0.30%	77.7	2.96E+06	(K)EAGPNISVK(G)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.07	2%	0.30%	82.9	2.23E+05	(K)TDFVPIFAK(A)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
14.07	2%	0.30%	85.6	2.32E+06	(K)LIDEFSK(Q)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.83	2%	0.40%	75.7	8.78E+04	(K)GYDVIEEIK(T)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]

13.7	2%	0.50%	61.2	2.36E+05	(K)EAGPNISVK(G)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.65	2%	0.50%	71.6	1.58E+04	(K)KCPGVVSCADIVSVSAR(D)	C:Carbamidomethylation	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.59	2%	0.50%	74.5	1.85E+06	(K)TEPVVQAmADKK(T)	m:Oxidized methionine	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.57	2%	0.50%	80.4	6.08E+05	(K)TDFVPIFAK(A)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.5	2%	0.50%	66.8	3.37E+05	(R)CFFIETDAAPIDPGYK(K)	C:Carbamidomethylation	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.42	2%	0.50%	76.8	1.99E+06	(K)TEPVVQAmADK(K)	m:Oxidized methionine	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.37	2%	0.50%	74.5	2.85E+06	(K)TEPVVQAmADKK(T)	m:Oxidized methionine	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.28	2%	0.50%	67.8	1.27E+05	(K)ADPGTAAGLLR(L)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.08	2%	0.60%	72.7	4.80E+05	(R)EDADNLPGPDIAVPK(L)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
13.06	2%	0.60%	73.8	6.19E+05	(K)KTDFVPIFAK(A)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
12.94	2%	0.60%	71.8	7.73E+04	(K)GYDVIEEIK(T)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
12.92	2%	0.60%	65.2	3.01E+05	(K)KCPGVVSCADIVSVSAR(D)	C:Carbamidomethylation	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
12.74	2%	0.60%	72.4	2.39E+05	(K)KTDFVPIFAK(A)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
12.34	2%	0.70%	81.3	2.20E+06	(K)TDFVPIFAK(A)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
12.33	2%	0.70%	67	4.66E+04	(K)GYDVIEEIK(T)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
12.16	3%	0.70%	79	5.65E+05	(R)DSLVSNREDADNLPGPDIAVPK(L)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
12.02	3%	0.80%	79.1	1.86E+05	(K)IIFGVVEK(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
11.95	3%	0.90%	82	1.57E+06	(R)EDADNLPGPDIAVPK(L)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
11.39	3%	1.00%	68	9.03E+05	(K)KmPLTIDR(L)	m:Oxidized methionine	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
11.33	3%	1.00%	64.2	7.05E+04	(K)GYDVIEEIKTELEK(K)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
11.19	3%	1%	67.7	4.91E+04	(K)KmPLTIDR(L)	m:Oxidized methionine	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
11.1	3%	1%	73.3	5.06E+05	(R)EDADNLPGPDIAVPK(L)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
10.9	3%	1%	69.5	7.56E+04	(K)LIDEFSK(Q)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
10.86	3%	1%	61.7	3.93E+05	(K)LTGGPEYSVPLGR(R)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
10.72	3%	1%	60.1	3.15E+05	(K)TEPVVQAMADK(K)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
10.69	3%	1%	60.4	1.69E+05	(K)DSGSVDmDSTSPNTFDGSYFGLVLEK(K)	m:Oxidized methionine	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
10.49	3%	1%	67.1	1.57E+04	(K)TSCPDAEK(I)	C:Carbamidomethylation	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
10.48	3%	1%	68.3	9.85E+05	(K)EAGPNISVK(G)		UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
10.23	3%	1%	63.9	7.65E+04	(K)TEPVVQAmADK(K)	m:Oxidized methionine	UG342	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g046800 [S bicolor] >gi|241922345|gb|EER95489.1| hypothet prot SORBIDRAFT_01g046800 [S bicolor]
22.34	<0.1%	<0.1%	91.7	1.50E+06	(R)GLGLLSTDEELWTDPR(T)		CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
21.29	<0.1%	<0.1%	97.7	3.85E+06	(R)TKPLVQLYASNPAAFFTDFGR(A)		CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
20.28	<0.1%	<0.1%	85.1	2.44E+05	(K)GFTVQELVALSGAHTLGFSHCNEFANR(L)	C:Carbamidomethylation	CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
20.2	<0.1%	<0.1%	92.9	4.23E+05	(R)TKPLVQLYASNPAAFFTDFGR(A)		CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
19.7	<0.1%	<0.1%	97	1.28E+06	(K)NYLKDPTIAAFNDImTPGK(F)	m:Oxidized methionine	CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
18.26	<0.1%	<0.1%	86.5	3.43E+05	(K)LALELECPGVVSCADILALASGVLVTmTGGPR(Y)	C:Carbamidomethylation m:Oxidized methionine	CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
18.24	<0.1%	<0.1%	82.3	2.14E+06	(K)GFTVQELVALSGAHTLGFSHCNEFANR(L)	C:Carbamidomethylation	CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
17.86	<0.1%	<0.1%	85.1	1.64E+05	(K)LALELECPGVVSCADILALASGVLVTmTGGPR(Y)	C:Carbamidomethylation m:Oxidized methionine	CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
17.82	<0.1%	<0.1%	83.6	4.86E+05	(K)FDNMYFVNLER(G)		CL1773.c1	S.halepenseF3	hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]

17.78 <0.1% <0.1% 82.1 1.47E+06 (R)TKPLVQLYASNPAAFFTDFGR(A) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
17.36 <0.1% <0.1% 83.6 1.72E+05 (K)LALELECPGVVSCADILALASGVLVTmTGGPR(Y) C:Carbamidomethylation m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
16.29 <0.1% <0.1% 81.7 2.04E+06 (K)FDNmYFVNLER(G) m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
16.25 <0.1% <0.1% 93.5 3.73E+06 (R)GLQDVCK(N) C:Carbamidomethylation CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
15.36 0.20% <0.1% 88.9 4.62E+06 (R)YPIPLGR(R) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
15.2 0.20% <0.1% 86 1.17E+06 (K)SEHDAEINHSLPGDAFDAVVR(A) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
14.37 2% <0.1% 81.7 3.04E+06 (K)SEHDAEINHSLPGDAFDAVVR(A) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
14.32 2% <0.1% 76.6 8.39E+05 (K)GFTVQELVALSGAHTLGFSHCNEFANR(L) C:Carbamidomethylation CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
14.26 2% <0.1% 87.2 3.20E+06 (R)YPIPLGR(R) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
14.18 2% 0.10% 77.3 3.73E+05 (R)NQGGKPEPFDPSMNPSYAR(G) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.98 2% 0.30% 74.5 2.11E+06 (K)QmANPTTAAGVLR(V) m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.89 2% 0.40% 83.8 6.17E+04 (K)TGADGEVR(R) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.86 2% 0.40% 87.3 2.35E+06 (K)LSLYGVK(T) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.83 2% 0.50% 81.7 5.38E+06 (R)IIAEVmQTK(Q) m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.59 2% 0.50% 87.8 1.01E+06 (R)LIQMFGAK(G) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.47 2% 0.50% 78.9 8.40E+05 (R)YPIPLGR(R) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.45 2% 0.50% 70.3 1.86E+05 (K)NYLKDPTIAAFNDImTPGK(F) m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.35 2% 0.50% 69.5 4.88E+04 (K)GFTVQELVALSGAHTLGFSHCNEFANR(L) C:Carbamidomethylation CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.34 2% 0.50% 77 8.48E+05 (R)IIAEVmQTK(Q) m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.23 2% 0.50% 80.2 4.82E+05 (R)GLGLLSTDEELWTDPR(T) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
13.19 2% 0.50% 77.2 5.16E+04 (K)DPTIAAFNDIMTPGK(F) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
12.91 2% 0.60% 75.5 3.58E+05 (K)SEHDAEINHSLPGDAFDAVVR(A) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
12.87 2% 0.60% 89.3 4.89E+06 (R)LYNFR(N) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
12.48 2% 0.60% 69.2 1.75E+05 (K)LALELECPGVVSCADILALASGVLVTmTGGPR(Y) C:Carbamidomethylation m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
12.29 2% 0.70% 70.4 1.33E+05 (R)VFFHDCFVSGCDASVLIASTQFQK(S) C:Carbamidomethylation CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
12.23 3% 0.70% 67.8 6.32E+05 (R)VFFHDCFVSGCDASVLIASTQFQK(S) C:Carbamidomethylation CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
12.2 3% 0.70% 73.1 2.32E+05 (K)FDNmYFVNLER(G) m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
11.84 3% 0.90% 78.8 8.98E+05 (R)GLQDVCK(N) C:Carbamidomethylation CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
11.79 3% 0.90% 62.6 3.09E+05 (K)GFTVQELVALSGAHTLGFSHCNEFANR(L) C:Carbamidomethylation CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
11.72 3% 0.90% 71.8 4.59E+04 (K)FDNMYFVNLER(G) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
11.46 3% 1.00% 71.3 8.90E+04 (K)LALELECPGVVSCADILALASGVLVTmTGGPR(Y) C:Carbamidomethylation m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
11.37 3% 1.00% 74.8 5.96E+05 (K)DPTIAAFNDImTPGK(F) m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
11.24 3% 1% 80 3.58E+05 (R)YPIPLGR(R) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
11.09 3% 1% 63.8 4.52E+05 (R)NQGGKPEPFDPSmNPSYAR(G) m:Oxidized methionine CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
11.08 3% 1% 75.1 2.32E+05 (K)SEHDAEINHSLPGDAFDAVVR(A) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
10.79 3% 1% 64.2 1.98E+05 (K)NYLKDPTIAAFNDIMTPGK(F) CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
10.77 3% 1% 66.1 2.51E+04 (K)GFTVQELVALSGAHTLGFSHCNEFANR(L) C:Carbamidomethylation CL1773.c1 S.halepenseF3 hypothet prot SORBIDRAFT_04g028340 [S bicolor] >gi|241934137|gb|EES07282.1| hypothet prot SORBIDRAFT_04g028340 [S bicolor]
10.63 3% 1% 69.9 4.53E+05 (K)FATTPLK(D) UG1665 S.halepenseF2 hypothet prot SORBIDRAFT_03g010530 [S bicolor] >gi|241929595|gb|EES02740.1| hypothet prot SORBIDRAFT_03g010530 [S bicolor]

23.12 <0.1% <0.1% 86.8 3.57E+05 (K)FTFCYDALHGVAGAYAK(H) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
22.31 <0.1% <0.1% 95 8.30E+05 (K)VTVFQQPHYLQNFVQSTFNALPADQVK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
22.27 <0.1% <0.1% 85.8 4.77E+04 (K)FFGNLmDAGmCSICGEESFGTGSDHIR(E) C:Carbamidomethylation m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
22.07 <0.1% <0.1% 95.2 8.19E+05 (K)VTVFQQPHYLQNFVQSTFNALPADQVK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
21.42 <0.1% <0.1% 79.4 2.24E+06 (K)FTFCYDALHGVAGAYAK(H) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
21.15 <0.1% <0.1% 81.3 3.09E+05 (K)FFGNLmDAGmCSICGEESFGTGSDHIR(E) C:Carbamidomethylation m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
21.06 <0.1% <0.1% 87.1 1.00E+06 (R)SDVSEVVAADEFEYKDPVDGSVSK(H) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
20.78 <0.1% <0.1% 93 1.39E+06 (R)SDVSEVVAADEFEYKDPVDGSVSK(H) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
20.31 <0.1% <0.1% 86 1.95E+06 (R)YDYENVDAGAAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
20.05 <0.1% <0.1% 97 1.88E+06 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
19.65 <0.1% <0.1% 88.6 2.64E+05 (K)SSSNVEPPEFGAAADGDADR(N) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
19.53 <0.1% <0.1% 84.9 1.41E+05 (K)YNmGNGGPAPESVTDK(I) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
19.45 <0.1% <0.1% 94.8 3.26E+05 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
19.36 <0.1% <0.1% 88.1 3.17E+05 (K)SSSNVEPPEFGAAADGDADR(N) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.86 <0.1% <0.1% 69.7 1.51E+06 (K)FTFCYDALHGVAGAYAK(H) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.82 <0.1% <0.1% 92.6 3.03E+06 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.61 <0.1% <0.1% 82 1.32E+04 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.59 <0.1% <0.1% 92.1 2.63E+05 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.5 <0.1% <0.1% 90.9 1.33E+06 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.27 <0.1% <0.1% 75.5 1.93E+05 (K)YNmGNGGPAPESVTDK(I) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.24 <0.1% <0.1% 81.1 1.59E+06 (R)YDYENVDAGAAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.12 <0.1% <0.1% 86.9 2.23E+06 (K)EDFGGGHPDPNLTYAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.04 <0.1% <0.1% 87.9 1.81E+06 (K)TIFDFEAIKK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.03 <0.1% <0.1% 83 1.63E+06 (R)YDYENVDAGAAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
18.02 <0.1% <0.1% 95.4 3.53E+06 (K)LVSVEDIVR(Q) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.93 <0.1% <0.1% 83.8 1.84E+06 (K)EDFGGGHPDPNLTYAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.75 <0.1% <0.1% 82.7 2.71E+05 (R)VWVGLNSLmSTPAVSAVIR(E) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.65 <0.1% <0.1% 88.8 9.43E+05 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.49 <0.1% <0.1% 88.3 2.11E+06 (K)HIFVEELGADESSLLNCVPK(E) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.41 <0.1% <0.1% 74.7 1.92E+05 (K)FTFCYDALHGVAGAYAK(H) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.37 <0.1% <0.1% 83.7 8.63E+05 (R)VWVGLNSLmSTPAVSAVIR(E) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.34 <0.1% <0.1% 91.5 6.09E+05 (K)ELmANLVSmQSSLSDVNK(L) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.3 <0.1% <0.1% 90.4 7.10E+05 (K)HIFVEELGADESSLLNCVPK(E) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.28 <0.1% <0.1% 91.4 3.36E+06 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.21 <0.1% <0.1% 82.3 1.95E+06 (K)FFEVPTGWK(F) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.09 <0.1% <0.1% 93 3.18E+06 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
17.06 <0.1% <0.1% 85.4 7.45E+05 (K)ATGAFILTASHNPGGPTEDFGIK(Y) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
16.98 <0.1% <0.1% 72.4 2.15E+05 (K)FTFCYDALHGVAGAYAK(H) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]

16.83 <0.1% <0.1% 86.7 1.24E+06 (R)LSGTGSVGATIR(V) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
16.78 <0.1% <0.1% 87.8 2.28E+05 (K)SSSNVEPPEFGAAADGDADR(N) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
16.72 <0.1% <0.1% 87.3 1.06E+06 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
16.64 <0.1% <0.1% 84 2.03E+06 (K)TIFDFEAIKK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
16.5 <0.1% <0.1% 80.1 2.29E+06 (R)VYIEQYEK(D) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
16.28 <0.1% <0.1% 83.6 3.65E+05 (K)ELmANLVSmQSSLSDVNK(L) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
16 <0.1% <0.1% 87.3 2.51E+05 (K)EDFGGGHPDPNLTYAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.97 <0.1% <0.1% 86.2 2.77E+06 (R)LSGTGSVGATIR(V) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.95 <0.1% <0.1% 72.9 4.53E+03 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.88 0.20% <0.1% 77.2 7.22E+05 (K)VTVFQQPHYLQNFVQSTFNALPADQVK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.84 0.20% <0.1% 91.7 4.64E+06 (K)LVSVEDIVR(Q) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.82 0.20% <0.1% 87.5 5.32E+06 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.78 0.20% <0.1% 86 2.25E+06 (K)GATIVVSGDGR(Y) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.66 0.20% <0.1% 61.7 1.70E+06 (R)SmPTSAALDVVAK(N) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.48 0.20% <0.1% 81.5 6.34E+05 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.48 0.20% <0.1% 69.5 1.46E+06 (K)ATTPFEGQKPGTSGLR(K) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.41 0.20% <0.1% 78.1 5.02E+05 (K)ATGAFILTASHNPGGPTEDFGIK(Y) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.38 0.20% <0.1% 87.6 2.31E+06 (K)DAVQIITK(M) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.35 0.20% <0.1% 83.4 2.76E+05 (K)TIFDFEAIKK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.3 0.20% <0.1% 76.8 1.34E+06 (R)VWVGLNSLmSTPAVSAVIR(E) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.27 0.20% <0.1% 85 2.02E+05 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.26 0.20% <0.1% 78.1 3.15E+06 (R)LSGTGSVGATIR(V) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.22 0.20% <0.1% 78.1 1.34E+06 (K)FFEVPTGWK(F) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.19 0.20% <0.1% 68.4 2.54E+06 (R)SmPTSAALDVVAK(N) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.18 0.20% <0.1% 70.7 1.58E+05 (K)SSSNVEPPEFGAAADGDADR(N) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.17 0.20% <0.1% 83 8.49E+05 (K)HIFVEELGADESSLLNCVPK(E) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.16 0.20% <0.1% 85.3 2.69E+06 (K)GATIVVSGDGR(Y) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.13 0.20% <0.1% 88.4 2.80E+05 (K)KVTVFQQPHYLQNFVQSTFNALPADQVK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.1 0.20% <0.1% 76.8 5.92E+04 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
15.09 0.20% <0.1% 75.3 1.99E+05 (K)DNLGGDKLVSVEDIVR(Q) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.98 0.20% <0.1% 77 1.09E+05 (K)YNmGNGGPAPESVTDK(I) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.96 0.20% <0.1% 65.2 1.32E+04 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.95 0.20% <0.1% 76.9 4.46E+05 (K)LVSVEDIVR(Q) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.77 0.20% <0.1% 78.2 3.71E+05 (R)LSGTGSVGATIR(V) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.75 0.20% <0.1% 81.7 2.88E+05 (K)EDFGGGHPDPNLTYAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.75 0.20% <0.1% 79.4 3.25E+05 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.67 2% <0.1% 77 6.01E+05 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.63 2% <0.1% 88.6 2.21E+06 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]

14.54 2% <0.1% 80.5 3.59E+05 (R)SMPTSAALDVVAK(N) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.54 2% <0.1% 89.9 5.89E+05 (K)LVSVEDIVR(Q) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.5 2% <0.1% 69.7 1.84E+06 (K)ATTPFEGQKPGTSGLR(K) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.42 2% <0.1% 80.7 2.07E+05 (R)RVWVGLNSLmSTPAVSAVIR(E) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.17 2% 0.20% 78 1.22E+06 (K)SSSNVEPPEFGAAADGDADRNmILGK(R) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14.13 2% 0.30% 78.5 5.63E+05 (R)LSGTGSVGATIR(V) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
14 2% 0.30% 74.6 4.58E+05 (K)TIFDFEAIKK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.74 2% 0.50% 81.2 1.60E+05 (K)KVTVFQQPHYLQNFVQSTFNALPADQVK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.61 2% 0.50% 65.3 2.76E+05 (R)YDYENVDAGAAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.59 2% 0.50% 82.1 2.52E+06 (K)GATIVVSGDGR(Y) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.58 2% 0.50% 84.3 1.10E+05 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.47 2% 0.50% 74.8 3.16E+05 (K)DAVQIITK(M) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.46 2% 0.50% 79.2 1.93E+04 (K)TIFDFEAIKK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.2 2% 0.50% 77 8.76E+05 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.18 2% 0.50% 66.8 1.90E+05 (R)QHWATYGR(H) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.11 2% 0.60% 75.9 3.32E+06 (R)VYIEQYEK(D) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.05 2% 0.60% 74.5 1.84E+06 (K)DAVQIITK(M) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
13.04 2% 0.60% 67.1 2.09E+05 (K)FTFCYDALHGVAGAYAK(H) C:Carbamidomethylation UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.98 2% 0.60% 64.8 5.40E+05 (R)VWVGLNSLmSTPAVSAVIR(E) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.92 2% 0.60% 68.9 1.94E+05 (R)YDYENVDAGAAK(E) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.88 2% 0.60% 84.6 1.99E+06 (R)YLFGDGSR(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.7 2% 0.60% 73.4 1.02E+04 (R)SMPTSAALDVVAK(N) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.63 2% 0.70% 74 1.19E+06 (K)VTVFQQPHYLQNFVQSTFNALPADQVK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.62 2% 0.70% 70.4 1.76E+05 (K)DNLGGDKLVSVEDIVR(Q) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.61 2% 0.70% 79.7 7.37E+04 (R)HYYTR(Y) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.23 3% 0.70% 73.7 2.36E+05 (K)DAVQIITK(M) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.21 3% 0.70% 81.4 4.81E+05 (R)RVWVGLNSLmSTPAVSAVIR(E) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.2 3% 0.70% 77.9 2.90E+06 (K)GATIVVSGDGR(Y) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
12.2 3% 0.70% 79 2.38E+06 (R)YLFGDGSR(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11.93 3% 0.90% 63.2 4.53E+03 (R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11.93 3% 0.90% 73.9 4.01E+05 (K)GATIVVSGDGR(Y) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11.83 3% 0.90% 75.7 1.08E+05 (K)YNmGNGGPAPESVTDK(I) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11.43 3% 1.00% 76.4 1.86E+05 (K)TIFDFEAIKK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11.33 3% 1.00% 64.6 3.44E+05 (R)SMPTSAALDVVAK(N) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11.13 3% 1% 70.4 9.99E+04 (R)DSQDALAPLVDVALK(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11.12 3% 1% 74.9 1.61E+06 (R)YLFGDGSR(L) UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11.08 3% 1% 66.1 2.08E+05 (K)SSSNVEPPEFGAAADGDADRNmILGK(R) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
11 3% 1% 66.2 1.04E+06 (K)SSSNVEPPEFGAAADGDADRNmILGK(R) m:Oxidized methionine UG1121 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]

10.88	3%	1%	63.4	1.84E+04	(R)FFVTPSDSVAIIAANAVQSIPYFASGLK(G)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.82	3%	1%	73.8	1.16E+05	(K)MQEYTGR(S)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.82	3%	1%	69.3	1.07E+06	(K)KATTPFEGQKPGTSGLR(K)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.66	3%	1%	75.3	1.19E+06	(K)ELmANLVSmQSSLSDVNK(L)	m:Oxidized methionine	UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.49	3%	1%	70.1	1.23E+06	(K)ELmANLVSmQSSLSDVNK(L)	m:Oxidized methionine	UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.46	3%	1%	68	1.02E+05	(K)ELMANLVSmQSSLSDVNK(L)	m:Oxidized methionine	UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.45	3%	1%	64.6	6.91E+05	(K)ELmANLVSmQSSLSDVNK(L)	m:Oxidized methionine	UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.44	3%	1%	64.1	1.53E+05	(K)SSSNVEPPEFGAAADGDADR(N)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.43	3%	1%	68.9	4.51E+05	(R)DSQDALAPLVDVALK(L)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.41	3%	1%	61.9	3.96E+05	(K)DAVQIITK(M)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.31	3%	1%	66.4	1.06E+06	(K)VTVFQQPHYLQNFVQSTFNALPADQVK(G)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.26	3%	1%	70.4	5.07E+05	(R)VYIEQYEK(D)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.23	3%	1%	63.8	2.35E+04	(R)YDYENVDAGAAK(E)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.2	3%	1%	63.7	1.85E+05	(R)DSQDALAPLVDVALK(L)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
10.17	3%	1%	68.2	1.09E+05	(K)LVSVEDIVR(Q)		UG1121	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g010280 [S bicolor] >gi|241920430|gb|EER93574.1| hypothet prot SORBIDRAFT_01g010280 [S bicolor]
16.08	<0.1%	<0.1%	75.6	5.95E+04	(R)FYKEEEK(N)		CL1997.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
13.37	2%	0.50%	75.6	1.98E+05	(R)FYKEEEK(N)		CL1997.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
12.53	2%	0.60%	72.2	5.79E+04	(R)AHASTEGVTK(F)		CL1997.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
10.33	3%	1%	77.8	2.49E+05	(R)AHASTEGVTK(F)		CL1997.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
15.16	0.20%	<0.1%	75.5	1.77E+06	(K)GVTTIIGGGDSVAAVEK(V)		UG7577	S.halepenseF2	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
13.39	2%	0.50%	76.8	5.60E+06	(K)GVTTIIGGGDSVAAVEK(V)		UG7577	S.halepenseF2	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
12.45	2%	0.60%	76.9	3.79E+06	(K)GVTTIIGGGDSVAAVEK(V)		UG7577	S.halepenseF2	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
11.99	3%	0.80%	76.5	1.47E+06	(K)GVTTIIGGGDSVAAVEK(V)		UG7577	S.halepenseF2	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
11.71	3%	0.90%	72.4	3.29E+05	(K)GVTTIIGGGDSVAAVEK(V)		UG7577	S.halepenseF2	hypothet prot SORBIDRAFT_09g024340 [S bicolor] >gi|241946598|gb|EES19743.1| hypothet prot SORBIDRAFT_09g024340 [S bicolor]
21.11	<0.1%	<0.1%	98	4.45E+06	(K)LVAALPEGGVLLLENVR(F)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
21.04	<0.1%	<0.1%	94.8	5.19E+06	(K)LASVADLYVNDAFGTAHR(A)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
20.49	<0.1%	<0.1%	94.2	2.35E+06	(K)YSLKPLVPR(L)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
20.04	<0.1%	<0.1%	89.5	2.08E+06	(K)LVAALPEGGVLLLENVR(F)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
19.81	<0.1%	<0.1%	88.4	6.54E+06	(K)LVAALPEGGVLLLENVR(F)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
18.34	<0.1%	<0.1%	90.5	6.33E+06	(K)KPFAAIVGGSK(V)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.63	<0.1%	<0.1%	84.9	4.30E+05	(R)FYKEEEKNEPEFAK(K)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.62	<0.1%	<0.1%	86.9	1.05E+06	(K)LASVADLYVNDAFGTAHR(A)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.61	<0.1%	<0.1%	82.5	2.77E+06	(K)LVAALPEGGVLLLENVR(F)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.42	<0.1%	<0.1%	86.5	1.60E+06	(R)FYKEEEKNEPEFAK(K)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.34	<0.1%	<0.1%	91.8	3.35E+05	(K)LVAALPEGGVLLLENVR(F)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.27	<0.1%	<0.1%	80.5	4.27E+05	(K)LASVADLYVNDAFGTAHR(A)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.24	<0.1%	<0.1%	90.4	1.65E+06	(K)LVAALPEGGVLLLENVR(F)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.22	<0.1%	<0.1%	89.9	1.21E+06	(K)LVAALPEGGVLLLENVR(F)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"

17.07	<0.1%	<0.1%	85.6	1.27E+06	(K)ELDYLVGAVANPK(K)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.07	<0.1%	<0.1%	84	1.64E+05	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.49	<0.1%	<0.1%	88.7	1.83E+05	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.42	<0.1%	<0.1%	79.7	5.90E+05	(K)KLASVADLYVNDAFGTAHR(A)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.15	<0.1%	<0.1%	84.6	5.74E+06	(K)ELDYLVGAVANPK(K)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.1	<0.1%	<0.1%	80.5	7.77E+05	(K)KPFAAIVGGSK(V)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.1	<0.1%	<0.1%	90.6	4.10E+06	(K)KPFAAIVGGSK(V)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.02	<0.1%	<0.1%	80.2	7.13E+06	(K)YSLKPLVPR(L)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16	<0.1%	<0.1%	84.2	1.13E+05	(K)ELDYLVGAVANPK(K)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
15.99	<0.1%	<0.1%	75.5	2.50E+06	(K)YSLKPLVPR(L)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
15.42	0.20%	<0.1%	80.7	1.36E+06	(K)YSLKPLVPR(L)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
15.23	0.20%	<0.1%	74.5	5.46E+06	(K)YSLKPLVPR(L)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.93	0.20%	<0.1%	80.7	1.03E+05	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.9	0.20%	<0.1%	78.8	2.29E+06	(R)ADLNVPLDDAQK(I)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.77	0.20%	<0.1%	86.1	2.48E+06	(R)SVGTLGEADLK(G)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.65	2%	<0.1%	85.7	4.03E+06	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.64	2%	<0.1%	87.5	3.75E+06	(R)ADLNVPLDDAQK(I)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.55	2%	<0.1%	84.7	1.13E+05	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.92	2%	0.40%	83.1	2.82E+05	(K)ELDYLVGAVANPK(K)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.84	2%	0.40%	81.9	1.57E+06	(K)YLKPAVAGFLMQK(E)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.67	2%	0.50%	67.7	8.40E+05	(K)YLKPAVAGFLmQK(E) m:Oxidized methionine	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.31	2%	0.50%	70.6	6.63E+05	(K)YSLKPLVPR(L)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.11	2%	0.60%	79.4	2.06E+05	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13	2%	0.60%	74.3	2.19E+05	(K)LASVADLYVNDAFGTAHR(A)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.99	2%	0.60%	68.3	5.07E+06	(K)YLKPAVAGFLmQK(E) m:Oxidized methionine	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.96	2%	0.60%	74.5	6.11E+06	(R)SVGTLGEADLK(G)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.87	2%	0.60%	85.1	1.82E+05	(R)ADLNVPLDDAQK(I)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.61	2%	0.70%	80.1	1.53E+06	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.51	2%	0.60%	65.9	1.73E+04	(K)KLASVADLYVNDAFGTAHR(A)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.49	2%	0.60%	80.5	7.67E+04	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.2	3%	0.70%	64.6	3.42E+05	(K)KPFAAIVGGSK(V)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.06	3%	0.80%	68.5	6.33E+04	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.96	3%	0.80%	66.4	5.10E+06	(R)FYKEEEKNEPEFAK(K)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.72	3%	0.90%	71.1	7.19E+04	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.54	3%	0.90%	75.6	2.89E+05	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.49	3%	1.00%	73.4	2.04E+05	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.46	3%	1.00%	68.4	1.05E+06	(K)ELDYLVGAVANPK(K)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.31	3%	1.00%	78.5	4.60E+04	(K)LVAALPEGGVLLLENVR(F)	CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"

11.27	3%	1%	67.3	4.33E+05	(K)YSLKPLVPR(L)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.93	3%	1%	61.6	1.25E+05	(K)YLKPAVAGFLMQK(E)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.86	3%	1%	73.5	1.67E+05	(R)ADLNVPLDDAQK(I)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.67	3%	1%	64	3.04E+05	(K)YLKPAVAGFLMQK(E)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.39	3%	1%	67.6	3.25E+05	(K)LASVADLYVNDAFGTAHR(A)		CL1997.c2	S.halepenseF3	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
20.89	<0.1%	<0.1%	94.2	2.72E+05	(K)GVSLLLPTDIVVADK(F)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
19.83	<0.1%	<0.1%	95.5	1.39E+06	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
19.63	<0.1%	<0.1%	85.3	1.23E+06	(K)TFNEALDTTQTIIWNGPmGVFEFPK(F)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
19.63	<0.1%	<0.1%	89.6	7.46E+06	(K)FAAGTEAIAK(K)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
19.6	<0.1%	<0.1%	82	1.43E+06	(K)SLVEEDKLELATSLIEK(A)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
19.42	<0.1%	<0.1%	94.7	3.03E+06	(K)FAADAESK(I)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
18.81	<0.1%	<0.1%	90.4	1.03E+05	(K)GVSLLLPTDIVVADK(F)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
18.58	<0.1%	<0.1%	94.2	2.46E+05	(K)IVPATAIPDDWMGLDVGPDATK(T)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
18.28	<0.1%	<0.1%	94.5	5.25E+06	(K)IGVIESLLAK(V)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.97	<0.1%	<0.1%	89.2	4.92E+05	(K)IVPATAIPDDWMGLDVGPDATK(T)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.59	<0.1%	<0.1%	83.6	4.13E+05	(K)SLVEEDKLELATSLIEK(A)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.19	<0.1%	<0.1%	83.5	2.27E+04	(K)VDILILGGGmIYTFYK(A)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.08	<0.1%	<0.1%	84.1	1.62E+06	(K)SLVEEDKLELATSLIEK(A)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.44	<0.1%	<0.1%	86.1	8.80E+05	(K)FAADAESK(I)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.23	<0.1%	<0.1%	85.3	1.79E+06	(K)IGVIESLLAK(V)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
16.11	<0.1%	<0.1%	89.4	6.32E+05	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
15.96	<0.1%	<0.1%	85.2	1.99E+05	(K)TFNEALDTTQTIIWNGPMGVFEFPK(F)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
15.9	0.20%	<0.1%	79.3	1.94E+05	(K)VDILILGGGmIYTFYK(A)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
15.6	0.20%	<0.1%	89	4.49E+05	(K)IGVIESLLAK(V)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
15.43	0.20%	<0.1%	85.2	6.42E+05	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.56	2%	<0.1%	79.3	1.06E+05	(K)IGVIESLLAK(V)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.25	2%	<0.1%	80.4	1.70E+06	(K)LAELTTTK(G)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
14.1	2%	0.30%	81.3	1.74E+05	(K)IGVIESLLAK(V)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.83	2%	0.50%	72.1	1.72E+05	(K)TFNEALDTTQTIIWNGPmGVFEFPK(F)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.82	2%	0.50%	81.8	2.34E+06	(K)FAAGTEAIAK(K)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.64	2%	0.50%	80.1	3.57E+05	(K)IGVIESLLAK(V)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.55	2%	0.50%	77.8	2.08E+06	(K)KLAELTTTK(G)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.41	2%	0.50%	79.9	9.20E+04	(K)IGVIESLLAK(V)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.24	2%	0.50%	70.1	2.73E+05	(K)SLVEEDKLELATSLIEK(A)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.19	2%	0.50%	87.5	1.63E+06	(K)GVSLLLPTDIVVADK(F)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
13.03	2%	0.60%	83.7	2.36E+05	(K)GVSLLLPTDIVVADKFAADAESK(I)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.96	2%	0.60%	76.3	2.11E+05	(K)IVPATAIPDDWmGLDVGPDATK(T)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.93	2%	0.60%	70.7	6.96E+04	(K)FAADAESK(I)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"

12.85	2%	0.60%	74.8	4.55E+06	(K)LAELTTTK(G)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.79	2%	0.60%	85.5	2.92E+06	(K)GVSLLLPTDIVVADK(F)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
12.52	2%	0.60%	67	3.75E+05	(K)FAAGTEAIAK(K)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.77	3%	0.90%	66.9	2.70E+05	(K)TFNEALDTTQTIIWNGPmGVFEFPK(F)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.64	3%	0.90%	64.7	1.15E+04	(K)SLVEEDKLELATSLIEK(A)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.59	3%	1.00%	73.7	1.06E+05	(K)IGVIESLLAK(V)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.5	3%	1.00%	60.1	6.40E+05	(K)KLAELTTTK(G)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.49	3%	1.00%	72.5	1.15E+04	(K)SLVEEDKLELATSLIEK(A)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.42	3%	1.00%	67.1	1.47E+05	(K)KLAELTTTK(G)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
11.22	3%	1%	66.9	2.69E+06	(K)AQGYSVGK(S)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.8	3%	1%	75	3.56E+06	(K)GVSLLLPTDIVVADK(F)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.7	3%	1%	72.6	8.19E+05	(K)AQGYSVGK(S)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.59	3%	1%	70.7	2.87E+05	(K)TFNEALDTTQTIIWNGPmGVFEFPK(F)	m:Oxidized methionine	UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.51	3%	1%	60.1	2.53E+05	(K)SLVEEDKLELATSLIEK(A)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
10.31	3%	1%	71.2	2.10E+04	(K)GVSLLLPTDIVVADK(F)		UG2835	S.halepenseF3RevF3Rev	"uncharacterized protein LOC100274579 [Zea mays] >gi|195632546|gb|ACG36709.1| phosphoglycerate kinase, cytosolic [Zea mays]"
17.43	<0.1%	<0.1%	84.4	1.67E+05	(R)TLTDETASPR(W)		UG2291	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g005220 [S bicolor] >gi|241945977|gb|EES19122.1| hypothet prot SORBIDRAFT_09g005220 [S bicolor]
10.52	3%	1%	62.5	2.69E+05	(K)IYATIGLGK(A)		UG2291	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g005220 [S bicolor] >gi|241945977|gb|EES19122.1| hypothet prot SORBIDRAFT_09g005220 [S bicolor]
10.06	5%	1%	62.8	1.40E+05	(R)KLVETVEDTVGVGK(G)		UG2291	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g005220 [S bicolor] >gi|241945977|gb|EES19122.1| hypothet prot SORBIDRAFT_09g005220 [S bicolor]
19.72	<0.1%	<0.1%	92.6	1.21E+06	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
19.71	<0.1%	<0.1%	92.7	2.82E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
19.64	<0.1%	<0.1%	91.3	3.86E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
19	<0.1%	<0.1%	89.2	7.92E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
17.17	<0.1%	<0.1%	90.6	5.05E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
16.35	<0.1%	<0.1%	82.3	9.16E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
16.02	<0.1%	<0.1%	74.5	3.93E+05	(R)QLGSTSADEVQR(M)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
15.18	0.20%	<0.1%	79.7	3.20E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
14.35	2%	<0.1%	73.6	3.22E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
13.87	2%	0.40%	70.3	3.76E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
11.83	3%	0.90%	70.9	3.62E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
11.75	3%	0.90%	76.3	1.63E+05	(K)ISLSELTDALR(Q)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
10.28	3%	1%	60.5	2.38E+05	(R)QLGSTSADEVQR(M)		UG451	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g023990 [S bicolor] >gi|241942023|gb|EES15168.1| hypothet prot SORBIDRAFT_07g023990 [S bicolor]
24.79	<0.1%	<0.1%	97.2	8.38E+05	(K)SPDPACAEIEEQR(A)	C:Carbamidomethylation	CL2052.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]
20.93	<0.1%	<0.1%	95.9	6.27E+05	(K)KSPDPACAEIEEQR(A)	C:Carbamidomethylation	CL2052.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]
20.49	<0.1%	<0.1%	93.6	1.29E+06	(K)LEIDQDHQEEICEVVLK(K)	C:Carbamidomethylation	CL2052.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]
19.6	<0.1%	<0.1%	87	8.87E+06	(R)YANPIAFFR(K)		CL2052.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]
19.25	<0.1%	<0.1%	87.2	1.41E+06	(K)AEATTDDFGWYK(L)		CL2052.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]
19.23	<0.1%	<0.1%	78.8	2.88E+05	(K)AEATTDDFGWYK(L)		CL2052.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]
17.9	<0.1%	<0.1%	81.5	2.08E+06	(R)YANPIAFFR(K)		CL2052.c1	S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]

17.88	<0.1%	<0.1%	89.1	4.08E+06	(K)SVAGATVEVVCR(H)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
17.41	<0.1%	<0.1%	80.5	5.18E+06	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
17.38	<0.1%	<0.1%	81.8	4.74E+05	(K)AEATTDDFGWYK(L)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
16.68	<0.1%	<0.1%	82.4	3.23E+05	(K)KSPDPACAEIEEQR(A)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
16.48	<0.1%	<0.1%	80.4	4.50E+04	(K)LEIDQDHQEEICEVVLK(K)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
16.21	<0.1%	<0.1%	81.8	2.50E+06	(K)KSPDPACAEIEEQR(A)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
16.19	<0.1%	<0.1%	81.9	1.18E+06	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
15.73	0.20%	<0.1%	71.6	4.12E+05	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
15.38	0.20%	<0.1%	81.7	3.05E+06	(K)AGGFVVTGR(V)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
14.87	0.20%	<0.1%	69.9	6.24E+05	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
14.79	0.20%	<0.1%	81.6	4.34E+04	(K)LEIDQDHQEEICEVVLK(K)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
14.72	0.20%	<0.1%	70.8	5.51E+05	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
14.14	2%	0.20%	75.9	1.38E+06	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
14.04	2%	0.30%	77.8	8.04E+05	(K)AGGFVVTGR(V)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
13.96	2%	0.30%	72.8	3.29E+05	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
13.71	2%	0.50%	88.9	2.14E+06	(R)VPLTSNNGIK(Q)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
13.42	2%	0.50%	72.8	3.11E+05	(R)KDPLKECGAILQK(Y)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
12.95	2%	0.60%	79.5	5.13E+04	(R)HFEASK(E)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
12.81	2%	0.60%	78.8	4.09E+05	(R)VPLTSNNGIK(Q)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
12.29	2%	0.70%	69.2	2.48E+05	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
11.86	3%	0.90%	74.6	1.13E+06	(R)KDPLKECGAILQK(Y)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
11.53	3%	0.90%	62.4	1.83E+05	(R)YANPIAFFR(K)		CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
11.46	3%	1.00%	64	1.78E+05	(K)KSPDPACAEIEEQR(A)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
11.04	3%	1%	65.7	3.76E+05	(K)SVAGATVEVVCR(H)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
10.75	3%	1%	62.6	1.60E+04	(K)SVAGATVEVVCR(H)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
10.24	3%	1%	67.4	1.93E+05	(K)LEIDQDHQEEICEVVLK(K)	C:Carbamidomethylation	CL2052.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g001020 [S bicolor] >gi|241926874|gb|EES00019.1| hypothet prot SORBIDRAFT_03g001020 [S bicolor]		
25.2	<0.1%	<0.1%	100	7.59E+06	(K)SPEADCAEIEVNR(D)	C:Carbamidomethylation	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
24.06	<0.1%	<0.1%	86.9	9.49E+05	(K)MEIAGDHQDEICDVR(L)	C:Carbamidomethylation	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
24	<0.1%	<0.1%	88.1	8.63E+05	(K)mEIAGDHQDEICDVR(L)	C:Carbamidomethylation m:Oxidized methionine	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
23.11	<0.1%	<0.1%	94.9	1.27E+06	(K)SPEADCAEIEVNR(D)	C:Carbamidomethylation	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
21.63	<0.1%	<0.1%	92.9	1.21E+05	(K)SPEADCAEIEVNR(D)	C:Carbamidomethylation	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
21.63	<0.1%	<0.1%	94.9	1.21E+05	(K)SPEADCAEIEVNR(D)	C:Carbamidomethylation	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
21.02	<0.1%	<0.1%	81.9	7.91E+06	(K)AQATTDAGGWYK(M)		UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
20.99	<0.1%	<0.1%	82.9	3.56E+06	(K)mEIAGDHQDEICDVR(L)	C:Carbamidomethylation m:Oxidized methionine	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
19.56	<0.1%	<0.1%	86.4	1.29E+05	(K)SPEADCAEIEVNR(D)	C:Carbamidomethylation	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
19.35	<0.1%	<0.1%	75.5	2.62E+05	(K)mEIAGDHQDEICDVR(L)	C:Carbamidomethylation m:Oxidized methionine	UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
18.51	<0.1%	<0.1%	97.2	9.40E+06	(R)VPLTGNDGIK(Q)		UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	
18.45	<0.1%	<0.1%	91.7	4.08E+06	(R)VPLTGNDGIK(Q)		UG540	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]	

18.3 <0.1% <0.1% 85.3 1.70E+05 (K)SPEADCAEIEVNR(D) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1|
hypothet prot SORBIDRAFT_09g007260 [S bicolor]
18.06 <0.1% <0.1% 86.7 4.65E+06 (K)MEIAGDHQDEICDVR(L) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor]
>gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
16.55 <0.1% <0.1% 78.9 1.53E+05 (K)SPEADCAEIEVNR(D) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1|
hypothet prot SORBIDRAFT_09g007260 [S bicolor]
16.21 <0.1% <0.1% 74.8 2.76E+05 (K)AQATTDAGGWYK(M) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
16.12 <0.1% <0.1% 75.6 1.18E+06 (K)AQATTDAGGWYK(M) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
15.75 0.20% <0.1% 87 3.09E+06 (R)HFESQQIHDK(A) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
15.55 0.20% <0.1% 69.5 1.98E+05 (K)mEIAGDHQDEICDVR(L) C:Carbamidomethylation m:Oxidized methionine UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor]
>gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
15.41 0.20% <0.1% 81.3 3.68E+05 (R)HFESQQIHDK(A) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
15.4 0.20% <0.1% 71.4 7.67E+05 (K)mEIAGDHQDEICDVR(L) C:Carbamidomethylation m:Oxidized methionine UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor]
>gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
14.62 2% <0.1% 69.4 1.83E+05 (K)AQATTDAGGWYK(M) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
14.49 2% <0.1% 73.2 1.47E+05 (K)MEIAGDHQDEICDVR(L) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor]
>gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
14.44 2% <0.1% 62.6 2.17E+05 (K)mEIAGDHQDEICDVR(L) C:Carbamidomethylation m:Oxidized methionine UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor]
>gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
14.17 2% 0.20% 79.3 7.65E+05 (K)MEIAGDHQDEICDVR(L) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor]
>gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
13.98 2% 0.30% 80.2 1.28E+06 (R)IYCDNCR(A) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1|
hypothet prot SORBIDRAFT_09g007260 [S bicolor]
13.69 2% 0.50% 72.6 1.88E+06 (R)VPLTGNDGIK(Q) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
13.61 2% 0.50% 80.6 3.21E+05 (R)HFESQQIHDK(A) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
13.6 2% 0.50% 80.6 1.06E+06 (K)SPEADCAEIEVNR(D) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1|
hypothet prot SORBIDRAFT_09g007260 [S bicolor]
13.52 2% 0.50% 65.6 1.84E+06 (K)AQATTDAGGWYK(M) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
11.52 3% 0.90% 75.4 1.49E+06 (R)CRVPLTGNDGIK(Q) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1|
hypothet prot SORBIDRAFT_09g007260 [S bicolor]
11.41 3% 1.00% 73.2 1.71E+04 (R)IYCDNCR(A) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1|
hypothet prot SORBIDRAFT_09g007260 [S bicolor]
10.98 3% 1% 61.4 2.17E+05 (K)mEIAGDHQDEICDVR(L) C:Carbamidomethylation m:Oxidized methionine UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor]
>gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
10.19 3% 1% 72.2 3.53E+06 (R)HFESQQIHDK(A) UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot
SORBIDRAFT_09g007260 [S bicolor]
10.17 3% 1% 69.4 5.78E+04 (R)IYCDNCR(A) C:Carbamidomethylation UG540 S.halepenseF1Rev hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1|
hypothet prot SORBIDRAFT_09g007260 [S bicolor]
23.24 <0.1% <0.1% 96 1.27E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
22.89 <0.1% <0.1% 93.9 3.78E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
21.32 <0.1% <0.1% 86.6 2.85E+06 (K)GATDFSDDLKESPAK(T) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
20.79 <0.1% <0.1% 92.5 2.68E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
20.66 <0.1% <0.1% 90.5 1.49E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
20.46 <0.1% <0.1% 89.5 4.93E+06 (K)DKGATDFSDDLK(E) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
20.17 <0.1% <0.1% 87.8 7.45E+06 (K)DKGATDFSDDLKESPAK(T) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
20.12 <0.1% <0.1% 90.9 7.32E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
19.79 <0.1% <0.1% 94.1 2.48E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
19.79 <0.1% <0.1% 91.2 1.64E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
19.68 <0.1% <0.1% 90.7 1.37E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
18.93 <0.1% <0.1% 90.7 1.46E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
18.78 <0.1% <0.1% 89.8 1.11E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
18.49 <0.1% <0.1% 84.9 7.01E+05 (K)TFTYESKEPIK(G) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
18.41 <0.1% <0.1% 89.1 1.70E+06 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]

18.39	<0.1%	<0.1%	89.6	3.46E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
18.21	<0.1%	<0.1%	71	7.79E+06	(K)GATDFSDDLKESPAK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
18.13	<0.1%	<0.1%	89.2	1.50E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
18.13	<0.1%	<0.1%	90.1	8.56E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
18.09	<0.1%	<0.1%	89.8	4.82E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.94	<0.1%	<0.1%	88.5	1.71E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.9	<0.1%	<0.1%	90.7	1.69E+06	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.84	<0.1%	<0.1%	89.2	9.89E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.81	<0.1%	<0.1%	89.6	6.52E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.73	<0.1%	<0.1%	80.1	1.17E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.71	<0.1%	<0.1%	88	1.86E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.49	<0.1%	<0.1%	89.3	5.80E+06	(K)EPIKGPLSVR(F)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.45	<0.1%	<0.1%	86.6	4.46E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.35	<0.1%	<0.1%	90.7	1.72E+06	(K)TFTYESK(E)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.35	<0.1%	<0.1%	86.1	2.34E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.26	<0.1%	<0.1%	84.7	1.92E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.24	<0.1%	<0.1%	89.1	2.05E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.08	<0.1%	<0.1%	89.8	2.25E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.03	<0.1%	<0.1%	83.1	1.94E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
17.01	<0.1%	<0.1%	83.9	1.31E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.93	<0.1%	<0.1%	85.4	1.18E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.8	<0.1%	<0.1%	93.9	2.53E+07	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.78	<0.1%	<0.1%	88.1	2.92E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.77	<0.1%	<0.1%	86.7	3.61E+05	(K)TFTYESKEPIKGPLSVR(F)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.75	<0.1%	<0.1%	92.9	2.10E+07	(K)TFTYESK(E)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.65	<0.1%	<0.1%	84.4	1.32E+06	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.62	<0.1%	<0.1%	81.7	5.83E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.57	<0.1%	<0.1%	77.3	5.00E+06	(K)GATDFSDDLK(E)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.53	<0.1%	<0.1%	87.9	7.49E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.46	<0.1%	<0.1%	87.1	1.88E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.45	<0.1%	<0.1%	91.7	1.24E+07	(K)TFTYESK(E)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.45	<0.1%	<0.1%	81.9	9.20E+06	(K)DKGATDFSDDLKESPAK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.37	<0.1%	<0.1%	90	9.00E+05	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.33	<0.1%	<0.1%	84.1	2.06E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.28	<0.1%	<0.1%	93.1	1.26E+06	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.21	<0.1%	<0.1%	81	2.07E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
16.08	<0.1%	<0.1%	84.5	4.85E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.77	0.20%	<0.1%	89.5	1.93E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]

15.77	0.20%	<0.1%	77.9	4.66E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.68	0.20%	<0.1%	74.2	7.52E+05	(K)TFTYESKEPIKGPLSVR(F)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.67	0.20%	<0.1%	82	3.09E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.65	0.20%	<0.1%	81.6	3.91E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.57	0.20%	<0.1%	81.3	3.05E+03	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.56	0.20%	<0.1%	83	2.14E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.47	0.20%	<0.1%	92.5	4.39E+06	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.37	0.20%	<0.1%	91.2	4.68E+06	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.27	0.20%	<0.1%	85.9	5.15E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.22	0.20%	<0.1%	76.1	2.15E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.21	0.20%	<0.1%	76.8	1.52E+06	(K)DKGATDFSDDLKESPAK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15.06	0.20%	<0.1%	79	9.48E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
15	0.20%	<0.1%	81	1.14E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.96	0.20%	<0.1%	82.8	1.64E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.74	0.20%	<0.1%	89.4	3.47E+06	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.74	0.20%	<0.1%	79.6	2.41E+05	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.69	0.20%	<0.1%	82.5	2.06E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.55	2%	<0.1%	81.4	2.92E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.55	2%	<0.1%	89.6	2.02E+06	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.47	2%	<0.1%	86.5	5.02E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.36	2%	<0.1%	79.5	1.36E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.32	2%	<0.1%	84.6	1.78E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.28	2%	<0.1%	70.2	2.08E+06	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.27	2%	<0.1%	83.4	5.26E+05	(R)TTDDVIPADFKPGSVYK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.2	2%	<0.1%	83.8	5.88E+04	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.19	2%	0.10%	80.4	1.36E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.16	2%	0.20%	87	2.55E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.12	2%	0.30%	79.8	2.08E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
14.07	2%	0.30%	82.4	2.49E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.98	2%	0.30%	78	5.48E+06	(K)DKGATDFSDDLK(E)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.85	2%	0.40%	79.7	2.04E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.79	2%	0.50%	81	1.12E+06	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.64	2%	0.50%	65.9	2.44E+05	(K)DKGATDFSDDLKESPAK(T)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.63	2%	0.50%	79.3	1.59E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.62	2%	0.50%	78.7	4.34E+04	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.58	2%	0.50%	73.9	8.75E+04	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.51	2%	0.50%	77.1	1.41E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.48	2%	0.50%	79.1	1.80E+05	(R)LVLVASADVSEVAVK(D)	CL1122.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot SORBIDRAFT_01g032080 [S bicolor]

13.43 2% 0.50% 79 3.83E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.34 2% 0.50% 78.3 2.10E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.28 2% 0.50% 77.3 1.08E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.23 2% 0.50% 87.9 4.18E+05 (R)TTDDVIPADFKPGSVYK(T) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.2 2% 0.50% 77.2 1.84E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.18 2% 0.50% 75.7 1.57E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
13.16 2% 0.50% 79.8 7.39E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
12.97 2% 0.60% 79.5 2.33E+06 (K)TFTYESKEPIK(G) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
12.92 2% 0.60% 69.2 2.86E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
12.71 2% 0.60% 75.4 2.24E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
12.71 2% 0.60% 79.7 6.32E+04 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
12.49 2% 0.60% 79.2 9.01E+04 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
12.36 2% 0.60% 81.2 5.65E+05 (R)TTDDVIPADFKPGSVYK(T) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
12.32 2% 0.70% 71.4 3.71E+05 (K)DKGATDFSDDLK(E) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
12.03 3% 0.80% 79.5 5.61E+05 (R)TTDDVIPADFKPGSVYK(T) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.94 3% 0.90% 77 1.42E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.87 3% 0.90% 74 3.90E+05 (K)TFTYESK(E) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
11.81 3% 0.90% 74.7 2.41E+05 (K)EPIKGPLSVR(F) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
11.77 3% 0.90% 77.6 3.58E+05 (R)TTDDVIPADFKPGSVYK(T) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.65 3% 0.90% 70.3 4.40E+04 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.5 3% 1.00% 70.8 1.39E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.49 3% 1.00% 75.5 3.29E+03 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.43 3% 1.00% 75.2 1.15E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.43 3% 1.00% 73.6 2.33E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.27 3% 1% 61.5 3.42E+05 (K)GATDFSDDLK(E) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
11.14 3% 1% 74.9 3.89E+04 (R)TTDDVIPADFKPGSVYK(T) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
11.02 3% 1% 70.1 2.07E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.84 3% 1% 69 1.88E+07 (K)EPIKGPLSVR(F) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
10.71 3% 1% 73.5 1.80E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.67 3% 1% 65.6 3.82E+05 (K)TFTYESK(E) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
10.65 3% 1% 69.4 1.40E+06 (K)TFTYESK(E) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1| hypothet prot
SORBIDRAFT_01g032080 [S bicolor]
10.59 3% 1% 74.1 1.34E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.47 3% 1% 66 5.43E+04 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.45 3% 1% 73.9 1.24E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.39 3% 1% 64.4 5.25E+04 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.32 3% 1% 78 6.49E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.23 3% 1% 72.4 1.96E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.23 3% 1% 73.9 4.88E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]

10.22 3% 1% 66.6 5.22E+03 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.07 5% 1% 73.9 1.09E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
10.04 5% 1% 65.5 1.17E+05 (R)LVLVASADVSEVAVK(D) CL1122.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_01g032080 [S bicolor] >gi|241921529|gb|EER94673.1|
hypothet prot SORBIDRAFT_01g032080 [S bicolor]
19.2 <0.1% <0.1% 82.2 1.66E+07 (K)GAAEFLDDmKESPAK(T) m:Oxidized methionine CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor]
>gi|241937137|gb|EES10282.1| hypothet prot SORBIDRAFT_05g027110 [S bicolor]
18.95 <0.1% <0.1% 74.6 1.48E+05 (K)GAAEFLDDmKESPAK(T) m:Oxidized methionine CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor]
>gi|241937137|gb|EES10282.1| hypothet prot SORBIDRAFT_05g027110 [S bicolor]
18.94 <0.1% <0.1% 80.9 3.22E+06 (K)GAAEFLDDMKESPAK(T) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
18.82 <0.1% <0.1% 82.7 4.28E+05 (K)GTTPTYTHLVLVANLPIHELAIR(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
18.77 <0.1% <0.1% 89.5 1.08E+06 (K)GAAEFLDDMKESPAK(T) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
18.43 <0.1% <0.1% 82.3 5.01E+06 (K)GAAEFLDDmKESPAK(T) m:Oxidized methionine CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor]
>gi|241937137|gb|EES10282.1| hypothet prot SORBIDRAFT_05g027110 [S bicolor]
18.1 <0.1% <0.1% 81.4 2.56E+06 (K)GTTPTYTHLVLVANLPIHELAIR(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
18.08 <0.1% <0.1% 82.3 2.94E+06 (K)GTTPTYTHLVLVANLPIHELAIR(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
17.95 <0.1% <0.1% 76.4 1.53E+06 (K)GTTPTYTHLVLVANLPIHELAIR(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
17.81 <0.1% <0.1% 76.5 4.78E+05 (K)GAAEFLDDmKESPAK(T) m:Oxidized methionine CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor]
>gi|241937137|gb|EES10282.1| hypothet prot SORBIDRAFT_05g027110 [S bicolor]
17.67 <0.1% <0.1% 76 1.46E+06 (K)GTTPTYTHLVLVANLPIHELAIR(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
17.35 <0.1% <0.1% 80 2.78E+06 (K)GAAEFLDDMK(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
17.32 <0.1% <0.1% 72.7 1.01E+07 (K)GTTPTYTHLVLVANLPIHELAIR(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
17.3 <0.1% <0.1% 85.9 2.72E+05 (K)GAAEFLDDMK(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
17.19 <0.1% <0.1% 79.6 1.97E+06 (K)GAAEFLDDmKESPAK(T) m:Oxidized methionine CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor]
>gi|241937137|gb|EES10282.1| hypothet prot SORBIDRAFT_05g027110 [S bicolor]
17.1 <0.1% <0.1% 98.2 4.72E+07 (K)GPLSVR(F) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
16.76 <0.1% <0.1% 75.3 1.19E+07 (K)GTTPTYTHLVLVANLPIHELAIR(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
15.21 0.20% <0.1% 76.3 1.60E+05 (K)GAAEFLDDMK(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
14.99 0.20% <0.1% 95.7 5.04E+07 (K)GPLSVR(F) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
14.48 2% <0.1% 69.2 7.93E+04 (R)EKGAAEFLDDMKESPAK(T) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
14.3 2% <0.1% 69.8 1.50E+06 (R)EKGAAEFLDDmKESPAK(T) m:Oxidized methionine CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor]
>gi|241937137|gb|EES10282.1| hypothet prot SORBIDRAFT_05g027110 [S bicolor]
14.21 2% <0.1% 71.2 3.52E+06 (K)GAAEFLDDmK(E) m:Oxidized methionine CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1|
hypothet prot SORBIDRAFT_05g027110 [S bicolor]
13.44 2% 0.50% 89.7 1.74E+06 (K)GPLSVR(F) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
12.67 2% 0.60% 72.2 4.83E+05 (K)GAAEFLDDmK(E) m:Oxidized methionine CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1|
hypothet prot SORBIDRAFT_05g027110 [S bicolor]
12.23 3% 0.70% 90.2 6.96E+06 (K)GPLSVR(F) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
11.91 3% 0.90% 63.7 6.68E+05 (K)GTTPTYTHLVLVANLPIHELAIR(E) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
11.69 3% 0.90% 77.8 1.87E+05 (K)TFTQDSK(A) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
10.41 3% 1% 80.2 3.35E+05 (K)GPLSVR(F) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
10.07 5% 1% 78.5 4.34E+05 (K)GPLSVR(F) CL1122.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g027110 [S bicolor] >gi|241937137|gb|EES10282.1| hypothet prot
SORBIDRAFT_05g027110 [S bicolor]
23.14 <0.1% <0.1% 94.1 1.11E+07 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1|
hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
23.12 <0.1% <0.1% 98.5 7.77E+06 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1|
hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
22.5 <0.1% <0.1% 92 1.99E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1|
hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
22.2 <0.1% <0.1% 95.2 1.11E+06 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1|
hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
21.38 <0.1% <0.1% 89 1.52E+07 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1|
hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
21.37 <0.1% <0.1% 94.1 5.47E+06 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1|
hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]

21.14 <0.1% <0.1% 89.7 2.00E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
21.1 <0.1% <0.1% 87.8 2.12E+07 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
21.01 <0.1% <0.1% 80.5 9.92E+06 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
20.8 <0.1% <0.1% 86.9 1.38E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
20.7 <0.1% <0.1% 78.6 4.49E+06 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
20.6 <0.1% <0.1% 88.2 1.29E+07 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
20.42 <0.1% <0.1% 88.8 4.22E+06 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
20.32 <0.1% <0.1% 87.6 4.91E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
20.15 <0.1% <0.1% 84.9 1.34E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
20.06 <0.1% <0.1% 77.1 2.09E+07 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
20.01 <0.1% <0.1% 80.6 2.86E+07 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.81 <0.1% <0.1% 86.2 1.50E+07 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.76 <0.1% <0.1% 80.8 7.34E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.74 <0.1% <0.1% 89.9 1.94E+07 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.66 <0.1% <0.1% 89.5 5.47E+06 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.61 <0.1% <0.1% 80 1.27E+07 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.55 <0.1% <0.1% 96.1 5.46E+07 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.54 <0.1% <0.1% 95.8 4.37E+07 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.48 <0.1% <0.1% 77.5 1.82E+06 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.48 <0.1% <0.1% 87.2 1.69E+07 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.31 <0.1% <0.1% 86.7 5.74E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.31 <0.1% <0.1% 89.5 3.21E+06 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.97 <0.1% <0.1% 89.4 3.02E+07 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.94 <0.1% <0.1% 93 7.74E+06 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.72 <0.1% <0.1% 86.1 1.02E+06 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.36 <0.1% <0.1% 86 2.23E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.34 <0.1% <0.1% 91.5 1.79E+07 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.32 <0.1% <0.1% 87.4 2.78E+06 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.31 <0.1% <0.1% 86 2.79E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.14 <0.1% <0.1% 75.1 6.46E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.11 <0.1% <0.1% 86.1 1.71E+07 (K)GATDFTDDLK(E) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
18.04 <0.1% <0.1% 85.9 1.95E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
17.86 <0.1% <0.1% 88.3 2.77E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
17.49 <0.1% <0.1% 83.8 1.43E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
17.34 <0.1% <0.1% 86.6 5.81E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
17.19 <0.1% <0.1% 82.8 5.26E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
17.09 <0.1% <0.1% 74.1 3.34E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.91 <0.1% <0.1% 82.3 4.05E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]

16.86 <0.1% <0.1% 87.3 3.73E+06 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.84 <0.1% <0.1% 89 9.09E+04 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.83 <0.1% <0.1% 78.5 1.53E+06 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.7 <0.1% <0.1% 85.3 1.21E+06 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.61 <0.1% <0.1% 80.7 9.58E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.42 <0.1% <0.1% 71.4 8.23E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.42 <0.1% <0.1% 84.9 1.09E+06 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.14 <0.1% <0.1% 82.1 2.86E+07 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.11 <0.1% <0.1% 80.5 8.82E+04 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16.05 <0.1% <0.1% 66.6 5.60E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
16 <0.1% <0.1% 82.2 1.07E+06 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
15.84 0.20% <0.1% 78.5 7.30E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
15.8 0.20% <0.1% 82 2.99E+06 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
15.79 0.20% <0.1% 71.3 4.04E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
15.79 0.20% <0.1% 76.7 6.47E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
15.69 0.20% <0.1% 80.2 1.14E+07 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
15.61 0.20% <0.1% 76.1 1.49E+06 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
15.45 0.20% <0.1% 66.9 4.96E+04 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
15.28 0.20% <0.1% 67.2 7.61E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.92 0.20% <0.1% 88.8 3.44E+05 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.71 0.20% <0.1% 75.9 2.12E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.69 0.20% <0.1% 77.2 1.25E+06 (K)GATDFTDDLK(E) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.67 2% <0.1% 68.7 3.71E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.54 2% <0.1% 84.5 8.06E+05 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.5 2% <0.1% 73.9 5.03E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.44 2% <0.1% 72.6 3.35E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.33 2% <0.1% 74.7 8.81E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.31 2% <0.1% 72 1.15E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.3 2% <0.1% 72.2 8.70E+05 (K)GATDFTDDLK(E) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.3 2% <0.1% 77.4 3.72E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
14.09 2% 0.30% 69.2 2.01E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.95 2% 0.30% 84.4 8.55E+05 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.92 2% 0.40% 80.5 4.78E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.91 2% 0.40% 75 8.21E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.85 2% 0.40% 69.1 2.08E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.8 2% 0.50% 76.7 1.39E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.76 2% 0.50% 75.2 1.42E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.65 2% 0.50% 68.2 7.85E+04 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]

13.6 2% 0.50% 72.5 4.60E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.56 2% 0.50% 74.4 1.27E+06 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.48 2% 0.50% 76.7 2.16E+05 (K)GATDFTDDLK(E) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.4 2% 0.50% 67.9 4.32E+05 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
13.16 2% 0.50% 69 2.84E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.9 2% 0.60% 77.6 9.53E+05 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.81 2% 0.60% 76.5 6.35E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.72 2% 0.60% 76.5 9.44E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.63 2% 0.70% 61.5 5.82E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.61 2% 0.70% 72.6 6.65E+05 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.58 2% 0.60% 71.6 7.13E+05 (R)VVDNAIPADFK(A) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.51 2% 0.60% 66.4 1.23E+05 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.27 2% 0.70% 68.1 5.93E+03 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
12.23 3% 0.70% 74.9 9.89E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.96 3% 0.80% 69.5 5.43E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.87 3% 0.90% 65.8 9.73E+04 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.84 3% 0.90% 71.8 5.87E+05 (K)TFTLDSKEPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.66 3% 0.90% 72.7 1.00E+06 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.59 3% 1.00% 62.3 6.73E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.59 3% 1.00% 68.3 3.12E+05 (K)EPIEGPIAFR(F) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.52 3% 0.90% 65.5 1.22E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.34 3% 1.00% 71 7.09E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
11.15 3% 1% 68.7 8.86E+04 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
10.89 3% 1% 65.2 1.10E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
10.79 3% 1% 61.7 1.07E+05 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
10.62 3% 1% 62.8 9.15E+04 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
10.52 3% 1% 66.7 2.55E+03 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
10.51 3% 1% 62 7.64E+05 (K)GATDFTDDLKESEPK(T) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
10.41 3% 1% 64.2 8.21E+04 (K)LSLITNVAISEVSVKPK(G) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
10.14 3% 1% 62.7 2.22E+05 (K)GATDFTDDLK(E) CL1695.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|242084680|ref|XP_002442765.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor] >gi|241943457|gb|EES16602.1| hypothet prot SORBIDRAFT_08g002450 [S bicolor] >gi|241943458|gb|EES16603.1| hypothet prot SORBIDRAFT_08g002460 [S bicolor]
19.42 <0.1% <0.1% 85.4 5.39E+05 (K)LSFATDVAISEVAVK(Q) UG551 S.halepenseF2 hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]
17.97 <0.1% <0.1% 82 4.34E+05 (K)LSFATDVAISEVAVK(Q) UG551 S.halepenseF2 hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]
16.79 <0.1% <0.1% 93.4 1.29E+06 (R)FADKDGGYHVLVDIIPADFK(A) UG551 S.halepenseF2 hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]
16.79 <0.1% <0.1% 92.4 3.24E+05 (K)DGGYHVLVDIIPADFK(A) UG551 S.halepenseF2 hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]
16.23 <0.1% <0.1% 92.8 4.51E+07 (K)TFTLDSK(D) UG551 S.halepenseF2 hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]
15.97 <0.1% <0.1% 93.4 5.06E+07 (K)TFTLDSK(D) UG551 S.halepenseF2 hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]
15.8 0.20% <0.1% 90 2.87E+06 (K)TFTLDSK(D) UG551 S.halepenseF2 hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]
13.63 2% 0.50% 81.6 4.40E+05 (R)FADKDGGYHVLVDIIPADFK(A) UG551 S.halepenseF2 hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]

13.12	2%	0.60%	79.8	1.99E+06	(K)TFTLDSK(D)		UG551	S.halepenseF2	hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]	
12.95	2%	0.60%	64.7	4.12E+05	(K)TFTLDSKDPIKGPITIR(F)		UG551	S.halepenseF2	hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]	
11.38	3%	1.00%	65.2	1.73E+05	(K)TFTLDSKDPIKGPITIR(F)		UG551	S.halepenseF2	hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]	
10.84	3%	1%	81.5	2.86E+06	(K)GPITIR(F)		UG551	S.halepenseF2	hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]	
10.49	3%	1%	62.5	1.29E+06	(K)TFTLDSK(D)		UG551	S.halepenseF2	hypothet prot SORBIDRAFT_08g002500 [S bicolor] >gi|241943461|gb|EES16606.1| hypothet prot SORBIDRAFT_08g002500 [S bicolor]	
14.01	2%	0.30%	74.6	5.31E+05	(K)ALVNLDDRDNCLGALRPAQK(T)	C:Carbamidomethylation	UG184	S.halepenseF3	Pollen-specific leucine-rich repeat extensin-like protein 4 [Arabidopsis thaliana] >gi|75318791|sp|O81765.1|PLRX4_ARATH RecName: Full=Pollen-specific leucine-rich repeat extensin-like protein 4; Short=AtPEX4; Short=Pollen-specific LRR/EXTENSIN4; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|3297821|emb|CAA19879.1| extensin-like protein [Arabidopsis thaliana] >gi|7270346|emb|CAB80114.1| extensin-like protein [Arabidopsis thaliana] >gi|332660902|gb|AEE86302.1| Pollen-specific leucine-rich repeat extensin-like protein 4 [Arabidopsis thaliana]	
18.19	<0.1%	<0.1%	86	5.72E+05	(R)AQVELVTDAGAGLATTVR(R)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
17.77	<0.1%	<0.1%	88.8	6.65E+05	(R)GAEEVCSVVLLSSPVPGCAEK(E)	C:Carbamidomethylation	UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
15.77	0.20%	<0.1%	87.3	1.19E+06	(R)HYMSASGAVER(S)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
15.54	0.20%	<0.1%	78.3	6.36E+05	(R)GAEEVCSVVLLSSPVPGCAEK(E)	C:Carbamidomethylation	UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
14.87	0.20%	<0.1%	82.3	7.39E+05	(K)SQPLPNCGEILK(S)	C:Carbamidomethylation	UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
14.62	2%	<0.1%	82.3	1.98E+06	(R)ANPLGFLK(S)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
14.44	2%	<0.1%	78.1	9.75E+04	(R)AQVELVTDAGAGLATTVR(R)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
13.3	2%	0.50%	77.5	2.17E+05	(R)ANPLGFLK(S)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
12.88	2%	0.60%	85.9	3.99E+06	(R)IELVDNR(G)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
12.35	2%	0.70%	64.2	1.46E+05	(R)SAEGATDAAGR(Y)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
12.16	3%	0.70%	78.7	1.04E+05	(R)ANPLGFLK(S)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
12.06	3%	0.80%	82.6	3.51E+06	(R)IELVDNR(G)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
11.88	3%	0.90%	66.7	1.94E+05	(R)GAEEVCSVVLLSSPVPGCAEK(E)	C:Carbamidomethylation	UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
11.7	3%	0.90%	68.7	8.52E+05	(R)IELVDNR(G)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
11.55	3%	1.00%	82.9	1.14E+06	(R)YRIELVDNR(G)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
11.37	3%	1.00%	71.9	1.53E+06	(K)SQPLPNCGEILK(S)	C:Carbamidomethylation	UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
11.23	3%	1%	68.5	9.57E+04	(R)AQVELVTDAGAGLATTVR(R)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
10.75	3%	1%	70.9	5.55E+06	(R)HYmSASGAVER(S)	m:Oxidized methionine	UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
10.62	3%	1%	74.3	8.63E+05	(K)SQPLPNCGEILK(S)	C:Carbamidomethylation	UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
10.44	3%	1%	69	2.73E+05	(R)IELVDNR(G)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
10.2	3%	1%	70.7	2.70E+05	(R)AQVELVTDAGAGLATTVR(R)		UG578	S.halepenseF3	hypothet prot SORBIDRAFT_02g012930 [S bicolor] >gi|241923256|gb|EER96400.1| hypothet prot SORBIDRAFT_02g012930 [S bicolor]	
14.93	0.20%	<0.1%	86.8	7.12E+05	(R)TLADYNIQK(E)		CL18.c5	S.halepenseF1	Ubiquitin [Medicago truncatula] >gi|355523917|gb|AET04371.1| Ubiquitin [Medicago truncatula]	
13.34	2%	0.50%	65.3	1.00E+05	(K)ESTLHLVLR(L)		CL18.c5	S.halepenseF1	Ubiquitin [Medicago truncatula] >gi|355523917|gb|AET04371.1| Ubiquitin [Medicago truncatula]	
11.57	3%	1.00%	65.8	4.29E+05	(K)ESTLHLVLR(L)		CL18.c5	S.halepenseF1	Ubiquitin [Medicago truncatula] >gi|355523917|gb|AET04371.1| Ubiquitin [Medicago truncatula]	
10.32	3%	1%	71.9	1.17E+06	(R)LIFAGK(Q)		CL18.c5	S.halepenseF1	Ubiquitin [Medicago truncatula] >gi|355523917|gb|AET04371.1| Ubiquitin [Medicago truncatula]	
17.69	<0.1%	<0.1%	91.9	2.05E+05	(K)VPIPPGQVYAINDALSAEGAADDYEACLK(Q)	C:Carbamidomethylation	UG7145	S.halepenseF2	hypothet prot SORBIDRAFT_02g030620 [S bicolor] >gi|241923932|gb|EER97076.1| hypothet prot SORBIDRAFT_02g030620 [S bicolor]	
15.71	0.20%	<0.1%	82.5	6.26E+05	(R)FDLQLLGmGPDGHIASLFPGHPLVNEK(E)	m:Oxidized methionine	UG7145	S.halepenseF2	hypothet prot SORBIDRAFT_02g030620 [S bicolor] >gi|241923932|gb|EER97076.1| hypothet prot SORBIDRAFT_02g030620 [S bicolor]	
11.96	3%	0.80%	67	1.40E+05	(R)FDLQLLGmGPDGHIASLFPGHPLVNEK(E)	m:Oxidized methionine	UG7145	S.halepenseF2	hypothet prot SORBIDRAFT_02g030620 [S bicolor] >gi|241923932|gb|EER97076.1| hypothet prot SORBIDRAFT_02g030620 [S bicolor]	
11.79	3%	0.90%	72.6	4.34E+05	(R)FDLQLLGMGPDGHIASLFPGHPLVNEK(E)		UG7145	S.halepenseF2	hypothet prot SORBIDRAFT_02g030620 [S bicolor] >gi|241923932|gb|EER97076.1| hypothet prot SORBIDRAFT_02g030620 [S bicolor]	
10.4	3%	1%	63.1	7.49E+06	(R)TFYTTK(F)		UG8423	S.halepenseF2	hypothet prot SORBIDRAFT_10g003920 [S bicolor] >gi|241914731|gb|EER87875.1| hypothet prot SORBIDRAFT_10g003920 [S bicolor]	
19.96	<0.1%	<0.1%	91.8	3.35E+05	(K)IGAILWAGYPGQAGGLAIAK(V)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]	
18.32	<0.1%	<0.1%	87.4	1.13E+05	(K)NLALEAALDGIVLLK(N)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]	
16.26	<0.1%	<0.1%	85.9	1.23E+06	(R)TTLLLPGNQQSLINAVANAAK(R)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]	

14.84	0.20%	<0.1%	79.4	4.35E+05	(K)LPNTWYPEEFTR(I)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
14.48	2%	<0.1%	76.8	1.13E+06	(K)NSAGVLPLKR(G)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
14.44	2%	<0.1%	70.9	7.45E+05	(R)TTLLLPGNQQSLINAVANAAK(R)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
13.86	2%	0.40%	72.2	2.45E+05	(K)LTQQDVDK(A)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
13.28	2%	0.50%	80.6	1.49E+05	(K)NSAGVLPLKR(G)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
12.87	2%	0.60%	76.6	7.33E+04	(K)IGAILWAGYPGQAGGLAIAK(V)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
12.73	2%	0.60%	65.9	1.09E+06	(R)NSQFYRPTAEDTVAATLK(A)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
12.58	2%	0.60%	64.3	5.61E+05	(K)FGYGLSYSK(F)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
12.2	3%	0.70%	75.2	9.83E+05	(K)FLAGCNK(A)	C:Carbamidomethylation	UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
11.85	3%	0.90%	69.5	1.24E+05	(K)IGAILWAGYPGQAGGLAIAK(V)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
11.76	3%	0.90%	72.6	1.54E+05	(R)TTLLLPGNQQSLINAVANAAK(R)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
11.5	3%	1.00%	65.5	1.09E+05	(R)GTVNSAAVIGHNANDVLALLGNYWGPPCAPTTPLQGIQGYVK(N)	C:Carbamidomethylation	UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
11.24	3%	1%	68.7	4.60E+04	(R)SCVVDGK(A)	C:Carbamidomethylation	UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
11.16	3%	1%	71.8	2.46E+05	(R)TTLLLPGNQQSLINAVANAAK(R)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
11.1	3%	1%	63.3	1.03E+04	(R)GTVNSAAVIGHNANDVLALLGNYWGPPCAPTTPLQGIQGYVK(N)	C:Carbamidomethylation	UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
11.05	3%	1%	68.6	4.18E+05	(K)LTQQDVDK(A)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
10.93	3%	1%	65.4	8.64E+04	(K)IGAILWAGYPGQAGGLAIAK(V)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
10.77	3%	1%	77.4	1.56E+05	(R)TTLLLPGNQQSLINAVANAAK(R)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
10.15	3%	1%	66.2	1.93E+05	(K)NSAGVLPLK(R)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
10.12	3%	1%	62.8	8.60E+04	(K)RPVILVLLTGGPVDITFAQANPK(I)		UG2241	S.halepenseF3	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
19.08	<0.1%	<0.1%	85.7	5.10E+05	(R)SATSFPQVLHTAASFNDNLWFR(I)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
19.07	<0.1%	<0.1%	89.6	1.92E+05	(R)AFYNIGQAEGLTmWSPNVNIFR(D)	m:Oxidized methionine	UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
18.54	<0.1%	<0.1%	91	2.61E+05	(R)GQETPGEDPAVASR(Y)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
18.29	<0.1%	<0.1%	90.7	2.20E+05	(R)GQETPGEDPAVASR(Y)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
18.06	<0.1%	<0.1%	90.8	2.63E+05	(K)ASQLGDIANGVPR(L)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
17.39	<0.1%	<0.1%	91	7.02E+05	(R)GQETPGEDPAVASR(Y)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
17.07	<0.1%	<0.1%	90.4	1.17E+06	(R)LGVPSYK(W)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
14.42	2%	<0.1%	81.3	2.87E+05	(R)LGVPSYK(W)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
14.29	2%	<0.1%	69.5	1.37E+04	(R)AFYNIGQAEGLTmWSPNVNIFR(D)	m:Oxidized methionine	UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
13.61	2%	0.50%	70.9	1.17E+04	(R)GQETPGEDPAVASR(Y)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
12.47	2%	0.60%	72.9	1.46E+05	(R)GQETPGEDPAVASR(Y)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
12.25	3%	0.70%	60.7	1.24E+05	(R)AFYNIGQAEGLTmWSPNVNIFR(D)	m:Oxidized methionine	UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
10.68	3%	1%	70.2	1.01E+04	(R)SATSFPQVLHTAASFNDNLWFR(I)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
10.42	3%	1%	63.3	1.23E+06	(R)YGAAFVR(G)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
10.27	3%	1%	65.8	1.18E+05	(R)SATSFPQVLHTAASFNDNLWFR(I)		UG4458	S.halepenseF1	hypothet prot SORBIDRAFT_0010s012040 [S bicolor] >gi|241946959|gb|EES20104.1| hypothet prot SORBIDRAFT_0010s012040 [S bicolor]
16.67	<0.1%	<0.1%	74.1	1.32E+05	(K)VFDVDGDGFISAAELQTVLK(K)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
15.8	0.20%	<0.1%	72.9	1.43E+05	(K)VFDVDGDGFISAAELQTVLK(K)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
15.72	0.20%	<0.1%	77.2	3.32E+05	(R)ALGDAFFGALADHQDDATDAGGK(K)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]

15.45	0.20%	<0.1%	79.3	1.21E+05	(R)AGLAATVGAYVPDGAAGLR(F)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
14.25	2%	<0.1%	76.1	1.95E+05	(R)AGLAATVGAYVPDGAAGLR(F)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
13.79	2%	0.50%	76.5	1.28E+05	(R)AGLAATVGAYVPDGAAGLR(F)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
13	2%	0.60%	70.3	2.19E+05	(R)AGLAATVGAYVPDGAAGLR(F)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
12.41	2%	0.70%	67.3	1.29E+05	(K)VFDVDGDGFISAAELQTVLK(K)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
11.85	3%	0.90%	86.6	2.39E+05	(R)VFDLFDR(N)		UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
10.58	3%	1%	64.3	2.67E+05	(K)LGLPEASSmANVR(E)	m:Oxidized methionine	UG832	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g043140 [S bicolor] >gi|241924599|gb|EER97743.1| hypothet prot SORBIDRAFT_02g043140 [S bicolor]
17.39	<0.1%	<0.1%	87.1	2.53E+05	(K)LTAPFDFPR(F)		UG681	S.halepenseF3	hypothet prot SORBIDRAFT_07g001680 [S bicolor] >gi|241941286|gb|EES14431.1| hypothet prot SORBIDRAFT_07g001680 [S bicolor]
15.19	0.20%	<0.1%	79.2	3.55E+05	(R)AHLKPEPFDRPLR(D)		UG681	S.halepenseF3	hypothet prot SORBIDRAFT_07g001680 [S bicolor] >gi|241941286|gb|EES14431.1| hypothet prot SORBIDRAFT_07g001680 [S bicolor]
12.07	3%	0.80%	77.6	2.04E+05	(R)EVDVAPDGTIR(Y)		UG681	S.halepenseF3	hypothet prot SORBIDRAFT_07g001680 [S bicolor] >gi|241941286|gb|EES14431.1| hypothet prot SORBIDRAFT_07g001680 [S bicolor]
10.58	3%	1%	65.8	1.39E+05	(R)LVSSLSTKDAYIVR(E)		UG722	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_02g000200 [S bicolor] >gi|241924661|gb|EER97805.1| hypothet prot SORBIDRAFT_02g000200 [S bicolor]
10.3	3%	1%	85	7.42E+05	(R)ILEPIK(A)		CL1211.c1	S.halepenseF2	hypothet prot SORBIDRAFT_08g021830 [S bicolor] >gi|241943248|gb|EES16393.1| hypothet prot SORBIDRAFT_08g021830 [S bicolor]
10.19	3%	1%	81.5	7.72E+05	(R)ILEPIK(A)		CL1211.c1	S.halepenseF2	hypothet prot SORBIDRAFT_08g021830 [S bicolor] >gi|241943248|gb|EES16393.1| hypothet prot SORBIDRAFT_08g021830 [S bicolor]
15.01	0.20%	<0.1%	75.8	3.40E+05	(R)LSSIGLDNTEPNR(Q)		UG12049	S.halepenseF1	hypothet prot SORBIDRAFT_03g008050 [S bicolor] >gi|241927276|gb|EES00421.1| hypothet prot SORBIDRAFT_03g008050 [S bicolor]
10.68	3%	1%	72.2	1.16E+06	(R)IEVAGR(A)		UG606	S.halepenseF2Rev	hypothet prot SORBIDRAFT_04g028460 [S bicolor] >gi|241932411|gb|EES05556.1| hypothet prot SORBIDRAFT_04g028460 [S bicolor]
22.03	<0.1%	<0.1%	92.1	2.52E+05	(K)DSHEEDICQVVLVQSPR(K)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
17.83	<0.1%	<0.1%	97.4	4.03E+06	(R)AGVLLTR(N)		CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
16.66	<0.1%	<0.1%	90.4	1.93E+06	(K)DVPLPVCAALLK(Q)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
16.57	<0.1%	<0.1%	85	3.12E+05	(K)DSHEEDICQVVLVQSPR(K)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
14.81	0.20%	<0.1%	73.5	9.92E+04	(R)AIDGVTDATGTYTIELK(D)		CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
13.86	2%	0.40%	74	7.01E+05	(K)DSHEEDICQVVLVQSPR(K)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
13.58	2%	0.50%	75.3	6.42E+05	(R)AIDGVTDATGTYTIELK(D)		CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
12.96	2%	0.60%	74.7	1.59E+05	(R)VYCDTCR(A)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
12.58	2%	0.60%	74.7	3.01E+05	(K)DVPLPVCAALLK(Q)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
12.36	2%	0.70%	74.4	1.60E+04	(K)DVPLPVCAALLK(Q)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
12.26	2%	0.70%	80.9	2.59E+05	(R)KDCDQTQPLR(D)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
11.87	3%	0.90%	73.2	5.23E+04	(K)DVPLPVCAALLK(Q)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
10.86	3%	1%	67.4	2.12E+06	(R)AGVLLTR(N)		CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
10.57	3%	1%	65.9	6.26E+05	(R)KDCDQTQPLR(D)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
10.52	3%	1%	63.6	4.10E+05	(K)DCDQTQPLR(D)	C:Carbamidomethylation	CL1754.c1	S.halepenseF1	hypothet prot SORBIDRAFT_06g014730 [S bicolor] >gi|241937546|gb|EES10691.1| hypothet prot SORBIDRAFT_06g014730 [S bicolor]
15.6	0.20%	<0.1%	72	5.43E+05	(K)LmTLPHFLDLAK(A)	m:Oxidized methionine	CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
15.39	0.20%	<0.1%	86.6	3.09E+05	(R)GIGIVEAVSSALTK(A)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
14.59	2%	<0.1%	73.6	1.09E+05	(R)GIGIVEAVSSALTK(A)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
13.37	2%	0.50%	79.5	2.32E+05	(K)EFAVGILVPK(T)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
13.3	2%	0.50%	81.3	1.79E+05	(K)DTLSYISSPEIEFLK(S)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
12.63	2%	0.70%	78	1.28E+05	(R)LLNEDIEEPSTK(K)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
12.11	3%	0.70%	69.3	9.26E+04	(K)LSSEDYILELPK(D)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
11.38	3%	1.00%	77.1	1.65E+05	(R)VLNIEAK(I)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
11.03	3%	1%	66.9	2.20E+05	(K)WLTLSGLPPLVIAR(G)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
10.54	3%	1%	77.5	1.75E+05	(K)DQYLAPSPTSLVK(D)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]

10.25	3%	1%	67.2	6.78E+04	(K)WLTLSGLPPLVIAR(G)		CL1829.c1	S.halepenseF2	glycerophosphoryl diester phosphodiesterase 2 precursor-like protein [Oryza sativa Japonica Group]
14.09	2%	0.30%	75.9	5.69E+05	(R)EIDDADKLVAAIQAK(K)		CL584.c2	S.halepenseF1Rev	uncharacterized protein LOC100501585 [Zea mays]
13.26	2%	0.50%	74.6	4.28E+05	(K)LTDFGTPGADSNNILYLR(E)		CL584.c2	S.halepenseF1Rev	uncharacterized protein LOC100501585 [Zea mays]
12.54	2%	0.60%	69.4	1.38E+05	(K)LTDFGTPGADSNNILYLR(E)		CL584.c2	S.halepenseF1Rev	uncharacterized protein LOC100501585 [Zea mays]
13.64	2%	0.50%	61	3.43E+05	(R)LPGFYVCVGSGGER(L)	C:Carbamidomethylation	CL584.c3	S.halepenseF1Rev	uncharacterized protein LOC100501585 [Zea mays]
12.2	3%	0.70%	73.8	8.87E+05	(K)EAVAPYERPALSK(G)		CL584.c3	S.halepenseF1Rev	uncharacterized protein LOC100501585 [Zea mays]
11.03	3%	1%	77.7	1.35E+05	(K)GIELILSTEIVK(A)		CL584.c3	S.halepenseF1Rev	uncharacterized protein LOC100501585 [Zea mays]
21.59	<0.1%	<0.1%	90.7	6.11E+05	(K)SIEGAIDTGFSFK(N)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
19.66	<0.1%	<0.1%	91.8	3.74E+06	(R)VILDLKPGAVFR(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
17.62	<0.1%	<0.1%	83.3	5.01E+05	(R)VILDLKPGAVFR(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
17.33	<0.1%	<0.1%	88.7	3.22E+05	(K)DGGKPVGTVGSATLAVESDYFTAYGVVLK(N)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
16.82	<0.1%	<0.1%	88.6	4.74E+05	(R)VILDLKPGAVFR(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
16.75	<0.1%	<0.1%	80.3	2.30E+06	(R)VILDLKPGAVFR(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
15.85	0.20%	<0.1%	88.3	1.00E+06	(R)VILDLKPGAVFR(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
14.87	0.20%	<0.1%	71.8	2.73E+05	(K)CFGPGADAK(R)	C:Carbamidomethylation	UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
14.66	2%	<0.1%	77.4	5.19E+03	(R)VILDLKPGAVFR(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
14.64	2%	<0.1%	78.4	1.35E+05	(K)SIEGAIDTGFSFK(N)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
14	2%	0.30%	85.1	2.24E+05	(R)VILDLKPGAVFR(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
13.52	2%	0.50%	80.8	1.48E+05	(K)NDAPLAKPGAK(G)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
12.56	2%	0.60%	79.7	1.35E+05	(R)GSVDFIFGFGR(S)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
12.35	2%	0.70%	77.5	1.47E+06	(K)GGQAVALR(L)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
12.3	2%	0.70%	87.9	3.00E+05	(K)SLQEAEAK(K)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
12.23	3%	0.70%	75.5	1.95E+05	(R)SFYEDCRIESVVK(E)	C:Carbamidomethylation	UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
11.94	3%	0.90%	74.8	1.61E+05	(R)VILDLKPGAVFR(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
11.7	3%	0.90%	82.1	1.37E+06	(R)IESVVK(E)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
11.67	3%	0.90%	68.5	1.01E+05	(K)SIEGAIDTGFSFK(N)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
11.5	3%	1.00%	73.6	7.07E+05	(R)SFYEDCR(I)	C:Carbamidomethylation	UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
11.2	3%	1%	73.5	3.91E+04	(R)GSVDFIFGFGR(S)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
11	3%	1%	75.7	4.67E+04	(K)SLQEAEAK(K)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
10.98	3%	1%	73.4	2.41E+05	(R)SFYEDCR(I)	C:Carbamidomethylation	UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
10.74	3%	1%	73.4	3.89E+05	(K)GGQAVALR(L)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
10.15	3%	1%	70.3	3.63E+05	(K)GGQAVALR(L)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
10.11	3%	1%	69.9	1.90E+06	(K)GGQIYLGR(A)		UG47	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_05g026816 [S bicolor] >gi|241937118|gb|EES10263.1| hypothet prot SORBIDRAFT_05g026816 [S bicolor]
24.31	<0.1%	<0.1%	89.4	3.93E+05	(K)AAFYDCTFDGGQDTLYDHR(G)	C:Carbamidomethylation	UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
22.3	<0.1%	<0.1%	90.2	5.15E+05	(R)SLYEDCAITSVTK(D)	C:Carbamidomethylation	UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
20.89	<0.1%	<0.1%	89.6	3.89E+05	(R)SLYEDCAITSVTK(D)	C:Carbamidomethylation	UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
20.11	<0.1%	<0.1%	94.2	6.56E+05	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
19.04	<0.1%	<0.1%	89.6	8.38E+05	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
19.01	<0.1%	<0.1%	84	8.13E+04	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
18.43	<0.1%	<0.1%	87.2	1.50E+05	(K)NAAPLAAPGTEGGQAVAVR(V)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
17.72	<0.1%	<0.1%	89.3	2.45E+05	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]

17.58	<0.1%	<0.1%	92.7	4.74E+05	(K)NAAPLAAPGTEGGQAVAVR(V)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
16.4	<0.1%	<0.1%	80	3.29E+05	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
16.03	<0.1%	<0.1%	81.6	1.35E+05	(K)VWDPELLAAQGmALR(Y)	m:Oxidized methionine	UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
15.96	<0.1%	<0.1%	73.7	2.28E+05	(R)IGSSTGAGQIYLGR(A)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
15.89	0.20%	<0.1%	75.3	3.73E+05	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
15.86	0.20%	<0.1%	76.3	6.25E+05	(R)IGSSTGAGQIYLGR(A)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
15.74	0.20%	<0.1%	80.5	9.11E+04	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
15.72	0.20%	<0.1%	87.1	7.77E+04	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
15.42	0.20%	<0.1%	75.1	1.75E+05	(K)VWDPELLAAQGmALR(Y)	m:Oxidized methionine	UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
15.32	0.20%	<0.1%	83.8	3.15E+05	(K)NAAPLAAPGTEGGQAVAVR(V)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
14.98	0.20%	<0.1%	78.9	1.99E+05	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
13.65	2%	0.50%	75.2	1.86E+05	(K)NAAPLAAPGTEGGQAVAVR(V)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
13.35	2%	0.50%	74.7	1.07E+05	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
12.61	2%	0.70%	79.7	3.31E+05	(K)DVAIVTAQQR(T)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
12.01	3%	0.80%	74.5	2.97E+05	(K)EVVPVGWDK(W)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
11.74	3%	0.90%	68.4	9.71E+05	(R)VVYAYTTmGK(E)	m:Oxidized methionine	UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
11.4	3%	1.00%	70.1	4.48E+05	(R)GLHYFK(S)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
11.38	3%	1.00%	62.3	5.64E+04	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
11.11	3%	1%	67.8	5.51E+05	(R)YVVSPDGK(G)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
10.54	3%	1%	65.7	1.11E+05	(R)VVYAYTTmGK(E)	m:Oxidized methionine	UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
10.41	3%	1%	68.2	2.70E+05	(R)YVVSPDGK(G)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
10.26	3%	1%	62.2	1.96E+05	(K)NAAPLAAPGTEGGQAVAVR(V)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
10.21	3%	1%	60.1	5.21E+04	(R)SIADALETGFSFLR(C)		UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
10.02	5%	1%	67.1	7.01E+05	(R)VVYAYTTmGK(E)	m:Oxidized methionine	UG548	S.halepenseF3	hypothet prot SORBIDRAFT_08g018360 [S bicolor] >gi|241944061|gb|EES17206.1| hypothet prot SORBIDRAFT_08g018360 [S bicolor]
11.51	3%	0.90%	77.8	1.47E+05	(K)VIIPENKPFIFVR(G)		CL1914.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g022950 [S bicolor] >gi|241929921|gb|EES03066.1| hypothet prot SORBIDRAFT_03g022950 [S bicolor]
10.91	3%	1%	72.2	1.32E+04	(R)VIFSDTYLSR(T)		CL1914.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g022950 [S bicolor] >gi|241929921|gb|EES03066.1| hypothet prot SORBIDRAFT_03g022950 [S bicolor]
18.11	<0.1%	<0.1%	92.2	3.12E+06	(K)VVAQDGSGDFK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
17.79	<0.1%	<0.1%	92	1.97E+06	(R)LGELLPEEAK(A)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
17.41	<0.1%	<0.1%	88.5	2.64E+06	(K)TISEAIAAVPK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
15.3	0.20%	<0.1%	87.1	1.43E+06	(K)TISEAIAAVPK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
14.03	2%	0.30%	80.4	9.48E+05	(K)VVAQDGSGDFK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
13.92	2%	0.40%	89.3	2.11E+06	(R)FVIYVK(S)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
13.55	2%	0.50%	80.6	5.50E+05	(K)TISEAIAAVPK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
13.22	2%	0.50%	78.6	1.20E+06	(R)FVIYVK(S)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
13.16	2%	0.50%	73.6	2.01E+06	(K)EYVTVPK(N)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.81	2%	0.60%	84.6	2.72E+05	(R)FVIYVK(S)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.74	2%	0.60%	85.4	1.25E+06	(R)FVIYVK(S)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.64	2%	0.70%	79.1	6.82E+05	(R)FVIYVK(S)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]

12.59	2%	0.60%	71.8	1.43E+06	(K)TISEAIAAVPK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.31	2%	0.70%	66.5	2.54E+06	(K)EYVTVPK(N)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.89	3%	0.90%	75.5	2.08E+05	(K)TISEAIAAVPK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.66	3%	0.90%	72.1	2.27E+05	(K)VVAQDGSGDFK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.44	3%	1.00%	75.7	1.16E+06	(K)VVAQDGSGDFK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.4	3%	1.00%	76.5	6.48E+05	(R)FVIYVK(S)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.29	3%	1.00%	69.9	1.48E+05	(R)FVIYVK(S)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.14	3%	1%	75	2.80E+06	(K)VVAQDGSGDFK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
10.89	3%	1%	67.6	1.91E+05	(R)FVIYVK(S)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
10.86	3%	1%	74.9	1.46E+04	(K)TISEAIAAVPK(T)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
10.66	3%	1%	68.6	2.49E+04	(R)LGELLPEEAK(A)		UG2181	S.halepenseF3	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
10.48	3%	1%	85.5	6.65E+04	(K)TVVTGDK(S)		UG2229	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.1	3%	1%	70.2	5.07E+05	(R)LASGGLAPSPGKLMR(E)		UG16200	S.halepenseF1	hypothet prot SORBIDRAFT_01g021330 [S bicolor] >gi|241921055|gb|EER94199.1| hypothet prot SORBIDRAFT_01g021330 [S bicolor]
25.17	<0.1%	<0.1%	100	4.73E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
23.4	<0.1%	<0.1%	95.1	3.38E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
21.89	<0.1%	<0.1%	79.9	3.53E+05	(R)VWVSGVMTYVYTCADGFEKPELK(E)	C:Carbamidomethylation	UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
20.98	<0.1%	<0.1%	93.6	5.23E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
20.47	<0.1%	<0.1%	92.7	7.64E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
20.37	<0.1%	<0.1%	94.2	1.10E+06	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
19.53	<0.1%	<0.1%	91.4	3.29E+05	(K)LLDDATEDLGAMSR(L)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
19.16	<0.1%	<0.1%	90.8	5.09E+05	(K)LLDDATEDLGAMSR(L)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
18.77	<0.1%	<0.1%	97.4	5.24E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
17.52	<0.1%	<0.1%	83.7	2.91E+04	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
17.19	<0.1%	<0.1%	86.7	8.54E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
17	<0.1%	<0.1%	90.2	2.65E+06	(R)LKPQDVVR(H)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
16.67	<0.1%	<0.1%	79.5	8.39E+05	(K)LLDDATEDLGAmSR(L)	m:Oxidized methionine	UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
16.41	<0.1%	<0.1%	83.7	4.11E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
16.23	<0.1%	<0.1%	86.5	4.10E+06	(R)LKPQDVVR(H)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
16.18	<0.1%	<0.1%	82.1	5.38E+05	(R)LKPQDVVR(H)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
15.51	0.20%	<0.1%	80.9	1.25E+05	(K)LLDDATEDLGAMSR(L)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
14.5	2%	<0.1%	85.1	8.84E+05	(R)LKPQDVVR(H)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
14.46	2%	<0.1%	68	1.36E+05	(R)VWVSGVMTYVYTCADGFEKPELK(E)	C:Carbamidomethylation	UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
13.35	2%	0.50%	74	5.51E+05	(K)LSTVCASTLYPQK(C)	C:Carbamidomethylation	UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.43	2%	0.60%	62.5	3.57E+05	(K)VDDNDAGGLFSSVK(L)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
12.28	2%	0.70%	66.6	3.57E+05	(K)VDDNDAGGLFSSVK(L)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.59	3%	1.00%	67	1.44E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.42	3%	1.00%	65.8	1.50E+06	(K)LSTVCASTLYPQK(C)	C:Carbamidomethylation	UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
11.38	3%	1.00%	62.6	2.33E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]

11.13	3%	1%	66.2	1.95E+05	(R)AAFNVALDEVAAAFQR(S)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
10.67	3%	1%	66.3	8.40E+05	(K)NAMEVCK(K)	C:Carbamidomethylation	UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
10.58	3%	1%	62.8	6.52E+03	(K)LLDDATEDLGAmSR(L)	m:Oxidized methionine	UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
10.37	3%	1%	65.4	1.11E+06	(R)LKPQDVVR(H)		UG3234	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g030310 [S bicolor] >gi|241938383|gb|EES11528.1| hypothet prot SORBIDRAFT_06g030310 [S bicolor]
14.69	0.20%	<0.1%	84.2	4.34E+05	(K)DVDLSTYK(G)		CL2279.c1	S.halepenseF3	unknown [Zea mays]
15.67	0.20%	<0.1%	81.3	2.46E+04	(R)IVGDVGNHPDER(Y)		UG1334	S.halepenseF2	hypothet prot SORBIDRAFT_03g028140 [S bicolor] >gi|241927940|gb|EES01085.1| hypothet prot SORBIDRAFT_03g028140 [S bicolor]
14.51	2%	<0.1%	69.8	3.63E+04	(R)IVGDVGNHPDER(Y)		UG1334	S.halepenseF2	hypothet prot SORBIDRAFT_03g028140 [S bicolor] >gi|241927940|gb|EES01085.1| hypothet prot SORBIDRAFT_03g028140 [S bicolor]
13.04	2%	0.60%	73.7	8.24E+04	(R)SALPIVDALTIK(N)		UG1334	S.halepenseF2	hypothet prot SORBIDRAFT_03g028140 [S bicolor] >gi|241927940|gb|EES01085.1| hypothet prot SORBIDRAFT_03g028140 [S bicolor]
11.28	3%	1%	65.7	6.19E+04	(R)SALPIVDALTIK(N)		UG1334	S.halepenseF2	hypothet prot SORBIDRAFT_03g028140 [S bicolor] >gi|241927940|gb|EES01085.1| hypothet prot SORBIDRAFT_03g028140 [S bicolor]
18.33	<0.1%	<0.1%	95.4	5.22E+05	(K)GVTSNVSPKPCPELGAEGKPCAFPVEELVIGPPALPK(C)	C:Carbamidomethylation	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
18.13	<0.1%	<0.1%	82.1	2.05E+05	(K)IEDCYIVSGDDCVAVK(S)	C:Carbamidomethylation	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
17.76	<0.1%	<0.1%	89.5	9.92E+05	(K)VTEYGAVGDGR(T)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
17.44	<0.1%	<0.1%	88.6	1.10E+06	(K)VTEYGAVGDGR(T)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
17.23	<0.1%	<0.1%	93.7	3.36E+05	(K)GVTSNVSPKPCPELGAEGKPCAFPVEELVIGPPALPK(C)	C:Carbamidomethylation	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
16.29	<0.1%	<0.1%	77.9	2.40E+05	(K)IEDCYIVSGDDCVAVK(S)	C:Carbamidomethylation	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
16.18	<0.1%	<0.1%	72.6	1.66E+06	(K)FNmPSQHIVIR(R)	m:Oxidized methionine	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
15.99	<0.1%	<0.1%	80.5	7.45E+05	(K)SGWDEYGIK(F)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
14.39	2%	<0.1%	62.1	6.24E+05	(K)SGWDEYGIK(F)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
14.12	2%	0.30%	78	3.51E+05	(R)LTCISPTSAmIALGSEmSGGIR(D)	C:Carbamidomethylation m:Oxidized methionine	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
13.95	2%	0.30%	69	4.14E+05	(K)FNMPSQHIVIR(R)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
13.92	2%	0.40%	76.7	2.56E+05	(R)LTCISPTSAmIALGSEmSGGIR(D)	C:Carbamidomethylation m:Oxidized methionine	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
13.88	2%	0.40%	78	8.44E+05	(R)DGGAALVVPPGK(W)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
13.22	2%	0.50%	80.1	1.63E+05	(R)AEDNIAINTESAVR(I)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
12.99	2%	0.60%	84.4	5.13E+05	(R)AEDNIAINTESAVR(I)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
12.98	2%	0.60%	79.2	7.19E+05	(R)AEDNIAINTESAVR(I)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
12.26	2%	0.70%	60.2	3.60E+05	(K)FNMPSQHIVIR(R)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
11.97	3%	0.80%	63.7	9.27E+04	(R)LSLHTmK(W)	m:Oxidized methionine	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
11.79	3%	0.90%	78.8	1.28E+06	(K)AVADLSR(R)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
11.72	3%	0.90%	75.3	8.37E+05	(R)DGGAALVVPPGK(W)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
11.53	3%	0.90%	64.3	9.21E+04	(R)LSLHTmK(W)	m:Oxidized methionine	UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
10.84	3%	1%	70.6	6.51E+05	(R)DGGAALVVPPGK(W)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
10.7	3%	1%	65.2	6.93E+05	(R)DGGAALVVPPGK(W)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
10.2	3%	1%	69.5	8.37E+05	(R)DGGAALVVPPGK(W)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
10.14	3%	1%	82.6	1.26E+06	(K)AVADLSR(R)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
10.06	5%	1%	64.3	4.06E+05	(R)AEDNIAINTESAVR(I)		UG552	S.halepenseF1	hypothet prot SORBIDRAFT_01g048880 [S bicolor] >gi|241922455|gb|EER95599.1| hypothet prot SORBIDRAFT_01g048880 [S bicolor]
13.37	2%	0.50%	81.6	2.80E+05	(K)GGQAIAVSR(D)		UG764	S.halepenseF3	hypothet prot SORBIDRAFT_04g003600 [S bicolor] >gi|241931380|gb|EES04525.1| hypothet prot SORBIDRAFT_04g003600 [S bicolor]
10.77	3%	1%	82.8	1.15E+05	(R)LEGLIK(M)		UG1259	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g047200 [S bicolor] >gi|241931146|gb|EES04291.1| hypothet prot SORBIDRAFT_03g047200 [S bicolor]
11.06	3%	1%	79.3	3.55E+05	(R)LNFIK(Y)		CL227.c1	S.halepenseF2	palmitoyltransferase PFA4 [Zea mays] >gi|195624214|gb|ACG33937.1| palmitoyltransferase PFA4 [Zea mays]
10.79	3%	1%	76.8	1.17E+05	(R)LNFIK(Y)		CL227.c1	S.halepenseF2	palmitoyltransferase PFA4 [Zea mays] >gi|195624214|gb|ACG33937.1| palmitoyltransferase PFA4 [Zea mays]
10.69	3%	1%	74.2	1.27E+05	(R)LNFIK(Y)		CL227.c1	S.halepenseF2	palmitoyltransferase PFA4 [Zea mays] >gi|195624214|gb|ACG33937.1| palmitoyltransferase PFA4 [Zea mays]

19.49	<0.1%	<0.1%	85.7	6.67E+05	(R)LIGPNCPGIIKPGECK(I)	C:Carbamidomethylation	UG1593	S.halepenseF3	hypothet prot SORBIDRAFT_02g037420 [S bicolor] >gi|241924294|gb|EER97438.1| hypothet prot SORBIDRAFT_02g037420 [S bicolor]
14.73	0.20%	<0.1%	82	6.45E+05	(R)EAGVTVVESPAK(I)		UG1593	S.halepenseF3	hypothet prot SORBIDRAFT_02g037420 [S bicolor] >gi|241924294|gb|EER97438.1| hypothet prot SORBIDRAFT_02g037420 [S bicolor]
14.29	2%	<0.1%	82.9	1.88E+05	(R)EAGVTVVESPAK(I)		UG1593	S.halepenseF3	hypothet prot SORBIDRAFT_02g037420 [S bicolor] >gi|241924294|gb|EER97438.1| hypothet prot SORBIDRAFT_02g037420 [S bicolor]
12.77	2%	0.60%	73.8	4.02E+05	(K)TQKPVVAFIAGLTAPPGR(R)		UG1593	S.halepenseF3	hypothet prot SORBIDRAFT_02g037420 [S bicolor] >gi|241924294|gb|EER97438.1| hypothet prot SORBIDRAFT_02g037420 [S bicolor]
10.86	3%	1%	68.3	3.49E+05	(K)KGGTEHLGLPVFNSVAEAK(A)		UG1593	S.halepenseF3	hypothet prot SORBIDRAFT_02g037420 [S bicolor] >gi|241924294|gb|EER97438.1| hypothet prot SORBIDRAFT_02g037420 [S bicolor]
12.89	2%	0.60%	77.2	5.53E+05	(K)YFSSYISSR(H)	CL2105.c1	S.halepenseF2	uncharacterized protein LOC100191287 [Zea mays]	
23.12	<0.1%	<0.1%	93.5	1.40E+06	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
22.19	<0.1%	<0.1%	87.9	5.02E+06	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
21.08	<0.1%	<0.1%	94.7	1.08E+06	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
20.95	<0.1%	<0.1%	87.2	1.59E+06	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
19.78	<0.1%	<0.1%	83.9	7.01E+05	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
19.78	<0.1%	<0.1%	84.8	3.10E+05	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
19.24	<0.1%	<0.1%	85.2	8.10E+05	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
18.54	<0.1%	<0.1%	78.9	1.25E+06	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
17.82	<0.1%	<0.1%	90.6	9.20E+06	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
17.5	<0.1%	<0.1%	80.7	6.44E+05	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
17.47	<0.1%	<0.1%	88.4	9.45E+05	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
16.73	<0.1%	<0.1%	72.7	4.67E+05	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
16.56	<0.1%	<0.1%	86.8	3.51E+05	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
16.12	<0.1%	<0.1%	85.7	1.38E+06	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
16.11	<0.1%	<0.1%	75	3.84E+05	(K)DFDEPGHLAPTGLFLGATK(Y)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
14.69	1%	<0.1%	71.3	7.49E+06	(K)YmVIQGEPGAVIR(G) m:Oxidized methionine		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
14.19	2%	0.10%	74	9.80E+06	(K)GSGGITVK(K)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
14.13	2%	0.30%	74.5	8.48E+05	(K)GSGGITVK(K)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
13.85	2%	0.40%	80.4	4.75E+05	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
13.76	2%	0.50%	82.5	3.66E+05	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
13.03	2%	0.60%	76.9	1.90E+06	(K)YmVIQGEPGAVIR(G) m:Oxidized methionine		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
12.35	2%	0.70%	70.5	3.77E+06	(K)GSGGITVK(K)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
12.06	3%	0.80%	73.6	1.07E+05	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
10.79	3%	1%	77.1	1.72E+05	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
10.71	3%	1%	66.6	1.14E+06	(K)GSGGITVK(K)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
10.51	3%	1%	70.4	2.71E+05	(K)YMVIQGEPGAVIR(G)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
10.46	3%	1%	65.9	1.27E+06	(K)GSGGITVK(K)		UG1043	S.halepenseF2Rev	hypothet prot SORBIDRAFT_09g026120 [S bicolor] >gi|241946693|gb|EES19838.1| hypothet prot SORBIDRAFT_09g026120 [S bicolor]
23.78	<0.1%	<0.1%	97.2	3.12E+05	(K)KTGQALVIGIYDEPMTPGQCNMVVER(L)	C:Carbamidomethylation	UG308	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
23.45	<0.1%	<0.1%	100	8.30E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)		UG308	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
22.31	<0.1%	<0.1%	98.3	2.69E+06	(K)DFDEPGFLAPTGLFLGPTK(Y)		UG308	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
22.31	<0.1%	<0.1%	98.3	9.34E+05	(K)DFDEPGFLAPTGLFLGPTK(Y)		UG308	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
22.11	<0.1%	<0.1%	98.5	1.18E+07	(K)DFDEPGFLAPTGLFLGPTK(Y)		UG308	S.halepenseF2Rev	hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]

21.98 <0.1% <0.1% 96.4 1.38E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
21.51 <0.1% <0.1% 97.1 2.55E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
21.47 <0.1% <0.1% 96.8 1.68E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
21.44 <0.1% <0.1% 95.9 2.27E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
21.06 <0.1% <0.1% 95.5 4.91E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
20.47 <0.1% <0.1% 91.6 1.06E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
20.32 <0.1% <0.1% 98 4.18E+05 (K)TGQALVIGIYDEPMTPGQCNMVVER(L) C:Carbamidomethylation UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
20.18 <0.1% <0.1% 95.6 2.48E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
19.27 <0.1% <0.1% 88.3 3.21E+04 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
19.26 <0.1% <0.1% 90.7 1.66E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
19.26 <0.1% <0.1% 93.9 2.06E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
19.02 <0.1% <0.1% 93.3 6.75E+05 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
18.41 <0.1% <0.1% 86.5 5.80E+05 (K)KTGQALVIGIYDEPmTPGQCNmVVER(L) C:Carbamidomethylation m:Oxidized methionine UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
18.22 <0.1% <0.1% 92.1 1.63E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
18.05 <0.1% <0.1% 84.2 3.70E+05 (K)KTGQALVIGIYDEPmTPGQCNMVVER(L) C:Carbamidomethylation m:Oxidized methionine UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
18.03 <0.1% <0.1% 86.6 5.25E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
17.36 <0.1% <0.1% 85.3 3.37E+05 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
17.26 <0.1% <0.1% 86 1.34E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
17.07 <0.1% <0.1% 86.8 1.69E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
17.05 <0.1% <0.1% 87.5 5.12E+05 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
16.67 <0.1% <0.1% 82.6 4.65E+05 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
16.66 <0.1% <0.1% 84.3 7.44E+05 (K)TGQALVIGIYDEPmTPGQCNMVVER(L) C:Carbamidomethylation m:Oxidized methionine UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
15.82 0.20% <0.1% 82.1 9.44E+05 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
14.87 0.20% <0.1% 77.6 1.25E+05 (K)TGQALVIGIYDEPMTPGQCNmVVER(L) C:Carbamidomethylation m:Oxidized methionine UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
14.01 2% 0.30% 87 4.15E+05 (K)TGQALVIGIYDEPmTPGQCNmVVER(L) C:Carbamidomethylation m:Oxidized methionine UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
13.51 2% 0.50% 79.2 2.65E+04 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
13.42 2% 0.50% 72.8 1.05E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
12.9 2% 0.60% 73.9 1.41E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
12.7 2% 0.60% 83.6 6.73E+04 (K)TGQALVIGIYDEPMTPGQCNmVVER(L) C:Carbamidomethylation m:Oxidized methionine UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
12.31 2% 0.70% 68.1 9.51E+05 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
12.07 3% 0.80% 69.2 4.11E+05 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
11.3 3% 1.00% 79.2 2.57E+05 (K)TGQALVIGIYDEPMTPGQCNMVVER(L) C:Carbamidomethylation UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
10.4 3% 1% 67.3 1.06E+06 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
10.4 3% 1% 74.4 1.94E+05 (K)TGQALVIGIYDEPmTPGQCNMVVER(L) C:Carbamidomethylation m:Oxidized methionine UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
10.11 3% 1% 67.5 1.52E+04 (K)DFDEPGFLAPTGLFLGPTK(Y) UG308 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g034110 [S bicolor] >gi|241928307|gb|EES01452.1| hypothet prot SORBIDRAFT_03g034110 [S bicolor]
17.11 <0.1% <0.1% 84.9 1.41E+05 (R)YLSPCGNCDWR(E) C:Carbamidomethylation CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
16.71 <0.1% <0.1% 77.2 9.79E+04 (R)LLVLSVTTFTADGQR(H) CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
16.53 <0.1% <0.1% 76.2 2.34E+05 (R)AFSYEFVPAEGQSNAQANPLQILR(D) CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]

16.01 <0.1% <0.1% 75.1 1.59E+05 (K)FTLQFSTPGQAVVQDDVK(V) CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
14.66 2% <0.1% 61.4 3.14E+04 (R)AFSYEFVPAEGQSNAQANPLQILR(D) CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
13.68 2% 0.50% 70.7 2.22E+05 (R)AFSYEFVPAEGQSNAQANPLQILR(D) CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
13.58 2% 0.50% 72 1.70E+05 (R)AFSYEFVPAEGQSNAQANPLQILR(D) CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
12.27 2% 0.70% 76.8 8.66E+04 (R)HTVTVDAPGKPELAPPGYYmLYVIAK(G) m:Oxidized methionine CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
12.06 3% 0.80% 70.2 2.07E+05 (R)FTPPYLSPELAANRPVIDVGTVPGDGmAYGAK(F) m:Oxidized methionine CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
11.99 3% 0.80% 68.5 5.09E+05 (K)VTLYAPPFTTHGYSmNQR(L) m:Oxidized methionine CL1272.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g028310 [S bicolor] >gi|241945525|gb|EES18670.1| hypothet prot SORBIDRAFT_09g028310 [S bicolor]
26.37 <0.1% <0.1% 93.8 3.85E+05 (K)AYTGTDGDASVSGGGSGGAK(A) UG252 S.halepenseF3RevF3Rev predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144579679|gb|ABO97741.1| predicted protein [Ostreococcus lucimarinus CCE9901]
25.41 <0.1% <0.1% 91 3.41E+05 (K)AYTGTDGDASVSGGGSGGAK(A) UG252 S.halepenseF3RevF3Rev predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144579679|gb|ABO97741.1| predicted protein [Ostreococcus lucimarinus CCE9901]
24.61 <0.1% <0.1% 94.9 7.16E+05 (K)AYTGTDGDASVSGGGSGGAK(A) UG252 S.halepenseF3RevF3Rev predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144579679|gb|ABO97741.1| predicted protein [Ostreococcus lucimarinus CCE9901]
21.64 <0.1% <0.1% 82.8 1.02E+05 (K)AYTGTDGDASVSGGGSGGAK(A) UG252 S.halepenseF3RevF3Rev predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144579679|gb|ABO97741.1| predicted protein [Ostreococcus lucimarinus CCE9901]
20.54 <0.1% <0.1% 84.4 4.33E+05 (K)AYTGTDGDASVSGGGSGGAK(A) UG252 S.halepenseF3RevF3Rev predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144579679|gb|ABO97741.1| predicted protein [Ostreococcus lucimarinus CCE9901]
20.37 <0.1% <0.1% 85.2 1.65E+05 (K)AYTGTDGDASVSGGGSGGAK(A) UG252 S.halepenseF3RevF3Rev predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144579679|gb|ABO97741.1| predicted protein [Ostreococcus lucimarinus CCE9901]
20.34 <0.1% <0.1% 81.7 2.22E+05 (K)AYTGTDGDASVSGGGSGGAK(A) UG252 S.halepenseF3RevF3Rev predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144579679|gb|ABO97741.1| predicted protein [Ostreococcus lucimarinus CCE9901]
14.6 2% <0.1% 62.8 8.05E+04 (K)AYTGTDGDASVSGGGSGGAK(A) UG252 S.halepenseF3RevF3Rev predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144579679|gb|ABO97741.1| predicted protein [Ostreococcus lucimarinus CCE9901]
19.34 <0.1% <0.1% 93.6 1.02E+06 (K)GTAFPDICTSTVGPEAASNPVLDPMAVLR(M) C:Carbamidomethylation UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
17.33 <0.1% <0.1% 81.1 7.49E+05 (K)GTAFPDICTSTVGPEAASNPVLDPMAVLR(M) C:Carbamidomethylation UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
16.17 <0.1% <0.1% 75.4 3.91E+04 (K)EAAmTASPK(A) m:Oxidized methionine UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
15.7 0.20% <0.1% 75.5 8.88E+04 (K)GTAFPDICTSTVGPEAASNPVLDPMAVLR(M) C:Carbamidomethylation UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
15.17 0.20% <0.1% 79 1.08E+06 (K)GTAFPDICTSTVGPEAASNPVLDPmAVLR(M) C:Carbamidomethylation m:Oxidized methionine UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
14.15 2% 0.20% 76.1 2.76E+06 (R)MQVDAFNQR(T) UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
12.88 2% 0.60% 66.5 3.75E+05 (K)GTAFPDICTSTVGPEAASNPVLDPMAVLR(M) C:Carbamidomethylation UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
12.48 2% 0.60% 72.6 4.50E+05 (R)MQVDAFNQR(T) UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
12.05 3% 0.80% 66 5.05E+05 (K)EAAMTASPK(A) UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
11.31 3% 1.00% 63.9 1.13E+06 (K)EAAMTASPK(A) UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
10.42 3% 1% 60.6 4.61E+06 (R)mQVDAFNQR(T) m:Oxidized methionine UG294 S.halepenseF1Rev hypothet prot SORBIDRAFT_03g009690 [S bicolor] >gi|241927357|gb|EES00502.1| hypothet prot SORBIDRAFT_03g009690 [S bicolor]
24.15 <0.1% <0.1% 95.7 7.78E+05 (K)ADADATAGGEAEASK(S) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.79 <0.1% <0.1% 91.4 6.13E+05 (K)ADADATAGGEAEASK(S) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.55 <0.1% <0.1% 86.1 5.18E+05 (K)ADADATAGGEAEASK(S) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
19.08 <0.1% <0.1% 79.9 2.30E+05 (K)SSSSSASGDAGGNEGGETDADATTSSGGEAGGSGK(G) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
18.57 <0.1% <0.1% 78.7 3.31E+05 (K)SSSSSASGDAGGNEGGETDADATTSSGGEAGGSGK(G) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
16.72 <0.1% <0.1% 86.2 1.06E+06 (K)GDVDATAGAGGEAK(A) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
16.58 <0.1% <0.1% 76.7 2.61E+05 (K)ADADATAGGEAEASK(S) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
16.29 <0.1% <0.1% 81.3 1.02E+06 (K)SSSISASGDVGGDAGGK(-) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
16.25 <0.1% <0.1% 81 5.89E+05 (K)SSSISASGDVGGDAGGK(-) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.87 0.20% <0.1% 79.5 1.56E+06 (K)GDVDATAGAGGEAK(A) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.77 0.20% <0.1% 80.1 1.68E+06 (K)GDVDATAGAGGEAK(A) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.7 0.20% <0.1% 81.1 3.94E+05 (K)ADADATAGGEAEASK(S) CL1735.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]

14.43	2%	<0.1%	69.3	1.30E+05	(K)ADADATAGGEAEASK(S)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.34	2%	<0.1%	74.2	6.31E+04	(K)ADADATAGGEAEASK(S)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.23	2%	<0.1%	79.7	8.20E+05	(K)SSSISASGDVGGDAGGK(-)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.14	2%	0.20%	61.5	7.30E+04	(K)SSSSSASGDAGGNEGGETDADATTSSGGEAGGSGK(G)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.03	2%	0.30%	71.3	1.34E+05	(K)SSSISASGDVGGDAGGK(-)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.67	2%	0.50%	69	1.22E+05	(K)ADADATAGGEAEASK(S)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.9	2%	0.60%	72.4	4.04E+05	(K)GDVDATAGAGGEAK(A)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.59	2%	0.60%	70.5	6.74E+04	(K)ADADATAGGEAEASK(S)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.28	2%	0.70%	65.6	7.74E+04	(K)ADADATAGGEAEASK(S)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.23	3%	0.70%	63.6	3.22E+05	(K)SSSSSASGDAGGNEGGETDADATTSSGGEAGGSGK(G)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.72	3%	0.90%	65.1	1.33E+04	(K)GDVDATAGAGGEAK(A)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.18	3%	1%	65.8	1.17E+05	(K)GDVDATAGAGGEAK(A)		CL1735.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.73	2%	0.50%	72.6	6.65E+04	(K)VAGmVITGVTDEELQLLDAFEDVEYTR(T)	m:Oxidized methionine	UG12091	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g029140 [S bicolor] >gi|241917189|gb|EER90333.1| hypothet prot SORBIDRAFT_10g029140 [S bicolor]
10.95	3%	1%	67.5	6.90E+04	(K)VAGmVITGVTDEELQLLDAFEDVEYTR(T)	m:Oxidized methionine	UG12091	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g029140 [S bicolor] >gi|241917189|gb|EER90333.1| hypothet prot SORBIDRAFT_10g029140 [S bicolor]
19.49	<0.1%	<0.1%	85.4	6.01E+05	(K)LDEGVVIANLDADKYR(D)		UG5446	S.halepenseF2Rev	PREDICTED: protein disulfide isomerase-like 2-2-like [Brachypodium distachyon]
18.74	<0.1%	<0.1%	85.1	2.13E+05	(K)EVLSSmEEEAAK(L)	m:Oxidized methionine	UG5446	S.halepenseF2Rev	PREDICTED: protein disulfide isomerase-like 2-2-like [Brachypodium distachyon]
15.92	<0.1%	<0.1%	69.6	5.14E+05	(K)YGVTGFPTLK(F)		UG5446	S.halepenseF2Rev	PREDICTED: protein disulfide isomerase-like 2-2-like [Brachypodium distachyon]
17.44	<0.1%	<0.1%	86	3.73E+05	(K)LATIPSSVVVLTPETFDSIVLDEAK(D)		UG6635	S.halepenseF2Rev	PREDICTED: protein disulfide isomerase-like 2-1-like [Brachypodium distachyon]
12.77	2%	0.60%	67.4	5.27E+04	(K)YGVSGYPTIQWFPK(G)		UG6635	S.halepenseF2Rev	PREDICTED: protein disulfide isomerase-like 2-1-like [Brachypodium distachyon]
10.92	3%	1%	68	1.91E+04	(R)TAEALAEFVNTEGGTNVK(L)		UG6635	S.halepenseF2Rev	PREDICTED: protein disulfide isomerase-like 2-1-like [Brachypodium distachyon]
10.41	3%	1%	71.7	6.52E+04	(R)LGASFK(K)		UG6635	S.halepenseF2Rev	PREDICTED: protein disulfide isomerase-like 2-1-like [Brachypodium distachyon]
15.01	0.20%	<0.1%	81.8	3.59E+04	(K)LAPEYETAAK(E)		UG6038	S.halepenseF1	protein disulfide isomerase [Triticum durum] >gi|12056121|emb|CAC21231.1| protein disulfide isomerase [Triticum durum]
10.39	3%	1%	65.7	1.71E+04	(K)LAPEYETAAK(E)		UG6038	S.halepenseF1	protein disulfide isomerase [Triticum durum] >gi|12056121|emb|CAC21231.1| protein disulfide isomerase [Triticum durum]
11.69	3%	0.90%	71.5	1.19E+04	(R)TADDIVDFIK(K)		UG7876	S.halepenseF2	protein disulfide isomerase [Oryza sativa]
15.92	<0.1%	<0.1%	80.1	7.93E+04	(K)DFDVAALLK(F)		UG9570	S.halepenseF2	protein disulfide isomerase [Zea mays]
12.51	2%	0.60%	71.6	9.87E+04	(K)DFDVAALLK(F)		UG9570	S.halepenseF2	protein disulfide isomerase [Zea mays]
11.89	3%	0.90%	68.3	4.15E+05	(R)VLKPFDELVVDTK(D)		UG9570	S.halepenseF2	protein disulfide isomerase [Zea mays]
10.29	3%	1%	74.4	1.50E+05	(K)LQVLLPQNLWCIK(G)	C:Carbamidomethylation	UG2517	S.halepenseF1Rev	predicted protein [Populus trichocarpa] >gi|222846750|gb|EEE84297.1| predicted protein [Populus trichocarpa]
20.18	<0.1%	<0.1%	86	5.89E+05	(R)VALGPSGDLSLTSR(I)		CL1509.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g007530 [S bicolor] >gi|241941622|gb|EES14767.1| hypothet prot SORBIDRAFT_07g007530 [S bicolor]
16.87	<0.1%	<0.1%	83.2	2.64E+05	(K)AFVDLILKPSEEDLK(I)		CL1509.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g007530 [S bicolor] >gi|241941622|gb|EES14767.1| hypothet prot SORBIDRAFT_07g007530 [S bicolor]
15.27	0.20%	<0.1%	77.1	2.32E+05	(R)VALGPSGDLSLTSR(I)		CL1509.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g007530 [S bicolor] >gi|241941622|gb|EES14767.1| hypothet prot SORBIDRAFT_07g007530 [S bicolor]
12.67	2%	0.60%	64.6	1.82E+04	(R)GGIPVCFPQFGTHGNLEQHGFAR(N)	C:Carbamidomethylation	CL1509.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g007530 [S bicolor] >gi|241941622|gb|EES14767.1| hypothet prot SORBIDRAFT_07g007530 [S bicolor]
12.66	2%	0.60%	63.1	2.63E+05	(K)IWPHSFEFR(L)		CL1509.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g007530 [S bicolor] >gi|241941622|gb|EES14767.1| hypothet prot SORBIDRAFT_07g007530 [S bicolor]
11.97	3%	0.80%	64	1.12E+05	(R)VEGLETmDYLDNLK(A)	m:Oxidized methionine	CL1509.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g007530 [S bicolor] >gi|241941622|gb|EES14767.1| hypothet prot SORBIDRAFT_07g007530 [S bicolor]
10.67	3%	1%	67.8	1.46E+05	(R)FWTIDNNPPPLPVNPAIK(A)		CL1509.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g007530 [S bicolor] >gi|241941622|gb|EES14767.1| hypothet prot SORBIDRAFT_07g007530 [S bicolor]
11.96	3%	0.80%	73.5	1.86E+05	(K)VGVVLSGGQAPGGHNVICGIFDYLQER(A)	C:Carbamidomethylation	UG15229	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g008850 [S bicolor] >gi|241916370|gb|EER89514.1| hypothet prot SORBIDRAFT_10g008850 [S bicolor]
10.5	3%	1%	65.8	8.92E+04	(K)VGVVLSGGQAPGGHNVICGIFDYLQER(A)	C:Carbamidomethylation	UG15229	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g008850 [S bicolor] >gi|241916370|gb|EER89514.1| hypothet prot SORBIDRAFT_10g008850 [S bicolor]
12.22	3%	0.70%	71.4	2.10E+05	(K)ELFEFLPK(T)		UG2999	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g008850 [S bicolor] >gi|241916370|gb|EER89514.1| hypothet prot SORBIDRAFT_10g008850 [S bicolor]
13.1	2%	0.60%	76.1	4.46E+04	(R)DVTTTPAELVTFFR(D)		UG1757	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g028450 [S bicolor] >gi|241932410|gb|EES05555.1| hypothet prot SORBIDRAFT_04g028450 [S bicolor]
11.89	3%	0.90%	78.5	3.75E+05	(K)LLLIGDSGVGK(S)		UG2123	S.halepenseF1Rev	hypothet prot SORBIDRAFT_01g003310 [S bicolor] >gi|241920051|gb|EER93195.1| hypothet prot SORBIDRAFT_01g003310 [S bicolor]
11.19	3%	1%	72.3	2.72E+05	(K)LQIWDTAGQER(F)		UG2123	S.halepenseF1Rev	hypothet prot SORBIDRAFT_01g003310 [S bicolor] >gi|241920051|gb|EER93195.1| hypothet prot SORBIDRAFT_01g003310 [S bicolor]
12.25	3%	0.70%	80.3	1.84E+05	(R)SLIPSYIR(D)		UG122	S.halepenseF1	ras-related protein Rab-6A [Zea mays] >gi|195637990|gb|ACG38463.1| ras-related protein Rab-6A [Zea mays]
23.87	<0.1%	<0.1%	100	3.87E+05	(K)VPIWLTEVDVTK(G)		CL2034.c2	S.halepenseF1Rev	hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]

23.42 <0.1% <0.1% 100 6.52E+05 (K)VPIWLTEVDVTK(G) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
22.01 <0.1% <0.1% 98.3 1.03E+06 (K)VPIWLTEVDVTK(G) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
19.65 <0.1% <0.1% 97 7.46E+05 (K)VPIWLTEVDVTK(G) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
17.46 <0.1% <0.1% 79.9 3.91E+04 (K)LDPKPILFmNEFNTIEQPCDK(A) C:Carbamidomethylation m:Oxidized methionine CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
16.72 <0.1% <0.1% 77.9 4.75E+05 (K)EPIVQTVDLDSK(S) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
16.11 <0.1% <0.1% 83.3 4.72E+05 (K)VPIWLTEVDVTK(G) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
15.73 0.20% <0.1% 85 3.05E+04 (K)NLPQGDLVDR(L) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
15.3 0.20% <0.1% 68.8 7.59E+05 (K)YGIGLESHFAKPNIPYmR(G) m:Oxidized methionine CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
14.63 2% <0.1% 84 7.07E+05 (K)HASLKEPIVQTVDLDSK(S) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
14.52 2% <0.1% 70.6 3.07E+05 (K)GCYVmCLTDNNFK(N) C:Carbamidomethylation m:Oxidized methionine CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
14.36 2% <0.1% 71.7 1.93E+05 (R)QIQSYPGNEDLK(Y) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
14.25 2% <0.1% 72.9 3.78E+05 (K)VPIWLTEVDVTK(G) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
14.16 2% 0.20% 66.8 2.06E+06 (R)GSLDTLAAAK(V) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
13.91 2% 0.40% 81.9 1.14E+06 (K)DASGEIFK(E) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
13.5 2% 0.50% 73.2 6.91E+05 (K)NLPQGDLVDR(L) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
13.22 2% 0.50% 69.8 2.75E+05 (R)QIQSYPGNEDLK(Y) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
12.86 2% 0.60% 70.8 1.46E+05 (K)GIVMWAAWHAK(G) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
12.72 2% 0.60% 67.5 1.24E+06 (R)EGFGHPGVK(G) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
12.7 2% 0.60% 76.3 8.03E+05 (K)APLPTK(Y) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
12.43 2% 0.60% 83.3 3.46E+05 (R)LLDEWR(K) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
12.28 2% 0.70% 86.5 7.93E+05 (R)LLDEWR(K) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.94 3% 0.90% 74.1 1.96E+05 (K)APLPTK(Y) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.62 3% 0.90% 67.9 1.10E+05 (K)VPIWLTEVDVTK(G) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.37 3% 1.00% 70.2 1.49E+05 (R)LLDEWR(K) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.36 3% 1.00% 78.7 4.74E+05 (R)LLDEWR(K) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.3 3% 1.00% 62.9 3.25E+05 (K)APLPTK(Y) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.29 3% 1.00% 66.1 5.27E+05 (K)DASGEIFK(E) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.26 3% 1% 62.3 2.68E+05 (R)QIQSYPGNEDLK(Y) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
11.22 3% 1% 75.6 4.16E+05 (R)LLDEWR(K) CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
10.36 3% 1% 66.2 5.54E+05 (K)YGIGLESHFAKPNIPYmR(G) m:Oxidized methionine CL2034.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g043730 [S bicolor] >gi|241919540|gb|EER92684.1| hypothet prot SORBIDRAFT_01g043730 [S bicolor]
26.15 <0.1% <0.1% 97.5 3.44E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
25.04 <0.1% <0.1% 97.8 3.21E+06 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
23.75 <0.1% <0.1% 94 1.22E+06 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
23.64 <0.1% <0.1% 91.4 4.99E+06 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
22.86 <0.1% <0.1% 91 1.04E+06 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
22.64 <0.1% <0.1% 93.6 2.18E+06 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
22.64 <0.1% <0.1% 96 4.14E+06 (R)SSPAYGSIWASTVR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
22.48 <0.1% <0.1% 88.5 1.07E+06 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]

22.18 <0.1% <0.1% 94.5 3.69E+06 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
22.04 <0.1% <0.1% 90 2.73E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
21.97 <0.1% <0.1% 95.3 3.68E+06 (R)SSPAYGSIWASTVR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
21.87 <0.1% <0.1% 95 2.63E+06 (R)SSPAYGSIWASTVR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
21.51 <0.1% <0.1% 90.1 6.47E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
21.51 <0.1% <0.1% 94.3 4.50E+06 (K)HGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
21.28 <0.1% <0.1% 89.1 4.62E+05 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
21.1 <0.1% <0.1% 90.2 8.01E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
21.01 <0.1% <0.1% 87.2 3.48E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
20.85 <0.1% <0.1% 89 1.48E+06 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
20.77 <0.1% <0.1% 93.6 2.78E+06 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
20.71 <0.1% <0.1% 94 1.94E+06 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
20.57 <0.1% <0.1% 87.1 1.26E+06 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
20.5 <0.1% <0.1% 91.3 9.15E+05 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.93 <0.1% <0.1% 75.9 5.92E+05 (R)STKPETFAVVDmSLLR(K) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.9 <0.1% <0.1% 79.1 4.81E+05 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.9 <0.1% <0.1% 93.9 1.32E+06 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.89 <0.1% <0.1% 83.7 2.39E+06 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.86 <0.1% <0.1% 86.7 4.28E+05 (R)DMYAFMEPYVTK(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.6 <0.1% <0.1% 81.3 9.65E+05 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.5 <0.1% <0.1% 82.3 1.77E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.43 <0.1% <0.1% 91.1 2.22E+04 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.32 <0.1% <0.1% 92.6 1.75E+06 (R)STKPETFAVVDMSLLR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.28 <0.1% <0.1% 88.4 5.01E+06 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.28 <0.1% <0.1% 90.6 4.27E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
19.01 <0.1% <0.1% 88.6 4.45E+06 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.82 <0.1% <0.1% 90.4 2.76E+06 (K)VVDANGNLLDR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.82 <0.1% <0.1% 85.8 2.71E+06 (K)GDFLACLTK(S) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.78 <0.1% <0.1% 87.4 4.96E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.74 <0.1% <0.1% 92.7 1.51E+06 (K)HGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.58 <0.1% <0.1% 93.5 3.63E+06 (K)YFSFNFER(L) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.48 <0.1% <0.1% 88.2 6.50E+05 (R)SSPAYGSIWASTVR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.19 <0.1% <0.1% 76.7 1.36E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.12 <0.1% <0.1% 72.8 2.76E+06 (R)DmYAFmEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
18.01 <0.1% <0.1% 97 7.41E+06 (R)FPELGVK(Q) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
17.95 <0.1% <0.1% 81.2 2.64E+06 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
17.89 <0.1% <0.1% 89.9 6.13E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
17.88 <0.1% <0.1% 79.1 9.91E+05 (K)DPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]

17.78	<0.1%	<0.1%	84	1.74E+05	(R)DLDLGVNQVVNDISTYESGK(V)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
17.75	<0.1%	<0.1%	92.5	5.23E+05	(K)WQQVAPSLPEDLMIR(I)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
17.65	<0.1%	<0.1%	94	5.96E+06	(R)FPELGVK(Q)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
17.59	<0.1%	<0.1%	85.3	1.20E+06	(R)STKPETFAVVDMSLLR(K)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
17.42	<0.1%	<0.1%	84.8	3.70E+05	(R)ILAmGGTAIFEGLFLGTCK(D)	C:Carbamidomethylation m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
17.42	<0.1%	<0.1%	79.8	4.84E+05	(K)EmSWVQSVAFIPmGDK(A)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
17.26	<0.1%	<0.1%	87.6	3.09E+05	(R)ILAmGGTAIFEGLFLGTCK(D)	C:Carbamidomethylation m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
17.21	<0.1%	<0.1%	83.7	1.13E+06	(R)DLDLGVNQVVNDISTYESGK(V)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
17.02	<0.1%	<0.1%	80.3	1.91E+06	(K)AATAWVDSGAQLGDIYYALGK(W)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.92	<0.1%	<0.1%	84.9	3.68E+05	(R)ILAmGGTAIFEGLFLGTCK(D)	C:Carbamidomethylation m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.9	<0.1%	<0.1%	86.1	3.46E+06	(K)GDFLACLTK(S)	C:Carbamidomethylation	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.87	<0.1%	<0.1%	77	3.09E+05	(R)SSPAYGSIWASTVR(N)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.86	<0.1%	<0.1%	91.4	1.11E+06	(K)DLLPLMASR(F)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.82	<0.1%	<0.1%	73.3	2.72E+04	(R)QGmLFNIQYVTYWSGEAAGAAPTQWSR(D)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.77	<0.1%	<0.1%	82.1	3.91E+05	(K)WQQVAPSLPEDLMIR(I)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.66	<0.1%	<0.1%	76.6	7.28E+05	(R)DLDLGVNQVVNDISTYESGK(V)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.61	<0.1%	<0.1%	82.5	3.72E+06	(K)GDFLACLTK(S)	C:Carbamidomethylation	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.45	<0.1%	<0.1%	64.4	1.46E+06	(K)TmGEDYFWAIR(G)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.35	<0.1%	<0.1%	86.6	4.91E+06	(R)FPELGVK(Q)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.3	<0.1%	<0.1%	80	1.17E+06	(K)SDYVKDPIAKPVWEK(I)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.29	<0.1%	<0.1%	88.3	3.32E+05	(K)WQQVAPSLPEDLMIR(I)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.28	<0.1%	<0.1%	77.4	3.47E+06	(R)STKPETFAVVDmSLLR(K)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.15	<0.1%	<0.1%	92.9	4.74E+06	(R)FPELGVK(Q)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
16.08	<0.1%	<0.1%	69.3	1.44E+05	(K)AATAWVDSGAQLGDIYYALGK(W)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.92	0.20%	<0.1%	90.1	3.70E+06	(K)DGAIDLIVK(W)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.88	0.20%	<0.1%	80.1	6.98E+05	(K)WQQVAPSLPEDLMIR(I)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.84	0.20%	<0.1%	73.7	1.32E+06	(K)AATAWVDSGAQLGDIYYALGK(W)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.82	0.20%	<0.1%	92.8	4.96E+06	(K)DGAIDLIVK(W)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.82	0.20%	<0.1%	90.1	1.21E+06	(R)STKPETFAVVDMSLLR(K)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.81	0.20%	<0.1%	76.3	5.61E+05	(K)EmSWVQSVAFIPmGDK(A)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.76	0.20%	<0.1%	85.3	3.27E+06	(K)HGLAVDNVVDAK(V)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.65	0.20%	<0.1%	85.7	2.96E+05	(R)FPELGVK(Q)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.58	0.20%	<0.1%	80.5	9.75E+05	(R)KTmGEDYFWAIR(G)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.57	0.20%	<0.1%	74.2	2.42E+04	(R)QGmLFNIQYVTYWSGEAAGAAPTQWSR(D)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.48	0.20%	<0.1%	73.1	4.32E+05	(K)GDFLACLTK(S)	C:Carbamidomethylation	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.4	0.20%	<0.1%	71.8	9.50E+05	(K)SDYVKDPIAKPVWEK(I)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.39	0.20%	<0.1%	76	7.09E+05	(K)EmSWVQSVAFIPmGDK(A)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		
15.37	0.20%	<0.1%	74.1	4.48E+05	(K)DPIAKPVWEK(I)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]		

15.37 0.20% <0.1% 74.7 1.66E+05 (R)ILAMGGTAIFEGLFLGTCK(D) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.36 0.20% <0.1% 75.5 2.79E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.34 0.20% <0.1% 88.4 1.09E+06 (K)DGAIDLIVK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.29 0.20% <0.1% 79.9 1.01E+06 (K)VVDANGNLLDR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.26 0.20% <0.1% 81.9 5.66E+06 (K)VVDANGNLLDR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.21 0.20% <0.1% 87.7 3.88E+06 (K)VDPTDYFR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.15 0.20% <0.1% 86.9 4.14E+05 (K)DGAIDLIVK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.15 0.20% <0.1% 69.4 2.32E+05 (K)EMSWVQSVAFIPmGDK(A) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.08 0.20% <0.1% 86.3 3.34E+05 (K)WQQVAPSLPEDLMIR(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.07 0.20% <0.1% 83 5.31E+06 (K)DGAIDLIVK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.06 0.20% <0.1% 70.2 4.59E+05 (K)DPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
15.02 0.20% <0.1% 82.4 3.96E+06 (K)VVDANGNLLDR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.96 0.20% <0.1% 93.6 6.60E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.88 0.20% <0.1% 79.4 7.51E+05 (K)HGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.86 0.20% <0.1% 78.8 1.33E+06 (K)DPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.82 0.20% <0.1% 77.9 7.19E+04 (R)STKPETFAVVDmSLLR(K) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.78 0.20% <0.1% 73.4 1.75E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.73 0.20% <0.1% 74.5 1.50E+06 (K)WQQVAPSLPEDLmIR(I) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.7 0.20% <0.1% 85.5 3.78E+06 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.69 0.20% <0.1% 66.3 2.27E+05 (R)DmYAFmEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.65 2% <0.1% 70.1 2.22E+06 (R)STKPETFAVVDmSLLR(K) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.63 2% <0.1% 76.2 2.78E+06 (K)VVDANGNLLDR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.62 2% <0.1% 84.5 7.40E+05 (K)VVDANGNLLDR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.55 2% <0.1% 68.1 1.74E+05 (K)EMSWVQSVAFIPMGDK(A) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.48 2% <0.1% 74.3 2.66E+06 (K)DLLPLmASR(F) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.47 2% <0.1% 93.9 7.35E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.47 2% <0.1% 70.6 1.24E+06 (R)FPELGVK(Q) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.41 2% <0.1% 70.4 2.11E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.34 2% <0.1% 80.1 4.21E+05 (K)VVDANGNLLDR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.34 2% <0.1% 85.1 5.41E+05 (K)DGAIDLIVK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.33 2% <0.1% 81.3 7.84E+05 (K)DPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.32 2% <0.1% 85.4 7.95E+05 (R)FPELGVK(Q) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.29 2% <0.1% 78.5 1.38E+05 (K)WQQVAPSLPEDLmIR(I) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.26 2% <0.1% 76.7 2.29E+05 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.24 2% <0.1% 82.7 3.56E+06 (K)DGAIDLIVK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.2 2% <0.1% 65.5 2.34E+05 (R)DmYAFmEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.2 2% <0.1% 93.3 4.14E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14.18 2% 0.10% 92.2 3.91E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]

14.18 2% 0.20% 77.7 1.19E+06 (R)KTmGEDYFWAIR(G) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
14 2% 0.30% 79 3.51E+06 (K)DLLPLmASR(F) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.99 2% 0.30% 64.2 3.16E+06 (R)DmYAFmEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.97 2% 0.30% 82.4 7.85E+05 (R)FPELGVK(Q) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.76 2% 0.50% 69 9.05E+05 (K)GDFLACLTK(S) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.73 2% 0.50% 67.8 2.56E+06 (K)YFSFNFER(L) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.7 2% 0.50% 80.6 7.50E+04 (R)FPELGVK(Q) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.68 2% 0.50% 63.5 1.05E+04 (K)EmSWVQSVAFIPMGDK(A) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.67 2% 0.50% 63.8 1.15E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.64 2% 0.50% 77 3.54E+06 (K)VDPTDYFR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.57 2% 0.50% 70.8 2.84E+05 (R)DmYAFMEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.53 2% 0.50% 76.8 5.49E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.51 2% 0.50% 82.7 2.80E+06 (R)KHGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.48 2% 0.50% 73.7 1.84E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.48 2% 0.50% 73.8 1.39E+06 (K)WQQVAPSLPEDLmIR(I) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.46 2% 0.50% 65.5 7.43E+04 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.46 2% 0.50% 87.4 2.45E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.4 2% 0.50% 71.5 2.10E+05 (K)YFSFNFER(L) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.35 2% 0.50% 90.1 7.22E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.34 2% 0.50% 62.6 4.74E+05 (R)DmYAFmEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.32 2% 0.50% 90.1 2.94E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.32 2% 0.50% 76.2 2.86E+05 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.31 2% 0.50% 71.5 2.15E+05 (R)STKPETFAVVDMSLLR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.24 2% 0.50% 79 3.49E+06 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.21 2% 0.50% 86.8 8.17E+05 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.19 2% 0.50% 75.9 2.34E+06 (R)KHGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.19 2% 0.50% 76.8 1.95E+06 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.12 2% 0.60% 75 3.23E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.12 2% 0.60% 72.2 1.29E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.11 2% 0.60% 71.6 3.43E+05 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.1 2% 0.60% 73.5 1.47E+06 (R)KHGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.1 2% 0.60% 68.8 8.92E+05 (R)KTmGEDYFWAIR(G) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.08 2% 0.60% 84.5 1.48E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.07 2% 0.60% 79.5 2.76E+05 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.02 2% 0.50% 68.8 1.38E+06 (R)FPELGVK(Q) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.02 2% 0.50% 75.9 1.73E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.02 2% 0.50% 76 3.75E+05 (R)DMYAFmEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
13.02 2% 0.50% 64.6 1.20E+05 (K)WQQVAPSLPEDLmIR(I) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]

13.01 2% 0.60% 72.1 7.10E+05 (K)GDFLACLTK(S) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.99 2% 0.60% 81.9 8.71E+05 (K)DGAIDLIVK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.98 2% 0.60% 70.6 2.24E+05 (K)HGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.93 2% 0.60% 80.5 2.84E+05 (K)DLLPLMASR(F) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.91 2% 0.60% 69.8 1.22E+06 (R)STKPETFAVVDmSLLR(K) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.88 2% 0.60% 80.8 6.61E+05 (K)DLLPLMASR(F) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.86 2% 0.60% 68.8 1.78E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.84 2% 0.60% 66.6 5.55E+03 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.8 2% 0.60% 79.1 3.74E+05 (K)DGAIDLIVK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.8 2% 0.60% 68.4 4.75E+05 (K)EmSWVQSVAFIPmGDK(A) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.73 2% 0.60% 72.2 6.39E+05 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.73 2% 0.60% 78.4 1.40E+06 (K)VTVLQMPR(S) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.72 2% 0.60% 77.1 1.00E+05 (K)TAKPLYIITPTEPAHIQATVACGR(K) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.72 2% 0.60% 86.7 2.99E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.72 2% 0.60% 66.5 1.41E+04 (K)WQQVAPSLPEDLMIR(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.72 2% 0.60% 63.3 1.52E+05 (K)EMSWVQSVAFIPMGDK(A) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.71 2% 0.60% 67.3 1.13E+06 (K)SDYVKDPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.68 2% 0.60% 85.9 1.33E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.65 2% 0.70% 75.1 2.38E+06 (K)VDPTDYFR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.63 2% 0.70% 75.5 1.74E+05 (K)WQQVAPSLPEDLMIR(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.63 2% 0.70% 61.8 3.23E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.59 2% 0.60% 66.2 1.31E+06 (K)WQQVAPSLPEDLmIR(I) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.56 2% 0.60% 60.1 2.62E+06 (K)YFSFNFER(L) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.55 2% 0.60% 65.1 1.20E+05 (K)DPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.49 2% 0.60% 64.1 1.72E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.48 2% 0.60% 74.2 9.08E+03 (K)WQQVAPSLPEDLMIR(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.42 2% 0.60% 72.1 1.82E+06 (K)HGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.42 2% 0.60% 87.1 9.84E+05 (K)DLLPLMASR(F) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.4 2% 0.60% 64.2 1.04E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.39 2% 0.60% 81.5 6.26E+05 (R)KVSLDGK(A) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.38 2% 0.60% 71.9 2.85E+06 (R)STKPETFAVVDmSLLR(K) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.38 2% 0.60% 64.6 9.87E+04 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.32 2% 0.70% 82.5 6.43E+05 (K)DLLPLMASR(F) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.31 2% 0.70% 69.8 1.63E+05 (R)DLDLGVNQVVNDISTYESGK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.28 2% 0.70% 69.2 2.78E+05 (R)DMYAFmEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.28 2% 0.70% 70.2 2.06E+05 (R)DMYAFMEPYVTK(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.24 3% 0.70% 78.3 4.31E+05 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.23 3% 0.70% 69.2 3.41E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]

12.15 3% 0.70% 68.1 3.77E+06 (K)VVDANGNLLDR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.09 3% 0.80% 64.8 1.47E+06 (K)SDYVKDPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.05 3% 0.80% 62.8 1.35E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
12.01 3% 0.80% 67.4 1.88E+06 (K)YFSFNFER(L) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.95 3% 0.90% 69.5 1.40E+06 (K)AKVDPTDYFR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.95 3% 0.80% 70.8 4.32E+06 (K)DLLPLmASR(F) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.94 3% 0.90% 73.8 8.28E+05 (K)AKVDPTDYFR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.93 3% 0.90% 62.7 4.81E+05 (R)STKPETFAVVDMSLLR(K) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.82 3% 0.90% 64.7 4.95E+05 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.79 3% 0.90% 69.7 1.19E+06 (R)NEQTIPPLFK(X) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.73 3% 0.90% 68.7 1.29E+05 (R)SSPAYGSIWASTVR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.72 3% 0.90% 73 7.18E+05 (K)HGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.72 3% 0.90% 70.4 1.35E+06 (K)AKVDPTDYFR(N) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.65 3% 0.90% 71.1 2.55E+06 (K)DLLPLmASR(F) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.52 3% 0.90% 71.9 2.80E+05 (R)KVSLDGK(A) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.38 3% 1.00% 76.5 3.75E+05 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.37 3% 1.00% 71.1 2.25E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.37 3% 1.00% 72.3 1.09E+06 (K)DPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.34 3% 1.00% 66.4 4.49E+05 (K)HGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.3 3% 1.00% 60.8 7.61E+05 (R)KHGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.3 3% 1.00% 63.8 2.12E+05 (K)DPIAKPVWEK(I) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.21 3% 1% 73.5 1.47E+06 (K)HGLAVDNVVDAK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.19 3% 1% 78.9 5.44E+05 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.18 3% 1% 60.2 1.37E+05 (R)DMYAFmEPYVTK(N) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.17 3% 1% 62.5 2.28E+05 (R)KTmGEDYFWAIR(G) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.16 3% 1% 61.5 4.58E+04 (K)GDFLACLTK(S) C:Carbamidomethylation UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.13 3% 1% 67.8 1.04E+06 (R)KVSLDGK(A) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.09 3% 1% 63.9 1.56E+05 (R)ILAmGGTAIFEGLFLGTCK(D) C:Carbamidomethylation m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.08 3% 1% 66.8 1.67E+05 (K)VVDANGNLLDRK(T) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.03 3% 1% 61.8 2.95E+05 (K)AATAWVDSGAQLGDIYYALGK(W) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11.02 3% 1% 61.9 2.53E+05 (R)STKPETFAVVDmSLLR(K) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
11 3% 1% 68.5 3.93E+06 (R)STKPETFAVVDmSLLR(K) m:Oxidized methionine UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.97 3% 1% 80.2 1.19E+06 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.88 3% 1% 90.1 1.01E+07 (K)ISAIPDR(A) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.78 3% 1% 78.3 3.91E+05 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.76 3% 1% 74.6 4.57E+05 (K)DLLPLMASR(F) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.74 3% 1% 76.6 5.07E+05 (K)LVPVPPK(V) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.66 3% 1% 91 4.54E+06 (K)ISAIPDR(A) UG808 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]

10.66	3%	1%	74.1	1.48E+06	(K)HGLAVDNVVDAK(V)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.65	3%	1%	62.6	4.71E+04	(R)ILAmGGTAIFEGLFLGTCK(D)	C:Carbamidomethylation m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.64	3%	1%	65.4	2.86E+04	(K)EmSWVQSVAFIPMGDK(A)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.64	3%	1%	69.5	5.47E+05	(R)KHGLAVDNVVDAK(V)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.61	3%	1%	62.1	1.56E+05	(R)ILAmGGTAIFEGLFLGTCK(D)	C:Carbamidomethylation m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.59	3%	1%	75.9	7.85E+05	(K)LVPVPPK(V)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.53	3%	1%	64.6	2.34E+05	(K)AATAWVDSGAQLGDIYYALGK(W)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.52	3%	1%	69.3	7.20E+05	(R)SSPAYGSIWASTVR(N)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.49	3%	1%	67.4	1.35E+05	(K)WQQVAPSLPEDLmIR(I)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.43	3%	1%	61.2	5.90E+05	(R)QAYVNYR(D)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.33	3%	1%	69.7	4.37E+05	(K)VSLDGK(A)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.3	3%	1%	65.3	2.35E+05	(R)SSPAYGSIWASTVR(N)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.27	3%	1%	68.8	2.77E+05	(K)VTVLQMPR(S)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.23	3%	1%	85.3	6.96E+06	(K)ISAIPDR(A)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.22	3%	1%	66.1	4.06E+06	(K)VDPTDYFR(N)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.2	3%	1%	66.2	1.28E+06	(K)VDPTDYFR(N)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.13	3%	1%	60.2	1.67E+05	(K)VDPTDYFR(N)		UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.12	3%	1%	65.7	4.81E+05	(K)EmSWVQSVAFIPmGDK(A)	m:Oxidized methionine	UG808	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_10g021680 [S bicolor] >gi|241916763|gb|EER89907.1| hypothet prot SORBIDRAFT_10g021680 [S bicolor]
10.56	3%	1%	68	3.58E+05	(R)IXFREXK(I)		CL1002.c1	S.halepenseF2	unknown protein [Oryza sativa Japonica Group] >gi|52353503|gb|AAU44069.1| putative polyprotein [Oryza sativa Japonica Group]
14.24	2%	<0.1%	87	4.98E+04	(K)GYAFALK(D)		CL1110.c2	S.halepenseF1Rev	Os01g0913600 [Oryza sativa Japonica Group] >gi|113534703|dbj|BAF07086.1| Os01g0913600 [Oryza sativa Japonica Group]
13.24	2%	0.50%	82.5	1.14E+05	(K)GYAFALK(D)		CL1110.c2	S.halepenseF1Rev	Os01g0913600 [Oryza sativa Japonica Group] >gi|113534703|dbj|BAF07086.1| Os01g0913600 [Oryza sativa Japonica Group]
18.15	<0.1%	<0.1%	88.1	3.28E+05	(K)HADGTDVEEEEEDEEGNKR(I)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
17.39	<0.1%	<0.1%	91.6	4.35E+05	(R)FSFIVSNNIVSGLK(Y)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
16.2	<0.1%	<0.1%	88.4	2.80E+05	(R)FSFIVSNNIVSGLK(Y)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
16.17	<0.1%	<0.1%	72.2	4.34E+03	(K)HADGTDVEEEEEDEEGNKR(I)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
15.83	0.20%	<0.1%	84.9	3.86E+05	(R)IVVLGPQVPLK(E)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
15.7	0.20%	<0.1%	74.5	1.61E+05	(K)mmLGTFSPQLEPYVYEGEEETTPAGIFAR(G)	m:Oxidized methionine	CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
15.55	0.20%	<0.1%	82.7	1.61E+05	(R)IVVLGPQVPLK(E)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
15.48	0.20%	<0.1%	75	4.89E+05	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
15.06	0.20%	<0.1%	83.5	1.23E+05	(R)FSFIVSNNIVSGLK(Y)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
14.96	0.20%	<0.1%	80	8.96E+03	(R)FSFIVSNNIVSGLK(Y)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
14.95	0.20%	<0.1%	76.4	1.80E+05	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
14.77	0.20%	<0.1%	85.8	1.82E+05	(R)IVVLGPQVPLK(E)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
14.26	2%	<0.1%	81.2	1.00E+06	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
14.01	2%	0.30%	79.5	2.71E+05	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
14.01	2%	0.30%	62.9	1.02E+05	(K)mmLGTFSPQLEPYVYEGEEETTPAGIFAR(G)	m:Oxidized methionine	CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
14	2%	0.30%	69.9	2.61E+05	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
12.47	2%	0.60%	65.3	2.16E+05	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]

12.23	3%	0.70%	68.8	1.03E+06	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
11.92	3%	0.90%	70.8	4.24E+05	(K)HADGTDVEEEEEDEEGNKR(I)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
11.56	3%	1.00%	80.9	9.82E+04	(R)IVVLGPQVPLK(E)	CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]	
11.41	3%	1.00%	66	4.34E+05	(K)EQLELDKDDESLRR(W)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
11.34	3%	1.00%	68.9	9.08E+04	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
11.17	3%	1%	74.2	1.55E+05	(K)VLNLTILSPGRPDLVLPIPFHADEK(G)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
11.09	3%	1%	71.1	1.56E+04	(R)FSFIVSNNIVSGLK(Y)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
10.69	3%	1%	68.4	4.79E+05	(R)FSFIVSNNIVSGLK(Y)		CL624.c1	S.halepenseF2	hypothet prot SORBIDRAFT_09g014630 [S bicolor] >gi|241944867|gb|EES18012.1| hypothet prot SORBIDRAFT_09g014630 [S bicolor]
16.08	<0.1%	<0.1%	89.1	1.48E+05	(R)VVVLGPQVPLK(E)	CL624.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g015030 [S bicolor] >gi|241944871|gb|EES18016.1| hypothet prot SORBIDRAFT_09g015030 [S bicolor]	
14.91	0.20%	<0.1%	74.7	1.72E+05	(R)FSFTVSNNIVSGLK(Y)		CL624.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g015030 [S bicolor] >gi|241944871|gb|EES18016.1| hypothet prot SORBIDRAFT_09g015030 [S bicolor]
14.57	2%	<0.1%	85.6	1.92E+05	(K)VLNLTILSPGRPDLVLPIPFQADDK(G)		CL624.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g015030 [S bicolor] >gi|241944871|gb|EES18016.1| hypothet prot SORBIDRAFT_09g015030 [S bicolor]
14.17	2%	0.20%	77.8	1.77E+05	(K)VLNLTILSPGRPDLVLPIPFQADDK(G)		CL624.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g015030 [S bicolor] >gi|241944871|gb|EES18016.1| hypothet prot SORBIDRAFT_09g015030 [S bicolor]
13.01	2%	0.60%	67.8	6.32E+04	(K)VLNLTILSPGRPDLVLPIPFQADDK(G)		CL624.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g015030 [S bicolor] >gi|241944871|gb|EES18016.1| hypothet prot SORBIDRAFT_09g015030 [S bicolor]
12.43	2%	0.60%	77.6	1.43E+05	(K)DGSLYSFR(F)	CL624.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g015030 [S bicolor] >gi|241944871|gb|EES18016.1| hypothet prot SORBIDRAFT_09g015030 [S bicolor]	
11.91	3%	0.90%	61.1	1.84E+04	(K)VLNLTILSPGRPDLVLPIPFQADDK(G)		CL624.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g015030 [S bicolor] >gi|241944871|gb|EES18016.1| hypothet prot SORBIDRAFT_09g015030 [S bicolor]
10.18	3%	1%	66	2.12E+05	(K)DGSLYSFR(F)	CL624.c2	S.halepenseF2	hypothet prot SORBIDRAFT_09g015030 [S bicolor] >gi|241944871|gb|EES18016.1| hypothet prot SORBIDRAFT_09g015030 [S bicolor]	
16.51	<0.1%	<0.1%	83.4	3.26E+05	(K)TIFHLNPSGR(F)	CL1260.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_09g002840 [S bicolor] >gi|241944520|gb|EES17665.1| hypothet prot SORBIDRAFT_09g002840 [S bicolor]	
13.03	2%	0.60%	74.8	2.22E+05	(K)TIFHLNPSGR(F)	CL1260.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_09g002840 [S bicolor] >gi|241944520|gb|EES17665.1| hypothet prot SORBIDRAFT_09g002840 [S bicolor]	
12.98	2%	0.60%	72.1	1.43E+05	(K)TIFHLNPSGR(F)	CL1260.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_09g002840 [S bicolor] >gi|241944520|gb|EES17665.1| hypothet prot SORBIDRAFT_09g002840 [S bicolor]	
10.38	3%	1%	72.9	1.29E+05	(K)TIFHLNPSGR(F)	CL1260.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_09g002840 [S bicolor] >gi|241944520|gb|EES17665.1| hypothet prot SORBIDRAFT_09g002840 [S bicolor]	
17.35	<0.1%	<0.1%	79.7	2.44E+05	(R)FVIGGPHGDAGLTGR(K)		CL1260.c3	S.halepenseF2	hypothet prot SORBIDRAFT_03g011930 [S bicolor] >gi|241929680|gb|EES02825.1| hypothet prot SORBIDRAFT_03g011930 [S bicolor]
16.76	<0.1%	<0.1%	79	2.03E+05	(R)FVIGGPHGDAGLTGR(K)		CL1260.c3	S.halepenseF2	hypothet prot SORBIDRAFT_03g011930 [S bicolor] >gi|241929680|gb|EES02825.1| hypothet prot SORBIDRAFT_03g011930 [S bicolor]
16.36	<0.1%	<0.1%	77	3.01E+05	(R)FVIGGPHGDAGLTGR(K)		CL1260.c3	S.halepenseF2	hypothet prot SORBIDRAFT_03g011930 [S bicolor] >gi|241929680|gb|EES02825.1| hypothet prot SORBIDRAFT_03g011930 [S bicolor]
13.93	2%	0.30%	72.8	2.75E+05	(R)FVIGGPHGDAGLTGR(K)		CL1260.c3	S.halepenseF2	hypothet prot SORBIDRAFT_03g011930 [S bicolor] >gi|241929680|gb|EES02825.1| hypothet prot SORBIDRAFT_03g011930 [S bicolor]
10.07	5%	1%	64.1	3.19E+05	(K)IWEAK(F)	UG287	S.halepenseF2Rev	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]	
23.59	<0.1%	<0.1%	89.2	4.36E+05	(R)VWVFSGDLDAmVPVIATK(Q)	m:Oxidized methionine	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
23.35	<0.1%	<0.1%	94.4	3.84E+05	(R)DTAYNQLGNIDVYNIYSGTCHDK(N)	C:Carbamidomethylation	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
21.43	<0.1%	<0.1%	96	9.95E+05	(K)DPEVAGYVIEYK(G)	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]	
21.4	<0.1%	<0.1%	95.8	6.68E+05	(K)DAAFQQYSGYVNLGDK(A)		UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
20.96	<0.1%	<0.1%	88.4	7.86E+05	(R)VWVFSGDLDAmVPVIATK(Q)	m:Oxidized methionine	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
20.45	<0.1%	<0.1%	82.6	3.32E+04	(K)VKPTGSNCmDLADPCAQYYVEAYLNQPEVLK(V)	C:Carbamidomethylation m:Oxidized methionine	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
18.97	<0.1%	<0.1%	82.8	1.17E+06	(R)DTAYNQLGNIDVYNIYSGTCHDK(N)	C:Carbamidomethylation	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
18.49	<0.1%	<0.1%	80.2	8.24E+05	(R)VWVFSGDLDAmVPVIATK(Q)	m:Oxidized methionine	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
18.46	<0.1%	<0.1%	79.7	1.53E+04	(R)VWVFSGDLDAmVPVIATK(Q)	m:Oxidized methionine	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
17.16	<0.1%	<0.1%	89.8	6.06E+05	(K)DPEVAGYVIEYK(G)	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]	
17.01	<0.1%	<0.1%	83	1.44E+06	(K)NAEDNSPLCSGAR(D)	C:Carbamidomethylation	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
16.85	<0.1%	<0.1%	78.1	3.23E+05	(K)DAAFQQYSGYVNLGDK(A)		UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
16.8	<0.1%	<0.1%	81.9	2.67E+05	(R)GSGHmVPIDSPAR(G)	m:Oxidized methionine	UG287	S.halepenseF3	hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]

16.8 <0.1% <0.1% 89.5 3.81E+05 (K)GRDFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
16.01 <0.1% <0.1% 87.7 7.85E+05 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
15.8 0.20% <0.1% 86.8 4.92E+05 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
15.78 0.20% <0.1% 82.2 6.55E+05 (R)DFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
15.65 0.20% <0.1% 90.5 1.13E+05 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
15.62 0.20% <0.1% 85.4 1.25E+06 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
15.29 0.20% <0.1% 74.4 5.46E+05 (R)VWVFSGDLDAmVPVIATK(Q) m:Oxidized methionine UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
15.03 0.20% <0.1% 74.2 1.34E+05 (R)DFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
14.87 0.20% <0.1% 86.7 1.12E+06 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
14.84 0.20% <0.1% 84.8 1.05E+05 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
14.83 0.20% <0.1% 85.1 1.84E+06 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
14.81 0.20% <0.1% 76.6 2.85E+05 (R)DFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
14.62 2% <0.1% 70.3 1.21E+06 (R)DFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
14.6 2% <0.1% 76.3 7.80E+05 (K)NAEDNSPLCSGAR(D) C:Carbamidomethylation UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
14.32 2% <0.1% 80.6 1.35E+05 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
14.22 2% <0.1% 71.3 4.70E+05 (K)LGLGVVADWRPWSIDPK(D) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.96 2% 0.30% 85 2.53E+06 (K)IAALPGQPK(D) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.91 2% 0.40% 83.5 1.35E+06 (K)IAALPGQPK(D) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.82 2% 0.50% 75 3.87E+05 (R)VWVFSGDLDAMVPVIATK(Q) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.8 2% 0.50% 76.5 1.33E+05 (R)DFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.69 2% 0.50% 64.2 1.16E+05 (R)VWVFSGDLDAMVPVIATK(Q) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.6 2% 0.50% 77.9 1.30E+05 (K)IAALPGQPK(D) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.53 2% 0.50% 82.3 6.07E+04 (K)DPEVAGYVIEYK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.5 2% 0.50% 80.8 6.18E+05 (K)GRDFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.47 2% 0.50% 70.3 2.63E+05 (K)WLDRFPEYK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
13.33 2% 0.50% 77.5 1.23E+06 (K)FGDSPTK(S) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.95 2% 0.60% 74.4 1.20E+06 (K)LGLGVVADWRPWSIDPK(D) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.91 2% 0.60% 74.8 1.14E+05 (R)DTAYNQLGNIDVYNIYSGTCHDK(N) C:Carbamidomethylation UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.88 2% 0.60% 72.9 2.09E+04 (R)DFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.79 2% 0.60% 86.1 2.92E+05 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.55 2% 0.60% 72.1 1.56E+05 (K)NAEDNSPLCSGAR(D) C:Carbamidomethylation UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.49 2% 0.60% 72.7 6.04E+05 (K)FGDSPTK(S) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.42 2% 0.60% 70 5.97E+05 (R)GSGHmVPIDSPAR(G) m:Oxidized methionine UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.27 2% 0.70% 64.6 1.29E+05 (R)DFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
12.26 2% 0.70% 69.3 5.74E+04 (K)NAEDNSPLCSGAR(D) C:Carbamidomethylation UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
11.95 3% 0.80% 64.6 1.05E+06 (R)DTAYNQLGNIDVYNIYSGTCHDK(N) C:Carbamidomethylation UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
11.85 3% 0.90% 72.7 8.97E+04 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
11.79 3% 0.90% 77.3 1.14E+06 (K)GVVFATVR(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]

11.64 3% 0.90% 73.5 7.84E+04 (R)GLALFSSFIK(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
11.55 3% 1.00% 69 6.70E+05 (K)EADKIAALPGQPK(D) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
11.54 3% 0.90% 74.9 1.89E+06 (K)GEPLPK(A) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
11.19 3% 1% 77.7 2.05E+06 (K)GVVFATVR(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
11.08 3% 1% 65.4 3.27E+04 (K)VKPTGSNCmDLADPCAQYYVEAYLNQPEVLK(V) C:Carbamidomethylation m:Oxidized methionine UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
10.89 3% 1% 75.1 2.11E+06 (K)TLCNFK(Y) C:Carbamidomethylation UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
10.82 3% 1% 62.8 4.80E+05 (K)NAEDNSPLCSGAR(D) C:Carbamidomethylation UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
10.72 3% 1% 61.4 3.32E+05 (K)GVVFATVR(G) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
10.48 3% 1% 66 8.73E+04 (K)FGDSPTK(S) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
10.43 3% 1% 64.6 1.13E+06 (K)GEPLPK(A) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
10.37 3% 1% 64.5 4.50E+04 (R)DFFIVGESYAGHYVPELATAIIAAK(N) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
10.36 3% 1% 79.4 2.25E+06 (K)AVVAGGVR(V) UG287 S.halepenseF3 hypothet prot SORBIDRAFT_01g044390 [S bicolor] >gi|241922209|gb|EER95353.1| hypothet prot SORBIDRAFT_01g044390 [S bicolor]
16.46 <0.1% <0.1% 84.1 1.45E+05 (K)NAVFGDSSALAPGGVR(I) CL599.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_05g014880 [S bicolor] >gi|241935307|gb|EES08452.1| hypothet prot SORBIDRAFT_05g014880 [S bicolor]
15.51 0.20% <0.1% 74.8 2.04E+05 (R)ImGLDLPSGGHLTHGYYTAGGK(K) m:Oxidized methionine CL599.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_05g014880 [S bicolor] >gi|241935307|gb|EES08452.1| hypothet prot SORBIDRAFT_05g014880 [S bicolor]
10.49 3% 1% 60.7 7.52E+04 (K)ISATSIYFESLPYK(V) CL599.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_05g014880 [S bicolor] >gi|241935307|gb|EES08452.1| hypothet prot SORBIDRAFT_05g014880 [S bicolor]
10.31 3% 1% 68.4 1.96E+05 (R)IGAPAmTSR(G) m:Oxidized methionine CL599.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_05g014880 [S bicolor] >gi|241935307|gb|EES08452.1| hypothet prot SORBIDRAFT_05g014880 [S bicolor]
11.6 3% 0.90% 84 1.44E+07 (R)LIATSVPR(H) CL1005.c1 S.halepenseF2Rev PREDICTED: uncharacterized protein LOC100839960 [Brachypodium distachyon]
13.19 2% 0.50% 75.9 1.25E+05 (K)HVHAAAAAAAAASK(A) CL417.c2 S.halepenseF2 hypothet prot SORBIDRAFT_05g012740 [S bicolor] >gi|241936552|gb|EES09697.1| hypothet prot SORBIDRAFT_05g012740 [S bicolor]
16.11 <0.1% <0.1% 82 2.72E+05 (K)VIEETNESWEK(L) UG4514 S.halepenseF3 hypothet prot SORBIDRAFT_04g034340 [S bicolor] >gi|241932717|gb|EES05862.1| hypothet prot SORBIDRAFT_04g034340 [S bicolor]
15.68 0.20% <0.1% 87.5 1.01E+05 (K)IPDGKPANR(F) UG4514 S.halepenseF3 hypothet prot SORBIDRAFT_04g034340 [S bicolor] >gi|241932717|gb|EES05862.1| hypothet prot SORBIDRAFT_04g034340 [S bicolor]
15.17 0.20% <0.1% 86.3 3.20E+05 (K)IVAISLDDPK(A) UG4514 S.halepenseF3 hypothet prot SORBIDRAFT_04g034340 [S bicolor] >gi|241932717|gb|EES05862.1| hypothet prot SORBIDRAFT_04g034340 [S bicolor]
12.83 2% 0.60% 77.6 3.83E+05 (K)AQGQPETLDYR(V) UG4514 S.halepenseF3 hypothet prot SORBIDRAFT_04g034340 [S bicolor] >gi|241932717|gb|EES05862.1| hypothet prot SORBIDRAFT_04g034340 [S bicolor]
22.84 <0.1% <0.1% 90.2 5.54E+05 (R)VLYSSVVYPHNYGFIPR(T) UG1505 S.halepenseF1 soluble inorganic pyrophosphatase [Zea mays] >gi|195625074|gb|ACG34367.1| soluble inorganic pyrophosphatase [Zea mays]
20.32 <0.1% <0.1% 85.7 7.66E+05 (R)VLYSSVVYPHNYGFIPR(T) UG1505 S.halepenseF1 soluble inorganic pyrophosphatase [Zea mays] >gi|195625074|gb|ACG34367.1| soluble inorganic pyrophosphatase [Zea mays]
13 2% 0.60% 72.4 1.44E+05 (K)IIAVCADDPEYR(H) C:Carbamidomethylation UG1505 S.halepenseF1 soluble inorganic pyrophosphatase [Zea mays] >gi|195625074|gb|ACG34367.1| soluble inorganic pyrophosphatase [Zea mays]
16.8 <0.1% <0.1% 74.1 9.06E+04 (R)SWQFLGLAGPGGVPR(G) CL459.c2 S.halepenseF1Rev hypothet prot OsI_06255 [Oryza sativa Indica Group]
14.37 2% <0.1% 77.3 1.31E+05 (R)SWQFLGLAGPGGVPR(G) CL459.c2 S.halepenseF1Rev hypothet prot OsI_06255 [Oryza sativa Indica Group]
18.02 <0.1% <0.1% 77.3 2.79E+05 (R)ALNPGLVYDLGDKDYLDFLCALK(Y) C:Carbamidomethylation UG1234 S.halepenseF1 hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
16.22 <0.1% <0.1% 80 2.76E+05 (R)EFPSYIVYDR(T) UG1234 S.halepenseF1 hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
15.79 0.20% <0.1% 70.5 1.80E+05 (K)DAQLCmIGALDPAK(V) C:Carbamidomethylation m:Oxidized methionine UG1234 S.halepenseF1 hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
14.9 0.20% <0.1% 90.1 3.85E+05 (R)TVHPQWSPAAIK(S) UG1234 S.halepenseF1 hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
14.85 0.20% <0.1% 78 3.97E+05 (K)GQSLSITTLPEK(T) UG1234 S.halepenseF1 hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
13.84 2% 0.40% 73.2 2.53E+05 (R)VAFNSQSGTSmSCPHVSGVVGLLR(T) C:Carbamidomethylation m:Oxidized methionine UG1234 S.halepenseF1 hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
12.74 2% 0.60% 72.3 5.27E+05 (K)TSYPLIDSVK(A) UG1234 S.halepenseF1 hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
10.8 3% 1% 64.7 3.58E+03 (R)ALNPGLVYDLGDKDYLDFLCALK(Y) C:Carbamidomethylation UG1234 S.halepenseF1 hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
20.97 <0.1% <0.1% 81.3 3.84E+05 (R)TVTNVGEAVSAYTAEVVAPPSVAVEVVPPR(L) UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
18.84 <0.1% <0.1% 84.6 2.64E+06 (R)TFGLmDGTSmAAPHLSGIAAVLK(R) m:Oxidized methionine UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
17.57 <0.1% <0.1% 89 1.77E+05 (K)DLNYPSFLVTLTAAAPVVEVR(R) UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
17.43 <0.1% <0.1% 92.8 5.41E+05 (R)TVTNVGEAVSAYTAEVVAPPSVAVEVVPPR(L) UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]

14.95 0.20% <0.1% 78.8 3.78E+05 (K)SAmmTTADVTHPDGTPITDEITGKPAGHLLmGSGIVNPTK(A) m:Oxidized methionine UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
14.42 2% <0.1% 72.8 5.94E+04 (K)DLNYPSFLVTLTAAAPVVEVR(R) UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
14.15 2% 0.20% 74.3 3.75E+05 (R)TFGLmDGTSmAAPHLSGIAAVLK(R) m:Oxidized methionine UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
13.25 2% 0.50% 75.3 2.97E+05 (R)TFGLMDGTSmAAPHLSGIAAVLK(R) m:Oxidized methionine UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
13.01 2% 0.60% 68.6 2.51E+06 (K)SAmmTTADVTHPDGTPITDEITGKPAGHLLmGSGIVNPTK(A) m:Oxidized methionine UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
12.37 2% 0.60% 69 1.34E+06 (R)TFGLmDGTSmAAPHLSGIAAVLK(R) m:Oxidized methionine UG1746 S.halepenseF3 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
21 <0.1% <0.1% 92.4 2.83E+05 (R)GILKPDLIGPGVNILAGVPSIEDVDQLR(D) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
20.86 <0.1% <0.1% 93.9 6.30E+05 (R)GILKPDLIGPGVNILAGVPSIEDVDQLR(D) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
19.9 <0.1% <0.1% 88.6 1.47E+06 (K)IILCEAGGDASTAK(A) C:Carbamidomethylation UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
18.42 <0.1% <0.1% 94 1.24E+06 (R)GILKPDLIGPGVNILAGVPSIEDVDQLR(D) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
17.74 <0.1% <0.1% 83.6 6.80E+05 (K)IILCEAGGDASTAK(A) C:Carbamidomethylation UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
15.94 <0.1% <0.1% 87.8 5.58E+05 (R)GILKPDLIGPGVNILAGVPSIEDVDQLR(D) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
15.49 0.20% <0.1% 80.7 4.39E+05 (K)IILCEAGGDASTAK(A) C:Carbamidomethylation UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
15.28 0.20% <0.1% 77.2 1.65E+05 (R)GILKPDLIGPGVNILAGVPSIEDVDQLR(D) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
11.84 3% 0.90% 78.4 4.76E+05 (R)FLASVK(L) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
11.57 3% 1.00% 67.1 6.25E+05 (R)GATATFVFK(G) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
11.5 3% 1.00% 68.2 4.98E+05 (R)AHIAFYQVCYQDK(G) C:Carbamidomethylation UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
11.29 3% 1.00% 72.6 8.56E+05 (K)SPmVAPFSSR(G) m:Oxidized methionine UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
11.27 3% 1% 73.2 3.48E+05 (R)GILKPDLIGPGVNILAGVPSIEDVDQLR(D) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.71 3% 1% 73.3 8.34E+05 (R)FLASVK(L) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.48 3% 1% 79 1.64E+05 (R)DAPVPR(F) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.1 3% 1% 74.7 1.64E+05 (R)DAPVPR(F) UG2075 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.46 3% 1% 75.6 2.12E+05 (K)TLHPDWSPSAIK(S) UG3984 S.halepenseF1 hypothet prot SORBIDRAFT_10g023870 [S bicolor] >gi|241915489|gb|EER88633.1| hypothet prot SORBIDRAFT_10g023870 [S bicolor]
14.55 2% <0.1% 86.6 8.39E+05 (R)SPLVVK(T) UG7484 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g023870 [S bicolor] >gi|241915489|gb|EER88633.1| hypothet prot SORBIDRAFT_10g023870 [S bicolor]
10.49 3% 1% 64.8 2.62E+05 (K)NVGPPGTYR(V) UG7484 S.halepenseF2Rev hypothet prot SORBIDRAFT_10g023870 [S bicolor] >gi|241915489|gb|EER88633.1| hypothet prot SORBIDRAFT_10g023870 [S bicolor]
17.26 <0.1% <0.1% 89.2 2.87E+05 (K)EALEADPSAMTR(L) CL808.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
12.57 2% 0.60% 76.2 4.84E+05 (K)EALEADPSAmTR(L) m:Oxidized methionine CL808.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.77 3% 1% 65.7 5.92E+05 (R)mTPEELDK(M) m:Oxidized methionine CL808.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
23.69 <0.1% <0.1% 94.2 6.20E+05 (K)VVFCDLSESTTLR(G) C:Carbamidomethylation UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
19.78 <0.1% <0.1% 90.5 2.10E+05 (K)VVFCDLSESTTLR(G) C:Carbamidomethylation UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
18.47 <0.1% <0.1% 93.5 7.42E+05 (R)SPILVTTGALPSAAATR(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
18.22 <0.1% <0.1% 84.9 5.35E+05 (R)ALTGPVEGEIK(W) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
17.99 <0.1% <0.1% 87.1 7.93E+05 (R)ALTGPVEGEIK(W) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
17.42 <0.1% <0.1% 91.2 1.36E+06 (R)KPILDVDGEPATLLALGAGHVNPK(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
17.33 <0.1% <0.1% 90.3 2.70E+06 (R)KPILDVDGEPATLLALGAGHVNPK(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
17.28 <0.1% <0.1% 83.1 5.25E+05 (R)KPILDVDGEPATLLALGAGHVNPK(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
17.03 <0.1% <0.1% 90.6 3.68E+05 (R)SPILVTTGALPSAAATR(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
16.9 <0.1% <0.1% 85.9 2.00E+05 (R)SPILVTTGALPSAAATR(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]

15.62 0.20% <0.1% 88 4.93E+05 (K)SALmTTAEPTDNLR(K) m:Oxidized methionine UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
15.53 0.20% <0.1% 81.1 2.29E+05 (K)SALmTTAEPTDNLR(K) m:Oxidized methionine UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
14.99 0.20% <0.1% 83.2 6.99E+05 (R)KPILDVDGEPATLLALGAGHVNPK(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
14.68 2% <0.1% 82 2.41E+05 (K)ALEEVLNYSVTIK(S) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
14.36 2% <0.1% 80.4 3.93E+05 (R)AAGGVGIIFFNDASGGR(V) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
13.63 2% 0.50% 76.2 3.67E+05 (K)VVFCDLSESTTLR(G) C:Carbamidomethylation UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
12.27 2% 0.70% 76.9 9.39E+05 (K)SALmTTAEPTDNLR(K) m:Oxidized methionine UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
11.61 3% 0.90% 69.8 1.09E+06 (R)AAGGVGIIFFNDASGGR(V) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
11.54 3% 0.90% 71.8 2.01E+06 (R)KPILDVDGEPATLLALGAGHVNPK(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.84 3% 1% 78.8 4.58E+05 (R)SPILVTTGALPSAAATR(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.76 3% 1% 72.4 2.30E+05 (R)SPILVTTGALPSAAATR(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.37 3% 1% 63.5 2.77E+05 (R)KPILDVDGEPATLLALGAGHVNPK(K) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
10.28 3% 1% 70.5 1.72E+05 (K)ALEEVLNYSVTIK(S) UG1745 S.halepenseF3 hypothet prot SORBIDRAFT_06g025100 [S bicolor] >gi|241938110|gb|EES11255.1| hypothet prot SORBIDRAFT_06g025100 [S bicolor]
18.65 <0.1% <0.1% 75.9 4.29E+05 (R)TPEGGQLVYSYQHVVSGFAAR(L) UG9653 S.halepenseF1 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
18.37 <0.1% <0.1% 93.8 7.39E+05 (R)HASYGDEGmPPPPAK(W) m:Oxidized methionine UG9653 S.halepenseF1 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
15.07 0.20% <0.1% 73.5 2.99E+05 (R)NmGEGVIVGVLDNGIDPR(H) m:Oxidized methionine UG9653 S.halepenseF1 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
11.57 3% 1.00% 71.3 8.11E+05 (R)NmGEGVIVGVLDNGIDPR(H) m:Oxidized methionine UG9653 S.halepenseF1 hypothet prot SORBIDRAFT_06g002950 [S bicolor] >gi|241938719|gb|EES11864.1| hypothet prot SORBIDRAFT_06g002950 [S bicolor]
17.3 <0.1% <0.1% 83.2 5.18E+05 (K)TAGPLIIACSK(G) C:Carbamidomethylation UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
17.07 <0.1% <0.1% 87.7 1.47E+05 (K)AILVNIFGGIMK(C) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
16.4 <0.1% <0.1% 93.3 1.03E+06 (K)VPIDVFK(G) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
16.15 <0.1% <0.1% 82.4 3.21E+05 (K)AILVNIFGGImK(C) m:Oxidized methionine UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
15.34 0.20% <0.1% 72.6 1.84E+05 (K)LHGGTPANFLDVGGSASEGQVVEAFK(I) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
14.77 0.20% <0.1% 78.3 8.84E+05 (K)VYLCEK(L) C:Carbamidomethylation UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
14.4 2% <0.1% 72.8 1.07E+06 (R)GAAAGSVQEVK(D) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
13.88 2% 0.40% 73.9 7.15E+05 (K)GITDEDAAK(V) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
13.36 2% 0.50% 70.1 1.03E+05 (K)VPIDVFK(G) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
12.77 2% 0.60% 75.4 7.58E+05 (K)AEEAESIASK(M) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
12.15 3% 0.70% 73.1 5.99E+04 (K)VPVVVR(L) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
11.89 3% 0.90% 85.1 1.44E+06 (K)VPVVVR(L) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
11.58 3% 1.00% 61.1 2.58E+05 (K)LYELFCK(C) C:Carbamidomethylation UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
11.4 3% 1.00% 64.3 7.96E+05 (K)LNFDDNAAFR(Q) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
11.17 3% 1% 61.6 8.59E+04 (K)VPIDVFK(G) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
10.58 3% 1% 68.9 9.51E+05 (K)YGINVPR(G) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
10.56 3% 1% 64.8 7.80E+04 (K)VPIDVFK(G) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
10.1 3% 1% 68 3.76E+05 (R)LEGTNVDQGK(R) UG923 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g026360 [S bicolor] >gi|241932302|gb|EES05447.1| hypothet prot SORBIDRAFT_04g026360 [S bicolor]
19.16 <0.1% <0.1% 81.9 1.98E+05 (K)IIYSGGQDLDILPQGAGK(G) UG2362 S.halepenseF1 hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]
15.45 0.20% <0.1% 79.8 1.48E+05 (R)LFITQTGSDSWVVR(F) UG2362 S.halepenseF1 hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]
14.46 2% <0.1% 77.5 1.90E+05 (R)FDLWESEGDVR(V) UG2362 S.halepenseF1 hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]

13.57	2%	0.50%	70.1	2.22E+05	(K)GQALAYLLK(K)		UG2362	S.halepenseF1	hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]
13.3	2%	0.50%	77.1	1.64E+05	(K)AESPEGFVLTHIQK(T)		UG2362	S.halepenseF1	hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]
12.51	2%	0.60%	71.3	3.88E+05	(K)FYVLYEK(W)		UG2362	S.halepenseF1	hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]
12.33	2%	0.70%	65.7	2.38E+05	(K)GQALAYLLK(K)		UG2362	S.halepenseF1	hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]
11	3%	1%	70.2	4.66E+05	(R)SPTLYK(E)		UG2362	S.halepenseF1	hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]
10.17	3%	1%	67.1	2.02E+05	(K)IIYSGGQDLDILPQGAGK(G)		UG2362	S.halepenseF1	hypothet prot SORBIDRAFT_04g020180 [S bicolor] >gi|241931958|gb|EES05103.1| hypothet prot SORBIDRAFT_04g020180 [S bicolor]
11.93	3%	0.90%	80.7	1.45E+07	(R)LSSSGVSPRR(V)		UG1009	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g043900 [S bicolor] >gi|241930966|gb|EES04111.1| hypothet prot SORBIDRAFT_03g043900 [S bicolor]
11.32	3%	1.00%	80.3	1.49E+07	(R)LSSSGVSPRR(V)		UG1009	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g043900 [S bicolor] >gi|241930966|gb|EES04111.1| hypothet prot SORBIDRAFT_03g043900 [S bicolor]
11.22	3%	1%	79.1	2.01E+07	(R)LSSSGVSPRR(V)		UG1009	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g043900 [S bicolor] >gi|241930966|gb|EES04111.1| hypothet prot SORBIDRAFT_03g043900 [S bicolor]
11.18	3%	1%	78.7	1.18E+07	(R)LSSSGVSPRR(V)		UG1009	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g043900 [S bicolor] >gi|241930966|gb|EES04111.1| hypothet prot SORBIDRAFT_03g043900 [S bicolor]
10.97	3%	1%	77.3	1.34E+07	(R)LSSSGVSPRR(V)		UG1009	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g043900 [S bicolor] >gi|241930966|gb|EES04111.1| hypothet prot SORBIDRAFT_03g043900 [S bicolor]
10.67	3%	1%	75.9	5.13E+06	(R)LSSSGVSPRR(V)		UG1009	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g043900 [S bicolor] >gi|241930966|gb|EES04111.1| hypothet prot SORBIDRAFT_03g043900 [S bicolor]
10.05	5%	1%	74.6	7.30E+06	(R)LSSSGVSPRR(V)		UG1009	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_03g043900 [S bicolor] >gi|241930966|gb|EES04111.1| hypothet prot SORBIDRAFT_03g043900 [S bicolor]
17.4	<0.1%	<0.1%	79.1	3.07E+05	(R)AVVVHADPDDLGK(G)		CL1619.c1	S.halepenseF3RevF3Rev	csd1 [Pleioblastus fortunei]
16.72	<0.1%	<0.1%	83.3	2.42E+06	(R)AVVVHADPDDLGK(G)		CL1619.c1	S.halepenseF3RevF3Rev	csd1 [Pleioblastus fortunei]
11.16	3%	1%	73.4	3.51E+05	(R)AVVVHADPDDLGK(G)		CL1619.c1	S.halepenseF3RevF3Rev	csd1 [Pleioblastus fortunei]
12.3	2%	0.70%	80.8	1.00E+06	(K)AVAVLGSSEGVK(G)		CL1331.c2	S.halepenseF2Rev	"Superoxide dismutase 1, putative, expressed [Oryza sativa Japonica Group] >gi|125586252|gb|EAZ26916.1| hypothet prot OsJ_10843 [Oryza sativa Japonica Group]"
17.35	<0.1%	<0.1%	86.6	2.63E+06	(R)AIAPLFVEHAK(K)		CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
16.89	<0.1%	<0.1%	86.4	3.88E+05	(R)AIAPLFVEHAK(K)		CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
16.33	<0.1%	<0.1%	89.4	3.19E+06	(K)VDVDELK(E)		CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
15.4	0.20%	<0.1%	75.1	2.39E+05	(K)IEAmPTFHFIK(N)	m:Oxidized methionine	CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
14.41	2%	<0.1%	87	1.36E+06	(K)KYTQAVFLK(V)		CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
13.73	2%	0.50%	75	1.12E+06	(K)IEAMPTFHFIK(N)		CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
13.59	2%	0.50%	74.9	1.47E+06	(K)EVTAEYK(I)		CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
12.86	2%	0.60%	68.7	5.09E+05	(R)AIAPLFVEHAK(K)		CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
11.3	3%	1.00%	74	1.61E+06	(K)IEAmPTFHFIK(N)	m:Oxidized methionine	CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
10.28	3%	1%	79	2.10E+05	(K)IEAMPTFHFIK(N)		CL1152.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g004850 [S bicolor] >gi|241924945|gb|EER98089.1| hypothet prot SORBIDRAFT_02g004850 [S bicolor]
14.28	2%	<0.1%	81.7	3.30E+05	(R)MIAPVFAELAK(K)		UG2745	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g024960 [S bicolor] >gi|241945326|gb|EES18471.1| hypothet prot SORBIDRAFT_09g024960 [S bicolor]
12.57	2%	0.60%	79.1	8.79E+05	(K)KHPNVVFLK(V)		UG2745	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g024960 [S bicolor] >gi|241945326|gb|EES18471.1| hypothet prot SORBIDRAFT_09g024960 [S bicolor]
10.68	3%	1%	77.7	3.72E+05	(R)mIAPVFAELAK(K)	m:Oxidized methionine	UG2745	S.halepenseF1Rev	hypothet prot SORBIDRAFT_09g024960 [S bicolor] >gi|241945326|gb|EES18471.1| hypothet prot SORBIDRAFT_09g024960 [S bicolor]
19.31	<0.1%	<0.1%	84.6	7.21E+04	(R)LVATGSLDTCAIVYEIDKPATSR(I)	C:Carbamidomethylation	UG4307	S.halepenseF2	hypothet prot SORBIDRAFT_03g007500 [S bicolor] >gi|241929424|gb|EES02569.1| hypothet prot SORBIDRAFT_03g007500 [S bicolor]
19.11	<0.1%	<0.1%	90.2	2.13E+05	(R)IYSISGDTLTEEALLEK(H)		UG4307	S.halepenseF2	hypothet prot SORBIDRAFT_03g007500 [S bicolor] >gi|241929424|gb|EES02569.1| hypothet prot SORBIDRAFT_03g007500 [S bicolor]
18.93	<0.1%	<0.1%	87.1	5.50E+04	(R)IYSISGDTLTEEALLEK(H)		UG4307	S.halepenseF2	hypothet prot SORBIDRAFT_03g007500 [S bicolor] >gi|241929424|gb|EES02569.1| hypothet prot SORBIDRAFT_03g007500 [S bicolor]
14.12	2%	0.30%	67.9	3.32E+05	(R)GAITSIHYSPDVSmFASADSNR(E)	m:Oxidized methionine	UG4307	S.halepenseF2	hypothet prot SORBIDRAFT_03g007500 [S bicolor] >gi|241929424|gb|EES02569.1| hypothet prot SORBIDRAFT_03g007500 [S bicolor]
11.59	3%	1.00%	66.8	4.85E+04	(R)INSLAWSPDSR(L)		UG4307	S.halepenseF2	hypothet prot SORBIDRAFT_03g007500 [S bicolor] >gi|241929424|gb|EES02569.1| hypothet prot SORBIDRAFT_03g007500 [S bicolor]
11.94	3%	0.90%	75.8	5.87E+04	(K)EYGITVESVIAAAK(S)		CL1167.c1	S.halepenseF3	hypothet prot SORBIDRAFT_10g002220 [S bicolor] >gi|241915985|gb|EER89129.1| hypothet prot SORBIDRAFT_10g002220 [S bicolor]
18.33	<0.1%	<0.1%	76.4	5.89E+05	(K)EGATDPTFLYFAHGLK(E)		UG1559	S.halepenseF2	hypothet prot SORBIDRAFT_04g000750 [S bicolor] >gi|241932971|gb|EES06116.1| hypothet prot SORBIDRAFT_04g000750 [S bicolor]
17.73	<0.1%	<0.1%	80.5	4.14E+05	(K)EIFDGVLWEVEGK(W)		UG1559	S.halepenseF2	hypothet prot SORBIDRAFT_04g000750 [S bicolor] >gi|241932971|gb|EES06116.1| hypothet prot SORBIDRAFT_04g000750 [S bicolor]
14.28	2%	<0.1%	82	1.06E+06	(R)VVDIVDTFR(L)		UG1559	S.halepenseF2	hypothet prot SORBIDRAFT_04g000750 [S bicolor] >gi|241932971|gb|EES06116.1| hypothet prot SORBIDRAFT_04g000750 [S bicolor]

13.53 2% 0.50% 88 1.07E+06 (K)TFVTNIK(R) UG1559 S.halepenseF2 hypothet prot SORBIDRAFT_04g000750 [S bicolor] >gi|241932971|gb|EES06116.1| hypothet prot SORBIDRAFT_04g000750 [S bicolor]
12.94 2% 0.60% 76.1 3.05E+05 (R)LQEQPTFDKK(T) UG1559 S.halepenseF2 hypothet prot SORBIDRAFT_04g000750 [S bicolor] >gi|241932971|gb|EES06116.1| hypothet prot SORBIDRAFT_04g000750 [S bicolor]
12.43 2% 0.60% 70.6 3.04E+04 (K)EIFDGVLWEVEGK(W) UG1559 S.halepenseF2 hypothet prot SORBIDRAFT_04g000750 [S bicolor] >gi|241932971|gb|EES06116.1| hypothet prot SORBIDRAFT_04g000750 [S bicolor]
12.14 3% 0.70% 68.6 2.84E+05 (R)VVDIVDTFR(L) UG1559 S.halepenseF2 hypothet prot SORBIDRAFT_04g000750 [S bicolor] >gi|241932971|gb|EES06116.1| hypothet prot SORBIDRAFT_04g000750 [S bicolor]
10.71 3% 1% 76 2.69E+05 (K)TFVTNIK(R) UG1559 S.halepenseF2 hypothet prot SORBIDRAFT_04g000750 [S bicolor] >gi|241932971|gb|EES06116.1| hypothet prot SORBIDRAFT_04g000750 [S bicolor]
14.31 2% <0.1% 70.4 2.41E+05 (R)ALLGESSDFVADK(V) UG12310 S.halepenseF2Rev "triosephosphate isomerase, cytosolic [Zea mays] >gi|195608616|gb|ACG26138.1| triosephosphate isomerase, cytosolic [Zea mays]"
14.06 2% 0.30% 76.6 9.75E+04 (R)LDFAVAAQNCWVR(K) C:Carbamidomethylation UG12310 S.halepenseF2Rev "triosephosphate isomerase, cytosolic [Zea mays] >gi|195608616|gb|ACG26138.1| triosephosphate isomerase, cytosolic [Zea mays]"
23.32 <0.1% <0.1% 94.4 2.70E+06 (K)VATPAQAQEVHASLR(D) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
22.81 <0.1% <0.1% 95.6 4.53E+06 (K)VATPAQAQEVHASLR(D) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
22.23 <0.1% <0.1% 95 2.89E+05 (K)VATPAQAQEVHASLR(D) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
21.23 <0.1% <0.1% 84.2 1.55E+05 (K)VATPAQAQEVHASLR(D) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
20.63 <0.1% <0.1% 89 2.70E+06 (R)IIYGGSVTAANCK(E) C:Carbamidomethylation UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
20.35 <0.1% <0.1% 93.5 1.61E+06 (K)INVSPEVAESTR(I) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
19.88 <0.1% <0.1% 94.5 2.35E+06 (K)INVSPEVAESTR(I) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
17.84 <0.1% <0.1% 85.1 1.77E+06 (R)IIYGGSVTAANCK(E) C:Carbamidomethylation UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
17.04 <0.1% <0.1% 88.3 6.32E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
16.04 <0.1% <0.1% 85.6 5.85E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
15.95 <0.1% <0.1% 86 3.43E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
15.94 <0.1% <0.1% 78.3 1.90E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
15.8 0.20% <0.1% 87.6 1.39E+06 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
14.2 2% <0.1% 82.5 8.58E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
13.49 2% 0.50% 75.5 1.07E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
12.88 2% 0.60% 73.9 1.46E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
11.8 3% 0.90% 82.2 1.10E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
11.46 3% 1.00% 67.1 1.07E+05 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
10.37 3% 1% 66 6.22E+04 (K)ELGAQPDVDGFLVGGASLKPEFIDIINAATVK(S) UG1149 S.halepenseF1 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
20.05 <0.1% <0.1% 97.9 2.57E+05 (K)KGGAFTGEVSAEmLVNLGVPWVILGHSER(R) m:Oxidized methionine UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
19.99 <0.1% <0.1% 91.9 7.66E+05 (R)ALLGESNEFVGDK(V) UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
18.83 <0.1% <0.1% 89.6 1.55E+06 (R)ALLGESNEFVGDK(V) UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
17.25 <0.1% <0.1% 83.7 6.31E+05 (R)ALLGESNEFVGDK(V) UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
16.96 <0.1% <0.1% 88.5 3.44E+05 (K)TLNEGQVPPADVVEVVVSPPYVFLTVVK(S) UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
16.62 <0.1% <0.1% 81.9 7.07E+05 (K)FFVGGNWK(C) UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
16.12 <0.1% <0.1% 75.3 5.44E+05 (K)SLLRPEFHVAAQNCWVK(K) C:Carbamidomethylation UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
16.02 <0.1% <0.1% 88.4 3.92E+04 (K)SLLRPEFHVAAQNCWVK(K) C:Carbamidomethylation UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
14.19 2% 0.10% 87.1 1.27E+05 (K)KGGAFTGEVSAEmLVNLGVPWVILGHSER(R) m:Oxidized methionine UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
13.6 2% 0.50% 67.9 8.36E+05 (R)EAGSTMEVVAAQTK(A) UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
13.23 2% 0.50% 72.4 4.73E+05 (R)EAGSTMEVVAAQTK(A) UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
13.08 2% 0.60% 75.7 1.25E+06 (K)SLLRPEFHVAAQNCWVK(K) C:Carbamidomethylation UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]

11.07 3% 1% 67.7 1.06E+05 (K)GGAFTGEVSAEmLVNLGVPWVILGHSER(R) m:Oxidized methionine UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
10.91 3% 1% 61.1 5.02E+04 (K)VAYALSQGLK(V) UG1896 S.halepenseF2 hypothet prot SORBIDRAFT_03g006130 [S bicolor] >gi|241927175|gb|EES00320.1| hypothet prot SORBIDRAFT_03g006130 [S bicolor]
11.78 3% 0.90% 72.6 1.59E+05 (R)LVSQVISSLTASLR(F) CL291.c3 S.halepenseF1 PREDICTED: tubulin alpha-1 chain-like [Brachypodium distachyon]
11.64 3% 0.90% 72.2 1.67E+04 (R)TVELIK(T) CL291.c3 S.halepenseF2 PREDICTED: tubulin alpha-1 chain-like [Brachypodium distachyon]
10.9 3% 1% 64.8 2.62E+04 (R)AIFVDLEPTVIDEVR(T) UG520 S.halepenseF1Rev putative tubulin alpha-3 chain [Miscanthus sinensis]
10.38 3% 1% 75.1 1.02E+05 (K)IREEYPDR(M) CL597.c1 S.halepenseF1 beta-tubulin 1 [x Doritaenopsis hybrid cultivar] >gi|357528289|gb|AET80383.1| beta-tubulin 2 [x Doritaenopsis hybrid cultivar]
16.09 <0.1% <0.1% 84.9 2.01E+05 (R)LHFFmVGFAPLTSR(G) m:Oxidized methionine CL597.c6 S.halepenseF1 hypothet prot SORBIDRAFT_10g027010 [S bicolor] >gi|241917061|gb|EER90205.1| hypothet prot SORBIDRAFT_10g027010 [S bicolor]
14.17 2% 0.20% 88.2 2.67E+05 (K)LAVNLIPFPR(L) CL597.c6 S.halepenseF1 hypothet prot SORBIDRAFT_10g027010 [S bicolor] >gi|241917061|gb|EER90205.1| hypothet prot SORBIDRAFT_10g027010 [S bicolor]
14.8 0.20% <0.1% 82.5 2.65E+05 (K)VLLSICSLLTDPNPDDPLVPEIAHmYK(T) C:Carbamidomethylation m:Oxidized methionine UG1041 S.halepenseF2 ubiquitin conjugating enzyme [Zea mays] >gi|2668744|gb|AAB88617.1| ubiquitin conjugating enzyme [Zea mays]
14.32 2% <0.1% 73.5 8.04E+03 (K)VLLSICSLLTDPNPDDPLVPEIAHMYK(T) C:Carbamidomethylation UG1041 S.halepenseF2 ubiquitin conjugating enzyme [Zea mays] >gi|2668744|gb|AAB88617.1| ubiquitin conjugating enzyme [Zea mays]
11.78 3% 0.90% 71.5 1.36E+05 (K)VLLSICSLLTDPNPDDPLVPEIAHMYK(T) C:Carbamidomethylation UG1041 S.halepenseF2 ubiquitin conjugating enzyme [Zea mays] >gi|2668744|gb|AAB88617.1| ubiquitin conjugating enzyme [Zea mays]
16.63 <0.1% <0.1% 88.7 1.99E+05 (K)VFSVPEAAPFTAVLK(Y) UG2475 S.halepenseF3 unknown [Zea mays]
10.73 3% 1% 73.9 2.91E+05 (R)IAAANPEGTR(W) UG6646 S.halepenseF2 hypothet prot SORBIDRAFT_01g040860 [S bicolor] >gi|241919398|gb|EER92542.1| hypothet prot SORBIDRAFT_01g040860 [S bicolor]
12.61 2% 0.70% 66.6 2.78E+05 (K)DINALEQHIK(N) CL1141.c2 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g038770 [S bicolor] >gi|241924365|gb|EER97509.1| hypothet prot SORBIDRAFT_02g038770 [S bicolor]
12.2 3% 0.70% 69.9 2.75E+05 (K)DINALEQHIK(N) CL1141.c2 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g038770 [S bicolor] >gi|241924365|gb|EER97509.1| hypothet prot SORBIDRAFT_02g038770 [S bicolor]
16 <0.1% <0.1% 72.2 1.45E+05 (R)ISSVNAISALCEATGADITEVAHSVGR(D) C:Carbamidomethylation CL183.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g014970 [S bicolor] >gi|241918108|gb|EER91252.1| hypothet prot SORBIDRAFT_01g014970 [S bicolor]
15.89 0.20% <0.1% 74.3 1.38E+04 (R)ISSVNAISALCEATGADITEVAHSVGR(D) C:Carbamidomethylation CL183.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g014970 [S bicolor] >gi|241918108|gb|EER91252.1| hypothet prot SORBIDRAFT_01g014970 [S bicolor]
14.16 2% 0.20% 72.3 1.76E+05 (R)ISSVNAISALCEATGADITEVAHSVGR(D) C:Carbamidomethylation CL183.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g014970 [S bicolor] >gi|241918108|gb|EER91252.1| hypothet prot SORBIDRAFT_01g014970 [S bicolor]
11.94 3% 0.90% 71.9 9.55E+04 (R)IITTNLWSAELSK(L) CL183.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g014970 [S bicolor] >gi|241918108|gb|EER91252.1| hypothet prot SORBIDRAFT_01g014970 [S bicolor]
10.82 3% 1% 72.9 5.93E+04 (R)LPIYEPGLDDVVK(Q) CL183.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g014970 [S bicolor] >gi|241918108|gb|EER91252.1| hypothet prot SORBIDRAFT_01g014970 [S bicolor]
19.38 <0.1% <0.1% 91.9 2.20E+05 (K)IAVLGFAFK(K) CL183.c2 S.halepenseF1 uncharacterized protein LOC100279549 [Zea mays]
17.41 <0.1% <0.1% 85 9.41E+04 (K)IAVLGFAFK(K) CL183.c2 S.halepenseF1 uncharacterized protein LOC100279549 [Zea mays]
15.16 0.20% <0.1% 74.2 1.89E+05 (K)LAANAFLAQR(I) CL183.c2 S.halepenseF1 uncharacterized protein LOC100279549 [Zea mays]
13.68 2% 0.50% 71.1 1.69E+05 (K)LAANAFLAQR(I) CL183.c2 S.halepenseF1 uncharacterized protein LOC100279549 [Zea mays]
13.23 2% 0.50% 82.5 5.55E+04 (K)IAVLGFAFK(K) CL183.c2 S.halepenseF1 uncharacterized protein LOC100279549 [Zea mays]
10.82 3% 1% 74.8 6.63E+03 (K)IVPSEVTIK(L) CL238.c2 S.halepenseF2Rev hypothet prot SORBIDRAFT_04g034900 [S bicolor] >gi|241932743|gb|EES05888.1| hypothet prot SORBIDRAFT_04g034900 [S bicolor]
18.01 <0.1% <0.1% 84.6 3.88E+05 (R)GILAGNIFDLGSAQLAEVFAK(D) UG11738 S.halepenseF1 hypothet prot SORBIDRAFT_10g012720 [S bicolor] >gi|241915190|gb|EER88334.1| hypothet prot SORBIDRAFT_10g012720 [S bicolor]
16.04 <0.1% <0.1% 86.8 3.38E+05 (R)AENDPTVPDAPAK(A) UG11738 S.halepenseF1 hypothet prot SORBIDRAFT_10g012720 [S bicolor] >gi|241915190|gb|EER88334.1| hypothet prot SORBIDRAFT_10g012720 [S bicolor]
11.52 3% 0.90% 70.5 2.02E+05 (K)DGmSFLASCQNLVSRPWVIDDLDAFK(S) C:Carbamidomethylation m:Oxidized methionine UG11738 S.halepenseF1 hypothet prot SORBIDRAFT_10g012720 [S bicolor] >gi|241915190|gb|EER88334.1| hypothet prot SORBIDRAFT_10g012720 [S bicolor]
12.47 2% 0.60% 70.5 3.79E+05 (R)AIETNLYAQmK(C) m:Oxidized methionine UG8358 S.halepenseF1Rev hypothet prot SORBIDRAFT_10g012720 [S bicolor] >gi|241915190|gb|EER88334.1| hypothet prot SORBIDRAFT_10g012720 [S bicolor]
12.72 2% 0.60% 71.6 1.09E+05 (R)LAPAVQGVDALIILTSAVPK(M) UG1693 S.halepenseF2Rev NAD-dependent epimerase/dehydratase [Zea mays] >gi|195623630|gb|ACG33645.1| NAD-dependent epimerase/dehydratase [Zea mays]
10.05 5% 1% 65.3 1.50E+05 (R)LAPAVQGVDALIILTSAVPK(M) UG1693 S.halepenseF2Rev NAD-dependent epimerase/dehydratase [Zea mays] >gi|195623630|gb|ACG33645.1| NAD-dependent epimerase/dehydratase [Zea mays]
10.86 3% 1% 63.4 5.46E+05 (R)IEATEPASFTVK(E) UG14240 S.halepenseF1 hypothet prot SORBIDRAFT_03g000440 [S bicolor] >gi|241929022|gb|EES02167.1| hypothet prot SORBIDRAFT_03g000440 [S bicolor]
24.16 <0.1% <0.1% 94.4 8.52E+05 (R)LFDSYGVGQVGVDMPR(Q) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
23.22 <0.1% <0.1% 96.5 9.24E+05 (K)VGGTVSPQYDLSSCmQVAQEGTDGCKEPLAK(L) C:Carbamidomethylation m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.86 <0.1% <0.1% 91.6 2.48E+05 (K)VVTQQDQDVADVKK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.84 <0.1% <0.1% 89.5 2.86E+06 (K)VVTQQDQDVADVK(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.79 <0.1% <0.1% 97.8 6.52E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.63 <0.1% <0.1% 93.2 4.27E+05 (R)KVGGTVSPQYDLSSCmQVAQEGTDGCKEPLAK(L) C:Carbamidomethylation m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.43 <0.1% <0.1% 96.8 6.08E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.83 <0.1% <0.1% 82.7 2.55E+06 (R)AAITAMVSELGAYAADLRK(V) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.74 <0.1% <0.1% 89.7 1.87E+05 (K)TNGQDYELGPCIQVIQEAAK(G) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]

20.73 <0.1% <0.1% 84.8 1.95E+06 (R)LFDSYGVGQVGVDmPR(Q) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.63 <0.1% <0.1% 94 7.66E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.32 <0.1% <0.1% 92.6 1.05E+07 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.24 <0.1% <0.1% 85.7 1.20E+06 (K)VVTQQDQDVADVK(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.09 <0.1% <0.1% 90.2 4.15E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.01 <0.1% <0.1% 78.5 2.29E+06 (R)AAITAmVSELGAYAADLRK(V) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.88 <0.1% <0.1% 85.1 1.05E+06 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.86 <0.1% <0.1% 91.8 1.05E+06 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.83 <0.1% <0.1% 81.7 4.60E+06 (R)LFDSYGVGQVGVDmPR(Q) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.7 <0.1% <0.1% 84.9 5.16E+05 (R)LFDSYGVGQVGVDmPR(Q) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.7 <0.1% <0.1% 83 1.11E+06 (R)AAITAMVSELGAYAADLRK(V) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.66 <0.1% <0.1% 89 8.37E+05 (K)TNGQDYELGPCIQVIQEAAK(G) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.59 <0.1% <0.1% 87.1 5.41E+05 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.59 <0.1% <0.1% 80.3 1.11E+06 (R)AAITAMVSELGAYAADLRK(V) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.55 <0.1% <0.1% 88.8 2.36E+06 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.35 <0.1% <0.1% 80.7 6.93E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.24 <0.1% <0.1% 84.2 5.06E+05 (K)VGGTVSPQYDLSSCMQVAQEGTDGCKEPLAK(L) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.12 <0.1% <0.1% 79.9 9.56E+06 (K)VVTQQDQDVADVKK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.05 <0.1% <0.1% 80.3 6.92E+05 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.03 <0.1% <0.1% 83.3 1.27E+06 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.02 <0.1% <0.1% 87.3 2.37E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.75 <0.1% <0.1% 86 1.11E+06 (R)LFDSYGVGQVGVDMPR(Q) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.72 <0.1% <0.1% 90.5 1.13E+07 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.69 <0.1% <0.1% 78.1 2.37E+06 (R)LFDSYGVGQVGVDmPR(Q) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.49 <0.1% <0.1% 75.4 1.71E+05 (K)TNGQDYELGPCIQVIQEAAK(G) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.37 <0.1% <0.1% 86.1 1.06E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.24 <0.1% <0.1% 84 1.51E+06 (K)CDYDIADVPR(S) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.08 <0.1% <0.1% 93.4 6.95E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.08 <0.1% <0.1% 66.1 7.20E+05 (K)VVTQQDQDVADVKK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.04 <0.1% <0.1% 76.9 2.52E+05 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.9 <0.1% <0.1% 89.9 4.47E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.82 <0.1% <0.1% 77.2 8.57E+05 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.81 <0.1% <0.1% 82.8 1.71E+06 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.71 <0.1% <0.1% 84.3 4.02E+05 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.69 <0.1% <0.1% 81.3 4.93E+05 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.61 <0.1% <0.1% 83.8 2.85E+05 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.61 <0.1% <0.1% 73.6 1.88E+04 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.51 <0.1% <0.1% 81.5 9.46E+05 (K)TNGQDYELGPCIQVIQEAAK(G) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]

17.3 <0.1% <0.1% 82.2 9.13E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.25 <0.1% <0.1% 79.2 4.59E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.14 <0.1% <0.1% 78.7 3.67E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.04 <0.1% <0.1% 74.6 1.08E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.03 <0.1% <0.1% 80.5 9.50E+05 (R)AAITAmVSELGAYAADLRK(V) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.02 <0.1% <0.1% 80.6 1.09E+06 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.97 <0.1% <0.1% 80.9 5.91E+05 (K)CDYDIADVPR(S) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.95 <0.1% <0.1% 79.6 2.93E+04 (K)CDYDIADVPR(S) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.86 <0.1% <0.1% 89.9 1.49E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.74 <0.1% <0.1% 81.6 2.45E+06 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.66 <0.1% <0.1% 85.1 2.03E+05 (K)CDYDIADVPR(S) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.5 <0.1% <0.1% 78.7 1.27E+06 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.46 <0.1% <0.1% 81.5 8.26E+04 (K)VVTQQDQDVADVK(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.43 <0.1% <0.1% 80.1 2.45E+05 (K)VVTQQDQDVADVK(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.42 <0.1% <0.1% 72.1 2.37E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.41 <0.1% <0.1% 75.9 2.90E+05 (R)LFDSYGVGQVGVDmPR(Q) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.35 <0.1% <0.1% 93.6 3.59E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.34 <0.1% <0.1% 80.3 1.30E+05 (K)VVTQQDQDVADVK(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.32 <0.1% <0.1% 71.3 2.72E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.32 <0.1% <0.1% 75.5 4.22E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.26 <0.1% <0.1% 83.2 2.18E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.11 <0.1% <0.1% 76.2 1.88E+05 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.92 <0.1% <0.1% 85.9 2.36E+06 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.88 0.20% <0.1% 79.6 3.70E+06 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.78 0.20% <0.1% 82.3 5.21E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.74 0.20% <0.1% 82.7 2.05E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.67 0.20% <0.1% 73.4 2.89E+04 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.66 0.20% <0.1% 65.5 5.29E+05 (R)AAITAmVSELGAYAADLRK(V) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.56 0.20% <0.1% 84.2 7.66E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.55 0.20% <0.1% 76.1 2.52E+05 (K)KVVTQQDQDVADVK(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.52 0.20% <0.1% 89.1 6.81E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.47 0.20% <0.1% 77.8 3.09E+06 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.47 0.20% <0.1% 76.9 2.11E+05 (K)VGGTVSPQYDLSSCmQVAQEGTDGCKEPLAK(L) C:Carbamidomethylation m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.41 0.20% <0.1% 75.9 1.03E+06 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.28 0.20% <0.1% 87.6 8.50E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.25 0.20% <0.1% 83.7 9.30E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.19 0.20% <0.1% 88.4 5.20E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.19 0.20% <0.1% 78.9 2.74E+05 (K)VGGTVSPQYDLSSCmQVAQEGTDGCK(E) C:Carbamidomethylation m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]

15.15 0.20% <0.1% 79.5 3.30E+04 (R)LFDSYGVGQVGVDMPR(Q) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.14 0.20% <0.1% 76.9 4.11E+05 (R)LFDSYGVGQVGVDmPR(Q) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.14 0.20% <0.1% 73.9 1.82E+06 (K)KVVTQQDQDVADVKK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.01 0.20% <0.1% 69 1.59E+06 (K)VGGTVSPQYDLSSCmQVAQEGTDGCKEPLAK(L) C:Carbamidomethylation m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15 0.20% <0.1% 83.6 5.50E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.73 0.20% <0.1% 78.1 1.15E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.64 2% <0.1% 82.9 3.31E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.59 2% <0.1% 81.8 2.46E+05 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.4 2% <0.1% 81.6 6.53E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.25 2% <0.1% 65.2 4.16E+04 (K)VVTQQDQDVADVKK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.08 2% 0.30% 70.8 1.26E+05 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.06 2% 0.30% 77.7 4.79E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.82 2% 0.50% 82.9 1.34E+05 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.78 2% 0.50% 80.3 1.35E+05 (K)VVTQQDQDVADVK(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.71 2% 0.50% 70.5 3.91E+06 (K)VVTQQDQDVADVKK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.69 2% 0.50% 65.9 2.81E+05 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.68 2% 0.50% 73.2 3.71E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.47 2% 0.50% 70.8 7.58E+05 (R)AAITAmVSELGAYAADLR(K) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.44 2% 0.50% 76.4 5.07E+03 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.97 2% 0.60% 77.6 1.39E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.94 2% 0.60% 69.9 2.81E+05 (K)GGEAELQLNAADDQHFSK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.93 2% 0.60% 71.2 2.78E+04 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.92 2% 0.60% 76.2 6.55E+04 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.81 2% 0.60% 79.4 3.83E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.58 2% 0.60% 77.2 1.07E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.51 2% 0.60% 61.9 7.61E+04 (R)AAITAMVSELGAYAADLRK(V) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.48 2% 0.60% 68.4 1.01E+06 (R)AAITAmVSELGAYAADLRK(V) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.3 2% 0.70% 72.5 6.07E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.28 2% 0.70% 61.9 1.21E+06 (R)LFDSYGVGQVGVDmPR(Q) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.26 3% 0.70% 77.8 1.56E+06 (R)SGVTVVVAELQALAK(S) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.19 3% 0.70% 76.5 1.12E+05 (R)SQVVLNAFAALAGIVSGGGAAGTPK(X) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.99 3% 0.80% 72.5 5.74E+05 (K)VVTQQDQDVADVKK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.94 3% 0.90% 67.2 1.18E+05 (R)AAITAMVSELGAYAADLR(K) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.94 3% 0.90% 68.2 6.02E+05 (K)KVVTQQDQDVADVKK(W) UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.85 3% 0.90% 67.9 1.09E+06 (R)LFDSYGVGQVGVDmPR(Q) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.78 3% 0.90% 63.9 4.32E+05 (K)VGGTVSPQYDLSSCmQVAQEGTDGCKEPLAK(L) C:Carbamidomethylation m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.75 3% 0.90% 61.6 2.51E+05 (K)TNGQDYELGPCIQVIQEAAK(G) C:Carbamidomethylation UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.56 3% 1.00% 63.1 5.26E+05 (R)AAITAmVSELGAYAADLRK(V) m:Oxidized methionine UG325 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]

11.49	3%	1.00%	63.3	1.55E+05	(R)AAITAMVSELGAYAADLRK(V)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.33	3%	1.00%	64.3	1.65E+05	(R)SQVVLNAFAALAGIVSGGGAAGTPK(X)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.25	3%	1%	68.1	8.44E+04	(R)QGmVSSSIDASSALVNDITMAAQAQHQQQQQPADAAAAR(D)	m:Oxidized methionine	UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.21	3%	1%	65.7	5.07E+03	(R)SQVVLNAFAALAGIVSGGGAAGTPK(X)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.14	3%	1%	62.5	2.08E+05	(K)WYQDAK(N)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.12	3%	1%	65.1	3.40E+05	(K)VVTQQDQDVADVKK(W)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.09	3%	1%	64.1	3.92E+04	(K)KVVTQQDQDVADVK(K)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.99	3%	1%	67.3	6.42E+05	(R)LFDSYGVGQVGVDmPR(Q)	m:Oxidized methionine	UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.98	3%	1%	68.8	2.74E+04	(K)KWLGNIIAK(S)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.82	3%	1%	72	1.37E+06	(K)KVVTQQDQDVADVK(K)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.81	3%	1%	64.7	2.43E+05	(R)LFDSYGVGQVGVDmPR(Q)	m:Oxidized methionine	UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.74	3%	1%	83.3	5.98E+04	(R)LEEEEK(K)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.74	3%	1%	77.7	1.30E+05	(R)SGVTVVVAELQALAK(S)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.67	3%	1%	71.5	4.68E+05	(R)SGVTVVVAELQALAK(S)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.58	3%	1%	69.9	1.52E+05	(R)SQVVLNAFAALAGIVSGGGAAGTPK(X)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.35	3%	1%	61	2.84E+05	(R)AAITAmVSELGAYAADLR(K)	m:Oxidized methionine	UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.11	3%	1%	60.5	1.46E+04	(R)AAITAmVSELGAYAADLR(K)	m:Oxidized methionine	UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.03	5%	1%	61.8	6.46E+05	(R)AAITAMVSELGAYAADLRK(V)		UG325	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.15	2%	0.50%	80.3	2.91E+05	(R)SIFCIVEK(A)	C:Carbamidomethylation	UG10227	S.halepenseF2Rev	hypothet prot SORBIDRAFT_07g015140 [S bicolor] >gi|241940566|gb|EES13711.1| hypothet prot SORBIDRAFT_07g015140 [S bicolor]
12.45	2%	0.60%	64.4	6.00E+05	(R)APHFVK(V)		UG10227	S.halepenseF2Rev	hypothet prot SORBIDRAFT_07g015140 [S bicolor] >gi|241940566|gb|EES13711.1| hypothet prot SORBIDRAFT_07g015140 [S bicolor]
12.13	3%	0.70%	71.4	2.13E+05	(K)LDLNDKVNVEASK(I)		UG10227	S.halepenseF2Rev	hypothet prot SORBIDRAFT_07g015140 [S bicolor] >gi|241940566|gb|EES13711.1| hypothet prot SORBIDRAFT_07g015140 [S bicolor]
22.96	<0.1%	<0.1%	96.1	3.83E+04	(K)KLmmmEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine	CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
20.26	<0.1%	<0.1%	100	2.76E+06	(R)VEIAAAIINAAPADKK(L)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
19.92	<0.1%	<0.1%	95.1	1.20E+07	(K)AADEVIAAAPADK(L)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
19.2	<0.1%	<0.1%	95	5.41E+06	(K)SIGDLNLEVEK(V)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
19.03	<0.1%	<0.1%	83.5	1.91E+06	(R)VEIAAAIINAAPADK(K)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
18.84	<0.1%	<0.1%	91.1	1.44E+07	(K)IAQVLAAYSK(A)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
18.62	<0.1%	<0.1%	90	7.09E+06	(K)AFDGVVAAAPVEK(R)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
18.61	<0.1%	<0.1%	94.2	1.33E+07	(K)AADEVIAAAPADK(L)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
18.53	<0.1%	<0.1%	86.7	8.49E+05	(K)AFDGVVAAAPVEK(R)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
18.39	<0.1%	<0.1%	85.1	1.37E+06	(K)AADEVIAAAPADK(L)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
18.24	<0.1%	<0.1%	87.3	3.24E+04	(K)LmmmEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine	CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
18.15	<0.1%	<0.1%	86.6	1.12E+07	(K)IAQVLAAYSK(A)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
17.94	<0.1%	<0.1%	88.4	2.13E+06	(R)VEIAAAIINAAPADKK(L)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
17.87	<0.1%	<0.1%	92	8.34E+05	(K)AADEVIAAAPADK(L)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
17.62	<0.1%	<0.1%	87.7	6.91E+06	(K)AFDGVVAAAPVEK(R)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
17.58	<0.1%	<0.1%	92.5	6.57E+06	(K)VIDVVVSAAPPAK(Q)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
17.12	<0.1%	<0.1%	91.3	3.93E+06	(K)SIGDLNLEVEK(V)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]

16.41 <0.1% <0.1% 83.6 1.95E+05 (K)VIDVVVSAAPPAK(Q) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
16.29 <0.1% <0.1% 87.9 1.44E+06 (R)VEIAAAIINAAPADKK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
16.23 <0.1% <0.1% 82.6 8.34E+03 (K)LmMmEDSFNSVAAPSPLDCPTVDK(A) C:Carbamidomethylation m:Oxidized methionine CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
16.18 <0.1% <0.1% 88.1 3.65E+05 (K)AADEVIAAAPADK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
16.02 <0.1% <0.1% 87.5 1.74E+05 (K)AADEVIAAAPADK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
15.92 <0.1% <0.1% 79.6 6.17E+05 (K)AFDGVVAAAPVEK(R) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
15.86 0.20% <0.1% 87.4 6.17E+06 (K)VIDVVVSAAPPAK(Q) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
15.82 0.20% <0.1% 83.3 2.75E+05 (K)IAQVLAAYSK(A) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
15.79 0.20% <0.1% 79.7 6.31E+06 (K)TMYTAGSTINK(A) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
15.73 0.20% <0.1% 78.4 3.38E+05 (K)VIDVVVSAAPPAK(Q) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
15.62 0.20% <0.1% 82.6 2.31E+05 (K)AADEVIAAAPADK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
15.61 0.20% <0.1% 86.1 8.40E+05 (K)AADEVIAAAPADKLTImEK(T) m:Oxidized methionine CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
15.45 0.20% <0.1% 87.4 7.24E+05 (K)KIAQVLAAYSK(A) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.68 2% <0.1% 74.1 5.42E+06 (K)TMYTAGSTINK(A) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.64 2% <0.1% 66.3 2.32E+05 (R)VEIAAAIINAAPADKK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.46 2% <0.1% 75.9 3.02E+05 (R)VEIAAAIINAAPADK(K) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.43 2% <0.1% 87.7 1.32E+06 (K)VIDVVVSAAPPAK(Q) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.3 2% <0.1% 80.5 1.39E+05 (K)VIDVVVSAAPPAK(Q) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.27 2% <0.1% 75.2 5.68E+05 (K)AFDGVVAAAPVEK(R) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.17 2% 0.20% 74.2 1.60E+05 (K)IAQVLAAYSK(A) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.17 2% 0.20% 72.1 8.44E+04 (K)AYCETDSK(I) C:Carbamidomethylation CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.16 2% 0.20% 81.4 6.34E+05 (K)KTmYTAGSTINK(A) m:Oxidized methionine CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.15 2% 0.20% 75.3 1.03E+05 (K)AYCETDSK(I) C:Carbamidomethylation CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
14.03 2% 0.30% 77.7 3.08E+04 (K)AYADGDEKK(I) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.86 2% 0.40% 81.9 5.04E+05 (K)AADEVIAAAPADK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.85 2% 0.40% 84.9 7.74E+04 (K)SIGDLNLEVEK(V) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.52 2% 0.50% 73.7 2.51E+06 (K)KTmYTAGSTINK(A) m:Oxidized methionine CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.44 2% 0.50% 64.6 1.96E+04 (K)IAQVLAAYSK(A) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.26 2% 0.50% 73.7 3.09E+05 (K)AFDGVVAAAPVEK(R) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.26 2% 0.50% 64.4 5.21E+06 (K)TmYTAGSTINK(A) m:Oxidized methionine CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.13 2% 0.60% 76.1 2.92E+04 (K)AYADGDEKK(I) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.04 2% 0.60% 81.1 1.58E+06 (R)VEIAAAIINAAPADKK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.04 2% 0.60% 70.8 2.08E+06 (R)VEIAAAIINAAPADK(K) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
12.9 2% 0.60% 82.6 5.34E+06 (K)LTIMEK(T) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
12.72 2% 0.60% 81.7 1.57E+06 (K)SIGDLNLEVEK(V) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
12.31 2% 0.70% 77.2 1.98E+05 (K)AADEVIAAAPADK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
11.75 3% 0.90% 70.6 2.85E+05 (R)VEIAAAIINAAPADKK(L) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
11.7 3% 0.90% 65.6 1.14E+06 (K)KIAQVLAAYSK(A) CL2015.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]

11.61	3%	0.90%	77.8	7.91E+04	(K)AADEVIAAAPADK(L)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
11.58	3%	1.00%	79.5	5.01E+06	(K)LTIMEK(T)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
11.28	3%	1%	81.3	1.10E+06	(K)VIDVVVSAAPPAK(Q)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
11.13	3%	1%	77.1	2.54E+05	(K)SIGDLNLEVEK(V)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
11.06	3%	1%	76.5	7.75E+06	(K)LTImEK(T)	m:Oxidized methionine	CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
10.75	3%	1%	64.5	1.29E+05	(K)SIGDLNLEVEK(V)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
10.58	3%	1%	62.6	2.77E+05	(K)AADEVIAAAPADK(L)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
10.54	3%	1%	70.2	2.45E+05	(K)AADEVIAAAPADKLTIMEK(T)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
10.34	3%	1%	69.2	1.50E+05	(K)AFDGVVAAAPVEK(R)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
10.05	5%	1%	65.8	4.04E+04	(K)AYADGDEK(K)		CL2015.c1	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g018320 [S bicolor] >gi|241937758|gb|EES10903.1| hypothet prot SORBIDRAFT_06g018320 [S bicolor]
13.52	2%	0.50%	77.3	5.67E+05	(R)LDVSLALAR(V)		UG1403	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g001956 [S bicolor] >gi|241934780|gb|EES07925.1| hypothet prot SORBIDRAFT_05g001956 [S bicolor]
20.87	<0.1%	<0.1%	98.4	1.61E+06	(K)KEETIDDVFLVNQEFAPTIR(A)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
20.44	<0.1%	<0.1%	93.8	9.35E+05	(K)TECHPNAEADKPFCETVSK(L)	C:Carbamidomethylation	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
17.46	<0.1%	<0.1%	88.7	3.92E+05	(K)INEVNLTLK(K)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
17.45	<0.1%	<0.1%	92.6	5.84E+05	(K)KEETIDDVFLVNQEFAPTIR(A)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
17.07	<0.1%	<0.1%	84.3	3.74E+05	(K)TECHPNAEADKPFCETVSK(L)	C:Carbamidomethylation	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
16.83	<0.1%	<0.1%	89.3	3.68E+06	(K)TECHPNAEADKPFCETVSK(L)	C:Carbamidomethylation	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
16.39	<0.1%	<0.1%	81.8	1.04E+06	(K)TECHPNAEADKPFCETVSK(L)	C:Carbamidomethylation	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
16.07	<0.1%	<0.1%	85.5	1.55E+06	(K)INEVNLTLK(K)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
16.03	<0.1%	<0.1%	77.1	3.13E+05	(K)AYADGDEKEIAAVLATYDK(C)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
16	<0.1%	<0.1%	75.3	4.56E+04	(R)mEELFNAmAAPNHK(T)	m:Oxidized methionine	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
15.92	<0.1%	<0.1%	82.4	2.46E+06	(K)LAmSYELSAR(I)	m:Oxidized methionine	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
15.22	0.20%	<0.1%	82.4	8.14E+05	(K)CADAILAAPLAEK(F)	C:Carbamidomethylation	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
14.43	2%	<0.1%	78.2	1.85E+06	(K)KQEAIDATTK(Q)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
13.99	2%	0.30%	80	6.94E+05	(K)KVFDDVIATAPPAK(K)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
13.92	2%	0.40%	72.8	1.03E+06	(K)VFDDVIATAPPAK(K)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
13.34	2%	0.50%	76.2	2.20E+05	(R)MEELFNAMAAPNHK(T)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
13.17	2%	0.50%	61.2	1.29E+06	(K)AYADGDEKEIAAVLATYDK(C)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
13.15	2%	0.50%	81.9	5.53E+06	(K)KQEAIDATTK(Q)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
13.08	2%	0.60%	78.4	1.91E+05	(K)INEVNLTLK(K)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
13.03	2%	0.60%	77.6	5.74E+05	(K)VFDDVIATAPPAK(K)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
13.03	2%	0.60%	78.7	9.01E+05	(K)KEETIDDVFLVNQEFAPTIR(A)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
12.95	2%	0.60%	77	1.53E+05	(K)KEETIDDVFLVNQEFAPTIR(A)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
12.95	2%	0.60%	74	7.74E+05	(K)LAmSYELSAR(I)	m:Oxidized methionine	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
12.88	2%	0.60%	72.3	1.22E+06	(K)LAMSYELSAR(I)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
12.1	3%	0.70%	70.3	1.47E+06	(R)IVTETPPAmKLER(M)	m:Oxidized methionine	UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
12.08	3%	0.80%	69.2	2.17E+05	(K)INEVNLTLKK(V)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
12.02	3%	0.80%	63.4	5.87E+05	(R)MEELFNAMAAPNHK(T)		UG397	S.halepenseF1Rev	hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]

11.92 3% 0.90% 82.9 3.25E+06 (R)IVTETPPAMK(L) UG397 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
11.87 3% 0.90% 71.5 6.28E+06 (K)ESIAAASR(A) UG397 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
11.65 3% 0.90% 66.1 2.13E+05 (K)INEVNLTLK(K) UG397 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
11.24 3% 1% 66.9 2.05E+05 (R)IVTETPPAmKLER(M) m:Oxidized methionine UG397 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
10.96 3% 1% 64.4 2.07E+05 (K)AYADGDEKEIAAVLATYDK(C) UG397 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
10.54 3% 1% 60.6 2.07E+05 (K)AYADGDEKEIAAVLATYDK(C) UG397 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
10.36 3% 1% 65.8 7.74E+05 (K)ESIAAASR(A) UG397 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
10.21 3% 1% 69.2 1.02E+06 (R)MEELFNAmAAPNHK(T) m:Oxidized methionine UG397 S.halepenseF1Rev hypothet prot SORBIDRAFT_04g021750 [S bicolor] >gi|241932039|gb|EES05184.1| hypothet prot SORBIDRAFT_04g021750 [S bicolor]
22.72 <0.1% <0.1% 100 5.38E+06 (K)AADAVIAAAPADK(L) UG7877 S.halepenseF3 hypothet prot SORBIDRAFT_08g023062 [S bicolor] >gi|241944355|gb|EES17500.1| hypothet prot SORBIDRAFT_08g023062 [S bicolor]
20.01 <0.1% <0.1% 97.4 5.03E+06 (K)AADAVIAAAPADK(L) UG7877 S.halepenseF3 hypothet prot SORBIDRAFT_08g023062 [S bicolor] >gi|241944355|gb|EES17500.1| hypothet prot SORBIDRAFT_08g023062 [S bicolor]
19.53 <0.1% <0.1% 91.8 3.48E+05 (K)AADAVIAAAPADK(L) UG7877 S.halepenseF3 hypothet prot SORBIDRAFT_08g023062 [S bicolor] >gi|241944355|gb|EES17500.1| hypothet prot SORBIDRAFT_08g023062 [S bicolor]
18.46 <0.1% <0.1% 89 3.76E+05 (K)AADAVIAAAPADK(L) UG7877 S.halepenseF3 hypothet prot SORBIDRAFT_08g023062 [S bicolor] >gi|241944355|gb|EES17500.1| hypothet prot SORBIDRAFT_08g023062 [S bicolor]
14.59 2% <0.1% 81.4 1.11E+05 (K)LDQISENEK(S) CL2284.c2 S.halepenseF3RevF3Rev UDP-glucose pyrophosphorylase [Saccharum officinarum]
13.42 2% 0.50% 76.9 2.59E+05 (R)IVTEDFLPLPSK(G) CL2284.c2 S.halepenseF3RevF3Rev UDP-glucose pyrophosphorylase [Saccharum officinarum]
12.85 2% 0.60% 75.6 1.57E+05 (R)IVTEDFLPLPSK(G) CL2284.c2 S.halepenseF3RevF3Rev UDP-glucose pyrophosphorylase [Saccharum officinarum]
12.8 2% 0.60% 74.6 1.82E+05 (K)LDILLAQGK(E) CL2284.c2 S.halepenseF3RevF3Rev UDP-glucose pyrophosphorylase [Saccharum officinarum]
12.01 3% 0.80% 64.9 3.92E+04 (K)LDQISENEK(S) CL2284.c2 S.halepenseF3RevF3Rev UDP-glucose pyrophosphorylase [Saccharum officinarum]
10.22 3% 1% 63 1.42E+05 (K)SGFLSLVSR(Y) CL2284.c2 S.halepenseF3RevF3Rev UDP-glucose pyrophosphorylase [Saccharum officinarum]
24.75 <0.1% <0.1% 95.1 3.07E+06 (K)YANSSIEIHTFNQSQYPR(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
22.56 <0.1% <0.1% 87.7 3.79E+05 (K)YANSSIEIHTFNQSQYPR(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
22.4 <0.1% <0.1% 95.1 2.96E+06 (R)ANPSNPSIELGPEFK(K) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
22.1 <0.1% <0.1% 93.1 2.01E+06 (K)IFNTNNLWVNLK(A) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
22.08 <0.1% <0.1% 97.4 3.51E+06 (K)SIPSIVELDSLK(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
21.27 <0.1% <0.1% 84.4 1.90E+05 (K)YANSSIEIHTFNQSQYPR(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
20.78 <0.1% <0.1% 97.9 9.60E+05 (K)IHTPTDEVVVPYDTLESPPEDIEATK(K) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
20.75 <0.1% <0.1% 95.7 3.54E+06 (K)LEIPDGAVLENK(D) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
20.41 <0.1% <0.1% 89.6 4.41E+05 (K)IHTPTDEVVVPYDTLESPPEDIEATKK(L) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
19.99 <0.1% <0.1% 80.8 3.10E+05 (K)IFNTNNLWVNLK(A) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
19.69 <0.1% <0.1% 88.7 5.48E+05 (R)ANPSNPSIELGPEFK(K) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
19.59 <0.1% <0.1% 94.5 2.53E+06 (K)IHTPTDEVVVPYDTLESPPEDIEATKK(L) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
19.36 <0.1% <0.1% 88.9 1.04E+06 (R)FFDHAIGINVPR(S) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
19.32 <0.1% <0.1% 88.5 1.20E+06 (R)FFDHAIGINVPR(S) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
19.18 <0.1% <0.1% 95.8 2.90E+05 (K)ATSDLQLVQSDLYTLVDGFVTR(N) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
19.09 <0.1% <0.1% 96.8 6.90E+06 (R)LVEADALK(M) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.93 <0.1% <0.1% 91 2.50E+05 (K)SIPSIVELDSLK(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.91 <0.1% <0.1% 84.9 5.72E+05 (K)LNGGLGTTmGCTGPK(S) C:Carbamidomethylation m:Oxidized methionine CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.51 <0.1% <0.1% 86.8 1.11E+05 (K)SIPSIVELDSLK(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.38 <0.1% <0.1% 80.6 5.37E+05 (K)YANSSIEIHTFNQSQYPR(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.38 <0.1% <0.1% 81.7 2.40E+06 (R)VQLLEIAQVPDAHVNEFK(S) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.37 <0.1% <0.1% 86 4.33E+05 (R)ANPSNPSIELGPEFK(K) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.31 <0.1% <0.1% 86.7 1.40E+05 (R)ANPSNPSIELGPEFK(K) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]

18.18	<0.1%	<0.1%	86.4	5.71E+05	(K)IFNTNNLWVNLK(A)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.17	<0.1%	<0.1%	79.7	3.85E+05	(K)IFNTNNLWVNLK(A)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
18.01	<0.1%	<0.1%	78.5	3.03E+05	(R)VVADEFLPWPSK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.96	<0.1%	<0.1%	91.1	4.40E+06	(K)LDLLLSQGK(E)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.92	<0.1%	<0.1%	94.5	1.08E+06	(K)VLQLETAAGAAIR(F)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.85	<0.1%	<0.1%	90.2	3.15E+06	(K)VLQLETAAGAAIR(F)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.85	<0.1%	<0.1%	90.7	8.70E+05	(K)YGSNVPLLLMNSFNTHEDTLK(I)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.82	<0.1%	<0.1%	86.5	6.52E+05	(R)FFDHAIGINVPR(S)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.71	<0.1%	<0.1%	81.4	7.08E+05	(K)SIPSIVELDSLK(V)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.59	<0.1%	<0.1%	85.1	5.78E+05	(K)VLQLETAAGAAIR(F)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.58	<0.1%	<0.1%	88.5	1.00E+06	(K)SIPSIVELDSLK(V)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.58	<0.1%	<0.1%	88.7	3.14E+06	(K)SGFLSLVGR(Y)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.57	<0.1%	<0.1%	87	5.93E+06	(R)FFDHAIGINVPR(S)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.49	<0.1%	<0.1%	81	1.79E+06	(R)VQLLEIAQVPDAHVNEFK(S)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.4	<0.1%	<0.1%	87.8	9.37E+05	(K)QNEYCmEVTPK(T) C:Carbamidomethylation m:Oxidized methionine	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.27	<0.1%	<0.1%	92.7	8.65E+04	(K)LEIPDGAVLENK(D)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.22	<0.1%	<0.1%	83.3	1.34E+06	(R)EATAGLTQISDNEK(S)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.11	<0.1%	<0.1%	82.3	1.93E+05	(K)ATSDLQLVQSDLYTLVDGFVTR(N)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.09	<0.1%	<0.1%	86.6	2.76E+06	(R)EATAGLTQISDNEK(S)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
17.02	<0.1%	<0.1%	88.8	4.94E+06	(R)VQLLEIAQVPDAHVNEFK(S)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.96	<0.1%	<0.1%	83	2.05E+05	(K)LEIPDGAVLENK(D)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.9	<0.1%	<0.1%	85.1	2.33E+05	(K)ATSDLQLVQSDLYTLVDGFVTR(N)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.88	<0.1%	<0.1%	87.7	1.73E+05	(K)VLQLETAAGAAIR(F)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.56	<0.1%	<0.1%	84	1.54E+06	(K)SIPSIVELDSLK(V)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.51	<0.1%	<0.1%	85.5	6.93E+05	(K)SGFLSLVGR(Y)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.38	<0.1%	<0.1%	82.2	1.46E+06	(R)VQLLEIAQVPDAHVNEFK(S)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.38	<0.1%	<0.1%	84.4	4.41E+05	(R)ANPSNPSIELGPEFK(K)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.26	<0.1%	<0.1%	84.8	1.30E+05	(K)IHTPTDEVVVPYDTLESPPEDIEATKK(L)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.25	<0.1%	<0.1%	85.4	9.89E+05	(R)VQLLEIAQVPDAHVNEFK(S)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.2	<0.1%	<0.1%	81.1	4.83E+05	(R)VVADEFLPWPSK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
16.2	<0.1%	<0.1%	82.3	1.29E+06	(R)YLSGDEELIEWAK(I)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.95	<0.1%	<0.1%	84.9	4.97E+05	(K)VSGDVWFGSGIVLK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.87	0.20%	<0.1%	86.5	3.48E+05	(K)ATSDLQLVQSDLYTLVDGFVTR(N)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.83	0.20%	<0.1%	80.9	1.06E+06	(R)VVADEFLPWPSK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.79	0.20%	<0.1%	88.9	2.64E+05	(K)LEIPDGAVLENK(D)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.74	0.20%	<0.1%	83.9	3.40E+05	(R)ANPSNPSIELGPEFK(K)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.69	0.20%	<0.1%	73.3	1.98E+05	(R)YLSGDEELIEWAK(I)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.65	0.20%	<0.1%	80.8	1.58E+05	(R)ANPSNPSIELGPEFK(K)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor]	>gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]

15.56	0.20%	<0.1%	85	1.96E+06	(K)SGFLSLVGR(Y)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.55	0.20%	<0.1%	90	2.49E+05	(K)VLQLETAAGAAIR(F)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.5	0.20%	<0.1%	86.2	1.60E+05	(K)SGFLSLVGR(Y)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.46	0.20%	<0.1%	79	5.86E+03	(K)SIPSIVELDSLK(V)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.44	0.20%	<0.1%	82.3	1.84E+05	(K)ATSDLQLVQSDLYTLVDGFVTR(N)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.38	0.20%	<0.1%	84	1.27E+05	(K)ATSDLQLVQSDLYTLVDGFVTR(N)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.29	0.20%	<0.1%	77.6	9.32E+05	(K)VLQLETAAGAAIR(F)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.27	0.20%	<0.1%	77.5	3.68E+05	(K)YANSSIEIHTFNQSQYPR(V)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.15	0.20%	<0.1%	86.3	5.86E+05	(K)VSGDVWFGSGIVLK(G)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.13	0.20%	<0.1%	67.6	1.16E+06	(R)ANPSNPSIELGPEFKK(V)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.09	0.20%	<0.1%	71	7.14E+05	(K)ILNHLIHK(Q)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.06	0.20%	<0.1%	80.5	4.12E+05	(K)LEIPDGAVLENK(D)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.06	0.20%	<0.1%	70.2	3.82E+05	(K)YANSSIEIHTFNQSQYPR(V)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15.02	0.20%	<0.1%	74.1	5.88E+05	(R)FFDHAIGINVPR(S)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15	0.20%	<0.1%	77.7	7.52E+03	(K)ATSDLQLVQSDLYTLVDGFVTR(N)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
15	0.20%	<0.1%	80.7	1.06E+05	(K)YGSNVPLLLMNSFNTHEDTLK(I)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.99	0.20%	<0.1%	85.6	4.76E+05	(R)VQLLEIAQVPDAHVNEFK(S)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.96	0.20%	<0.1%	78.4	3.56E+06	(K)ILNHLIHK(Q)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.93	0.20%	<0.1%	76.1	3.53E+05	(K)IFNTNNLWVNLK(A)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.91	0.20%	<0.1%	84.9	4.87E+05	(R)LVEADALK(M)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.9	0.20%	<0.1%	66	9.76E+05	(K)YANSSIEIHTFNQSQYPR(V)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.66	2%	<0.1%	80.5	3.03E+05	(R)VVADEFLPWPSK(G)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.55	2%	<0.1%	73.8	4.97E+05	(K)VLQLETAAGAAIR(F)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.52	2%	<0.1%	85.5	2.63E+05	(K)SGFLSLVGR(Y)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.49	2%	<0.1%	66.7	5.55E+05	(K)YANSSIEIHTFNQSQYPR(V)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.48	2%	<0.1%	88.4	1.19E+06	(R)LVEADALK(M)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.48	2%	<0.1%	85.6	7.90E+05	(K)LDLLLSQGK(E)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.22	2%	<0.1%	80.2	2.76E+05	(K)LEIPDGAVLENK(D)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.21	2%	<0.1%	88.8	7.59E+05	(R)VQLLEIAQVPDAHVNEFK(S)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.1	2%	0.30%	79.3	7.25E+05	(K)SGFLSLVGR(Y)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.02	2%	0.30%	80.3	1.39E+05	(K)VLQLETAAGAAIR(F)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
14.02	2%	0.30%	74.8	1.89E+05	(R)YLSGDEELIEWAK(I)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.61	2%	0.50%	63.5	1.18E+04	(K)IFNTNNLWVNLK(A)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.56	2%	0.50%	63.1	2.52E+05	(K)RLVEADALK(M)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.49	2%	0.50%	73	1.44E+05	(R)EATAGLTQISDNEK(S)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.43	2%	0.50%	75.9	1.81E+05	(R)FFDHAIGINVPR(S)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.42	2%	0.50%	76.3	1.60E+05	(R)VVADEFLPWPSK(G)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.4	2%	0.50%	78.1	6.55E+05	(R)EATAGLTQISDNEK(S)	CL2284.c1	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]

13.35 2% 0.50% 72 1.86E+05 (R)FFDHAIGINVPR(S) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.34 2% 0.50% 78.6 5.16E+05 (K)IHTPTDEVVVPYDTLESPPEDIEATKK(L) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.27 2% 0.50% 80.2 5.03E+05 (R)LVEADALK(M) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.18 2% 0.50% 77.3 3.65E+05 (K)SGFLSLVGR(Y) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.09 2% 0.60% 71.2 3.41E+05 (K)LDLLLSQGK(E) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.02 2% 0.50% 76.3 1.37E+05 (R)VQLLEIAQVPDAHVNEFK(S) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
13.02 2% 0.50% 93.6 6.53E+06 (K)SVIEVR(N) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.79 2% 0.60% 74.9 1.95E+05 (K)SGFLSLVGR(Y) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.73 2% 0.60% 81.3 8.36E+05 (R)LVEADALK(M) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.64 2% 0.70% 68.5 3.79E+05 (K)YANSSIEIHTFNQSQYPR(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.52 2% 0.60% 80.8 3.93E+05 (R)EATAGLTQISDNEK(S) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.52 2% 0.60% 72.4 6.50E+05 (K)VLQLETAAGAAIR(F) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.5 2% 0.60% 79.1 2.02E+05 (K)SIPSIVELDSLK(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.47 2% 0.60% 68.4 3.83E+05 (R)VVADEFLPWPSK(G) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.4 2% 0.60% 67 4.62E+05 (K)mEIIPNPK(E) m:Oxidized methionine CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.3 2% 0.70% 73.5 2.95E+05 (K)SGFLSLVGR(Y) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.16 3% 0.70% 88.6 1.12E+06 (K)SVIEVR(N) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.14 3% 0.70% 71.2 4.11E+05 (K)EYVFIANSDNLGAIVDmK(I) m:Oxidized methionine CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.12 3% 0.70% 73.3 2.74E+05 (R)VQLLEIAQVPDAHVNEFK(S) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.08 3% 0.80% 78 2.02E+06 (K)YGSNVPLLLmNSFNTHEDTLK(I) m:Oxidized methionine CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
12.01 3% 0.80% 67.1 4.65E+05 (K)LDLLLSQGK(E) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.96 3% 0.80% 66.5 3.40E+04 (K)SIPSIVELDSLK(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.95 3% 0.90% 69.1 2.22E+05 (K)VLQLETAAGAAIR(F) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.74 3% 0.90% 66.8 1.35E+05 (K)QNEYCmEVTPK(T) C:Carbamidomethylation m:Oxidized methionine CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.73 3% 0.90% 63.6 4.24E+03 (K)ATSDLQLVQSDLYTLVDGFVTR(N) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.7 3% 0.90% 66.7 9.70E+05 (K)LDLLLSQGK(E) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.68 3% 0.90% 69.7 3.22E+06 (K)mEIIPNPK(E) m:Oxidized methionine CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.52 3% 0.90% 71.7 5.06E+05 (K)ILNHLIHK(Q) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.48 3% 1.00% 71.1 6.72E+05 (K)YGSNVPLLLmNSFNTHEDTLK(I) m:Oxidized methionine CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.27 3% 1% 88.4 6.69E+06 (K)TLADVK(G) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.16 3% 1% 63.7 1.81E+05 (K)YANSSIEIHTFNQSQYPR(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.16 3% 1% 74.1 1.60E+04 (K)IHTPTDEVVVPYDTLESPPEDIEATK(K) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.12 3% 1% 86 4.76E+06 (K)TLADVK(G) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
11.1 3% 1% 64.6 4.55E+05 (K)SIPSIVELDSLK(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.98 3% 1% 86.6 9.37E+05 (K)TLADVK(G) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.98 3% 1% 65.7 5.57E+04 (K)SIPSIVELDSLK(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.96 3% 1% 75.5 6.25E+06 (K)GGTLISYEGR(V) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.85 3% 1% 71.9 1.04E+05 (R)VQLLEIAQVPDAHVNEFK(S) CL2284.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]

10.77	3%	1%	79.5	2.93E+05	(K)TLADVK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.76	3%	1%	78.1	7.86E+05	(K)TLADVK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.75	3%	1%	80	7.59E+06	(R)FLPVK(A)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.72	3%	1%	65.6	1.35E+05	(K)QNEYCmEVTPK(T)	C:Carbamidomethylation m:Oxidized methionine CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.72	3%	1%	79.1	8.57E+05	(R)LVEADALK(M)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.7	3%	1%	76.9	2.73E+05	(K)TLADVK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.69	3%	1%	66.1	8.06E+04	(K)LDLLLSQGK(E)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.6	3%	1%	71.6	2.28E+05	(K)IHTPTDEVVVPYDTLESPPEDIEATKK(L)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.39	3%	1%	77.8	3.76E+05	(K)SVIEVR(N)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.37	3%	1%	70.1	4.65E+05	(K)LDLLLSQGK(E)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.34	3%	1%	72.4	2.94E+05	(K)KVGCFLSR(F)	C:Carbamidomethylation CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.32	3%	1%	65.2	3.20E+06	(R)VVADEFLPWPSK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
10.2	3%	1%	80.7	5.25E+05	(K)TLADVK(G)	CL2284.c1 S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g001320 [S bicolor] >gi|241933016|gb|EES06161.1| hypothet prot SORBIDRAFT_04g001320 [S bicolor]
24.75	<0.1%	<0.1%	100	8.10E+05	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
24.5	<0.1%	<0.1%	100	1.69E+06	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
23.76	<0.1%	<0.1%	94.5	9.30E+05	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
21.88	<0.1%	<0.1%	75.8	2.01E+06	(R)VMEQTFSAVAAAAHQPAAAAK(A)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
21.59	<0.1%	<0.1%	89.4	1.99E+06	(K)ATASGDENNFVSVAGAYEK(A)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
21.56	<0.1%	<0.1%	94.8	6.03E+06	(R)LGFTDVVLK(Q)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
20.78	<0.1%	<0.1%	93.7	3.34E+06	(R)LGFTDVVLK(Q)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
20.41	<0.1%	<0.1%	80.9	1.79E+05	(K)ATASGDENNFVSVAGAYEK(A)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
19.64	<0.1%	<0.1%	93.5	2.27E+06	(R)ALPAEWATAIK(Y)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
19.6	<0.1%	<0.1%	76.4	2.94E+06	(R)VMEQTFSAVAAAAHQPAAAAK(A)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
19.36	<0.1%	<0.1%	89	1.42E+06	(R)CTAAAAADKPFCETYAK(T)	C:Carbamidomethylation CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
19.15	<0.1%	<0.1%	100	8.59E+05	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
18.72	<0.1%	<0.1%	93	1.41E+07	(R)LATDAAINK(A)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
18.53	<0.1%	<0.1%	89.7	1.70E+05	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
17.83	<0.1%	<0.1%	91.4	4.71E+06	(R)ALPAEWATAIK(Y)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
17.57	<0.1%	<0.1%	89	6.58E+06	(R)LATDAAINK(A)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
17.33	<0.1%	<0.1%	62.6	1.72E+06	(R)VmEQTFSAVAAAAHQPAAAAK(A)	m:Oxidized methionine CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
17.32	<0.1%	<0.1%	93.6	8.34E+06	(K)AADAVIAASPANK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
16.72	<0.1%	<0.1%	83.1	4.60E+05	(R)CTAAAAADKPFCETYAK(T)	C:Carbamidomethylation CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
16.71	<0.1%	<0.1%	89.9	4.88E+06	(K)AADAVIAASPANK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
16.7	<0.1%	<0.1%	85.7	2.14E+05	(R)LGFTDVVLK(Q)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
16.38	<0.1%	<0.1%	84.4	2.51E+05	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
16.31	<0.1%	<0.1%	72.1	1.18E+05	(R)VMEQTFSAVAAAAHQPAAAAK(A)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
16.14	<0.1%	<0.1%	86.5	5.50E+06	(K)AFAGVIATGDSPR(T)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
15.94	<0.1%	<0.1%	88.9	1.30E+05	(K)AADAVIAASPANK(L)	CL962.c1 S.halepenseF1	hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]

15.93 <0.1% <0.1% 65.8 1.53E+06 (R)VmEQTFSAVAAAAHQPAAAAK(A) m:Oxidized methionine CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
15.74 0.20% <0.1% 81.9 7.82E+03 (K)ILAAYAQAADAVAAAAPPEK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
15.67 0.20% <0.1% 84.4 2.72E+04 (K)ILAAYAQAADAVAAAAPPEK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
15.32 0.20% <0.1% 80.9 2.84E+06 (K)ILAAYAQAADAVAAAAPPEK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
15.24 0.20% <0.1% 82.7 9.88E+04 (R)LGFTDVVLK(Q) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
15.12 0.20% <0.1% 80.9 1.63E+05 (K)ILAAYAQAADAVAAAAPPEK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
15.09 0.20% <0.1% 88.3 3.36E+05 (K)RSEAVEAVLQQQLNmDVSLGK(A) m:Oxidized methionine CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
14.78 0.20% <0.1% 85.1 7.73E+04 (K)RSEAVEAVLQQQLNMDVSLGK(A) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
14.48 2% <0.1% 69.5 1.32E+06 (K)ATASGDENNFVSVAGAYEK(A) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
14.48 2% <0.1% 83.8 1.20E+05 (K)AADAVIAASPANK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
14.43 2% <0.1% 71.8 1.15E+05 (R)LGFTDVVLK(Q) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
14.13 2% 0.30% 73.6 2.64E+06 (R)CTAAAAADKPFCETYAK(T) C:Carbamidomethylation CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
13.98 2% 0.30% 72.8 2.65E+05 (K)ILAAYAQAADAVAAAAPPEK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
13.96 2% 0.30% 74.7 4.81E+05 (K)ATASGDENNFVSVAGAYEK(A) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
13.77 2% 0.50% 68.4 3.41E+05 (K)AFAGVIATGDSPR(T) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
13.73 2% 0.50% 78.2 4.99E+06 (K)AFAGVIATGDSPR(T) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
13.6 2% 0.50% 78.3 2.25E+05 (R)SEAVEAVLQQQLNmDVSLGK(A) m:Oxidized methionine CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
13.12 2% 0.60% 61.7 1.43E+05 (R)VmEQTFSAVAAAAHQPAAAAK(A) m:Oxidized methionine CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
13.09 2% 0.60% 77.1 1.43E+05 (R)SEAVEAVLQQQLNmDVSLGK(A) m:Oxidized methionine CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
12.99 2% 0.60% 65.2 1.84E+05 (R)VmEQTFSAVAAAAHQPAAAAK(A) m:Oxidized methionine CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
12.21 3% 0.70% 67.6 6.25E+05 (K)ATASGDENNFVSVAGAYEK(A) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
11.93 3% 0.90% 67.4 1.01E+05 (K)ILAAYAQAADAVAAAAPPEK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
11.85 3% 0.90% 61.6 1.61E+05 (K)AYAEGDKDK(I) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
11.26 3% 1% 73.4 8.19E+05 (K)AADAVIAASPANK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
10.88 3% 1% 62.9 2.24E+05 (R)VMEQTFSAVAAAAHQPAAAAK(A) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
10.8 3% 1% 74.2 2.55E+05 (K)AFAGVIATGDSPR(T) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
10.4 3% 1% 70.4 6.03E+05 (K)AADAVIAASPANK(L) CL962.c1 S.halepenseF1 hypothet prot SORBIDRAFT_05g001953 [S bicolor] >gi|241934779|gb|EES07924.1| hypothet prot SORBIDRAFT_05g001953 [S bicolor]
18.46 <0.1% <0.1% 86.5 2.23E+05 (K)LNSGDISSNVSSK(L) UG4208 S.halepenseF1 hypothet prot SORBIDRAFT_02g041640 [S bicolor] >gi|241924523|gb|EER97667.1| hypothet prot SORBIDRAFT_02g041640 [S bicolor]
14.67 2% <0.1% 85.6 1.39E+05 (K)VSAELRPVIGTLTR(L) UG4208 S.halepenseF1 hypothet prot SORBIDRAFT_02g041640 [S bicolor] >gi|241924523|gb|EER97667.1| hypothet prot SORBIDRAFT_02g041640 [S bicolor]
17.9 <0.1% <0.1% 81 1.43E+05 (K)TDYPDLCTSAITK(Q) C:Carbamidomethylation UG481 S.halepenseF1 hypothet prot SORBIDRAFT_08g018210 [S bicolor] >gi|241944053|gb|EES17198.1| hypothet prot SORBIDRAFT_08g018210 [S bicolor]
14.46 2% <0.1% 76.7 1.53E+05 (K)TDYPDLCTSAITK(Q) C:Carbamidomethylation UG481 S.halepenseF1 hypothet prot SORBIDRAFT_08g018210 [S bicolor] >gi|241944053|gb|EES17198.1| hypothet prot SORBIDRAFT_08g018210 [S bicolor]
12.65 2% 0.70% 62.2 1.00E+05 (R)TDVDTCDQGFEER(K) C:Carbamidomethylation UG481 S.halepenseF1 hypothet prot SORBIDRAFT_08g018210 [S bicolor] >gi|241944053|gb|EES17198.1| hypothet prot SORBIDRAFT_08g018210 [S bicolor]
11.4 3% 1.00% 72 1.31E+05 (K)LSSNCLAIATAAGLR(X) C:Carbamidomethylation UG481 S.halepenseF1 hypothet prot SORBIDRAFT_08g018210 [S bicolor] >gi|241944053|gb|EES17198.1| hypothet prot SORBIDRAFT_08g018210 [S bicolor]
11.04 3% 1% 77.4 2.68E+05 (R)LAMSAVR(A) UG481 S.halepenseF1 hypothet prot SORBIDRAFT_08g018210 [S bicolor] >gi|241944053|gb|EES17198.1| hypothet prot SORBIDRAFT_08g018210 [S bicolor]
15.93 <0.1% <0.1% 90 1.99E+05 (R)TVGDTVQDACSK(T) C:Carbamidomethylation UG485 S.halepenseF1 hypothet prot SORBIDRAFT_02g007560 [S bicolor] >gi|241922993|gb|EER96137.1| hypothet prot SORBIDRAFT_02g007560 [S bicolor]
12.24 3% 0.70% 79 3.49E+06 (R)VPIDPK(V) UG6359 S.halepenseF3RevF3Rev predicted protein [Hordeum vulgare subsp. vulgare]
17.45 <0.1% <0.1% 89.6 9.31E+05 (K)STDPVSGIDYK(R) CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]
15.71 0.20% <0.1% 80.4 2.07E+05 (K)EPPQFVALFQPmVILK(G) m:Oxidized methionine CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]

15.53 0.20% <0.1% 76.9 1.88E+05 (K)YVQHAVAFEGISPDVPLYK(V) CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]
15.36 0.20% <0.1% 82.9 1.26E+05 (R)ETYLVDSEFETVFGmTR(E) m:Oxidized methionine CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]
14.87 0.20% <0.1% 84.7 1.56E+06 (R)EEFYGQPR(W) CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]
12.45 2% 0.60% 74.1 2.86E+05 (K)EPPQFVALFQPmVILK(G) m:Oxidized methionine CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]
11.95 3% 0.90% 74 2.30E+05 (K)VAEFLK(T) CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]
11.86 3% 0.90% 77.4 6.96E+05 (R)EEFYGQPR(W) CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]
11.59 3% 1.00% 74.9 4.63E+05 (K)STDPVSGIDYK(R) CL623.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g034950 [S bicolor] >gi|241921691|gb|EER94835.1| hypothet prot SORBIDRAFT_01g034950 [S bicolor]
18.44 <0.1% <0.1% 87.4 4.12E+05 (R)AFVVEPAGVSVVVNPSVLK(F) UG1957 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
16.09 <0.1% <0.1% 86 2.97E+05 (R)AFVVEPAGVSVVVNPSVLK(F) UG1957 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
12.31 2% 0.70% 75.7 2.22E+05 (K)GFEVQFK(V) UG1957 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g006740 [S bicolor] >gi|241933318|gb|EES06463.1| hypothet prot SORBIDRAFT_04g006740 [S bicolor]
10.15 3% 1% 71.7 1.24E+05 (K)LGIRGQVEVQR(M) UG7267 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g022810 [S bicolor] >gi|241933821|gb|EES06966.1| hypothet prot SORBIDRAFT_04g022810 [S bicolor]
14.51 2% <0.1% 84.8 3.49E+06 (R)XCXASIVCK(X) C:Carbamidomethylation CL1058.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_04g012950 [S bicolor] >gi|241931825|gb|EES04970.1| hypothet prot SORBIDRAFT_04g012950 [S bicolor]
11.47 3% 1.00% 60.2 6.59E+04 (R)SARWSLVDmLCSWVNDYALSTIHFKImLEYK(I) C:Carbamidomethylation m:Oxidized methionine CL1298.c2 S.halepenseF1 hypothet prot SORBIDRAFT_01g046880 [S bicolor] >gi|241919698|gb|EER92842.1| hypothet prot SORBIDRAFT_01g046880 [S bicolor]
11.92 3% 0.90% 71.9 1.93E+05 (K)LDLHWR(W) CL162.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g050320 [S bicolor] >gi|241919883|gb|EER93027.1| hypothet prot SORBIDRAFT_01g050320 [S bicolor]
10.76 3% 1% 65.1 1.29E+05 (K)FASSLGVSPEDCVK(K) C:Carbamidomethylation CL1896.c1 S.halepenseF1Rev hypothet prot [Zea mays]
12.32 2% 0.70% 81.4 3.32E+06 (K)LFXYSK(Q) CL1987.c1 S.halepenseF3 hypothet prot SORBIDRAFT_05g025380 [S bicolor] >gi|241937018|gb|EES10163.1| hypothet prot SORBIDRAFT_05g025380 [S bicolor]
12.18 3% 0.70% 78.3 1.03E+06 (K)LFXYSK(Q) CL1987.c1 S.halepenseF3 hypothet prot SORBIDRAFT_05g025380 [S bicolor] >gi|241937018|gb|EES10163.1| hypothet prot SORBIDRAFT_05g025380 [S bicolor]
10.02 5% 1% 73.2 5.70E+05 (K)LFXYSK(Q) CL1987.c1 S.halepenseF3 hypothet prot SORBIDRAFT_05g025380 [S bicolor] >gi|241937018|gb|EES10163.1| hypothet prot SORBIDRAFT_05g025380 [S bicolor]
22.32 <0.1% <0.1% 98 1.56E+06 (K)VIDVVVSAAPPDK(Q) CL2015.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_08g023062 [S bicolor] >gi|241944355|gb|EES17500.1| hypothet prot SORBIDRAFT_08g023062 [S bicolor]
19.19 <0.1% <0.1% 94.3 1.14E+06 (K)VIDVVVSAAPPDK(Q) CL2015.c2 S.halepenseF1Rev hypothet prot SORBIDRAFT_08g023062 [S bicolor] >gi|241944355|gb|EES17500.1| hypothet prot SORBIDRAFT_08g023062 [S bicolor]
24.64 <0.1% <0.1% 95.6 4.19E+05 (K)LGPGASAQIFQQVGQLDR(N) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
24.22 <0.1% <0.1% 95.9 1.21E+06 (K)LGPGASAQIFQQVGQLDR(N) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
23.7 <0.1% <0.1% 92.4 9.66E+05 (K)LGVGLESHFSTPNIPYMR(S) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
21.09 <0.1% <0.1% 91.9 6.57E+05 (K)LPmWLTEVDVVK(G) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
20.97 <0.1% <0.1% 100 1.72E+05 (R)NPILFMNEFNTLEQPGDPNPTPAK(Y) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
20.01 <0.1% <0.1% 96.2 9.32E+05 (K)VIHWDVVNENLHFNFFETK(L) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
19.58 <0.1% <0.1% 91.4 1.32E+06 (K)LKLPmWLTEVDVVK(G) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
19.26 <0.1% <0.1% 84.5 3.58E+05 (K)LGVGLESHFSTPNIPYMR(S) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
18.49 <0.1% <0.1% 85.6 4.27E+05 (K)LGPGASAQIFQQVGQLDR(N) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
18.47 <0.1% <0.1% 89.1 1.63E+05 (K)LPMWLTEVDVVK(G) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
18.02 <0.1% <0.1% 84.3 5.92E+05 (K)LPMWLTEVDVVK(G) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
17.88 <0.1% <0.1% 91.5 3.37E+06 (K)VIHWDVVNENLHFNFFETK(L) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
17.44 <0.1% <0.1% 74.8 2.15E+06 (K)LGVGLESHFSTPNIPYmR(S) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
17.4 <0.1% <0.1% 83.8 4.28E+05 (K)LGVGLESHFSTPNIPYMR(S) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
16.72 <0.1% <0.1% 87.8 8.11E+05 (R)NPILFmNEFNTLEQPGDPNPTPAK(Y) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
16.42 <0.1% <0.1% 82.3 3.40E+05 (K)LKLPMWLTEVDVVK(G) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
16.09 <0.1% <0.1% 83.5 3.86E+05 (K)LGPGASAQIFQQVGQLDR(N) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
15.52 0.20% <0.1% 80.1 3.77E+05 (K)LGPGASAQIFQQVGQLDR(N) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]

15.21 0.20% <0.1% 84.3 6.00E+05 (K)VIHWDVVNENLHFNFFETK(L) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
14.95 0.20% <0.1% 71.7 1.97E+05 (K)LPmWLTEVDVVK(G) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
14.53 2% <0.1% 67.3 4.67E+05 (R)EGYGHPGVNGIVMWAAWHAK(G) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
14.3 2% <0.1% 64.2 3.44E+05 (K)LGPGASAQIFQQVGQLDR(N) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
14.07 2% 0.30% 89.8 7.72E+06 (R)SSLDTLAK(L) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.98 2% 0.30% 78.8 3.26E+05 (K)LKLPmWLTEVDVVK(G) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.8 2% 0.50% 80 1.05E+06 (K)LGPGASAQIFQQVGQLDR(N) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.73 2% 0.50% 81.1 1.54E+05 (K)VIHWDVVNENLHFNFFETK(L) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.57 2% 0.50% 67.9 8.29E+05 (K)VIHWDVVNENLHFNFFETK(L) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.56 2% 0.50% 69.4 2.67E+05 (K)LGVGLESHFSTPNIPYmR(S) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.48 2% 0.50% 71.4 1.31E+05 (K)LPmWLTEVDVVK(G) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.39 2% 0.50% 66.4 4.46E+06 (K)NLEQVLR(E) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
12.99 2% 0.60% 70.7 2.23E+05 (K)LKLPmWLTEVDVVK(G) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
12.51 2% 0.60% 71 5.38E+05 (K)LGVGLESHFSTPNIPYmR(S) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
12.38 2% 0.60% 72.6 2.15E+05 (R)NPILFmNEFNTLEQPGDPNPTPAK(Y) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
11.62 3% 0.90% 65.9 1.62E+05 (K)LKLPmWLTEVDVVK(G) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
11.62 3% 0.90% 82.7 1.45E+06 (R)SYPGNGGLK(L) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
10.94 3% 1% 66.1 1.00E+05 (K)LKLPMWLTEVDVVK(G) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
10.55 3% 1% 70.2 7.56E+04 (R)NPILFMNEFNTLEQPGDPNPTPAK(Y) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
10.2 3% 1% 60.2 2.02E+05 (K)LGPGASAQIFQQVGQLDR(N) CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
10.1 3% 1% 68.8 1.99E+05 (R)NPILFmNEFNTLEQPGDPNPTPAK(Y) m:Oxidized methionine CL2034.c1 S.halepenseF2Rev hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
27.9 <0.1% <0.1% 98.4 4.23E+06 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
25.95 <0.1% <0.1% 100 2.00E+05 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
25.79 <0.1% <0.1% 86 2.26E+06 (R)AmAGDVADQmTIVGQQHPTVASADIVAALR(L) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
22.36 <0.1% <0.1% 95.9 1.35E+06 (K)AVVEAVADAQAIDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
21.49 <0.1% <0.1% 93.6 2.30E+06 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
21.08 <0.1% <0.1% 96.1 3.12E+05 (K)AVVEAVADAQAIDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.99 <0.1% <0.1% 90.7 5.22E+06 (R)VETESQALAR(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.87 <0.1% <0.1% 96 2.97E+06 (R)VAAGVDINAR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.85 <0.1% <0.1% 94.7 5.94E+06 (R)VAAGVDINAR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.74 <0.1% <0.1% 90.5 5.43E+06 (K)AISLDAAmPENEKYELVK(G) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.73 <0.1% <0.1% 93.5 1.12E+06 (K)AIAAAEASAGPGGEAK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.72 <0.1% <0.1% 86.1 1.50E+05 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.46 <0.1% <0.1% 91.6 1.69E+06 (R)DLSTVAGNIAISmSSLAEDAVGVSGR(V) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
20.29 <0.1% <0.1% 92.3 8.01E+05 (K)AVVEAVADAQAIDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
19.99 <0.1% <0.1% 88.1 2.18E+05 (R)DLSTVAGNIAISMSSLAEDAVGVSGR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
19.92 <0.1% <0.1% 88.7 1.70E+05 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
19.9 <0.1% <0.1% 89.8 6.10E+05 (R)DLSTVAGNIAISmSSLAEDAVGVSGR(V) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]

19.52	<0.1%	<0.1%	89.4	7.07E+05	(K)AIAAAEASAGPGGEAK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
19.5	<0.1%	<0.1%	83.6	7.46E+05	(K)AVVEAVADAQAIDKAEDK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
19.38	<0.1%	<0.1%	91.1	2.41E+06	(K)AIAAAEASAGPGGEAK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
19.17	<0.1%	<0.1%	92.7	5.94E+06	(R)VAAGVDINAR(V)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
19.13	<0.1%	<0.1%	91.4	4.97E+06	(K)AIAAAEASAGPGGEAK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
18.95	<0.1%	<0.1%	91.6	5.34E+05	(K)AVVEAVADAQAIDKAEDK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
18.56	<0.1%	<0.1%	87.3	6.70E+05	(K)AIAAAEASAGPGGEAK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
18.45	<0.1%	<0.1%	83.2	2.70E+05	(R)DLSTVAGNIAISMSSLAEDAVGVSGR(V)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
18.29	<0.1%	<0.1%	85.9	2.56E+05	(R)DLSTVAGNIAISMSSLAEDAVGVSGR(V)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
18.07	<0.1%	<0.1%	91.3	2.67E+06	(R)VETESQALAR(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
17.94	<0.1%	<0.1%	94.5	7.37E+05	(K)HIQTIVVSPQIALQMK(L)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
17.83	<0.1%	<0.1%	84	6.51E+05	(K)AISLDAAmPENEK(Y) m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
17.58	<0.1%	<0.1%	82.3	3.73E+05	(R)DLSTVAGNIAISmSSLAEDAVGVSGR(V)	m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
17.37	<0.1%	<0.1%	88.7	4.96E+06	(K)AAGEATVVLK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
17.35	<0.1%	<0.1%	79	3.16E+05	(K)AVVEAVADAQAIDKAEDK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
17.2	<0.1%	<0.1%	90.1	3.81E+06	(R)VETESQALAR(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
17.07	<0.1%	<0.1%	77.7	1.43E+06	(K)ASTPDAEFSK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
16.83	<0.1%	<0.1%	83.4	1.33E+06	(R)VETESQALAR(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
16.56	<0.1%	<0.1%	85.8	9.60E+04	(R)DLSTVAGNIAISMSSLAEDAVGVSGR(V)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
16.32	<0.1%	<0.1%	87	4.27E+06	(R)LQQEILK(K)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
16.3	<0.1%	<0.1%	71.7	2.44E+06	(R)AmAGDVADQmTIVGQQHPTVASADIVAALR(L)	m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
16.25	<0.1%	<0.1%	80.6	3.37E+06	(K)ASTPDAEFSK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
16.09	<0.1%	<0.1%	86.8	4.41E+05	(K)AVVEAVADAQAIDK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
16.05	<0.1%	<0.1%	80.8	4.42E+05	(R)DLSTVAGNIAISmSSLAEDAVGVSGR(V)	m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
15.96	<0.1%	<0.1%	84.9	1.34E+05	(K)AISLDAAMPENEKYELVK(G)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
15.88	0.20%	<0.1%	63.3	1.86E+05	(R)AmAGDVADQMTIVGQQHPTVASADIVAALR(L)	m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
15.85	0.20%	<0.1%	82.2	2.10E+06	(R)DLSTVAGNIAISmSSLAEDAVGVSGR(V)	m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
15.81	0.20%	<0.1%	68.2	7.34E+05	(R)AmAGDVADQmTIVGQQHPTVASADIVAALR(L)	m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
15.79	0.20%	<0.1%	86.3	1.40E+05	(R)VAAGVDINAR(V)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
15.67	0.20%	<0.1%	80.5	6.23E+05	(K)AISLDAAmPENEKYELVK(G)	m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
15.18	0.20%	<0.1%	86.8	1.38E+06	(R)VAAGVDINAR(V)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
14.68	2%	<0.1%	78.1	9.69E+04	(K)AIAAAEASAGPGGEAK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
14.59	2%	<0.1%	75.7	2.01E+05	(K)AVVEAVADAQAIDK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
14.55	2%	<0.1%	87.6	3.02E+05	(K)HIQTIVVSPQIALQMK(L)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
14.51	2%	<0.1%	74.7	6.39E+05	(K)AISLDAAMPENEKYELVK(G)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
14.46	2%	<0.1%	74.3	1.70E+05	(K)AVVEAVADAQAIDKAEDK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	
14.39	2%	<0.1%	76.5	4.22E+05	(R)DLSTVAGNIAISmSSLAEDAVGVSGR(V)	m:Oxidized methionine	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.34	2%	<0.1%	75.2	8.81E+04	(K)AIAAAEASAGPGGEAK(A)	CL2521.c1 S.halepenseF1	hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]	

14.25 2% <0.1% 77.2 3.83E+05 (R)DLSTVAGNIAISmSSLAEDAVGVSGR(V) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.03 2% 0.40% 83.8 3.27E+05 (R)VAAGVDINAR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.92 2% 0.40% 86 1.49E+06 (K)HIQTIVVSPQIALQmK(L) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.77 2% 0.50% 67 3.73E+04 (R)DLSTVAGNIAISmSSLAEDAVGVSGR(V) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.6 2% 0.50% 80.1 2.09E+06 (R)LQQEILK(K) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.52 2% 0.50% 78.9 5.28E+05 (K)AISLDAAmPENEK(Y) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.52 2% 0.50% 69.1 5.31E+05 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.4 2% 0.50% 80.9 4.28E+06 (K)HIQTIVVSPQIALQmK(L) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.4 2% 0.50% 83.8 5.24E+04 (K)AISLDAAMPENEKYELVK(G) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.35 2% 0.50% 68.9 8.23E+04 (R)AmAGDVADQmTIVGQQHPTVASADIVAALR(L) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
13.3 2% 0.50% 66.9 5.04E+05 (K)ASTPDAEFSK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.83 2% 0.60% 62.5 1.03E+05 (R)DLSTVAGNIAISMSSLAEDAVGVSGR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.82 2% 0.60% 61.1 3.61E+05 (R)AmAGDVADQmTIVGQQHPTVASADIVAALR(L) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.81 2% 0.60% 69.2 2.41E+06 (K)AAGEATVVLK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.8 2% 0.60% 73.7 4.32E+05 (K)AISLDAAmPENEK(Y) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.66 2% 0.60% 70.5 7.86E+04 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.65 2% 0.60% 73.1 1.22E+06 (R)VAAGVDINAR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.52 2% 0.60% 72.9 8.14E+05 (K)AVVEAVADAQAIDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.52 2% 0.60% 77.3 2.40E+05 (K)AVVEAVADAQAIDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.38 2% 0.60% 67.9 1.20E+06 (K)AAGEATVVLK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.34 2% 0.70% 69.8 3.13E+05 (K)AISLDAAmPENEKYELVK(G) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.24 3% 0.70% 76.6 1.57E+04 (K)AISLDAAMPENEKYELVK(G) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.16 3% 0.70% 65.5 2.59E+05 (K)HIQTIVVSPQIALQmK(L) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.11 3% 0.70% 72.5 1.30E+05 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.99 3% 0.80% 77 5.90E+05 (R)DLSTVAGNIAISmSSLAEDAVGVSGR(V) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.92 3% 0.90% 68.9 1.58E+04 (K)AVVEAVADAQAIDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.85 3% 0.90% 65.8 9.18E+05 (R)VETESQALAR(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.81 3% 0.90% 63.5 6.25E+05 (K)HIQTIVVSPQIALQmK(L) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.79 3% 0.90% 73.9 4.27E+04 (R)DLSTVAGNIAISmSSLAEDAVGVSGR(V) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.72 3% 0.90% 64.5 1.92E+05 (R)AmAGDVADQMTIVGQQHPTVASADIVAALR(L) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.68 3% 0.90% 77.3 1.93E+06 (K)AISLDAAmPENEKYELVK(G) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.65 3% 0.90% 63.9 1.60E+06 (K)AAGEATVVLK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.43 3% 1.00% 75.3 2.47E+05 (K)SAEFMR(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.38 3% 1.00% 64.3 3.02E+05 (R)DLSTVAGNIAISmSSLAEDAVGVSGR(V) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
11.23 3% 1% 74.1 5.40E+05 (R)VAAGVDINAR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.98 3% 1% 60.6 1.02E+05 (R)DLSTVAGNIAISMSSLAEDAVGVSGR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.87 3% 1% 72.4 1.92E+05 (K)AISLDAAMPENEKYELVK(G) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.78 3% 1% 68.2 4.87E+04 (K)AISLDAAMPENEKYELVK(G) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]

10.6 3% 1% 64.8 6.28E+05 (K)SAEFmR(A) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.55 3% 1% 63.1 1.44E+06 (K)SAEFmR(A) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.34 3% 1% 69.3 4.37E+04 (R)DLSTVAGNIAISmSSLAEDAVGVSGR(V) m:Oxidized methionine CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.24 3% 1% 62.1 1.66E+05 (K)AVVEAVADAQAIDKAEDK(A) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.22 3% 1% 70.9 1.95E+05 (R)VAAGVDINAR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
10.17 3% 1% 68.8 4.64E+05 (R)VAAGVDINAR(V) CL2521.c1 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
15.6 0.20% <0.1% 84.8 3.56E+05 (K)ISVDATPGLVGDIK(Q) CL257.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
14.2 2% <0.1% 71.7 8.04E+04 (K)ISVDATPGLVGDIK(Q) CL257.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
13.96 2% 0.30% 80.7 1.61E+05 (K)LLLPPAVNLGWDPK(K) CL257.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
11.65 3% 0.90% 66.3 2.24E+05 (K)GESHLNSLLRPVLLVALVK(L) CL257.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
11.54 3% 0.90% 75.6 1.23E+05 (K)ISVDATPGLVGDIK(Q) CL257.c1 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
18.25 <0.1% <0.1% 88.6 2.83E+04 (K)mGAPPKPDVPVITPQELAEADGILFGFPTR(F) m:Oxidized methionine CL547.c1 S.halepenseF2 LOC100283201 [Zea mays] >gi|195628168|gb|ACG35914.1| minor allergen Alt a 7 [Zea mays]
10.63 3% 1% 74.7 9.44E+04 (K)IWQVPETLPEEVLGK(M) CL547.c1 S.halepenseF2 LOC100283201 [Zea mays] >gi|195628168|gb|ACG35914.1| minor allergen Alt a 7 [Zea mays]
13.5 2% 0.50% 76.5 2.07E+05 (K)AFFDATGGLWR(E) CL547.c2 S.halepenseF1Rev LOC100285601 [Zea mays] >gi|195651379|gb|ACG45157.1| flavoprotein wrbA [Zea mays]
16.69 <0.1% <0.1% 69.6 2.91E+05 (K)YGLDDNTIDFIGHAVALHR(D) CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
15.65 0.20% <0.1% 71.2 2.59E+05 (K)VCGVTSEGETAK(C) C:Carbamidomethylation CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
14.87 0.20% <0.1% 62.3 6.69E+05 (R)FKGEQTPPAHIGASR(D) CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
14.17 2% 0.20% 74 3.31E+05 (R)DYNVDmVPK(F) m:Oxidized methionine CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
13.68 2% 0.50% 77.9 1.94E+05 (R)DDSYLTEPAIDTVK(R) CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
13.28 2% 0.50% 75.1 4.18E+05 (R)AIAImSHPIPNTAESHSVQIILPQK(Q) m:Oxidized methionine CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
12.5 2% 0.60% 66.6 3.19E+05 (R)FQGGSPYIYPLYGLGELPQGFAR(L) CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
11.54 3% 0.90% 65 1.08E+05 (K)ELKPGIDLLGTVDELFIDTYDR(Y) CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
11.32 3% 1.00% 74.1 1.85E+05 (K)ECILSGLLSVDR(L) C:Carbamidomethylation CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
10.43 3% 1% 64.5 8.73E+05 (R)VLIHTGVTK(Y) CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
10.06 5% 1% 61.3 2.04E+04 (K)FFLYVQDYK(E) CL581.c1 S.halepenseF1Rev hypothet prot SORBIDRAFT_02g008810 [S bicolor] >gi|241925202|gb|EER98346.1| hypothet prot SORBIDRAFT_02g008810 [S bicolor]
17.77 <0.1% <0.1% 85.3 2.13E+05 (R)CEGFTSSIPVDAK(L) C:Carbamidomethylation CL641.c1 S.halepenseF2 hypothet prot SORBIDRAFT_05g018000 [S bicolor] >gi|241935375|gb|EES08520.1| hypothet prot SORBIDRAFT_05g018000 [S bicolor]
16.95 <0.1% <0.1% 85.6 2.51E+05 (K)AGVDTVFEVIVR(N) CL641.c1 S.halepenseF2 hypothet prot SORBIDRAFT_05g018000 [S bicolor] >gi|241935375|gb|EES08520.1| hypothet prot SORBIDRAFT_05g018000 [S bicolor]
16.4 <0.1% <0.1% 84.4 5.91E+05 (R)EGNDYLVDDGGR(I) CL641.c1 S.halepenseF2 hypothet prot SORBIDRAFT_05g018000 [S bicolor] >gi|241935375|gb|EES08520.1| hypothet prot SORBIDRAFT_05g018000 [S bicolor]
13.57 2% 0.50% 74.1 1.88E+05 (K)AGVDTVFEVIVR(N) CL641.c1 S.halepenseF2 hypothet prot SORBIDRAFT_05g018000 [S bicolor] >gi|241935375|gb|EES08520.1| hypothet prot SORBIDRAFT_05g018000 [S bicolor]
13.61 2% 0.50% 76.8 1.79E+05 (R)TPFFSR(V) CL694.c1 S.halepenseF3 hypothet prot SORBIDRAFT_08g000270 [S bicolor] >gi|241942348|gb|EES15493.1| hypothet prot SORBIDRAFT_08g000270 [S bicolor]
10.83 3% 1% 73.9 3.71E+05 (R)TPFFSR(V) CL694.c1 S.halepenseF3 hypothet prot SORBIDRAFT_08g000270 [S bicolor] >gi|241942348|gb|EES15493.1| hypothet prot SORBIDRAFT_08g000270 [S bicolor]
23.01 <0.1% <0.1% 92.5 2.17E+06 (K)AVmYPSILVVQGLVSGYTPPR(S) m:Oxidized methionine CL994.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
22.53 <0.1% <0.1% 97.5 4.54E+06 (K)AVmYPSILVVQGLVSGYTPPR(S) m:Oxidized methionine CL994.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.73 <0.1% <0.1% 87.7 3.71E+06 (K)AVMYPSILVVQGLVSGYTPPR(S) CL994.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.69 <0.1% <0.1% 90.7 1.20E+06 (K)AVmYPSILVVQGLVSGYTPPR(S) m:Oxidized methionine CL994.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.18 <0.1% <0.1% 87.8 8.99E+05 (K)AVMYPSILVVQGLVSGYTPPR(S) CL994.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
21.14 <0.1% <0.1% 89.5 1.05E+06 (K)AVMYPSILVVQGLVSGYTPPR(S) CL994.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.7 <0.1% <0.1% 89.9 2.11E+06 (K)AVMYPSILVVQGLVSGYTPPR(S) CL994.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
20.57 <0.1% <0.1% 97.6 5.20E+06 (K)AVmYPSILVVQGLVSGYTPPR(S) m:Oxidized methionine CL994.c1 S.halepenseF2 hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]

20.01	<0.1%	<0.1%	91	4.62E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.97	<0.1%	<0.1%	85.5	1.55E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.66	<0.1%	<0.1%	86.5	8.32E+04	(R)ALAAmGDDNKVEYVYDISSWMDEMDMK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.48	<0.1%	<0.1%	89.3	2.56E+06	(K)CAEQAAEFEPGPGK(K)	C:Carbamidomethylation	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
19.39	<0.1%	<0.1%	92.9	1.72E+05	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.73	<0.1%	<0.1%	84.5	2.53E+06	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.19	<0.1%	<0.1%	89.1	6.12E+06	(K)AVPDADKLLPTK(A)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
18.02	<0.1%	<0.1%	90.8	4.74E+06	(K)AVPDADKLLPTK(A)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.76	<0.1%	<0.1%	89.3	3.82E+06	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.44	<0.1%	<0.1%	79.6	2.54E+06	(R)CSPSVMPK(V)	C:Carbamidomethylation	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.38	<0.1%	<0.1%	87.7	1.28E+06	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.3	<0.1%	<0.1%	88.7	5.67E+06	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.15	<0.1%	<0.1%	83.9	2.54E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
17.07	<0.1%	<0.1%	85.8	1.84E+06	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.99	<0.1%	<0.1%	89	1.60E+06	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.93	<0.1%	<0.1%	86.1	1.73E+06	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.85	<0.1%	<0.1%	83.3	2.88E+05	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.8	<0.1%	<0.1%	79.8	3.39E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.65	<0.1%	<0.1%	82.4	3.71E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.61	<0.1%	<0.1%	85	7.45E+05	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.61	<0.1%	<0.1%	81.5	1.05E+06	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.61	<0.1%	<0.1%	86.3	2.38E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.47	<0.1%	<0.1%	82.2	1.42E+06	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.45	<0.1%	<0.1%	98	9.74E+06	(R)SLLAELR(K)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.37	<0.1%	<0.1%	86	2.60E+05	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
16.13	<0.1%	<0.1%	95.6	7.84E+06	(R)SLLAELR(K)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.96	<0.1%	<0.1%	83.8	2.65E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.59	0.20%	<0.1%	87.5	1.53E+06	(R)ALAAMGDDNK(V)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.48	0.20%	<0.1%	90.9	2.87E+05	(K)AVPDADK(L)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.46	0.20%	<0.1%	79.1	1.58E+06	(K)CAEQAAEFEPGPGKK(E)	C:Carbamidomethylation	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.44	0.20%	<0.1%	84.8	3.34E+06	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
15.36	0.20%	<0.1%	80.1	2.48E+05	(K)AVPDADKLLPTK(A)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.78	0.20%	<0.1%	76.5	4.86E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.56	2%	<0.1%	79.2	1.75E+04	(R)ALAAmGDDNKVEYVYDISSWMDEmDmK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.53	2%	<0.1%	71.2	1.91E+06	(R)CSPSVMPK(V)	C:Carbamidomethylation	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.43	2%	<0.1%	77.6	1.23E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.18	2%	0.10%	85.1	5.42E+05	(K)CAEQAAEFEPGPGK(K)	C:Carbamidomethylation	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
14.04	2%	0.30%	73.9	1.24E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]

13.93	2%	0.40%	82.4	2.31E+06	(K)AVPDADKLLPTK(A)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.83	2%	0.50%	93.9	8.59E+06	(R)SLLAELR(K)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.73	2%	0.50%	74.8	4.28E+05	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.69	2%	0.50%	72.6	8.32E+04	(R)ALAAmGDDNKVEYVYDISSWMDEMDMK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.45	2%	0.50%	90	8.17E+06	(R)SLLAELR(K)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.41	2%	0.50%	84	2.04E+06	(R)ALAAMGDDNK(V)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.33	2%	0.50%	72.9	1.76E+06	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.27	2%	0.50%	68.9	3.57E+05	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.2	2%	0.50%	66.7	1.97E+05	(R)ALAAMGDDNKVEYVYDISSWMDEMDMK(F)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.87	2%	0.60%	67.5	6.67E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.83	2%	0.60%	73.3	1.89E+04	(R)ALAAmGDDNKVEYVYDISSWmDEmDmK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.66	2%	0.60%	71.8	6.03E+05	(R)ALAAmGDDNKVEYVYDISSWmDEmDmK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.47	2%	0.60%	64.9	6.05E+03	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
12.01	3%	0.80%	71.4	1.38E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.78	3%	0.90%	68.8	2.69E+03	(R)VIGAATELMVANFR(S)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.73	3%	0.90%	74.1	8.32E+04	(R)ALAAMGDDNKVEYVYDISSWMDEMDmK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
11.13	3%	1%	60.6	5.21E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.9	3%	1%	80.7	8.88E+04	(R)ALAAMGDDNKVEYVYDISSWMDEmDmK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.84	3%	1%	67.3	3.71E+05	(K)AVPDADK(L)		CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.65	3%	1%	64.1	3.80E+04	(R)ALAAMGDDNKVEYVYDISSWMDEmDmK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.21	3%	1%	68.7	1.61E+04	(R)ALAAMGDDNKVEYVYDISSWmDEmDmK(F)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
10.03	5%	1%	65.3	1.66E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.c1	S.halepenseF2	hypothet prot SORBIDRAFT_10g001700 [S bicolor] >gi|241915964|gb|EER89108.1| hypothet prot SORBIDRAFT_10g001700 [S bicolor]
13.85	2%	0.40%	91.3	1.66E+06	(R)VVDILR(K)		UG10693	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g008450 [S bicolor] >gi|241931669|gb|EES04814.1| hypothet prot SORBIDRAFT_04g008450 [S bicolor]
11.75	3%	0.90%	82.5	2.09E+05	(R)VVDILR(K)		UG10693	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g008450 [S bicolor] >gi|241931669|gb|EES04814.1| hypothet prot SORBIDRAFT_04g008450 [S bicolor]
23.34	<0.1%	<0.1%	82.3	2.09E+06	(R)YCDGSSFTGDVEAVDTAK(N)	C:Carbamidomethylation	UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
22.42	<0.1%	<0.1%	84.6	2.18E+06	(K)YALLSGCSAGGLAAILHCDR(F)	C:Carbamidomethylation	UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
21.92	<0.1%	<0.1%	100	7.73E+05	(R)TPLFILNAAYDSWQVK(N)		UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
21.7	<0.1%	<0.1%	97.8	2.14E+06	(R)TPLFILNAAYDSWQVK(N)		UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
21.65	<0.1%	<0.1%	84.8	2.37E+06	(K)SCSPSQLTTLQNFR(T)	C:Carbamidomethylation	UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
20.71	<0.1%	<0.1%	75.5	9.02E+04	(K)GAVCLDGSPPVYHFSPGSGSGADNWVVHMEGGGWCR(N)	C:Carbamidomethylation	UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
19.67	<0.1%	<0.1%	86.7	7.58E+05	(K)CFSDAGYFFDGK(D)	C:Carbamidomethylation	UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
19.36	<0.1%	<0.1%	87	2.48E+06	(R)TPLFILNAAYDSWQVK(N)		UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
19.03	<0.1%	<0.1%	73.8	9.02E+04	(K)GAVCLDGSPPVYHFSPGSGSGADNWVVHMEGGGWCR(N)	C:Carbamidomethylation	UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
17.52	<0.1%	<0.1%	79.6	2.07E+06	(R)AImDDLLTVR(G)	m:Oxidized methionine	UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
17.37	<0.1%	<0.1%	92.2	4.78E+06	(K)DISGNYYAR(S)		UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
16.3	<0.1%	<0.1%	89	3.51E+06	(K)AVGDWYFDR(E)		UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
16.16	<0.1%	<0.1%	84.1	7.70E+05	(R)QIDCPYPCNPTCK(N)	C:Carbamidomethylation	UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
15.35	0.20%	<0.1%	93.9	5.65E+06	(K)NVLAPSPADPK(K)		UG1172	S.halepenseF1	hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]

15.11 0.20% <0.1% 72.7 1.00E+07 (K)NVVNLHGSAK(N) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
14.9 0.20% <0.1% 78.4 3.82E+06 (R)DLFPATTK(V) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
14.89 0.20% <0.1% 78.6 1.68E+06 (K)SNPDFYNWNR(I) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
14.29 2% <0.1% 66.8 2.37E+06 (K)SNPDFYNWNR(I) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
14.28 2% <0.1% 84.4 3.54E+06 (K)NLPASCTSK(Q) C:Carbamidomethylation UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
14.11 2% 0.30% 78.4 4.25E+06 (R)TDFLAALPK(T) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
13.52 2% 0.50% 76.3 2.71E+06 (R)NPDECAVR(K) C:Carbamidomethylation UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
13.28 2% 0.50% 71.3 2.76E+05 (R)AImDDLLTVR(G) m:Oxidized methionine UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
12.83 2% 0.60% 69.5 3.23E+05 (K)QPELCmFPQYVVPTmR(T) C:Carbamidomethylation m:Oxidized methionine UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
12.51 2% 0.60% 66.8 1.30E+06 (K)SCSPSQLTTLQNFR(T) C:Carbamidomethylation UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
12.49 2% 0.60% 76 1.43E+06 (K)NVLAPSPADPKK(T) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
12.43 2% 0.60% 65.4 1.06E+06 (R)TPLFILNAAYDSWQVK(N) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
12.2 3% 0.70% 87.6 3.02E+06 (K)NLPASCTSK(Q) C:Carbamidomethylation UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
11.69 3% 0.90% 81.4 1.24E+06 (R)FRDLFPATTK(V) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
11.43 3% 1.00% 64.4 5.17E+06 (K)FmRPLSFSGILGGSQK(S) m:Oxidized methionine UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
11.22 3% 1% 64.6 1.29E+05 (R)TPLFILNAAYDSWQVK(N) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
11.08 3% 1% 69 3.10E+06 (R)AIMDDLLTVR(G) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
10.67 3% 1% 83.3 3.97E+05 (R)FRDLFPATTK(V) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
10.39 3% 1% 61.4 1.36E+05 (R)AIMDDLLTVR(G) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
10.02 5% 1% 69.5 1.72E+06 (K)NVVNLHGSAK(N) UG1172 S.halepenseF1 hypothet prot SORBIDRAFT_06g027560 [S bicolor] >gi|241938233|gb|EES11378.1| hypothet prot SORBIDRAFT_06g027560 [S bicolor]
11.12 3% 1% 71.4 8.55E+04 (R)AFLHK(G) UG11835 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g022150 [S bicolor] >gi|241921110|gb|EER94254.1| hypothet prot SORBIDRAFT_01g022150 [S bicolor]
13.26 2% 0.50% 67.4 3.01E+05 (K)SCLIXR(Q) C:Carbamidomethylation UG12140 S.halepenseF1 hypothet prot SORBIDRAFT_01g014880 [S bicolor] >gi|241918101|gb|EER91245.1| hypothet prot SORBIDRAFT_01g014880 [S bicolor]
14.29 2% <0.1% 72 9.52E+04 (K)IPVSLSDLDWILGK(T) UG12523 S.halepenseF3 hypothet prot SORBIDRAFT_06g014260 [S bicolor] >gi|241937503|gb|EES10648.1| hypothet prot SORBIDRAFT_06g014260 [S bicolor]
13.83 2% 0.40% 69.3 3.81E+04 (K)IPVSLSDLDWILGK(T) UG12523 S.halepenseF3 hypothet prot SORBIDRAFT_06g014260 [S bicolor] >gi|241937503|gb|EES10648.1| hypothet prot SORBIDRAFT_06g014260 [S bicolor]
11.43 3% 1.00% 66.2 2.88E+04 (K)IPVSLSDLDWILGK(T) UG12523 S.halepenseF3 hypothet prot SORBIDRAFT_06g014260 [S bicolor] >gi|241937503|gb|EES10648.1| hypothet prot SORBIDRAFT_06g014260 [S bicolor]
11.47 3% 1.00% 75.3 3.67E+06 (R)XYGXSIAK(K) UG1263 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035690 [S bicolor] >gi|241928376|gb|EES01521.1| hypothet prot SORBIDRAFT_03g035690 [S bicolor]
11.27 3% 1% 75.6 4.62E+06 (R)XYGXSIAK(K) UG1263 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g035690 [S bicolor] >gi|241928376|gb|EES01521.1| hypothet prot SORBIDRAFT_03g035690 [S bicolor]
10.47 3% 1% 72.6 2.91E+05 (K)XHEVILHK(R) UG12660 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_10g028510 [S bicolor] >gi|241917155|gb|EER90299.1| hypothet prot SORBIDRAFT_10g028510 [S bicolor]
10.01 5% 1% 67.1 1.71E+07 (R)VTVAPSLR(W) UG12721 S.halepenseF3 #N/A
12.26 3% 0.70% 68 2.61E+04 (R)LGHNETINEGVR(R) UG13389 S.halepenseF1 predicted protein [Hordeum vulgare subsp. vulgare]
19.09 <0.1% <0.1% 92.4 4.43E+05 (K)SmADVLVNLPSGQDDmNPYFTFIK(G) m:Oxidized methionine UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
19.04 <0.1% <0.1% 85.8 8.69E+05 (K)TSSSSSADETSIVDK(F) UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
18.78 <0.1% <0.1% 83.9 2.79E+06 (K)TSSSSSADETSIVDK(F) UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
17.16 <0.1% <0.1% 78.3 2.86E+05 (K)FHDIWTVVK(V) UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
16.93 <0.1% <0.1% 80.4 6.97E+05 (K)TSSSSSADETSIVDKFHDIWTVVK(V) UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
15.01 0.20% <0.1% 76.6 1.66E+06 (K)TSSSSSADETSIVDKFHDIWTVVK(V) UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
14.75 0.20% <0.1% 77.8 1.11E+05 (K)FKHERPPACEK(N) C:Carbamidomethylation UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
14.57 2% <0.1% 82.1 6.27E+05 (K)SMADVLVNLPSGQDDMNPYFTFIK(G) UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
13.84 2% 0.40% 75.8 6.13E+05 (K)TSSSSSADETSIVDKFHDIWTVVK(V) UG1387 S.halepenseF2Rev hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]

13.6	2%	0.50%	60.4	2.91E+06	(K)FKHERPPACEK(N)	C:Carbamidomethylation	UG1387	S.halepenseF2Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
13.6	2%	0.50%	80.1	1.05E+06	(K)FHDIWTVVK(V)		UG1387	S.halepenseF2Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
13.3	2%	0.50%	82.8	2.17E+05	(K)SMADVLVNLPSGQDDMNPYFTFIK(G)		UG1387	S.halepenseF2Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
13.08	2%	0.60%	73.2	3.93E+05	(K)SMADVLVNLPSGQDDmNPYFTFIK(G)	m:Oxidized methionine	UG1387	S.halepenseF2Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
13.04	2%	0.60%	78	6.05E+05	(K)FHDIWTVVK(V)		UG1387	S.halepenseF2Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
12.46	2%	0.60%	73.7	5.14E+04	(K)SMADVLVNLPSGQDDmNPYFTFIK(G)	m:Oxidized methionine	UG1387	S.halepenseF2Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
11.92	3%	0.90%	63.6	1.31E+06	(K)FKHERPPACEK(N)	C:Carbamidomethylation	UG1387	S.halepenseF2Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
10.11	3%	1%	66.8	4.56E+05	(K)FHDIWTVVK(V)		UG1387	S.halepenseF2Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
12.36	2%	0.70%	84.6	1.24E+07	(K)LLSSAXPR(E)		UG14950	S.halepenseF3RevF3Rev	#N/A
11.29	3%	1%	82.6	8.24E+06	(K)LLSSAXPR(E)		UG14950	S.halepenseF3RevF3Rev	#N/A
13.1	2%	0.60%	75	4.34E+05	(K)YFPAPAPAR(S)		UG14985	S.halepenseF1Rev	unknown [Oryza sativa Indica Group]
19.96	<0.1%	<0.1%	94.4	8.15E+06	(R)VASDSPSCIK(V)	C:Carbamidomethylation	UG1499	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
18.25	<0.1%	<0.1%	92.3	8.15E+06	(R)VASDSPSCIK(V)	C:Carbamidomethylation	UG1499	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
17.68	<0.1%	<0.1%	89.8	1.10E+06	(K)VIGSIPGIQEVDINNAGK(I)		UG1499	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
17.37	<0.1%	<0.1%	88	2.90E+06	(R)VASDSPSCIK(V)	C:Carbamidomethylation	UG1499	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
16.58	<0.1%	<0.1%	91.8	6.02E+05	(K)VIGSIPGIQEVDINNAGK(I)		UG1499	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
15.28	0.20%	<0.1%	87.7	9.34E+05	(K)VIGSIPGIQEVDINNAGK(I)		UG1499	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
13.69	2%	0.50%	86.5	2.38E+06	(K)VIGSIPGIQEVDINNAGK(I)		UG1499	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g000890 [S bicolor] >gi|241934726|gb|EES07871.1| hypothet prot SORBIDRAFT_05g000890 [S bicolor]
10.02	5%	1%	65.2	1.22E+05	(R)LSLAVSGXCRR(R)	C:Carbamidomethylation	UG15017	S.halepenseF1Rev	hypothet prot SORBIDRAFT_08g004950 [S bicolor] >gi|241943615|gb|EES16760.1| hypothet prot SORBIDRAFT_08g004950 [S bicolor]
10.99	3%	1%	71	5.88E+05	(R)XGYSVXNINFGWYHGAmGGTNYSIXWK(X)	m:Oxidized methionine	UG15067	S.halepenseF1Rev	hypothet prot SORBIDRAFT_07g006030 [S bicolor] >gi|241940373|gb|EES13518.1| hypothet prot SORBIDRAFT_07g006030 [S bicolor]
16.6	<0.1%	<0.1%	67.3	1.95E+05	(K)NLPVGDVVDKLIAEWK(T)		UG1523	S.halepenseF1	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
15.68	0.20%	<0.1%	73	8.65E+05	(-)GCYVMCLTDNSFK(N)	C:Carbamidomethylation	UG1523	S.halepenseF1	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
15.13	0.20%	<0.1%	69.1	9.08E+05	(-)GCYVmCLTDNSFK(N)	C:Carbamidomethylation m:Oxidized methionine	UG1523	S.halepenseF1	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
12.41	2%	0.70%	61.1	2.14E+04	(-)GCYVmCLTDNSFK(N)	C:Carbamidomethylation m:Oxidized methionine	UG1523	S.halepenseF1	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
12.14	3%	0.70%	80.5	3.19E+06	(K)LIAEWK(T)		UG1523	S.halepenseF1	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
11.46	3%	1.00%	83	8.36E+05	(K)LIAEWK(T)		UG1523	S.halepenseF1	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
10.04	5%	1%	60.3	3.28E+04	(-)GCYVMCLTDNSFK(N)	C:Carbamidomethylation	UG1523	S.halepenseF1	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
10.34	3%	1%	60.3	2.59E+06	(-)PFPHR(I)		UG1588	S.halepenseF1Rev	uncharacterized protein LOC100279445 [Zea mays]
10.25	3%	1%	73	7.46E+05	(R)XDSEIK(M)		UG1640	S.halepenseF1Rev	hypothet prot SORBIDRAFT_02g003750 [S bicolor] >gi|241924885|gb|EER98029.1| hypothet prot SORBIDRAFT_02g003750 [S bicolor]
12.16	3%	0.70%	75.7	1.20E+05	(R)TLDAIALAK(E)		UG16835	S.halepenseF3	uncharacterized protein LOC100277067 [Zea mays]
10.34	3%	1%	73.8	4.11E+04	(R)NILLSLPIR(K)		UG1990	S.halepenseF1	hypothet prot SORBIDRAFT_03g047380 [S bicolor] >gi|241929001|gb|EES02146.1| hypothet prot SORBIDRAFT_03g047380 [S bicolor]
18.32	<0.1%	<0.1%	89.1	9.26E+05	(R)FTVATFENEMK(W)		UG2235	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
15.19	0.20%	<0.1%	78	3.76E+05	(R)FTVATFENEmK(W)	m:Oxidized methionine	UG2235	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.81	2%	0.50%	74.9	4.03E+05	(R)FTVATFENEMK(W)		UG2235	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
13.56	2%	0.50%	74	7.75E+05	(R)FTVATFENEMK(W)		UG2235	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
12.31	2%	0.70%	75.7	1.02E+06	(K)EITELPAYEK(W)		UG2235	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
12.25	3%	0.70%	74.7	2.36E+06	(R)mGFPFGNAATK(E)	m:Oxidized methionine	UG2235	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
12.08	3%	0.80%	77.2	7.75E+05	(R)MGFPFGNAATK(E)		UG2235	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
11.18	3%	1%	74.6	1.03E+06	(R)MLSLMQR(H)		UG2235	S.halepenseF2Rev	hypothet prot SORBIDRAFT_02g004490 [S bicolor] >gi|241924922|gb|EER98066.1| hypothet prot SORBIDRAFT_02g004490 [S bicolor]
23.63	<0.1%	<0.1%	97.2	7.89E+06	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
22.75	<0.1%	<0.1%	100	2.30E+07	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
22.4	<0.1%	<0.1%	88.7	3.54E+06	(K)VQDSFCATLCQGR(K)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]

22.23	<0.1%	<0.1%	94.8	6.83E+06	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
20.74	<0.1%	<0.1%	88.9	4.63E+06	(K)KVQDSFCATLCQGR(K)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
20.26	<0.1%	<0.1%	91	5.78E+06	(K)KPAESVAAAGEAAEAKK(V)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
20.18	<0.1%	<0.1%	85.5	1.34E+05	(K)VQDSFCATLCQGR(K)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
18.77	<0.1%	<0.1%	90.9	9.30E+06	(K)KPAESVAAAGEAAEAKK(V)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
18.49	<0.1%	<0.1%	92.8	1.72E+07	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
18.04	<0.1%	<0.1%	81.9	9.67E+06	(K)KVQDSFCATLCQGR(K)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
17.57	<0.1%	<0.1%	87.5	1.85E+05	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
17.4	<0.1%	<0.1%	77.8	1.17E+06	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
17.05	<0.1%	<0.1%	78.6	3.56E+05	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
16.73	<0.1%	<0.1%	82.9	1.09E+07	(K)KKPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
16.41	<0.1%	<0.1%	83.9	1.40E+05	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
16.31	<0.1%	<0.1%	79.8	4.04E+05	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
15.95	<0.1%	<0.1%	86	5.64E+06	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
15.89	0.20%	<0.1%	75.2	2.89E+07	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
15.72	0.20%	<0.1%	85.5	2.63E+06	(R)KGMDLIVCK(E)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
15.6	0.20%	<0.1%	85.6	3.22E+05	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
15.6	0.20%	<0.1%	90.3	1.45E+07	(K)GITAPAMK(V)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
15.43	0.20%	<0.1%	76	3.16E+05	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
15.43	0.20%	<0.1%	74.1	2.33E+06	(K)GMDLIVCK(E)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
15.3	0.20%	<0.1%	71	5.17E+05	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.6	2%	<0.1%	86.9	2.33E+07	(R)SNLVLYGR(I)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.54	2%	<0.1%	74.2	5.20E+06	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.49	2%	<0.1%	75.2	2.22E+06	(K)KKPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.32	2%	<0.1%	70	2.47E+05	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.28	2%	<0.1%	79.1	1.40E+07	(K)KKPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.23	2%	<0.1%	79.7	2.41E+05	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.19	2%	0.10%	76.1	9.18E+05	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.17	2%	0.20%	77.5	7.81E+06	(R)KGmDLIVCK(E)	C:Carbamidomethylation m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
14.16	2%	0.20%	83.5	2.72E+07	(K)GITAPAmK(V)	m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.93	2%	0.40%	67.7	9.72E+03	(K)VCEEQCDK(D)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.88	2%	0.40%	84.3	1.33E+07	(R)SNLVLYGR(I)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.68	2%	0.50%	73.3	1.62E+05	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.58	2%	0.50%	73.8	1.76E+05	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.4	2%	0.50%	66	2.28E+05	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.38	2%	0.50%	69.3	1.02E+05	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.37	2%	0.50%	69.2	1.96E+05	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.28	2%	0.50%	65.4	3.75E+06	(R)KGmDLIVCK(E)	C:Carbamidomethylation m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
13.01	2%	0.60%	81.7	2.36E+06	(R)SNLVLYGR(I)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.97	2%	0.60%	69.5	3.14E+05	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.97	2%	0.60%	80.5	1.84E+07	(K)GITAPAmK(V)	m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.92	2%	0.60%	71.4	1.58E+05	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.76	2%	0.60%	80.2	7.72E+06	(R)KGmDLIVCK(E)	C:Carbamidomethylation m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.71	2%	0.60%	77.9	1.25E+07	(R)KGmDLIVCK(E)	C:Carbamidomethylation m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.58	2%	0.60%	71.7	4.07E+05	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.39	2%	0.60%	77.3	1.07E+06	(K)GITAPAmK(V)	m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.19	3%	0.70%	67.8	1.41E+05	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.09	3%	0.70%	67.5	3.42E+05	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.09	3%	0.80%	79.6	4.29E+05	(K)GITAPAMK(V)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12.02	3%	0.80%	77.2	1.52E+06	(R)SNLVLYGR(I)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
12	3%	0.80%	61.5	1.69E+05	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.99	3%	0.80%	62.5	3.19E+05	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.96	3%	0.80%	61.4	3.73E+05	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.91	3%	0.90%	60.9	1.78E+05	(K)ESCELSQR(S)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.79	3%	0.90%	71.6	1.58E+05	(K)AAEVTAACNK(T)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.73	3%	0.90%	69.9	5.85E+06	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.72	3%	0.90%	69.6	3.64E+05	(K)GITAPAmK(V)	m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.7	3%	0.90%	73.9	1.69E+05	(K)VCEEQCDKDYVVK(A)	C:Carbamidomethylation	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.46	3%	1.00%	69.3	2.76E+05	(K)GITAPAmK(V)	m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11.04	3%	1%	73.9	2.74E+05	(K)GITAPAmK(V)	m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
11	3%	1%	66.4	3.13E+05	(K)KPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
10.62	3%	1%	68.4	5.08E+04	(K)KKPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
10.36	3%	1%	73.4	4.37E+05	(R)SNLVLYGR(I)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
10.32	3%	1%	66.8	4.64E+05	(K)KKPAESVAAAGEAAEAK(K)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
10.26	3%	1%	71.1	1.54E+06	(K)GITAPAmK(V)	m:Oxidized methionine	UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
10.11	3%	1%	70.3	5.03E+05	(R)SNLVLYGR(I)		UG295	S.halepenseF3RevF3Rev	uncharacterized protein LOC100276692 precursor [Zea mays]
24.15	<0.1%	<0.1%	91	7.03E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
22.57	<0.1%	<0.1%	84.5	3.51E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
22.47	<0.1%	<0.1%	85.4	9.89E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
21.84	<0.1%	<0.1%	93.8	4.68E+05	(K)SSGGGSDFGYGASSK(E)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
19.38	<0.1%	<0.1%	77.4	3.42E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
19.2	<0.1%	<0.1%	80.8	2.70E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]

19.01	<0.1%	<0.1%	77.3	2.62E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
17.54	<0.1%	<0.1%	75.1	3.42E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
17.31	<0.1%	<0.1%	82.4	3.12E+05	(K)SSGGGSDFGYGASSK(E)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
16.82	<0.1%	<0.1%	74.4	9.00E+04	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
14.5	2%	<0.1%	76.3	1.08E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
14.43	2%	<0.1%	72	8.45E+04	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
13.63	2%	0.50%	64.5	1.11E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
13.14	2%	0.60%	69.2	4.66E+05	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
11.82	3%	0.90%	61.1	6.74E+04	(K)GDAGGSGDAAASTSAEAK(A)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
10.9	3%	1%	65.4	1.91E+05	(K)SSGGGSDFGYGASSK(E)		UG310	S.halepenseF2Rev	hypothet prot [Zea mays]
15.9	0.20%	<0.1%	79.7	3.46E+05	(R)AAGAVQQAAEQVAQTVQGAAAAVK(D)			UG312	S.halepenseF1	hypothet prot [Zea mays]
13.31	2%	0.50%	71.5	2.45E+05	(R)AAGAVQQAAEQVAQTVQGAAAAVK(D)			UG312	S.halepenseF1	hypothet prot [Zea mays]
13.3	2%	0.50%	73.6	2.96E+05	(R)AAGAVQQAAEQVAQTVQGAAAAVK(D)			UG312	S.halepenseF1	hypothet prot [Zea mays]
11.43	3%	1.00%	73.1	1.75E+05	(R)AAGAVQQAAEQVAQTVQGAAAAVK(D)			UG312	S.halepenseF1	hypothet prot [Zea mays]
10.42	3%	1%	68.9	3.15E+05	(R)AAGAVQQAAEQVAQTVQGAAAAVK(D)			UG312	S.halepenseF1	hypothet prot [Zea mays]
14.37	2%	<0.1%	69.8	1.26E+05	(K)AAEFSSFFATR(K)		UG3167	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
13.23	2%	0.50%	71	3.62E+05	(R)LAQTVQDLLR(R)		UG3167	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
12.17	3%	0.70%	67.8	1.91E+05	(R)LAQTVQDLLR(R)		UG3167	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
11.33	3%	1.00%	69.8	1.88E+05	(R)YVTTLFTSNEK(A)		UG3167	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_02g022933 [S bicolor] >gi|241923489|gb|EER96633.1| hypothet prot SORBIDRAFT_02g022933 [S bicolor]
13.1	2%	0.60%	63.2	3.18E+05	(R)ATmGmAAQDmQNCDEQFR(Q)	C:Carbamidomethylation m:Oxidized methionine		UG321	S.halepenseF1	unknown [Zea mays]
26.17	<0.1%	<0.1%	100	7.72E+06	(K)VAEITASCHTVCTK(V)	C:Carbamidomethylation		UG359	S.halepenseF2	uncharacterized protein LOC100276692 precursor [Zea mays]
20.81	<0.1%	<0.1%	86.8	1.11E+06	(K)VAEITASCHTVCTK(V)	C:Carbamidomethylation		UG359	S.halepenseF2	uncharacterized protein LOC100276692 precursor [Zea mays]
16.24	<0.1%	<0.1%	85.5	9.08E+05	(K)EQLAIEECKK(I)	C:Carbamidomethylation		UG359	S.halepenseF2	uncharacterized protein LOC100276692 precursor [Zea mays]
14.11	2%	0.30%	77.2	2.52E+06	(K)ICTPSLIFK(E)	C:Carbamidomethylation		UG359	S.halepenseF2	uncharacterized protein LOC100276692 precursor [Zea mays]
13.3	2%	0.50%	76.7	2.54E+06	(K)EQLAIEECKK(I)	C:Carbamidomethylation		UG359	S.halepenseF2	uncharacterized protein LOC100276692 precursor [Zea mays]
13.04	2%	0.60%	67.6	9.86E+04	(K)KHGFGTPDSK(S)		UG359	S.halepenseF2	uncharacterized protein LOC100276692 precursor [Zea mays]
11.78	3%	0.90%	68.4	3.28E+04	(K)KICTPSLIFK(E)	C:Carbamidomethylation		UG359	S.halepenseF2	uncharacterized protein LOC100276692 precursor [Zea mays]
11.5	3%	1.00%	67.9	1.42E+06	(K)VWIEAVQCSLK(C)	C:Carbamidomethylation		UG359	S.halepenseF2	uncharacterized protein LOC100276692 precursor [Zea mays]
17.65	<0.1%	<0.1%	87.4	1.20E+06	(K)LTPEQVAALK(K)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
17.56	<0.1%	<0.1%	91.9	4.31E+06	(K)APAQGVNYK(A)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
16.88	<0.1%	<0.1%	80.6	4.34E+05	(K)HPAVLQALPEVK(Y)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
14.91	0.20%	<0.1%	85.5	2.00E+06	(K)AVASGFAAK(L)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
14.7	0.20%	<0.1%	79.1	1.41E+06	(K)LTPEQVAALKK(H)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
14.7	0.20%	<0.1%	79	3.73E+05	(K)QAAATSVYVVmVK(A)	m:Oxidized methionine	UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
14.29	2%	<0.1%	82.1	2.69E+06	(K)AVASGFAAK(L)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
13.59	2%	0.50%	90	2.98E+06	(R)ILATALGSEEK(A)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
13.08	2%	0.60%	85.4	7.64E+05	(K)HPAVLQALPEVK(Y)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
12.17	3%	0.70%	63.2	8.70E+04	(K)AVASGFAAK(L)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
10.78	3%	1%	64.3	1.87E+05	(K)QAAATSVYVVMVK(A)		UG373	S.halepenseF1	hypothet prot SORBIDRAFT_02g010480 [S bicolor] >gi|241923156|gb|EER96300.1| hypothet prot SORBIDRAFT_02g010480 [S bicolor]
10.05	5%	1%	74.6	1.22E+07	(K)QXLmPYNR(H)	m:Oxidized methionine	UG3800	S.halepenseF1Rev	hypothet prot SORBIDRAFT_06g033140 [S bicolor] >gi|241938519|gb|EES11664.1| hypothet prot SORBIDRAFT_06g033140 [S bicolor]
20.67	<0.1%	<0.1%	87.5	1.72E+05	(K)SMAEVLVNLPAGQDDMNAYQTYK(E)		UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
20.04	<0.1%	<0.1%	87.1	3.32E+06	(K)TSSSSSSAADIVDK(F)		UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
18.94	<0.1%	<0.1%	96.5	2.15E+04	(K)SMAEVLVNLPAGQDDmNAYQTYK(E)	m:Oxidized methionine	UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
18.1	<0.1%	<0.1%	80.3	3.28E+06	(K)WCQVASDSPSCVK(V)	C:Carbamidomethylation	UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
18.06	<0.1%	<0.1%	81.1	1.30E+06	(K)TSSSSSSAADIVDKFHDIWNVAK(V)		UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
17.07	<0.1%	<0.1%	79.5	1.39E+06	(K)TSSSSSSAADIVDK(F)		UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
14.79	0.20%	<0.1%	78	2.27E+05	(K)TSSSSSSAADIVDK(F)		UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
14.7	0.20%	<0.1%	79.4	4.24E+05	(K)TSSSSSSAADIVDKFHDIWNVAK(V)		UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
14.64	2%	<0.1%	79.1	4.68E+04	(K)SMAEVLVNLPAGQDDMNAYQTYK(E)		UG388	S.halepenseF2	hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]

14.01 2% 0.30% 85 8.74E+05 (K)VIESIPGIQEVDYNNAGK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
13.83 2% 0.50% 72.8 3.81E+05 (K)FKNEKPPACEK(D) C:Carbamidomethylation UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
13.79 2% 0.50% 79.6 1.48E+06 (K)VIESIPGIQEVDYNNAGK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
13.22 2% 0.50% 79.2 6.03E+05 (K)FHDIWNVAK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
12.52 2% 0.60% 83.5 1.38E+06 (K)VIESIPGIQEVDYNNAGK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
12.47 2% 0.60% 67.9 7.93E+05 (K)TSSSSSSAADIVDKFHDIWNVAK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
12.42 2% 0.60% 73.9 6.65E+05 (K)FHDIWNVAK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
12.21 3% 0.70% 63.8 1.42E+05 (K)GAADTLLAAEK(G) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
12.19 3% 0.70% 66.8 2.28E+06 (K)TSSSSSSAADIVDKFHDIWNVAK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
12.15 3% 0.70% 68.8 2.17E+05 (K)SMAEVLVNLPAGQDDmNAYQTYK(E) m:Oxidized methionine UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
11.69 3% 0.90% 66 2.04E+04 (K)FHDIWNVAK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
11.65 3% 0.90% 61.3 2.06E+06 (K)WCQVASDSPSCVK(V) C:Carbamidomethylation UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
11.63 3% 0.90% 73 9.32E+05 (K)TSSSSSSAADIVDKFHDIWNVAK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
11.26 3% 1% 67.3 7.15E+06 (K)FKNEKPPACEK(D) C:Carbamidomethylation UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
11.2 3% 1% 62.1 4.56E+04 (K)SmAEVLVNLPAGQDDmNAYQTYK(E) m:Oxidized methionine UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
11 3% 1% 73.6 5.58E+05 (K)FHDIWNVAK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
10.53 3% 1% 64.4 3.11E+05 (K)VIESIPGIQEVDYNNAGK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
10.45 3% 1% 67.5 5.41E+05 (K)FHDIWNVAK(V) UG388 S.halepenseF2 hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|242067217|ref|XP_002448885.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor] >gi|241934727|gb|EES07872.1| hypothet prot SORBIDRAFT_05g000910 [S bicolor] >gi|241934728|gb|EES07873.1| hypothet prot SORBIDRAFT_05g000920 [S bicolor]
18.56 <0.1% <0.1% 87.6 1.36E+06 (R)TPFPEVCK(S) C:Carbamidomethylation UG393 S.halepenseF3RevF3Rev hypothet prot SORBIDRAFT_09g009790 [S bicolor] >gi|241944812|gb|EES17957.1| hypothet prot SORBIDRAFT_09g009790 [S bicolor]
10.08 5% 1% 66.8 1.32E+05 (R)VAFTSLK(D) UG4189 S.halepenseF1Rev hypothet prot SORBIDRAFT_01g002240 [S bicolor] >gi|241920002|gb|EER93146.1| hypothet prot SORBIDRAFT_01g002240 [S bicolor]
10.91 3% 1% 76.6 2.61E+05 (R)SAVEFLR(A) UG4386 S.halepenseF2Rev hypothet prot SORBIDRAFT_01g028280 [S bicolor] >gi|241921305|gb|EER94449.1| hypothet prot SORBIDRAFT_01g028280 [S bicolor]
21.63 <0.1% <0.1% 86.2 5.21E+05 (K)AAEDFCITSCADKK(E) C:Carbamidomethylation UG477 S.halepenseF3RevF3Rev uncharacterized protein LOC100276692 precursor [Zea mays]
17.89 <0.1% <0.1% 83.5 1.68E+06 (K)AAEVTASCNAVCSK(V) C:Carbamidomethylation UG477 S.halepenseF3RevF3Rev uncharacterized protein LOC100276692 precursor [Zea mays]
12.54 2% 0.60% 74.8 5.94E+05 (R)SDLVFFESVTCLGK(C) C:Carbamidomethylation UG477 S.halepenseF3RevF3Rev uncharacterized protein LOC100276692 precursor [Zea mays]
14.4 2% <0.1% 90.7 6.42E+05 (R)SIVLIK(I) UG5060 S.halepenseF3 hypothet prot SORBIDRAFT_04g005940 [S bicolor] >gi|241931523|gb|EES04668.1| hypothet prot SORBIDRAFT_04g005940 [S bicolor]
12.47 2% 0.60% 85.7 2.04E+06 (R)SIVLIK(I) UG5060 S.halepenseF3 hypothet prot SORBIDRAFT_04g005940 [S bicolor] >gi|241931523|gb|EES04668.1| hypothet prot SORBIDRAFT_04g005940 [S bicolor]
12.41 2% 0.70% 85.7 2.99E+06 (K)FLIEK(S) UG5064 S.halepenseF1 hypothet prot SORBIDRAFT_04g034890 [S bicolor] >gi|241932742|gb|EES05887.1| hypothet prot SORBIDRAFT_04g034890 [S bicolor]
11.98 3% 0.80% 80.9 9.97E+05 (K)FLIEK(S) UG5064 S.halepenseF1 hypothet prot SORBIDRAFT_04g034890 [S bicolor] >gi|241932742|gb|EES05887.1| hypothet prot SORBIDRAFT_04g034890 [S bicolor]
10.18 3% 1% 75.8 2.64E+05 (K)FLIEK(S) UG5064 S.halepenseF1 hypothet prot SORBIDRAFT_04g034890 [S bicolor] >gi|241932742|gb|EES05887.1| hypothet prot SORBIDRAFT_04g034890 [S bicolor]
18.96 <0.1% <0.1% 84.8 1.88E+05 (R)DLEEFFQSTAGK(F) UG535 S.halepenseF2Rev LOC100281836 precursor [Zea mays] >gi|195616818|gb|ACG30239.1| HDDC2 protein [Zea mays]
17.05 <0.1% <0.1% 86.3 1.43E+06 (R)KDPLPNCGELLR(A) C:Carbamidomethylation UG595 S.halepenseF2 hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
16.07 <0.1% <0.1% 84.1 3.34E+05 (R)KDPLPNCGELLR(A) C:Carbamidomethylation UG595 S.halepenseF2 hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
15.17 0.20% <0.1% 82.7 1.99E+05 (R)KDPLPNCGELLR(A) C:Carbamidomethylation UG595 S.halepenseF2 hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
12.46 2% 0.60% 65.1 2.53E+06 (R)KDPLPNCGELLR(A) C:Carbamidomethylation UG595 S.halepenseF2 hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
10.47 3% 1% 61.4 1.18E+06 (K)DPLPNCGELLR(A) C:Carbamidomethylation UG595 S.halepenseF2 hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
10.13 3% 1% 61.9 2.73E+05 (R)KDPLPNCGELLR(A) C:Carbamidomethylation UG595 S.halepenseF2 hypothet prot SORBIDRAFT_09g007260 [S bicolor] >gi|241946096|gb|EES19241.1| hypothet prot SORBIDRAFT_09g007260 [S bicolor]
19.49 <0.1% <0.1% 86.7 2.47E+05 (K)IFQGDYSTGLPVDK(A) UG6651 S.halepenseF1Rev unknown [Zea mays]
13.67 2% 0.50% 76.8 2.17E+05 (K)VAAQVPDSGPCVTYIGK(G) C:Carbamidomethylation UG6651 S.halepenseF1Rev unknown [Zea mays]
20.72 <0.1% <0.1% 89.5 4.87E+05 (K)AImFDTVTTGPSLLR(L) m:Oxidized methionine UG691 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g031030 [S bicolor] >gi|241928105|gb|EES01250.1| hypothet prot SORBIDRAFT_03g031030 [S bicolor]
13.48 2% 0.50% 74.6 1.60E+05 (K)AImFDTVTTGPSLLR(L) m:Oxidized methionine UG691 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g031030 [S bicolor] >gi|241928105|gb|EES01250.1| hypothet prot SORBIDRAFT_03g031030 [S bicolor]

12.63 2% 0.70% 65.3 2.29E+05 (K)AImFDTVTTGPSLLR(L) m:Oxidized methionine UG691 S.halepenseF2Rev hypothet prot SORBIDRAFT_03g031030 [S bicolor] >gi|241928105|gb|EES01250.1| hypothet prot SORBIDRAFT_03g031030 [S bicolor]
19.69 <0.1% <0.1% 87 5.45E+05 (K)TDADATISSGGK(V) UG762 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
16.79 <0.1% <0.1% 82.7 4.61E+05 (K)TDADATISSGGK(V) UG762 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
16.52 <0.1% <0.1% 85.6 1.84E+06 (K)TDADATISSGGK(V) UG762 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
14.44 2% <0.1% 73.7 1.43E+06 (K)TDADATISSGGK(V) UG762 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
12.56 2% 0.60% 74.3 2.18E+05 (K)TDADATISSGGK(V) UG762 S.halepenseF1 hypothet prot SORBIDRAFT_03g024470 [S bicolor] >gi|241929951|gb|EES03096.1| hypothet prot SORBIDRAFT_03g024470 [S bicolor]
24.93 <0.1% <0.1% 88.3 1.31E+06 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
24.45 <0.1% <0.1% 86.8 6.43E+05 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
23.7 <0.1% <0.1% 86.8 8.16E+05 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
23.17 <0.1% <0.1% 100 1.30E+06 (R)FQGGSPYIYPLYGLGELPQAFAR(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
22.48 <0.1% <0.1% 79.3 4.58E+06 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
22.3 <0.1% <0.1% 84.2 8.65E+04 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
21.76 <0.1% <0.1% 83.1 3.17E+06 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
20.37 <0.1% <0.1% 94.7 1.88E+06 (K)IVCDPSYLPEK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
19.97 <0.1% <0.1% 90.1 2.34E+05 (R)FQGGSPYIYPLYGLGELPQAFAR(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
19.53 <0.1% <0.1% 78.4 4.50E+05 (R)KSDmYVFCCSYAHNVAPK(G) C:Carbamidomethylation m:Oxidized methionine UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
19.24 <0.1% <0.1% 91.3 5.51E+05 (R)FQGGSPYIYPLYGLGELPQAFAR(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
18.77 <0.1% <0.1% 74.5 2.40E+05 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
18.33 <0.1% <0.1% 79.3 3.63E+05 (R)FQGGSPYIYPLYGLGELPQAFAR(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
18.11 <0.1% <0.1% 88 1.02E+06 (R)DDSYLDEPAIDTVKR(M) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
18.01 <0.1% <0.1% 85.4 1.36E+05 (R)VLIHTSVTK(Y) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
17.79 <0.1% <0.1% 80.4 3.59E+05 (K)FFIYVQDYEEDDPKSHEGLDLTK(V) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
17.77 <0.1% <0.1% 91 1.08E+06 (R)DDSYLDEPAIDTVK(R) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
17.59 <0.1% <0.1% 72 1.87E+05 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
17.54 <0.1% <0.1% 80.8 5.13E+05 (K)SDmYVFCCSYAHNVAPK(G) C:Carbamidomethylation m:Oxidized methionine UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
17.44 <0.1% <0.1% 83.8 2.49E+05 (K)IVCDPSYLPEK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
17.23 <0.1% <0.1% 87 4.68E+05 (R)LSAVYGGTYMLNKPECK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
17.07 <0.1% <0.1% 75.3 7.62E+05 (R)FKGNDSPPEHLGISK(E) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
16.96 <0.1% <0.1% 79.7 1.70E+05 (R)FQGGSPYIYPLYGLGELPQAFAR(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
16.82 <0.1% <0.1% 88.5 2.77E+06 (K)AYGVTSEGETAK(C) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
16.19 <0.1% <0.1% 94.3 4.44E+06 (K)LYAESLAR(F) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
15.65 0.20% <0.1% 67.1 1.09E+05 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
15.4 0.20% <0.1% 71.2 4.10E+05 (K)EYNVDMVPK(F) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
15.07 0.20% <0.1% 64 2.80E+05 (R)LSAVYGGTYmLNKPECK(V) C:Carbamidomethylation m:Oxidized methionine UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
15.06 0.20% <0.1% 79.5 8.04E+05 (R)LSAVYGGTYmLNKPECK(V) C:Carbamidomethylation m:Oxidized methionine UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
14.97 0.20% <0.1% 73 8.20E+04 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
14.97 0.20% <0.1% 85.1 1.59E+06 (K)DVLALYNK(I) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
14.86 0.20% <0.1% 68.8 1.25E+05 (K)VPATDVEALK(S) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]

14.84 0.20% <0.1% 81.5 2.98E+05 (K)KIVCDPSYLPEK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
14.63 2% <0.1% 78.3 2.30E+06 (K)VEFDESGK(A) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
14.6 2% <0.1% 75.8 7.30E+06 (R)VLIHTSVTK(Y) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
14.28 2% <0.1% 71.4 6.81E+04 (R)FQGGSPYIYPLYGLGELPQAFAR(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
13.53 2% 0.50% 67.2 1.46E+05 (R)FQGGSPYIYPLYGLGELPQAFAR(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
13.41 2% 0.50% 82.7 1.43E+06 (K)HPIPDTK(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
13.34 2% 0.50% 80.7 1.35E+06 (K)VEFDESGK(A) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
13.23 2% 0.50% 67.3 5.64E+06 (K)VPATDVEALK(S) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
13.12 2% 0.60% 76.1 1.18E+06 (R)NDYYGGESSSLNLIK(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
13.09 2% 0.60% 77.2 2.27E+06 (K)ECIISGLLSVDGLK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
13.07 2% 0.60% 69.8 2.44E+05 (K)VEFDESGK(A) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
13.02 2% 0.60% 73 2.24E+06 (K)DSHSVQIILPK(K) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.91 2% 0.60% 75.9 2.47E+05 (R)YEPINNPEEDSCFLTNSYDSTTHFETTVK(D) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.88 2% 0.60% 78.2 1.11E+06 (K)DSHSVQIILPK(K) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.77 2% 0.60% 80.9 3.11E+05 (K)KIVCDPSYLPEK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.61 2% 0.70% 76.7 1.08E+06 (R)VLIHTSVTK(Y) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.6 2% 0.70% 60.9 1.07E+04 (K)YGLEDDTVDFIGHALALHR(D) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.55 2% 0.60% 71.4 3.65E+05 (K)ECIISGLLSVDGLK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.4 2% 0.60% 82 1.98E+05 (R)DDSYLDEPAIDTVK(R) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.33 2% 0.70% 73 3.36E+05 (K)SNLmGLFEK(R) m:Oxidized methionine UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.2 3% 0.70% 76 1.88E+06 (K)EYNVDmVPK(F) m:Oxidized methionine UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.17 3% 0.70% 63.9 1.32E+04 (R)FQGGSPYIYPLYGLGELPQAFAR(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.16 3% 0.70% 77.9 2.43E+04 (K)DSHSVQIILPK(K) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.14 3% 0.70% 69.4 2.25E+05 (K)FFIYVQDYEEDDPK(S) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.12 3% 0.80% 69.3 4.01E+05 (K)VLHmDRNDYYGGESSSLNLIK(L) m:Oxidized methionine UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.01 3% 0.80% 71.9 4.39E+05 (K)DSHSVQIILPK(K) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.86 3% 0.90% 74 6.96E+05 (K)LYAESLAR(F) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.78 3% 0.90% 66.4 1.86E+04 (R)NDYYGGESSSLNLIK(L) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.7 3% 0.90% 72.5 2.29E+05 (R)DDSYLDEPAIDTVKR(M) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.55 3% 1.00% 63.3 2.98E+05 (K)IVCDPSYLPEK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.54 3% 0.90% 72.9 2.20E+05 (K)DVLALYNK(I) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.51 3% 0.90% 71.3 2.56E+06 (R)AICImK(H) C:Carbamidomethylation m:Oxidized methionine UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.42 3% 1.00% 75.2 8.97E+05 (K)SHEGLDLTK(V) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.29 3% 1.00% 77.5 2.43E+06 (K)YLNFK(A) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.23 3% 1% 67.2 8.22E+04 (K)SHEGLDLTK(V) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.23 3% 1% 65.4 7.89E+05 (R)VLIHTSVTK(Y) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
11.14 3% 1% 69 2.45E+05 (K)IVCDPSYLPEK(V) C:Carbamidomethylation UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.89 3% 1% 70.6 1.95E+05 (R)DDSYLDEPAIDTVK(R) UG781 S.halepenseF3 hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]

10.8	3%	1%	63.8	3.49E+05	(K)DVLALYNK(I)		UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.71	3%	1%	66.4	1.76E+06	(K)SNLmGLFEK(R)	m:Oxidized methionine	UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.54	3%	1%	67.5	4.17E+05	(K)AYGVTSEGETAK(C)		UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.37	3%	1%	60.1	5.50E+04	(K)SHEGLDLTK(V)		UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.37	3%	1%	61.7	1.95E+05	(R)KFFIYVQDYEEDDPKSHEGLDLTK(V)		UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.34	3%	1%	61.8	5.67E+05	(R)KSDmYVFCCSYAHNVAPK(G)	C:Carbamidomethylation m:Oxidized methionine	UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.27	3%	1%	66.1	1.35E+05	(K)ECIISGLLSVDGLK(V)	C:Carbamidomethylation	UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.27	3%	1%	75.5	5.33E+05	(R)AICIMK(H)	C:Carbamidomethylation	UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
10.21	3%	1%	63.7	1.80E+05	(R)KFFIYVQDYEEDDPK(S)		UG781	S.halepenseF3	hypothet prot SORBIDRAFT_01g031830 [S bicolor] >gi|241918939|gb|EER92083.1| hypothet prot SORBIDRAFT_01g031830 [S bicolor]
12.41	2%	0.60%	71	9.01E+04	(R)SSHVVLK(T)		UG7840	S.halepenseF3RevF3Rev	hypothet prot SORBIDRAFT_04g006510 [S bicolor] >gi|241933305|gb|EES06450.1| hypothet prot SORBIDRAFT_04g006510 [S bicolor]
14.55	2%	<0.1%	77.3	2.51E+05	(K)TVSSLVFFTK(S)		UG7889	S.halepenseF3	hypothet prot SORBIDRAFT_03g007500 [S bicolor] >gi|241929424|gb|EES02569.1| hypothet prot SORBIDRAFT_03g007500 [S bicolor]
23.02	<0.1%	<0.1%	97	8.78E+06	(K)LSGVYDAWVAADK(F)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
22.85	<0.1%	<0.1%	80.3	8.14E+04	(K)VmYSEGPIGPCECNCPEPCSADESAAVKK(L)	C:Carbamidomethylation m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
22.39	<0.1%	<0.1%	90.1	2.32E+06	(K)NAVWYPQHESVVKPPPALESVINDCR(T)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
21.52	<0.1%	<0.1%	96.7	1.82E+06	(K)LSGVYDAWVAADK(F)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
21.18	<0.1%	<0.1%	95	1.07E+07	(K)AIIAGPELAAAK(L)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
21.16	<0.1%	<0.1%	93	9.89E+05	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
21.1	<0.1%	<0.1%	94.5	2.64E+06	(R)ATIHSYVQGDGK(K)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
20.66	<0.1%	<0.1%	89.4	3.57E+06	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
20.65	<0.1%	<0.1%	86.6	5.88E+05	(K)NAVWYPQHESVVKPPPALESVINDCR(T)		C:Carbamidomethylation	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
20.63	<0.1%	<0.1%	89.4	7.23E+06	(K)NAVWYPQHESVVKPPPALESVINDCR(T)		C:Carbamidomethylation	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
20.37	<0.1%	<0.1%	94.6	1.12E+06	(K)NAVWYPQHESVVKPPPALESVINDCR(T)		C:Carbamidomethylation	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
20.07	<0.1%	<0.1%	93.2	2.33E+07	(K)AIIAGPELAAAK(L)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
19.95	<0.1%	<0.1%	92.5	1.19E+07	(R)ELIDSGGDLDSEEK(K)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
19.95	<0.1%	<0.1%	90.4	7.42E+06	(R)ELIDSGGDLDSEEK(K)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
19.91	<0.1%	<0.1%	98.1	7.23E+06	(K)FLTELLPPAEVK(G)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
19.79	<0.1%	<0.1%	89.7	4.13E+06	(K)NAVWYPQHESVVKPPPALESVINDCR(T)		C:Carbamidomethylation	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
19.39	<0.1%	<0.1%	84	3.84E+04	(K)NAVWYPQHESVVKPPPALESVINDCR(T)		C:Carbamidomethylation	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
19.27	<0.1%	<0.1%	87.4	1.70E+05	(K)LSGVYDAWVAADK(F)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
19.12	<0.1%	<0.1%	69.5	3.22E+06	(K)SMDSGVLHVTCGLTK(Q)		C:Carbamidomethylation	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
19.07	<0.1%	<0.1%	66	8.53E+06	(K)SmDSGVLHVTCGLTK(Q)		C:Carbamidomethylation m:Oxidized methionine	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
18.98	<0.1%	<0.1%	88.9	8.01E+05	(K)SMDSGVLHVTCGLTK(Q)		C:Carbamidomethylation	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
18.78	<0.1%	<0.1%	86.7	1.84E+06	(K)NAVWYPQHESVVKPPPALESVINDCR(T)		C:Carbamidomethylation	UG807	S.halepenseF1 hypothet prot OsI_01937 [Oryza sativa Indica Group]
18.75	<0.1%	<0.1%	89.3	1.86E+06	(K)LKSDSCITECAK(V)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
18.75	<0.1%	<0.1%	91.1	1.83E+05	(K)LSGVYDAWVAADK(F)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
18.63	<0.1%	<0.1%	81	1.57E+06	(K)SDSCITECAK(V)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
18.5	<0.1%	<0.1%	63.5	3.85E+06	(K)SmDSGVLHVTCGLTK(Q)	C:Carbamidomethylation m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
18.33	<0.1%	<0.1%	89.2	6.68E+06	(K)AIIAGPELAAAK(L)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
18.02	<0.1%	<0.1%	83.4	4.73E+06	(K)SDSCITECAK(V)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.97	<0.1%	<0.1%	88.3	5.20E+05	(K)LSGVYDAWVAADK(F)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.96	<0.1%	<0.1%	88.3	2.42E+05	(K)LSGVYDAWVAADKFLTELLPPAEVK(G)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.89	<0.1%	<0.1%	91.2	4.70E+06	(K)LGEATGSMR(V)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.87	<0.1%	<0.1%	82.4	6.96E+04	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.84	<0.1%	<0.1%	95.8	9.37E+06	(K)FLTELLPPAEVK(G)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.78	<0.1%	<0.1%	82.5	1.88E+06	(R)ELIDSGGDLDSEEKK(A)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.77	<0.1%	<0.1%	93.7	2.13E+06	(K)FLTELLPPAEVK(G)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.73	<0.1%	<0.1%	87.5	3.52E+05	(R)ELIDSGGDLDSEEKKAEAAEmEK(S)	m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.61	<0.1%	<0.1%	87.9	1.22E+05	(K)KAEAAEMEK(S)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.55	<0.1%	<0.1%	89.9	3.34E+06	(R)ELIDSGGDLDSEEK(K)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.52	<0.1%	<0.1%	69.2	2.38E+06	(K)SmDSGVLHVTCGLTK(Q)	C:Carbamidomethylation m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.28	<0.1%	<0.1%	95.5	2.72E+06	(K)FLTELLPPAEVK(G)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17.06	<0.1%	<0.1%	90.3	1.48E+05	(K)FLTELLPPAEVK(G)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
17	<0.1%	<0.1%	79.3	5.37E+06	(K)SDSCITECAK(V)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.86	<0.1%	<0.1%	62.3	3.09E+06	(K)SMDSGVLHVTCGLTK(Q)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.84	<0.1%	<0.1%	85.7	3.03E+06	(K)ADEEALNVLNGYLNEK(V)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.82	<0.1%	<0.1%	81.9	7.07E+05	(K)LSGVYDAWVAADK(F)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.75	<0.1%	<0.1%	89	6.54E+06	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.41	<0.1%	<0.1%	74	3.84E+06	(K)SmDSGVLHVTCGLTK(Q)	C:Carbamidomethylation m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.33	<0.1%	<0.1%	91.3	1.74E+06	(K)FLTELLPPAEVK(G)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.1	<0.1%	<0.1%	84.8	8.42E+03	(K)LSGVYDAWVAADKFLTELLPPAEVK(G)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.07	<0.1%	<0.1%	82.2	8.59E+06	(K)LKSDSCITECAK(V)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
16.07	<0.1%	<0.1%	82.7	2.01E+05	(R)ELIDSGGDLDSEEKK(A)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
15.97	<0.1%	<0.1%	82.2	6.28E+04	(K)VMYSEGPIGPCECNCPEPCSADESAAVK(K)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
15.96	<0.1%	<0.1%	77.1	3.20E+06	(K)CSDELSALAK(T)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]

15.79	0.20%	<0.1%	76.7	1.49E+06	(K)ADEEALNVLNGYLNEK(V)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
15.71	0.20%	<0.1%	69.9	4.16E+06	(R)ATIHSYVQGDGK(K)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
15.67	0.20%	<0.1%	84.2	1.65E+06	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
15.49	0.20%	<0.1%	84.2	7.60E+05	(K)FLTELLPPAEVK(G)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
15.34	0.20%	<0.1%	68	3.39E+04	(K)KAEAAEmEK(S)	m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
15.16	0.20%	<0.1%	74.9	1.70E+06	(K)LKSDSCITECAK(V)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
15.16	0.20%	<0.1%	76.6	4.47E+05	(K)AIIAGPELAAAK(L)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
15.04	0.20%	<0.1%	76.2	5.51E+05	(R)ELIDSGGDLDSEEK(K)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
14.86	0.20%	<0.1%	92.4	2.44E+06	(K)FLTELLPPAEVK(G)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
14.84	0.20%	<0.1%	71.4	1.49E+07	(R)ATIHSYVQGDGK(K)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
14.7	0.20%	<0.1%	87.9	3.92E+05	(K)VVDEATSK(A)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
14.67	2%	<0.1%	77.2	1.45E+05	(R)ELIDSGGDLDSEEK(K)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
14.41	2%	<0.1%	84.7	1.03E+06	(K)LGEATGSMR(V)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
13.84	2%	0.40%	86.5	8.62E+04	(K)VVDEATSK(A)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
13.2	2%	0.50%	73.5	7.92E+05	(R)ATIHSYVQGDGK(K)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
13.04	2%	0.60%	77.6	6.76E+04	(K)LGEATGSMR(V)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
12.98	2%	0.60%	65.8	2.13E+06	(K)ADEEALNVLNGYLNEK(V)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
12.86	2%	0.60%	70.3	3.68E+06	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
12.85	2%	0.60%	80	5.29E+05	(K)FLTELLPPAEVK(G)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
12.66	2%	0.60%	72.3	3.84E+05	(K)LKSDSCITECAK(V)	C:Carbamidomethylation	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
12.44	2%	0.60%	76.2	1.24E+05	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
12.39	2%	0.60%	73.1	1.21E+06	(R)ELIDSGGDLDSEEK(K)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
12.26	2%	0.70%	88.9	4.63E+05	(K)TLAETK(A)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
12.07	3%	0.80%	73.7	2.75E+05	(K)AIIAGPELAAAK(L)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
12.01	3%	0.80%	63.2	1.20E+06	(K)SmDSGVLHVTCGLTK(Q)	C:Carbamidomethylation m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
11.75	3%	0.90%	66.3	1.07E+05	(K)AIIAGPELAAAK(L)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
11.59	3%	1.00%	80	1.37E+05	(K)FLTELLPPAEVK(G)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
11.1	3%	1%	73.7	6.33E+05	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
10.98	3%	1%	61.3	2.94E+05	(K)LGEATGSmR(V)	m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
10.88	3%	1%	73.3	1.31E+05	(K)FLTELLPPAEVK(G)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
10.85	3%	1%	70.5	3.11E+05	(K)FLTELLPPAEVK(G)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
10.78	3%	1%	61.7	8.83E+04	(R)ELIDSGGDLDSEEK(K)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
10.76	3%	1%	72.2	1.34E+04	(K)VVDEATSK(A)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
10.53	3%	1%	67.6	1.04E+06	(K)LGEATGSmR(V)	m:Oxidized methionine	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
10.46	3%	1%	61.3	8.88E+05	(K)LSGVYDAWVAADK(F)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
10.41	3%	1%	72.7	5.29E+06	(K)NLAEIR(A)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
10.23	3%	1%	67	1.20E+05	(R)TAIEAVNQEIYSAESQLK(N)		UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]
10.14	3%	1%	64.5	2.00E+05	(K)AIIAGPELAAAK(L)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
10.1	3%	1%	70.8	1.55E+05	(K)FLTELLPPAEVK(G)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
10.05	5%	1%	71.4	1.82E+07	(K)NLAEIR(A)	UG807	S.halepenseF1	hypothet prot OsI_01937 [Oryza sativa Indica Group]	
16.48	<0.1%	<0.1%	88.9	2.83E+05	(R)IEASPEAAQK(A)	UG827	S.halepenseF3	unknown [Zea mays]	
10.02	5%	1%	70.3	4.84E+06	(R)NLSSHVWR(E)	UG9604	S.halepenseF1Rev	hypothet prot SORBIDRAFT_05g021720 [S bicolor] >gi|241936805|gb|EES09950.1| hypothet prot SORBIDRAFT_05g021720 [S bicolor]	

Table E7 Identification of putative allergen components of JGP; transcriptome, proteome and allergome search for matches with grass pollen allergens. (June 26)

Hit	filename	reading_frame_of_match	nr_annotation	SwissProt_annotation		Iteration_query-ID	Iteration_query-def	Hit_num	Hit_accession	Hit_len
	Hsp_num	Hsp_bit-score	Hsp_score	Hsp_evalue	Hsp_query-from	Hsp_query-to	Hsp_hit-from	Hsp_hit-to	Hsp_identity	Hsp_positive
	Hsp_gaps	Hsp_align-len	%ID	%ID/(AL-GL)	AL-GL/QL					
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2		S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor]			>gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_4099	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	11	87282	246	1	51.2174	121	2.58E-07	163	261	53	147	30	53	6	100	0.3	0.319148936	0.358778626
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2		S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor]			>gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_4100	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	11	87282	246	1	51.2174	121	2.55E-07	163	261	53	147	30	53	6	100	0.3	0.319148936	0.358778626
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3		S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]			>gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_2140	"Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	10	35050	252	1	45.8246	107	1.43E-05	167	255	72	158	27	47	4	90	0.3	0.313953488	0.326996198
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3		S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]			>gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_2131	"Dac g 1 (""Grasses, Group 1;Expansin"")"	11	35050	252	1	44.2838	103	0.000050132	168	256	72	158	27	46	4	90	0.3	0.313953488	0.325757576
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3		S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]			>gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_2119	"Hol l 1 (""Grasses, Group 1;Expansin"")"	10	35050	252	1	45.8246	107	0.00001759	167	255	72	158	27	47	4	90	0.3	0.313953488	0.326996198
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3		S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]			>gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_2139	"Poa p 1 (""Grasses, Group 1;Expansin"")"	10	35050	252	1	46.595	109	8.74E-06	167	255	72	158	27	47	4	90	0.3	0.313953488	0.326996198
Unigene492	20120710_JGPPBS_1_7.8636.8708.2		S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]			>gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2		Query_1920	"Bra di 2 (""Grasses, Group 2"")"	1	39.2762	90	0.000176667	23	102	25	103	24	41	1	80	0.3	0.303797468	0.738317757	6	47854	201
Unigene492	20120710_JGPPBS_1_7.8636.8708.2		S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]			>gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2		Query_2121	"Tri ur 2 (""Grasses, Group 2"")"	1	45.4394	106	7.34E-07	21	90	40	103	21	39	6	70	0.3	0.328125	0.711111111	3	47854	201
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3		S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]			>gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_6111	"Lol p 3 (""Grasses, Group 3"")"	7	35050	252	1	34.6538	78	0.00760904	2	89	74	160	27	40	5	90	0.3	0.317647059	0.87628866
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3		S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]			>gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_6112	"Lol p 3 (""Grasses, Group 3"")"	7	35050	252	1	34.6538	78	0.00760904	2	89	74	160	27	40	5	90	0.3	0.317647059	0.87628866
Unigene551	20120710_JGPPBS_1_8.8266.8340.2		S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]			>gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_2122	"Hol l 1 (""Grasses, Group 1;Expansin"")"	10	48366	255	1	45.0542	105	2.94E-05	173	264	90	177	28	47	6	93	0.301075269	0.32183908	0.328301887
Unigene551	20120710_JGPPBS_1_8.8266.8340.2		S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]			>gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_2123	"Hol l 1 (""Grasses, Group 1;Expansin"")"	10	48366	255	1	45.0542	105	2.94E-05	173	264	90	177	28	47	6	93	0.301075269	0.32183908	0.328301887
Unigene552	20120710_JGPPBS_1_3.8565.8570.4		S.halepenseFrame1	hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor]			>gi|241922455|gb|EER95599.1| hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor]	Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1		Query_1781	"Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"	7	13553	604	1	83.5741	205	6.39E-17	69	310	104	372	84	128	47	279	0.301075269	0.362068966	0.543325527
Unigene492	20120710_JGPPBS_1_7.8636.8708.2		S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]			>gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2		Query_4450	"Ory s 2 (""Grasses, Group 2"")"	1	38.5058	88	0.0002764	3	90	17	109	28	45	5	93	0.301075269	0.318181818	0.977777778	5	47854	201
Unigene551	20120710_JGPPBS_1_8.8266.8340.2		S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]			>gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_1989	"Tri a 3 (""Grasses, Group 3"")"	1	48366	255	1	48.9062	115	1.38E-07	25	115	89	176	28	44	7	93	0.301075269	0.325581395	0.728813559
Unigene551	20120710_JGPPBS_1_8.8266.8340.2		S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]			>gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1		Query_2120	"Tri ur 3 (""Grasses, Group 3"")"	1																					

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        48366   255     1       51.2174 121     1.93E-08        26      116     89      176     28      46      7       93      0.301075269     0.325581395
        0.722689076
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3      S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_482 "Lol p 2 (""Grasses, Group 2"")"       8       35050   252
        1       35.039  79      0.00470402      26      87      98      160     19      34      1       63      0.301587302     0.306451613     0.704545455
Unigene552      20120710_JGPPBS_1_3.8565.8570.4      S.halepenseFrame1   hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor] >gi|241922455|gb|EER95599.1| hypothetical protein
SORBIDRAFT_01g048880 [Sorghum bicolor]  Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1              Query_4436      "Zea m 13 (""Polygalacturonase;Grasses,
Group 13"")"     8       13553   604     1       77.0258 188     2.68E-15        7       200     173     372     64      103     30      212     0.301886792
        0.351648352     0.574132492
Unigene7876     20120710_JGPPBS_1_4.7246.7246.2      S.halepenseFrame2   protein disulfide isomerase [Oryza sativa]       Protein disulfide-isomerase OS=Zea mays GN=PDI PE=2 SV=1
        Query_1234      Tri a 25 (Thioredoxin)      18      50396   154     1       31.9574 71      0.0940237       49      98      1       52      16      25      4
        53      0.301886792     0.326530612     0.392
Unigene7876     20120710_JGPPBS_1_4.7246.7246.2      S.halepenseFrame2   protein disulfide isomerase [Oryza sativa]       Protein disulfide-isomerase OS=Zea mays GN=PDI PE=2 SV=1
        Query_1240      Zea m 25 (Thioredoxin)      19      50396   154     1       31.5722 70      0.143778        52      101     1       52      16      25      4
        53      0.301886792     0.326530612     0.3828125
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_929 "Dac g 1 (""Grasses, Group 1;Expansin"")"      12
        88192   280     1       40.0466 92      0.00125431      144     238     58      148     29      47      6       96      0.302083333     0.322222222
        0.375
Unigene552      20120710_JGPPBS_1_3.8565.8570.4      S.halepenseFrame1   hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor] >gi|241922455|gb|EER95599.1| hypothetical protein
SORBIDRAFT_01g048880 [Sorghum bicolor]  Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1              Query_1454      "Bra di 13 (""Polygalacturonase;Grasses,
Group 13"")"     6       13553   604     1       92.8189 229     5.13E-20        45      241     97      311     68      115     38      225     0.302222222
        0.363636364     0.453883495
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3      S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2121      "Tri ur 2 (""Grasses, Group 2"")"        10
        35050   252     1       27.7202 60      1.47908 48      90      127     169     13      19      0       43      0.302325581     0.302325581
        0.477777778
Unigene335      20120710_JGPPBS_1_7.5768.5772.2      S.halepenseFrame2Rev        unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_1540      "Tri a 1 (""Grasses, Group 1;Expansin"")"        7       63886   454     1       93.5893 231     2.51E-21        42      272     100     309     72
        106     35      238     0.302521008     0.354679803     0.743589744
Unigene335      20120710_JGPPBS_1_7.5768.5772.2      S.halepenseFrame2Rev        unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2944      "Sor b 1 (""Grasses, Group 1;Expansin"")"        6       63886   454     1       100.908 250     5.41E-24        22      266     79      309     76
        111     26      251     0.302788845     0.337777778     0.845864662
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4099      "Cyn d 1 (""CCD-bearing Protein
(XF);Grasses, Group 1;Expansin"")"      12      88192   280     1       48.521  114     2.41E-06        164     261     59      152     30      51      6       99
        0.303030303     0.322580645     0.354961832
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4100      "Cyn d 1 (""CCD-bearing Protein
(XF);Grasses, Group 1;Expansin"")"      12      88192   280     1       48.521  114     2.38E-06        164     261     59      152     30      51      6       99
        0.303030303     0.322580645     0.354961832
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_1587      "Tri ur 1 (""Grasses, Group 1;Expansin;CCD-
bearing Protein (XF)"")"     9       87282   246     1       44.669  104     4.47E-06        29      126     52      145     30      46      6       99      0.303030303
        0.322580645     0.720930233
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2130      "Tri ur 1 (""Grasses, Group 1;Expansin;CCD-
bearing Protein (XF)"")"     10      87282   246     1       45.0542 105     1.49E-05        106     203     52      145     30      46      6       99      0.303030303
        0.322580645     0.451456311
Unigene492      20120710_JGPPBS_1_7.8636.8708.2      S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2074      "Bra di 2 (""Grasses, Group 2"")"       3       47854   201     1
        45.4394 106     1.73E-06        19      113     5       103     30      49      4       99      0.303030303     0.315789474     0.805084746
Unigene551      20120710_JGPPBS_1_8.8266.8340.2      S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_1922      "Bra di 2 (""Grasses, Group 2"")"       4
        48366   255     1       53.9138 128     2.34E-09        26      124     87      180     30      48      5       99      0.303030303     0.319148936
        0.758064516
Unigene551      20120710_JGPPBS_1_8.8266.8340.2      S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2112      "Hor v 2 (""Grasses, Group 2"")"       4
        48366   255     1       48.1358 113     3.04E-07        22      116     83      175     30      50      10      99      0.303030303     0.337078652
        0.741666667
Unigene492      20120710_JGPPBS_1_7.8636.8708.2      S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2044      "Ory s 3 (""Grasses, Group 3"")"       6       47854   201     1
        56.6102 135     1.38E-10        23      116     10      108     30      55      5       99      0.303030303     0.319148936     0.796610169
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CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_2727 "Ory s 2 (""Grasses, Group 2"")" 7 70550 436 1
44.2838 103 5.53E-06 3 86 207 295 27 43 5 89 0.303370787 0.321428571 0.933333333
CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_1926 "Ory s 2 (""Grasses, Group 2"")" 7 70550 436 1
43.5134 101 9.74E-06 12 95 207 295 27 43 5 89 0.303370787 0.321428571 0.848484848
Unigene397 20120710_JGPPBS_1_7.9063.9133.3 S.halepenseFrame1Rev hypothetical protein SORBIDRAFT_04g021750 [Sorghum bicolor] >gi|241932039|gb|EES05184.1| hypothetical protein SORBIDRAFT_04g021750 [Sorghum bicolor] Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1 Query_2548 "Aeg ta 5 (""Grasses, Group 5"")" 5 29611 319 1 55.0694 131 4.89E-09 1 176 59 250 59 97 20 194 0.304123711
0.33908046 0.961325967
CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_2042 "Ory s 2 (""Grasses, Group 2"")" 6 70550 436 2
43.5134 101 0.000082215 136 222 202 293 28 43 5 92 0.304347826 0.32183908 0.381578947
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_6267 "Dac g 3 (""Grasses, Group 3"")" 4
48366 255 1 48.9062 115 9.97E-08 3 92 89 175 28 45 7 92 0.304347826 0.329411765
0.885416667
Unigene6038 20120710_JGPPBS_1_4.2924.2934.2 S.halepenseFrame1 protein disulfide isomerase [Triticum durum] >gi|12056121|emb|CAC21231.1| protein disulfide isomerase [Triticum durum] Protein disulfide-isomerase OS=Zea mays GN=PDI PE=2 SV=1 Query_1140 Tri a Trx (Thioredoxin) 13 14005 183 1 48.1358 113
1.14E-07 30 104 72 153 25 42 7 82 0.304878049 0.333333333 0.63559322
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_4099 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")" 10 35050 252 1 52.373 124 9.93E-08 166 262 75 169 30 50 4 98 0.306122449
0.319148936 0.358778626
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_4100 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")" 10 35050 252 1 52.373 124 9.74E-08 166 262 75 169 30 50 4 98 0.306122449
0.319148936 0.358778626
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_4098 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")" 11 35050 252 1 48.9062 115 1.45E-06 166 262 75 169 30 50 4 98 0.306122449
0.319148936 0.358778626
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2138 "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")" 12 87282 246 1 42.3578 98 0.000222188 167 263 53 145 30 48 6 98
0.306122449 0.326086957 0.349809886
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2129 "Tri a 1 (""Grasses, Group 1;Expansin"")" 10 87282 246 1 44.2838 103 0.000046531 171 267 53 145 30 46 6 98 0.306122449
0.326086957 0.340740741
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2046 "Ory s 2 (""Grasses, Group 2"")" 5 47854 201 1
48.521 114 1.10E-07 25 117 12 109 30 50 5 98 0.306122449 0.322580645 0.794871795
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_1774 "Ory s 2 (""Grasses, Group 2"")" 5 47854 201 1
49.2914 116 5.77E-08 25 117 12 109 30 50 5 98 0.306122449 0.322580645 0.794871795
CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_2563 "Ory s 2 (""Grasses, Group 2"")" 7 70550 436 1
35.8094 81 0.00397516 40 101 234 295 19 31 0 62 0.306451613 0.306451613 0.59047619
CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_2573 "Ory s 2 (""Grasses, Group 2"")" 7 70550 436 1
43.5134 101 1.41E-05 21 109 202 295 29 45 5 94 0.308510638 0.325842697 0.787610619
CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_2575 "Ory s 2 (""Grasses, Group 2"")" 7 70550 436 1
44.669 104 5.74E-06 21 109 202 295 29 46 5 94 0.308510638 0.325842697 0.787610619
CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_2038 "Ory s 2 (""Grasses, Group 2"")" 7 70550 436 1
47.7506 112 5.26E-07 25 113 202 295 29 47 5 94 0.308510638 0.325842697 0.760683761
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2042 "Ory s 2 (""Grasses, Group 2"")" 5 47854 201 2
45.8246 107 1.01E-05 25 113 12 105 29 49 5 94 0.308510638 0.325842697 0.390350877
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_6111 "Lol p 3 (""Grasses, Group 3"")" 3
88192 280 1 46.9802 110 4.49E-07 5 92 61 147 29 48 13 94 0.308510638 0.358024691
0.835051546

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CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_6112          "Lol p 3 (""Grasses, Group 3"")"        3
          88192     280       1         46.9802   110       4.49E-07  5         92        61        147       29        48        94        0.308510638         0.358024691
          0.835051546
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2563          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
          40.0466   92        0.000115165         29        105       29        109       25        39        4         81        0.308641975         0.324675325         0.733333333
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_1634          "Ory s 1 (""Grasses, Group 1;Expansin"")"        11
          35050     252       1         48.9062   115       1.59E-07  32        127       74        167       30        49        4         97        0.309278351         0.322580645
          0.715384615
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_1921          "Bra di 2 (""Grasses, Group 2"")"       4
          87282     246       1         58.5362   140       5.86E-11  1         123       13        146       43        67        21        139       0.309352518         0.36440678
          0.951612903
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_1920          "Bra di 2 (""Grasses, Group 2"")"       3
          88192     280       1         41.9726   97        2.79E-05  36        106       81        151       22        38        0         71        0.309859155         0.309859155
          0.663551402
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_192 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"       12        87282     246       1         51.9878   123       1.04E-07  145       243       53        147       31        54        6         100       0.31      0.329787234
          0.385245902
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_193 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"       12        87282     246       1         52.373    124       8.67E-08  145       243       53        147       31        54        6         100       0.31      0.329787234
          0.385245902
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_164 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"       10        88192     280       1         55.0694   131       1.18E-08  145       243       58        152       31        55        6         100       0.31      0.329787234
          0.382113821
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4098          "Cyn d 1 (""CCD-bearing Protein
(XF);Grasses, Group 1;Expansin"")"       12        87282     246       1         48.9062   115       1.59E-06  163       261       53        147       31        53        6         100
          0.31      0.329787234         0.358778626
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2124          "Tri ur 3 (""Grasses, Group 3"")"       7
          35050     252       1         30.8018   68        0.265938  1         114       49        160       36        51        6         116       0.310344828         0.327272727
          0.909090909
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2138          "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"       10        35050     252       1         45.8246   107       1.51E-05  167       255       72        158       28        46        4         90        0.311111111
          0.325581395         0.326996198
Unigene552          20120710_JGPPBS_1_3.8565.8570.4         S.halepenseFrame1   hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor] >gi|241922455|gb|EER95599.1| hypothetical protein
SORBIDRAFT_01g048880 [Sorghum bicolor]  Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1              Query_2276          "Pas n 13 (""Grasses, Group
13;Polygalacturonase"")"      6         13553     604       1         90.5077   223       2.70E-19  56        252       97        311       70        113       38        225       0.311111111
          0.374331551         0.475826972
Unigene552          20120710_JGPPBS_1_3.8565.8570.4         S.halepenseFrame1   hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor] >gi|241922455|gb|EER95599.1| hypothetical protein
SORBIDRAFT_01g048880 [Sorghum bicolor]  Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1              Query_2277          "Pas n 13 (""Grasses, Group
13;Polygalacturonase"")"      6         13553     604       1         90.5077   223       2.70E-19  56        252       97        311       70        113       38        225       0.311111111
          0.374331551         0.475826972
Unigene552          20120710_JGPPBS_1_3.8565.8570.4         S.halepenseFrame1   hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor] >gi|241922455|gb|EER95599.1| hypothetical protein
SORBIDRAFT_01g048880 [Sorghum bicolor]  Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1              Query_2278          "Pas n 13 (""Grasses, Group
13;Polygalacturonase"")"      6         13553     604       1         90.1225   222       2.88E-19  56        252       97        311       70        113       38        225       0.311111111
          0.374331551         0.475826972
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_6267          "Dac g 3 (""Grasses, Group 3"")"        7
          35050     252       1         37.7354   86        0.000588857         2         89        74        160       28        40        5         90        0.311111111         0.329411765
          0.885416667
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_287 "Phl p 3 (""Grasses, Group 3"")"       7         35050     252
          1         37.7354   86        0.000589709         3         90        74        160       28        40        5         90        0.311111111         0.329411765         0.87628866
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CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_6111          "Lol p 3 (""Grasses, Group 3"")"        2         70550     436       1
         56.9954   136       2.58E-10  2         93        202       294       29        50        1         93        0.311827957         0.315217391         0.948453608
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_6112          "Lol p 3 (""Grasses, Group 3"")"        2         70550     436       1
         56.9954   136       2.58E-10  2         93        202       294       29        50        1         93        0.311827957         0.315217391         0.948453608
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_288 "Phl p 3 (""Grasses, Group 3"")"        3         47854     201       1
         51.9878   123       3.69E-09  3         94        12        104       29        48        1         93        0.311827957         0.315217391         0.948453608
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2114          "Ory s 1 (""Grasses, Group 1;Expansin"")"        12
         35050     252       1         50.0618   118       6.18E-07  170       264       75        167       30        50        4         96        0.3125    0.326086957         0.344569288
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2115          "Ory s 1 (""Grasses, Group 1;Expansin"")"        12
         35050     252       1         50.0618   118       6.18E-07  170       264       75        167       30        50        4         96        0.3125    0.326086957         0.344569288
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                  Query_2041          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
         48.521    114       1.14E-07  25        115       12        107       30        50        5         96        0.3125    0.32967033          0.777777778
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                  Query_2043          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
         48.521    114       1.17E-07  25        115       12        107       30        50        5         96        0.3125    0.32967033          0.777777778
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_6267          "Dac g 3 (""Grasses, Group 3"")"        5
         88192     280       1         44.669    104       3.01E-06  3         96        61        151       30        47        7         96        0.3125    0.337078652         0.927083333
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_192 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"      10        88192     280       1         53.9138   128       3.26E-08  146       243       59        152       31        53        6         99        0.313131313
         0.333333333         0.381147541
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_193 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"      11        88192     280       1         53.9138   128       2.69E-08  146       243       59        152       31        53        6         99        0.313131313
         0.333333333         0.381147541
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4098          "Cyn d 1 (""CCD-bearing Protein
(XF);Grasses, Group 1;Expansin"")"      10        88192     280       1         50.0618   118       6.72E-07  164       261       59        152       31        52        6         99
         0.313131313         0.333333333         0.354961832
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_1921          "Bra di 2 (""Grasses, Group 2"")"        5
         48366     255       1         56.9954   136       2.05E-10  26        124       87        180       31        49        5         99        0.313131313         0.329787234
         0.758064516
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2248          "Zea m 1 (""Grasses, Group 1;Expansin"")"        13
         35050     252       1         46.2098   108       1.37E-05  175       262       73        158       28        46        4         89        0.314606742         0.329411765
         0.314814815
Unigene681          20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1126          Bra di 7 (Polcalcin;CBP)        36
         84312     325       1         36.1946   82        0.00181306          11        63        130       183       17        30        1         54        0.314814815         0.320754717
         0.6625
Unigene681          20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1339          Hor v 7 (Polcalcin;CBP)         27
         84312     325       2         35.4242   80        0.00314183          9         61        130       183       17        29        1         54        0.314814815         0.320754717
         0.679487179
Unigene681          20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1137          Ory s 7 (Polcalcin;CBP)         27
         84312     325       2         35.8094   81        0.00207771          13        65        130       183       17        30        1         54        0.314814815         0.320754717
         0.646341463
Unigene681          20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1338          Phl p 7 (Polcalcin;CBP)         29
         84312     325       2         35.8094   81        0.0019347 9         61        130       183       17        30        1         54        0.314814815         0.320754717
         0.679487179
Unigene681          20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1375          Sor b 7 (Polcalcin;CBP)         33
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        84312   325     2       35.8094 81      0.0021574 11      63      130     183     17      29      1       54      0.314814815       0.320754717
        0.6625
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1          Query_1246          Zea m 7 (Polcalcin;CBP)       28
        84312   325     2       36.965  84      0.000972564       11      63      130     183     17      30      1       54      0.314814815       0.320754717
        0.6625
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1          Query_1376          Zea m 7 (Polcalcin;CBP)       34
        84312   325     1       36.965  84      0.000972564       11      63      130     183     17      30      1       54      0.314814815       0.320754717
        0.6625
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1              Query_2074          "Bra di 2 (""Grasses, Group 2"")"       4       70550   436     1
        44.669  104     5.75E-06        24      113     202     293     29      46      2       92      0.315217391       0.322222222       0.762711864
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2112          "Hor v 2 (""Grasses, Group 2"")"       3       47854   201     1
        48.521  114     1.15E-07        26      117     13      104     29      47      0       92      0.315217391       0.315217391       0.766666667
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1              Query_287 "Phl p 3 (""Grasses, Group 3"")"       2       70550   436     1
        59.6918 143     3.57E-11        3       93      202     293     29      51      1       92      0.315217391       0.318681319       0.93814433
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1              Query_5365          "Zea m 1 (""Grasses, Group 1;Expansin"")"
        12      88192   280     1       43.1282 100     0.000122836       173     266     58      147     30      47      6       95      0.315789474
        0.337078652       0.330855019
Unigene552      20120710_JGPPBS_1_3.8565.8570.4          S.halepenseFrame1   hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor] >gi|241922455|gb|EER95599.1| hypothetical protein
SORBIDRAFT_01g048880 [Sorghum bicolor]  Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1              Query_5492          "Zea m 13 (""Polygalacturonase;Grasses,
Group 13"")"     7       13553   604     1       68.1662 165     1.40E-12  100     227     191     317     42      73      11      133     0.315789474
        0.344262295       0.423611111
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1              Query_2074          "Bra di 2 (""Grasses, Group 2"")"       2
        88192   280     1       51.2174 121     2.56E-08  20      113     56      147     30      51      4       95      0.315789474       0.32967033
        0.771186441
Unigene492      20120710_JGPPBS_1_7.8636.8708.2          S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2727          "Ory s 2 (""Grasses, Group 2"")"       5       47854   201     1
        48.521  114     6.69E-08        1       90      15      109     30      48      5       95      0.315789474       0.333333333       1
Unigene6038     20120710_JGPPBS_1_4.2924.2934.2          S.halepenseFrame1   protein disulfide isomerase [Triticum durum] >gi|12056121|emb|CAC21231.1| protein disulfide isomerase [Triticum
durum]    Protein disulfide-isomerase OS=Zea mays GN=PDI PE=2 SV=1              Query_1998          Zea m 25 (Thioredoxin)        8       14005   183     1       54.299  129
        7.69E-10  30      116     72      166     30      51      8       95      0.315789474       0.344827586       0.713114754
Unigene492      20120710_JGPPBS_1_7.8636.8708.2          S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_287 "Phl p 3 (""Grasses, Group 3"")"       3       47854   201     1
        50.8322 120     1.04E-08        3       96      12      100     30      50      7       95      0.315789474       0.340909091       0.907216495
Unigene6635     20120710_JGPPBS_1_6.11090.11155.3        S.halepenseFrame2Rev          PREDICTED: protein disulfide isomerase-like 2-1-like [Brachypodium distachyon]  Protein disulfide
isomerase-like 2-2 OS=Oryza sativa subsp. japonica GN=PDIL2-2 PE=2 SV=1               Query_1140          Tri a Trx (Thioredoxin)       26      66747   104     1       25.7942 55
        9.96655 55      92      8       45      12      17      0       38      0.315789474       0.315789474       0.322033898
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3          S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1              Query_192 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"    11      35050   252     1       53.5286 127     3.97E-08  148     244     75      169     31      51      4       98      0.316326531
        0.329787234       0.385245902
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3          S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1              Query_193 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"    10      35050   252     1       54.299  129     1.65E-08  148     244     75      169     31      51      4       98      0.316326531
        0.329787234       0.385245902
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1              Query_5701          "Hor v 1 (""Grasses, Group 1;Expansin"")"
        10      87282   246     1       44.669  104     4.02E-06  25      121     53      145     31      49      6       98      0.316326531       0.336956522
        0.760330579
Unigene492      20120710_JGPPBS_1_7.8636.8708.2          S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2337          "Ory s 2 (""Grasses, Group 2"")"       5       47854   201     1
        53.5286 127     1.01E-09        4       96      12      109     31      53      5       98      0.316326531       0.333333333       0.96875
Unigene492      20120710_JGPPBS_1_7.8636.8708.2          S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2039          "Ory s 2 (""Grasses, Group 2"")"       5       47854   201     1
        54.299  129     9.69E-10        25      117     12      109     31      53      5       98      0.316326531       0.333333333       0.794871795
Unigene492      20120710_JGPPBS_1_7.8636.8708.2          S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2036          "Ory s 3 (""Grasses, Group 3"")"       5       47854   201     1
        56.6102 135     1.44E-10        25      117     12      109     31      54      5       98      0.316326531       0.333333333       0.794871795
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Unigene1334	20120710_JGPPBS_1_4.2209.2212.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_03g028140 [Sorghum bicolor] >gi|241927940|gb|EES01085.1| hypothetical protein
SORBIDRAFT_03g028140 [Sorghum bicolor]	Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1	Query_1769	"Sor b 13 (""Grasses, Group
13;Polygalacturonase"")"	9	41643	396	1	74.3294	181	3.62E-14	139	305	47	220	57	88	19	180	0.316666667
	0.354037267	0.381516588
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2121	"Tri ur 2 (""Grasses, Group 2"")"	5	70550	436	1
	43.8986	102	7.55E-06	25	84	234	293	19	34	0	60	0.316666667	0.316666667	0.666666667
Unigene335	20120710_JGPPBS_1_7.5768.5772.2	S.halepenseFrame2Rev	unknown [Zea mays]	Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
	Query_2942	"Pas n 1 (""Grasses, Group 1;Expansin"")"	6	63886	454	1	107.842	268	2.41E-26	42	265	100	309	73
	102	26	230	0.317391304	0.357843137	0.769811321
Unigene335	20120710_JGPPBS_1_7.5768.5772.2	S.halepenseFrame2Rev	unknown [Zea mays]	Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
	Query_2129	"Tri a 1 (""Grasses, Group 1;Expansin"")"	6	63886	454	1	100.908	250	7.45E-24	45	270	100	309	73
	110	24	230	0.317391304	0.354368932	0.762962963
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_6111	"Lol p 3 (""Grasses, Group 3"")"	5
	48366	255	1	45.8246	107	1.24E-06	29	92	110	175	21	36	2	66	0.318181818	0.328125	0.659793814
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_6112	"Lol p 3 (""Grasses, Group 3"")"	5
	48366	255	1	45.8246	107	1.24E-06	29	92	110	175	21	36	2	66	0.318181818	0.328125	0.659793814
Unigene335	20120710_JGPPBS_1_7.5768.5772.2	S.halepenseFrame2Rev	unknown [Zea mays]	Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
	Query_5701	"Hor v 1 (""Grasses, Group 1;Expansin"")"	7	63886	454	1	57.3806	137	4.13E-10	8	119	198	304	36
	53	7	113	0.318584071	0.339622642	0.876033058
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2120	"Tri ur 3 (""Grasses, Group 3"")"	6
	35050	252	1	35.4242	80	0.00686491	2	112	51	160	36	52	5	113	0.318584071	0.333333333
	0.907563025
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2128	"Bra di 1 (""Grasses, Group 1;Expansin"")"	10
	35050	252	1	52.7582	125	8.95E-08	169	258	72	159	29	49	4	91	0.318681319	0.333333333
	0.328301887
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_5701	"Hor v 1 (""Grasses, Group 1;Expansin"")"	9
	35050	252	1	45.8246	107	1.62E-06	25	114	72	159	29	47	4	91	0.318681319	0.333333333
	0.719008264
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2113	"Hor v 1 (""Grasses, Group 1;Expansin"")"	10
	35050	252	1	46.595	109	9.77E-06	166	255	72	159	29	47	4	91	0.318681319	0.333333333
	0.332061069
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_5365	"Zea m 1 (""Grasses, Group 1;Expansin"")"	11
	35050	252	1	50.8322	120	3.87E-07	173	262	72	159	29	49	4	91	0.318681319	0.333333333
	0.323420074
Unigene335	20120710_JGPPBS_1_7.5768.5772.2	S.halepenseFrame2Rev	unknown [Zea mays]	Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
	Query_5365	"Zea m 1 (""Grasses, Group 1;Expansin"")"	6	63886	454	1	98.5969	244	4.11E-23	44	268	94	305	73
	112	21	229	0.318777293	0.350961538	0.773234201
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_4829	"Dac g 2 (""Grasses, Group 2"")"	4
	48366	255	1	53.1434	126	5.58E-09	28	118	87	175	30	53	8	94	0.319148936	0.348837209
	0.704918033
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_4834	"Hol l 2 (""Grasses, Group 2"")"	4
	48366	255	1	53.1434	126	5.11E-09	28	118	87	175	30	53	8	94	0.319148936	0.348837209
	0.704918033
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2112	"Hor v 2 (""Grasses, Group 2"")"	2	70550	436	1
	55.8398	133	1.13E-09	26	119	203	296	30	48	0	94	0.319148936	0.319148936	0.783333333
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_4830	"Lol m 2 (""Grasses, Group 2"")"	4
	48366	255	1	53.1434	126	5.11E-09	28	118	87	175	30	53	8	94	0.319148936	0.348837209
	0.704918033
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2337	"Ory s 2 (""Grasses, Group 2"")"	7	70550	436	1
	50.8322	120	3.33E-08	4	92	202	295	30	48	5	94	0.319148936	0.337078652	0.927083333
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2039	"Ory s 2 (""Grasses, Group 2"")"	7	70550	436	1
	51.2174	121	3.58E-08	25	113	202	295	30	48	5	94	0.319148936	0.337078652	0.760683761
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CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2051          "Ory s 2 (""Grasses, Group 2"")"        7         70550     436       1
         50.0618   118       1.08E-07  25        113       202       295       30        48        5         94        0.319148936         0.337078652         0.760683761
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2046          "Ory s 2 (""Grasses, Group 2"")"        7         70550     436       1
         45.4394   106       2.95E-06  25        113       202       295       30        46        5         94        0.319148936         0.337078652         0.760683761
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_4831          "Phl p 2 (""Grasses, Group 2"")"        4
         48366     255       1         53.1434   126       5.11E-09  28        118       87        175       30        53        8         94        0.319148936         0.348837209
         0.704918033
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_4833          "Poa p 2 (""Grasses, Group 2"")"        4
         48366     255       1         53.1434   126       5.11E-09  28        118       87        175       30        53        8         94        0.319148936         0.348837209
         0.704918033
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_4832          "Tri a 2 (""Grasses, Group 2"")"        4
         48366     255       1         53.1434   126       5.11E-09  28        118       87        175       30        53        8         94        0.319148936         0.348837209
         0.704918033
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2053          "Ory s 2 (""Grasses, Group 2"")"        7         70550     436       1
         52.373    124       1.48E-08  22        113       199       295       31        49        5         97        0.319587629         0.336956522         0.786324786
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2036          "Ory s 3 (""Grasses, Group 3"")"        6         70550     436       1
         52.373    124       1.65E-08  22        113       199       295       31        47        5         97        0.319587629         0.336956522         0.786324786
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2114          "Ory s 1 (""Grasses, Group 1;Expansin"")"
         11        88192     280       1         51.6026   122       2.02E-07  168       266       59        153       32        55        6         100       0.32      0.340425532
         0.352059925
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2115          "Ory s 1 (""Grasses, Group 1;Expansin"")"
         11        88192     280       1         51.6026   122       2.02E-07  168       266       59        153       32        55        6         100       0.32      0.340425532
         0.352059925
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2248          "Zea m 1 (""Grasses, Group 1;Expansin"")"        11
         48366     255       1         46.595    109       8.33E-06  171       269       83        177       32        49        6         100       0.32      0.340425532         0.348148148
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_1922          "Bra di 2 (""Grasses, Group 2"")"       5
         87282     246       1         51.6026   122       1.53E-08  24        123       52        146       32        53        5         100       0.32      0.336842105         0.766129032
Unigene1403         20120710_JGPPBS_1_8.6880.6965.2         S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_05g001956 [Sorghum bicolor] >gi|241934780|gb|EES07925.1| hypothetical
protein SORBIDRAFT_05g001956 [Sorghum bicolor]    Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1           Query_2548          "Aeg ta 5 (""Grasses,
Group 5"")"         6         24831     253       2         40.817    94        0.00036042          81        172       45        143       32        57        9         100       0.32
         0.351648352         0.502762431
Unigene335          20120710_JGPPBS_1_7.5768.5772.2         S.halepenseFrame2Rev        unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
         Query_2114          "Ory s 1 (""Grasses, Group 1;Expansin"")"        6         63886     454       1         106.301   264       6.93E-26  39        262       98        305       73
         107       24        228       0.320175439         0.357843137         0.764044944
Unigene335          20120710_JGPPBS_1_7.5768.5772.2         S.halepenseFrame2Rev        unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
         Query_2115          "Ory s 1 (""Grasses, Group 1;Expansin"")"        6         63886     454       1         106.301   264       6.93E-26  39        262       98        305       73
         107       24        228       0.320175439         0.357843137         0.764044944
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2562          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
         42.3578   98        1.38E-05  29        105       29        109       26        40        4         81        0.320987654         0.337662338         0.733333333
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2574          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
         41.5874   96        0.000149418         118       194       29        109       26        40        4         81        0.320987654         0.337662338         0.396907216
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_6111          "Lol p 3 (""Grasses, Group 3"")"        4         47854     201       1
         45.8246   107       6.28E-07  2         84        12        95        27        41        1         84        0.321428571         0.325301205         0.855670103
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_6112          "Lol p 3 (""Grasses, Group 3"")"        4         47854     201       1
         45.8246   107       6.28E-07  2         84        12        95        27        41        1         84        0.321428571         0.325301205         0.855670103
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_5535          "Zea m 1 (""Grasses, Group 1;Expansin"")"        11
         35050     252       1         46.9802   110       6.41E-06  167       255       72        158       29        47        4         90        0.322222222         0.337209302
         0.326996198
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CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_288 "Phl p 3 (""Grasses, Group 3"")"        7         35050     252
        1         40.0466   92        9.37E-05  3         90        74        160       29        41        5         90        0.322222222         0.341176471         0.87628866
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_12  "Lol p 2 (""Grasses, Group 2"")"        4         48366     255
        1         56.9954   136       1.17E-10  4         95        89        176       30        51        6         93        0.322580645         0.344827586         0.896907216
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2562          "Ory s 2 (""Grasses, Group 2"")"        7         70550     436       1
        38.5058   88        0.000488312         40        101       234       295       20        32        0         62        0.322580645         0.322580645         0.59047619
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_287 "Phl p 3 (""Grasses, Group 3"")"        4         48366     255
        1         50.8322   120       1.72E-08  4         94        89        176       30        46        7         93        0.322580645         0.348837209         0.886597938
Unigene552          20120710_JGPPBS_1_3.8565.8570.4         S.halepenseFrame1   hypothetical protein SORBIDRAFT_01g048880 [Sorghum bicolor] >gi|241922455|gb|EER95599.1| hypothetical protein
SORBIDRAFT_01g048880 [Sorghum bicolor]  Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1      Query_741 "Phl p 13 (""Grasses, Group 13;Polygalacturonase"")"
        6         13553     604       1         93.5893   231       2.26E-20  26        223       97        311       73        112       39        226       0.32300885          0.390374332
        0.474619289
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2968          "Hor v 2 (""Grasses, Group 2"")"        4
        48366     255       1         53.1434   126       4.05E-09  22        116       83        176       32        52        9         99        0.323232323         0.355555556
        0.75
Unigene7876         20120710_JGPPBS_1_4.7246.7246.2         S.halepenseFrame2   protein disulfide isomerase [Oryza sativa]          Protein disulfide-isomerase OS=Zea mays GN=PDI PE=2 SV=1
        Query_1140          Tri a Trx (Thioredoxin)         17        50396     154       1         38.891    89        0.00022423          39        105       1         70        23        31
        5         71        0.323943662         0.348484848         0.559322034
Unigene335          20120710_JGPPBS_1_7.5768.5772.2          S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2113          "Hor v 1 (""Grasses, Group 1;Expansin"")"        6         63886     454       1         102.449   254       1.51E-24  40        260       100       304       73
        110       24        225       0.324444444         0.36318408          0.767175573
Unigene335          20120710_JGPPBS_1_7.5768.5772.2          S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_4235          "Ory s 1 (""Grasses, Group 1;Expansin"")"        6         63886     454       1         112.079   279       2.05E-27  85        314       92        305       76
        110       24        234       0.324786325         0.361904762         0.65830721
Unigene335          20120710_JGPPBS_1_7.5768.5772.2          S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_1634          "Ory s 1 (""Grasses, Group 1;Expansin"")"        6         63886     454       1         61.2326   147       2.19E-11  7         125       194       305       39
        55        9         120       0.325     0.351351351         0.853846154
Unigene335          20120710_JGPPBS_1_7.5768.5772.2          S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2950          "Zea m 1 (""Grasses, Group 1;Expansin"")"        6         63886     454       1         57.3806   137       1.42E-09  43        169       100       215       43
        60        21        132       0.325757576         0.387387387         0.531100478
Unigene335          20120710_JGPPBS_1_7.5768.5772.2          S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_5535          "Zea m 1 (""Grasses, Group 1;Expansin"")"        6         63886     454       1         99.3673   246       1.86E-23  43        262       100       305       73
        108       22        224       0.325892857         0.361386139         0.768060837
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2042          "Ory s 2 (""Grasses, Group 2"")"        6         70550     436       1
        46.595    109       1.00E-05  25        111       202       293       30        45        5         92        0.326086957         0.344827586         0.381578947
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_288 "Phl p 3 (""Grasses, Group 3"")"        4         48366     255
        1         51.9878   123       8.40E-09  4         93        89        175       30        46        7         92        0.326086957         0.352941176         0.87628866
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2113          "Hor v 1 (""Grasses, Group 1;Expansin"")"
        11        87282     246       1         45.0542   105       2.50E-05  166       262       53        145       32        49        6         98        0.326530612         0.347826087
        0.351145038
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2038          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
        54.6842   130       5.74E-10  25        117       12        109       32        52        5         98        0.326530612         0.344086022         0.794871795
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2040          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
        54.6842   130       6.88E-10  25        117       12        109       32        53        5         98        0.326530612         0.344086022         0.794871795
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2053          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
        54.299    129       8.94E-10  25        117       12        109       32        52        5         98        0.326530612         0.344086022         0.794871795
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2051          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
        54.299    129       9.30E-10  25        117       12        109       32        52        5         98        0.326530612         0.344086022         0.794871795
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2042          "Ory s 2 (""Grasses, Group 2"")"        5         47854     201       1
        50.8322   120       1.30E-07  136       228       12        109       32        52        5         98        0.326530612         0.344086022         0.407894737
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_1189          "Ory s 3 (""Grasses, Group 3"")"        5         47854     201       1
        52.373    124       3.69E-09  13        105       12        109       32        52        5         98        0.326530612         0.344086022         0.877358491
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Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2037	"Ory s 3 (""Grasses, Group 3"")"	5	47854	201	1	52.373	124	4.43E-09	25	117	12	109	32	52	5	98	0.326530612	0.344086022	0.788135593
Unigene5446	20120710_JGPPBS_1_6.7085.7089.3	S.halepenseFrame2Rev	PREDICTED: protein disulfide isomerase-like 2-2-like [Brachypodium distachyon]	Protein disulfide isomerase-like 2-2 OS=Oryza sativa subsp. japonica GN=PDIL2-2 PE=2 SV=1	Query_1234	Tri a 25 (Thioredoxin)	12	65726	284	1	51.2174	121	3.05E-08	39	102	21	87	22	37	3	67	0.328358209	0.34375	0.512
Unigene5446	20120710_JGPPBS_1_6.7085.7089.3	S.halepenseFrame2Rev	PREDICTED: protein disulfide isomerase-like 2-2-like [Brachypodium distachyon]	Protein disulfide isomerase-like 2-2 OS=Oryza sativa subsp. japonica GN=PDIL2-2 PE=2 SV=1	Query_1240	Zea m 25 (Thioredoxin)	13	65726	284	1	50.0618	118	8.11E-08	42	105	21	87	22	38	3	67	0.328358209	0.34375	0.5
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_482	"Lol p 2 (""Grasses, Group 2"")"	4	88192	280	1	56.225	134	1.92E-10	2	88	61	145	29	53	4	88	0.329545455	0.345238095	0.954545455
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_482	"Lol p 2 (""Grasses, Group 2"")"	5	48366	255	1	54.299	129	8.43E-10	2	88	91	173	29	49	6	88	0.329545455	0.353658537	0.931818182
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_1244	"Bra di 1 (""Grasses, Group 1;Expansin"")"	10	35050	252	1	47.7506	112	4.04E-06	169	258	72	159	30	46	4	91	0.32967033	0.344827586	0.327067669
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2102	"Bra sy 1 (""Grasses, Group 1;Expansin"")"	10	35050	252	1	47.3654	111	4.40E-06	167	256	72	159	30	46	4	91	0.32967033	0.344827586	0.329545455
CL2015.Contig1	20120710_JGPPBS_1_8.6546.6551.3	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_06g018320 [Sorghum bicolor] >gi|241937758|gb|EES10903.1| hypothetical protein SORBIDRAFT_06g018320 [Sorghum bicolor]	Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1	Query_1581	Ory s 23 (Not given)	1	19028	415	2	33.113	74	0.0580182	40	128	71	161	30	45	2	91	0.32967033	0.337078652	0.664179104
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_4099	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	13	48366	255	1	46.9802	110	7.06E-06	166	258	89	177	31	49	6	94	0.329787234	0.352272727	0.335877863
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_4100	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	13	48366	255	1	46.9802	110	6.69E-06	166	258	89	177	31	49	6	94	0.329787234	0.352272727	0.335877863
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2128	"Bra di 1 (""Grasses, Group 1;Expansin"")"	11	48366	255	1	51.6026	122	1.75E-07	172	264	89	177	31	49	6	94	0.329787234	0.352272727	0.332075472
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_1921	"Bra di 2 (""Grasses, Group 2"")"	3	47854	201	1	58.151	139	4.07E-11	27	120	12	104	31	54	1	94	0.329787234	0.333333333	0.75
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_4828	"Cyn d 2 (""Grasses, Group 2"")"	4	48366	255	1	54.299	129	2.13E-09	28	118	87	175	31	53	8	94	0.329787234	0.360465116	0.704918033
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2040	"Ory s 2 (""Grasses, Group 2"")"	7	70550	436	1	51.6026	122	3.29E-08	25	113	202	295	31	49	5	94	0.329787234	0.348314607	0.760683761
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_1774	"Ory s 2 (""Grasses, Group 2"")"	6	70550	436	1	48.9062	115	2.38E-07	25	113	202	295	31	46	5	94	0.329787234	0.348314607	0.760683761
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2041	"Ory s 2 (""Grasses, Group 2"")"	7	70550	436	1	47.7506	112	6.03E-07	25	113	202	295	31	47	5	94	0.329787234	0.348314607	0.760683761
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2043	"Ory s 2 (""Grasses, Group 2"")"	7	70550	436	1	47.7506	112	5.92E-07	25	113	202	295	31	47	5	94	0.329787234	0.348314607	0.760683761
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2054	"Zea m 2 (""Grasses, Group 2"")"	5	47854	201	1	51.6026	122	7.63E-09	27	119	13	108	32	48	5	97	0.329896907	0.347826087	0.766666667
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_1634	"Ory s 1 (""Grasses, Group 1;Expansin"")"
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        10      88192   280     1       50.8322 120     4.81E-08 31     129     59      153     33      56      6       100     0.33    0.35106383
        0.723076923
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2  S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1        Query_1922      "Bra di 2 (""Grasses, Group 2"")"       2       70550   436     1
        66.6254 161     2.99E-13 13     122     186     296     37      63      3       112     0.330357143     0.339449541     0.879032258
CL2015.Contig1  20120710_JGPPBS_1_8.6546.6551.3  S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_06g018320 [Sorghum bicolor] >gi|241937758|gb|EES10903.1| hypothetical
protein SORBIDRAFT_06g018320 [Sorghum bicolor]  Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1       Query_2548      "Aeg ta 5 (""Grasses,
Group 5"")"     1       19028   415     1       70.0922 170     4.98E-14 1       176     77      263     62      103     11      187     0.331550802
        0.352272727     0.972375691
Unigene335      20120710_JGPPBS_1_7.5768.5772.2  S.halepenseFrame2Rev    unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_5509      "Ory s 1 (""Grasses, Group 1;Expansin"")"       6       63886   454     1       111.694 278     7.44E-28 26     247     100     305     75
        112     24      226     0.331858407     0.371287129     0.801587302
Unigene335      20120710_JGPPBS_1_7.5768.5772.2  S.halepenseFrame2Rev    unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_5510      "Ory s 1 (""Grasses, Group 1;Expansin"")"       6       63886   454     1       114.005 284     1.17E-28 26     247     100     305     75
        112     24      226     0.331858407     0.371287129     0.801587302
Unigene335      20120710_JGPPBS_1_7.5768.5772.2  S.halepenseFrame2Rev    unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2092      "Ory s 1 (""Grasses, Group 1;Expansin"")"       6       63886   454     1       111.694 278     8.41E-28 41     262     100     305     75
        112     24      226     0.331858407     0.371287129     0.756554307
Unigene335      20120710_JGPPBS_1_7.5768.5772.2  S.halepenseFrame2Rev    unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2119      "Hol l 1 (""Grasses, Group 1;Expansin"")"       5       63886   454     1       110.153 274     3.40E-27 38     262     97      305     76
        111     24      229     0.331877729     0.370731707     0.779467681
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1       Query_1634      "Ory s 1 (""Grasses, Group 1;Expansin"")"
        9       87282   246     1       51.2174 121     3.03E-08 29     129     52      148     34      52      6       102     0.333333333     0.354166667
        0.738461538
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3  S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1       Query_2184      "Cyn d 15 (""Grasses, Group 15;Expansin"")"      8
        35050   252     1       46.2098 108     1.15E-06 29     102     83      160     26      45      4       78      0.333333333     0.351351351
        0.660714286
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2        Query_1922      "Bra di 2 (""Grasses, Group 2"")"       3       47854   201     1
        56.225  134     2.03E-10 27     119     12      103     31      53      1       93      0.333333333     0.336956522     0.741935484
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3  S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1       Query_2074      "Bra di 2 (""Grasses, Group 2"")"       7
        35050   252     1       38.5058 88      0.000471237     21      110     71      160     31      44      6       93      0.333333333     0.356321839
        0.737288136
Unigene551      20120710_JGPPBS_1_8.8266.8340.2  S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1       Query_1920      "Bra di 2 (""Grasses, Group 2"")"       1
        48366   255     1       48.1358 113     1.85E-07 36     107     109     180     24      37      0       72      0.333333333     0.333333333
        0.672897196
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1       Query_2968      "Hor v 2 (""Grasses, Group 2"")"       7
        88192   280     1       38.891  89      0.000380548     75      119     107     151     15      27      0       45      0.333333333     0.333333333
        0.375
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2        Query_2573      "Ory s 2 (""Grasses, Group 2"")"       5       47854   201     1
        49.2914 116     6.26E-08 21     111     12      107     32      51      5       96      0.333333333     0.351648352     0.805309735
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2        Query_2575      "Ory s 2 (""Grasses, Group 2"")"       5       47854   201     1
        50.447  119     1.97E-08 21     111     12      107     32      52      5       96      0.333333333     0.351648352     0.805309735
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2  S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1       Query_4450      "Ory s 2 (""Grasses, Group 2"")"       7       70550   436     1
        38.5058 88      0.000428308     25      84      234     293     20      31      0       60      0.333333333     0.333333333     0.666666667
Unigene8760     20120710_JGPPBS_1_1.10441.10441.3  S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_03g034200 [Sorghum bicolor] >gi|241928310|gb|EES01455.1| hypothetical
protein SORBIDRAFT_03g034200 [Sorghum bicolor]  Elongation factor 2 OS=Beta vulgaris PE=2 SV=1       Query_2563      "Ory s 2 (""Grasses, Group 2"")"       9       68587   150
        1       26.1794 56      8.35532 8       67      69      136     23      33      10      69      0.333333333     0.389830508     0.561904762
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2  S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1       Query_2574      "Ory s 2 (""Grasses, Group 2"")"       6       70550   436     1
        35.4242 80      0.029853 129     188     234     293     20      31      0       60      0.333333333     0.333333333     0.309278351
Unigene551      20120710_JGPPBS_1_8.8266.8340.2  S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1       Query_2121      "Tri ur 2 (""Grasses, Group 2"")"       2
        48366   255     1       47.7506 112     2.19E-07 2      85      97      176     29      47      10      87      0.333333333     0.376623377
        0.855555556
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Unigene6038 20120710_JGPPBS_1_4.2924.2934.2 S.halepenseFrame1 protein disulfide isomerase [Triticum durum] >gi|12056121|emb|CAC21231.1| protein disulfide isomerase [Triticum durum] Protein disulfide-isomerase OS=Zea mays GN=PDI PE=2 SV=1 Query_1234 Tri a 25 (Thioredoxin) 13 14005 183 1 49.6766 117 3.69E-08 31 101 63 140 26 44 7 78 0.333333333 0.366197183 0.568

Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_6267 "Dac g 3 (""Grasses, Group 3"")" 3 47854 201 1 56.225 134 1.07E-10 2 93 12 104 31 48 1 93 0.333333333 0.336956522 0.958333333

CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_288 "Phl p 3 (""Grasses, Group 3"")" 2 70550 436 1 63.5438 153 1.59E-12 3 94 202 294 31 53 1 93 0.333333333 0.336956522 0.948453608

Unigene1403 20120710_JGPPBS_1_8.6880.6965.2 S.halepenseFrame1Rev hypothetical protein SORBIDRAFT_05g001956 [Sorghum bicolor] >gi|241934780|gb|EES07925.1| hypothetical protein SORBIDRAFT_05g001956 [Sorghum bicolor] Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1 Query_6073 "Phl p 6 (""Grasses, Group 6"")" 2 24831 253 1 26.1794 56 8.46954 1 42 107 148 14 21 0 42 0.333333333 0.333333333 0.396226415

Unigene681 20120710_JGPPBS_1_8.7556.7561.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1 Query_1127 Bra di 7 (Polcalcin;CBP) 29 84312 325 1 37.7354 86 0.000471013 11 63 130 183 18 30 1 54 0.333333333 0.339622642 0.6625

Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1 Query_2248 "Zea m 1 (""Grasses, Group 1;Expansin"")" 6 63886 454 1 103.219 256 1.04E-24 50 269 100 305 75 110 22 224 0.334821429 0.371287129 0.748148148

Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1 Query_2139 "Poa p 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 110.538 275 2.49E-27 38 262 97 305 77 111 24 229 0.336244541 0.375609756 0.779467681

CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_2044 "Ory s 3 (""Grasses, Group 3"")" 7 70550 436 1 58.5362 140 1.52E-10 23 118 200 300 34 54 5 101 0.336633663 0.354166667 0.813559322

CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2128 "Bra di 1 (""Grasses, Group 1;Expansin"")" 9 87282 246 1 55.0694 131 1.38E-08 169 265 53 145 33 56 6 98 0.336734694 0.358695652 0.347169811

CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_1244 "Bra di 1 (""Grasses, Group 1;Expansin"")" 9 87282 246 1 51.2174 121 2.23E-07 169 265 53 145 33 51 6 98 0.336734694 0.358695652 0.345864662

CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2102 "Bra sy 1 (""Grasses, Group 1;Expansin"")" 9 87282 246 1 51.2174 121 2.36E-07 167 263 53 145 33 51 6 98 0.336734694 0.358695652 0.348484848

CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_441 "Dac g 2 (""Grasses, Group 2"")" 5 88192 280 1 57.3806 137 6.95E-10 5 98 60 151 32 55 4 95 0.336842105 0.351648352 0.464285714

Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_164 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")" 13 48366 255 1 43.5134 101 9.36E-05 148 238 89 175 31 48 6 92 0.336956522 0.360465116 0.349593496

CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2117 "Ory s 1 (""Grasses, Group 1;Expansin"")" 10 87282 246 1 51.9878 123 1.01E-07 137 227 59 148 31 48 3 92 0.336956522 0.348314607 0.390350877

Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1 Query_2122 "Hol l 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 110.923 276 1.89E-27 40 264 97 305 78 110 28 231 0.337662338 0.384236453 0.766037736

Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1 Query_2123 "Hol l 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 110.923 276 1.89E-27 40 264 97 305 78 110 28 231 0.337662338 0.384236453 0.766037736

Unigene7876 20120710_JGPPBS_1_4.7246.7246.2 S.halepenseFrame2 protein disulfide isomerase [Oryza sativa] Protein disulfide-isomerase OS=Zea mays GN=PDI PE=2 SV=1 Query_1998 Zea m 25 (Thioredoxin) 14 50396 154 1 45.0542 105 1.27E-06 39 111 1 76 26 41 5 77 0.337662338 0.361111111 0.590163934

Unigene1334 20120710_JGPPBS_1_4.2209.2212.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_03g028140 [Sorghum bicolor] >gi|241927940|gb|EES01085.1| hypothetical protein SORBIDRAFT_03g028140 [Sorghum bicolor] Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1 Query_1287 "Sor b 13 (""Grasses, Group 13;Polygalacturonase"")" 9 41643 396 1 70.0922 170 8.49E-13 119 247 36 166 45 74 6 133 0.338345865 0.354330709 0.309756098

Unigene1334 20120710_JGPPBS_1_4.2209.2212.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_03g028140 [Sorghum bicolor] >gi|241927940|gb|EES01085.1| hypothetical protein SORBIDRAFT_03g028140 [Sorghum bicolor] Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1 Query_5492 "Zea m 13 (""Polygalacturonase;Grasses,

```
Group 13"")"	6	41643	396	1	71.633	174	8.95E-14	99	244	36	180	51	80	9	150	0.34	0.361702128
	0.489583333
Unigene1334	20120710_JGPPBS_1_4.2209.2212.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_03g028140 [Sorghum bicolor] >gi|241927940|gb|EES01085.1| hypothetical protein
SORBIDRAFT_03g028140 [Sorghum bicolor]	Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1	Query_1285	"Zea m 13 (""Polygalacturonase;Grasses,
Group 13"")"	7	41643	396	1	73.9442	180	1.88E-14	119	264	36	180	51	81	9	150	0.34	0.361702128
	0.457792208
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2074	"Bra di 2 (""Grasses, Group 2"")"	5
	87282	246	1	44.2838	103	6.05E-06	20	117	51	146	34	51	6	100	0.34	0.361702128	0.796610169
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_441	"Dac g 2 (""Grasses, Group 2"")"	7
	87282	246	1	48.9062	115	6.96E-07	4	98	56	146	33	54	8	97	0.340206186	0.370786517
	0.454081633
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2073	"Zea m 2 (""Grasses, Group 2"")"	7	47854	201	1
	55.8398	133	2.79E-10	27	119	13	108	33	49	5	97	0.340206186	0.358695652	0.766666667
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2075	"Zea m 2 (""Grasses, Group 2"")"	5	47854	201	1
	54.6842	130	6.80E-10	27	119	13	108	33	49	5	97	0.340206186	0.358695652	0.766666667
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2077	"Zea m 2 (""Grasses, Group 2"")"	5	47854	201	1
	54.6842	130	5.85E-10	27	119	13	108	33	49	5	97	0.340206186	0.358695652	0.766666667
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2079	"Zea m 2 (""Grasses, Group 2"")"	5	47854	201	1
	54.6842	130	6.03E-10	27	119	13	108	33	49	5	97	0.340206186	0.358695652	0.766666667
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2080	"Zea m 2 (""Grasses, Group 2"")"	5	47854	201	1
	54.6842	130	5.79E-10	27	119	13	108	33	49	5	97	0.340206186	0.358695652	0.766666667
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2082	"Zea m 2 (""Grasses, Group 2"")"	5	47854	201	1
	57.3806	137	8.25E-11	27	119	13	108	33	50	5	97	0.340206186	0.358695652	0.766666667
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2081	"Zea m 3 (""Grasses, Group 3"")"	5	47854	201	1
	57.3806	137	8.25E-11	27	119	13	108	33	50	5	97	0.340206186	0.358695652	0.766666667
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_192	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"	13	48366	255	1	46.9802	110	5.72E-06	148	240	89	177	32	49	6	94	0.340425532
	0.363636364	0.360655738
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_193	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"	13	48366	255	1	47.3654	111	4.11E-06	148	240	89	177	32	49	6	94	0.340425532
	0.363636364	0.360655738
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_12	"Lol p 2 (""Grasses, Group 2"")"	6
	87282	246	1	45.8246	107	1.04E-06	4	95	56	143	32	52	8	94	0.340425532	0.372093023
	0.886597938
Unigene335	20120710_JGPPBS_1_7.5768.5772.2	S.halepenseFrame2Rev	unknown [Zea mays]	Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
	Query_929	"Dac g 1 (""Grasses, Group 1;Expansin"")"	5	63886	454	1	111.309	277	7.27E-28	15	239	97	305	78	112
	24	229	0.340611354	0.380487805	0.854166667
Unigene335	20120710_JGPPBS_1_7.5768.5772.2	S.halepenseFrame2Rev	unknown [Zea mays]	Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
	Query_2131	"Dac g 1 (""Grasses, Group 1;Expansin"")"	6	63886	454	1	111.694	278	8.77E-28	39	263	97	305	78
	112	24	229	0.340611354	0.380487805	0.776515152
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_12	"Lol p 2 (""Grasses, Group 2"")"	5
	88192	280	1	55.8398	133	4.09E-10	6	95	61	148	31	54	4	91	0.340659341	0.356321839
	0.896907216
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2574	"Ory s 2 (""Grasses, Group 2"")"	5	47854	201	2
	41.2022	95	0.00023638	21	88	12	84	25	41	5	73	0.342465753	0.367647059	0.350515464
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_4829	"Dac g 2 (""Grasses, Group 2"")"	7
	35050	252	1	44.2838	103	6.44E-06	3	109	49	154	37	54	3	108	0.342592593	0.352380952
	0.860655738
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_4834	"Hol l 2 (""Grasses, Group 2"")"	7
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        35050   252     1       44.669  104     4.79E-06  3       109     49      154     37      54      3       108     0.342592593     0.352380952
        0.860655738
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3      S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4830          "Lol m 2 (""Grasses, Group 2"")"        7
        35050   252     1       44.669  104     4.79E-06  3       109     49      154     37      54      3       108     0.342592593     0.352380952
        0.860655738
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3      S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4831          "Phl p 2 (""Grasses, Group 2"")"        7
        35050   252     1       44.669  104     4.79E-06  3       109     49      154     37      54      3       108     0.342592593     0.352380952
        0.860655738
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3      S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4833          "Poa p 2 (""Grasses, Group 2"")"        7
        35050   252     1       44.669  104     4.79E-06  3       109     49      154     37      54      3       108     0.342592593     0.352380952
        0.860655738
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3      S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4832          "Tri a 2 (""Grasses, Group 2"")"        7
        35050   252     1       44.669  104     4.79E-06  3       109     49      154     37      54      3       108     0.342592593     0.352380952
        0.860655738
Unigene335          20120710_JGPPBS_1_7.5768.5772.2       S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2138          "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    5       63886   454     1       112.849 281     4.04E-28  39      262     98
        305     78      109     22      227     0.343612335       0.380487805       0.779467681
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_482 "Lol p 2 (""Grasses, Group 2"")"       6
        87282   246     1       43.1282 100     7.24E-06  26      88      77      140     22      40      1       64      0.34375   0.349206349     0.715909091
Unigene551          20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_441 "Dac g 2 (""Grasses, Group 2"")"       3       48366   255
        1       64.6994 156     1.42E-12  4       95      89      176     32      53      6       93      0.344086022       0.367816092       0.443877551
Unigene335          20120710_JGPPBS_1_7.5768.5772.2       S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2135          "Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"    5       63886   454     1       111.309 277     1.41E-27  38      262     97
        305     79      110     24      229     0.344978166       0.385365854       0.779467681
Unigene335          20120710_JGPPBS_1_7.5768.5772.2       S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2136          "Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"    5       63886   454     1       111.309 277     1.41E-27  38      262     97
        305     79      110     24      229     0.344978166       0.385365854       0.779467681
Unigene681          20120710_JGPPBS_1_8.7556.7561.2       S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_788 Cyn d 7 (Polcalcin;CBP)       25
        84312   325     1       39.6614 91      0.000115986       3       56      129     183     19      31      1       55      0.345454545       0.351851852
        0.739726027
Unigene5446         20120710_JGPPBS_1_6.7085.7089.3       S.halepenseFrame2Rev          PREDICTED: protein disulfide isomerase-like 2-2-like [Brachypodium distachyon]  Protein disulfide
isomerase-like 2-2 OS=Oryza sativa subsp. japonica GN=PDIL2-2 PE=2 SV=1                 Query_1140          Tri a Trx (Thioredoxin)       10      65726   284     1       55.8398   133
        6.72E-10  29      103     21      98      27      40      3       78      0.346153846       0.36      0.63559322
CL962.Contig1       20120710_JGPPBS_1_8.7811.7897.2       S.halepenseFrame1   hypothetical protein SORBIDRAFT_05g001953 [Sorghum bicolor] >gi|241934779|gb|EES07924.1| hypothetical protein
SORBIDRAFT_05g001953 [Sorghum bicolor]  Vegetative cell wall protein gp1 OS=Chlamydomonas reinhardtii GN=GP1 PE=2 SV=1            Query_1757          Cyn d 23 (Not given)          3
        3929    436     1       57.7658 138     2.90E-10  19      114     76      173     34      56      2       98      0.346938776       0.354166667
        0.813559322
Unigene492          20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_1926          "Ory s 2 (""Grasses, Group 2"")"        5       47854   201     1
        48.521  114     6.76E-08  11      99      16      109     33      51      7       95      0.347368421       0.375     0.888888889
Unigene492          20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2968          "Hor v 2 (""Grasses, Group 2"")"        3       47854   201     1
        56.9954 136     1.07E-10  27      116     13      104     32      49      2       92      0.347826087       0.355555556       0.75
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2       S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2054          "Zea m 2 (""Grasses, Group 2"")"        6       70550   436     1
        50.8322 120     4.95E-08  27      114     203     293     32      46      5       92      0.347826087       0.367816092       0.725
Unigene335          20120710_JGPPBS_1_7.5768.5772.2       S.halepenseFrame2Rev          unknown [Zea mays]  Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_5801          "Sec c 1 (""Grasses, Group 1;Expansin"")"        6       63886   454     1       108.227 269     8.19E-27  19      238     97      300     78
        109     24      224     0.348214286       0.39      0.836820084
Unigene551          20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2074          "Bra di 2 (""Grasses, Group 2"")"       1
        48366   255     1       57.7658 138     1.01E-10  26      113     90      175     31      48      4       89      0.348314607       0.364705882
        0.720338983
Unigene681          20120710_JGPPBS_1_8.7556.7561.2       S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1126          Bra di 7 (Polcalcin;CBP)      36
        84312   325     2       35.4242 80      0.00319733        7       69      55      116     22      30      1       63      0.349206349       0.35483871
        0.775
Unigene681          20120710_JGPPBS_1_8.7556.7561.2       S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1352          Cyn d 7 (Polcalcin;CBP)       27
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84312 325 2 36.1946 82 0.00156603 7 69 55 116 22 31 1 63 0.349206349 0.35483871
0.775
Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
Query_2140 "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")" 5 63886 454 1 113.62 283 1.73E-28 38 262 97
305 80 113 24 229 0.349344978 0.390243902 0.779467681
Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
Query_2133 "Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")" 5 63886 454 1 114.005 284 1.44E-28 38 262 97
305 80 112 24 229 0.349344978 0.390243902 0.779467681
Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
Query_2132 "Fes p 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 113.62 283 1.68E-28 38 262 97 305 80
113 24 229 0.349344978 0.390243902 0.779467681
Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
Query_2134 "Fes p 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 113.235 282 2.83E-28 38 262 97 305 80
112 24 229 0.349344978 0.390243902 0.779467681
Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
Query_2137 "Fes p 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 113.62 283 1.75E-28 38 262 97 305 80
113 24 229 0.349344978 0.390243902 0.779467681
Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
Query_1244 "Bra di 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 112.849 281 3.59E-28 42 264 100 305 79
109 23 226 0.349557522 0.389162562 0.763157895
Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
Query_2102 "Bra sy 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 112.464 280 4.73E-28 40 262 100 305 79
109 23 226 0.349557522 0.389162562 0.768939394
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2114 "Ory s 1 (""Grasses, Group 1;Expansin"")"
10 87282 246 1 51.9878 123 1.65E-07 168 266 54 148 35 52 6 100 0.35 0.372340426
0.352059925
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2115 "Ory s 1 (""Grasses, Group 1;Expansin"")"
10 87282 246 1 51.9878 123 1.65E-07 168 266 54 148 35 52 6 100 0.35 0.372340426
0.352059925
Unigene681 20120710_JGPPBS_1_8.7556.7561.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor] Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1 Query_788 Cyn d 7 (Polcalcin;CBP) 25
84312 325 2 35.039 79 0.00329213 3 62 58 116 21 31 1 60 0.35 0.355932203
0.808219178
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2076 "Zea m 2 (""Grasses, Group 2"")" 5 47854 201 1
57.3806 137 6.20E-11 27 119 13 108 34 50 5 97 0.350515464 0.369565217 0.766666667
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_1455 "Zea m 2 (""Grasses, Group 2"")" 5 47854 201 1
55.0694 131 4.12E-10 27 119 13 108 34 49 5 97 0.350515464 0.369565217 0.766666667
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2078 "Zea m 2 (""Grasses, Group 2"")" 5 47854 201 1
55.4546 132 3.88E-10 27 119 13 108 34 50 5 97 0.350515464 0.369565217 0.766666667
Unigene335 20120710_JGPPBS_1_7.5768.5772.2 S.halepenseFrame2Rev unknown [Zea mays] Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
Query_2128 "Bra di 1 (""Grasses, Group 1;Expansin"")" 5 63886 454 1 117.472 293 9.49E-30 41 264 98 305 80
113 24 228 0.350877193 0.392156863 0.769811321
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_4098 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")" 13 48366 255 1 46.2098 108 1.29E-05 166 258 89 177 33 49 6 94 0.35106383
0.375 0.335877863
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2121 "Tri ur 2 (""Grasses, Group 2"")" 1
88192 280 1 48.521 114 1.37E-07 15 85 75 148 26 41 3 74 0.351351351 0.366197183
0.788888889
Unigene6635 20120710_JGPPBS_1_6.11090.11155.3 S.halepenseFrame2Rev PREDICTED: protein disulfide isomerase-like 2-1-like [Brachypodium distachyon] Protein disulfide
isomerase-like 2-2 OS=Oryza sativa subsp. japonica GN=PDIL2-2 PE=2 SV=1 Query_1998 Zea m 25 (Thioredoxin) 23 66747 104 1 27.335 59
2.80591 55 91 8 44 13 18 0 37 0.351351351 0.351351351 0.303278689
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_788 Cyn d 7 (Polcalcin;CBP) 8
68206 407 3 25.0238 53 9.75101 19 55 158 194 13 16 0 37 0.351351351 0.351351351
0.506849315
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_1339 Hor v 7 (Polcalcin;CBP)

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        7       68206   407     3       26.1794 56      4.44028 24      60      158     194     13      17      0       37      0.351351351     0.351351351
        0.474358974
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_441 "Dac g 2 (""Grasses, Group 2"")"       4       47854   201     1
        63.5438 153     2.16E-12  4       94      13      103     32      53      0       91      0.351648352     0.351648352     0.464285714
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2968      "Hor v 2 (""Grasses, Group 2"")"       2       70550   436     1
        60.4622 145     2.84E-11  27      115     203     293     32      51      2       91      0.351648352     0.359550562     0.741666667
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_12  "Lol p 2 (""Grasses, Group 2"")"       3       47854   201     1
        60.4622 145     2.86E-12  4       94      13      103     32      53      0       91      0.351648352     0.351648352     0.93814433
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_4828      "Cyn d 2 (""Grasses, Group 2"")"       7
        35050   252     1       45.4394 106     2.51E-06  3       109     49      154     38      54      3       108     0.351851852     0.361904762
        0.860655738
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1            Query_1352      Cyn d 7 (Polcalcin;CBP)       27
        84312   325     1       38.891  89      0.000191039     11      63      130     183     19      30      1       54      0.351851852     0.358490566
        0.6625
CL2015.Contig2  20120710_JGPPBS_1_8.5835.5928.2         S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_08g023062 [Sorghum bicolor] >gi|241944355|gb|EES17500.1| hypothetical
protein SORBIDRAFT_08g023062 [Sorghum bicolor]  #N/A             Query_1581      Ory s 23 (Not given)        10      19029   136     1       35.4242  80      0.00526921
        55      128     4       79      27      38      2       76      0.355263158     0.364864865     0.552238806
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_482 "Lol p 2 (""Grasses, Group 2"")"       3       47854   201     1
        55.4546 132     1.76E-10  2       88      15      101     31      49      0       87      0.356321839     0.356321839     0.988636364
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_482 "Lol p 2 (""Grasses, Group 2"")"       2       70550   436     1
        60.8474 146     1.01E-11  2       88      205     291     31      47      0       87      0.356321839     0.356321839     0.988636364
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2117      "Ory s 1 (""Grasses, Group 1;Expansin"")"       13
        35050   252     1       44.669  104     2.91E-05  157     225     98      167     25      39      1       70      0.357142857     0.362318841
        0.302631579
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1            Query_786 Cyn d 7 (Polcalcin;CBP)       25
        84312   325     2       33.113  74      0.0147161 5     60      62      116     20      29      1       56      0.357142857     0.363636364
        0.774647887
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1            Query_786 Cyn d 7 (Polcalcin;CBP)       25
        84312   325     1       37.7354 86      0.000382374     3       54      131     183     19      29      1       53      0.358490566     0.365384615
        0.732394366
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2075      "Zea m 2 (""Grasses, Group 2"")"       6       70550   436     1
        54.299  129     3.89E-09  27      114     203     293     33      47      5       92      0.358695652     0.379310345     0.725
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2077      "Zea m 2 (""Grasses, Group 2"")"       6       70550   436     1
        54.299  129     4.00E-09  27      114     203     293     33      47      5       92      0.358695652     0.379310345     0.725
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2079      "Zea m 2 (""Grasses, Group 2"")"       6       70550   436     1
        53.9138 128     4.81E-09  27      114     203     293     33      47      5       92      0.358695652     0.379310345     0.725
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2080      "Zea m 2 (""Grasses, Group 2"")"       6       70550   436     1
        53.9138 128     4.81E-09  27      114     203     293     33      47      5       92      0.358695652     0.379310345     0.725
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_1455      "Zea m 2 (""Grasses, Group 2"")"       6       70550   436     1
        55.0694 131     1.97E-09  27      114     203     293     33      47      5       92      0.358695652     0.379310345     0.725
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2078      "Zea m 2 (""Grasses, Group 2"")"       6       70550   436     1
        55.8398 133     1.13E-09  27      114     203     293     33      48      5       92      0.358695652     0.379310345     0.725
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_164 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"   11      87282   246     1       51.6026 122     1.72E-07  145     243     53      147     36      56      6       100     0.36    0.382978723
        0.382113821
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2117      "Ory s 1 (""Grasses, Group 1;Expansin"")"
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        11      88192   280     1       50.0618 118     5.02E-07        157     227     82      153     26      44      1       72      0.361111111     0.366197183
        0.311403509
Unigene551      20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2       hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_1634      "Ory s 1 (""Grasses, Group 1;Expansin"")"        7
        48366   255     1       54.6842 130     1.55E-09        33      125     89      177     34      51      6       94      0.361702128     0.386363636
        0.676923077
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_1921      "Bra di 2 (""Grasses, Group 2"")"        2       70550   436     1
        66.2402 160     4.18E-13        27      120     202     294     34      57      1       94      0.361702128     0.365591398     0.75
Unigene1334     20120710_JGPPBS_1_4.2209.2212.3         S.halepenseFrame2       hypothetical protein SORBIDRAFT_03g028140 [Sorghum bicolor] >gi|241927940|gb|EES01085.1| hypothetical protein
SORBIDRAFT_03g028140 [Sorghum bicolor]  Probable polygalacturonase OS=Vitis vinifera GN=GSVIVT00026920001 PE=1 SV=1            Query_4436      "Zea m 13 (""Polygalacturonase;Grasses,
Group 13"")"     7       41643   396     1       76.6406 187     2.42E-15        8       152     25      160     53      76      11      146     0.363013699
        0.392592593     0.425867508
Unigene335      20120710_JGPPBS_1_7.5768.5772.2         S.halepenseFrame2Rev    unknown [Zea mays]      Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_4204      "Pha a 1 (""Grasses, Group 1;Expansin"")"        5       63886   454     1       110.153 274     4.04E-27        44      269     97      307     85
        113     31      234     0.363247863     0.418719212     0.75464684
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1127      Bra di 7 (Polcalcin;CBP)        29
        84312   325     2       37.3502 85      0.000643655     7       69      55      116     23      31      1       63      0.365079365     0.370967742
        0.775
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1339      Hor v 7 (Polcalcin;CBP)         27
        84312   325     1       37.7354 86      0.000497793     5       67      55      116     23      31      1       63      0.365079365     0.370967742
        0.794871795
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1338      Phl p 7 (Polcalcin;CBP)         29
        84312   325     1       37.3502 85      0.000732249     5       67      55      116     23      31      1       63      0.365079365     0.370967742
        0.794871795
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_6267      "Dac g 3 (""Grasses, Group 3"")"         2       70550   436     1
        68.9366 167     2.31E-14        2       93      202     294     34      54      1       93      0.365591398     0.369565217     0.958333333
Unigene397      20120710_JGPPBS_1_7.9063.9133.3         S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g021750 [Sorghum bicolor] >gi|241932039|gb|EES05184.1| hypothetical
protein SORBIDRAFT_04g021750 [Sorghum bicolor]  Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1          Query_1757      Cyn d 23 (Not given)
        8       29611   319     1       46.9802 110     7.64E-07        1       114     16      141     47      66      16      128     0.3671875       0.419642857
        0.949152542
Unigene335      20120710_JGPPBS_1_7.5768.5772.2         S.halepenseFrame2Rev    unknown [Zea mays]      Expansin-A26 OS=Oryza sativa subsp. japonica GN=EXPA26 PE=2 SV=1
        Query_2116      "Ory s 1 (""Grasses, Group 1;Expansin"")"        4       63886   454     1       50.0618 118     1.10E-07        26      101     85      159     28
        39      1       76      0.368421053     0.373333333     0.641025641
Unigene681      20120710_JGPPBS_1_8.7556.7561.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein
SORBIDRAFT_07g001680 [Sorghum bicolor]  Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1             Query_1137      Ory s 7 (Polcalcin;CBP)         27
        84312   325     1       38.891  89      0.000242792     7       71      53      116     24      32      1       65      0.369230769     0.375
        0.780487805
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2076      "Zea m 2 (""Grasses, Group 2"")"         6       70550   436     1
        57.7658 138     2.91E-10        27      114     203     293     34      48      5       92      0.369565217     0.390804598     0.725
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2082      "Zea m 2 (""Grasses, Group 2"")"         7       70550   436     1
        56.225  134     9.63E-10        27      114     203     293     34      48      5       92      0.369565217     0.390804598     0.725
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3       hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2081      "Zea m 3 (""Grasses, Group 3"")"         7       70550   436     1
        56.225  134     9.63E-10        27      114     203     293     34      48      5       92      0.369565217     0.390804598     0.725
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2184      "Cyn d 15 (""Grasses, Group 15;Expansin"")"
        4       87282   246     1       51.2174 121     1.72E-08        40      108     73      145     27      48      4       73      0.369863014     0.391304348
        0.616071429
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2       hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2052      "Ory s 2 (""Grasses, Group 2"")"         4
        35050   252     1       26.9498 58      1.1488  1       59      49      110     23      34      3       62      0.370967742     0.389830508     1
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2       hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2184      "Cyn d 15 (""Grasses, Group 15;Expansin"")"       1       47854   201
        1       58.151  139     2.88E-11        22      111     13      109     36      56      7       97      0.371134021     0.4     0.803571429
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_1920      "Bra di 2 (""Grasses, Group 2"")"        2
        87282   246     1       46.595  109     6.66E-07        37      106     77      146     26      39      0       70      0.371428571     0.371428571
        0.654205607
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Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2114          "Ory s 1 (""Grasses, Group 1;Expansin"")"         9
          48366     255       1         55.8398   133       8.22E-09  170       262       89        177       35        51        6         94        0.372340426         0.397727273
          0.329588015
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2115          "Ory s 1 (""Grasses, Group 1;Expansin"")"         9
          48366     255       1         55.8398   133       8.22E-09  170       262       89        177       35        51        6         94        0.372340426         0.397727273
          0.329588015
Unigene397          20120710_JGPPBS_1_7.9063.9133.3         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g021750 [Sorghum bicolor] >gi|241932039|gb|EES05184.1| hypothetical
protein SORBIDRAFT_04g021750 [Sorghum bicolor]    Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1            Query_1757          Cyn d 23 (Not given)
          8         29611     319       2         36.5798   83        0.00227098          23        113       161       248       35        48        9         94        0.372340426
          0.411764706         0.720338983
CL962.Contig1       20120710_JGPPBS_1_8.7811.7897.2         S.halepenseFrame1   hypothetical protein SORBIDRAFT_05g001953 [Sorghum bicolor] >gi|241934779|gb|EES07924.1| hypothetical protein
SORBIDRAFT_05g001953 [Sorghum bicolor]  Vegetative cell wall protein gp1 OS=Chlamydomonas reinhardtii GN=GP1 PE=2 SV=1            Query_2548          "Aeg ta 5 (""Grasses, Group 5"")"        4
          3929      436       1         60.8474   146       7.28E-11  1         173       90        276       70        101       16        188       0.372340426         0.406976744
          0.950276243
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_12  "Lol p 2 (""Grasses, Group 2"")"        2         70550     436       1
          68.1662   165       4.45E-14  4         94        203       293       34        51        0         91        0.373626374         0.373626374         0.93814433
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2121          "Tri ur 2 (""Grasses, Group 2"")"        7
          87282     246       1         41.5874   96        2.28E-05  15        85        70        143       28        41        3         74        0.378378378         0.394366197
          0.788888889
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                Query_5492          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"         5         91018     470       1         140.198   352       2.20E-37  63        287       121       340       86        118       9         227
          0.378854626         0.394495413         0.756944444
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_1775          "Ory s 2 (""Grasses, Group 2"")"         4
          35050     252       1         38.5058   88        0.000993382         18        72        67        124       22        34        3         58        0.379310345         0.4
          0.392857143
Unigene397          20120710_JGPPBS_1_7.9063.9133.3         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g021750 [Sorghum bicolor] >gi|241932039|gb|EES05184.1| hypothetical
protein SORBIDRAFT_04g021750 [Sorghum bicolor]    Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1            Query_1581          Ory s 23 (Not given)
          5         29611     319       1         53.5286   127       6.41E-09  40        125       53        139       33        52        1         87        0.379310345         0.38372093
          0.641791045
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2073          "Zea m 2 (""Grasses, Group 2"")"         5         70550     436       1
          60.077    144       4.03E-11  27        114       203       293       35        49        5         92        0.380434783         0.402298851         0.725
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2117          "Ory s 1 (""Grasses, Group 1;Expansin"")"         8
          48366     255       1         53.1434   126       3.36E-08  142       223       94        177       32        46        2         84        0.380952381         0.390243902
          0.359649123
Unigene1403         20120710_JGPPBS_1_8.6880.6965.2         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_05g001956 [Sorghum bicolor] >gi|241934780|gb|EES07925.1| hypothetical
protein SORBIDRAFT_05g001956 [Sorghum bicolor]    Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1            Query_2548          "Aeg ta 5 (""Grasses,
Group 5"")"         6         24831     253       1         53.5286   127       1.26E-08  1         79        63        143       31        51        2         81        0.382716049
          0.392405063         0.436464088
CL1715.Contig1      20120710_JGPPBS_1_8.6904.6909.3         S.halepenseFrame1   hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein
SORBIDRAFT_02g043510 [Sorghum bicolor]  Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2              Query_1339          Hor v 7 (Polcalcin;CBP)       10        1167      415       2
          44.669    104       3.13E-06  3         61        180       239       23        36        1         60        0.383333333         0.389830508         0.756410256
CL1715.Contig1      20120710_JGPPBS_1_8.6904.6909.3         S.halepenseFrame1   hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein
SORBIDRAFT_02g043510 [Sorghum bicolor]  Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2              Query_1338          Phl p 7 (Polcalcin;CBP)       7         1167      415       2
          46.9802   110       5.14E-07  3         61        180       239       23        36        1         60        0.383333333         0.389830508         0.756410256
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_441 "Dac g 2 (""Grasses, Group 2"")"         1         70550     436       1
          70.4774   171       5.55E-14  4         94        203       293       35        51        0         91        0.384615385         0.384615385         0.464285714
CL1715.Contig1      20120710_JGPPBS_1_8.6904.6909.3         S.halepenseFrame1   hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein
SORBIDRAFT_02g043510 [Sorghum bicolor]  Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2              Query_1126          Bra di 7 (Polcalcin;CBP)      8         1167      415       2
          48.521    114       1.60E-07  3         63        178       239       24        37        1         62        0.387096774         0.393442623         0.7625
CL1715.Contig1      20120710_JGPPBS_1_8.6904.6909.3         S.halepenseFrame1   hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein
SORBIDRAFT_02g043510 [Sorghum bicolor]  Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2              Query_1137          Ory s 7 (Polcalcin;CBP)       5         1167      415       2
          46.9802   110       4.73E-07  5         65        178       239       24        36        1         62        0.387096774         0.393442623         0.743902439
CL1715.Contig1      20120710_JGPPBS_1_8.6904.6909.3         S.halepenseFrame1   hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein
SORBIDRAFT_02g043510 [Sorghum bicolor]  Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2              Query_1375          Sor b 7 (Polcalcin;CBP)       7         1167      415       2
          46.2098   108       1.00E-06  6         63        181       239       23        35        1         59        0.389830508         0.396551724         0.725
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CL1715.Contig1      20120710_JGPPBS_1_8.6904.6909.3         S.halepenseFrame1   hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein
SORBIDRAFT_02g043510 [Sorghum bicolor]  Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2              Query_1246          Zea m 7 (Polcalcin;CBP)       8         1167      415       2
         44.2838   103       3.69E-06  6         63        181       239       23        35        1         59        0.389830508         0.396551724         0.725
CL2015.Contig1      20120710_JGPPBS_1_8.6546.6551.3         S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_06g018320 [Sorghum bicolor] >gi|241937758|gb|EES10903.1| hypothetical
protein SORBIDRAFT_06g018320 [Sorghum bicolor]    Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1           Query_1757          Cyn d 23 (Not given)
         5         19028     415       1         55.8398   133       1.03E-09  16        111       161       259       39        59        5         100       0.39      0.410526316
         0.805084746
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_4829          "Dac g 2 (""Grasses, Group 2"")"        3         70550     436       1
         70.8626   172       9.79E-15  29        118       202       293       36        52        2         92        0.391304348         0.4       0.737704918
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_4834          "Hol l 2 (""Grasses, Group 2"")"        3         70550     436       1
         70.8626   172       9.42E-15  29        118       202       293       36        52        2         92        0.391304348         0.4       0.737704918
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_4830          "Lol m 2 (""Grasses, Group 2"")"        3         70550     436       1
         70.8626   172       9.42E-15  29        118       202       293       36        52        2         92        0.391304348         0.4       0.737704918
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_6313          "Ory s 2 (""Grasses, Group 2"")"        4
         35050     252       1         62.003    149       2.01E-12  8         96        69        160       36        50        3         92        0.391304348         0.404494382
         0.847619048
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_4831          "Phl p 2 (""Grasses, Group 2"")"        3         70550     436       1
         70.8626   172       9.42E-15  29        118       202       293       36        52        2         92        0.391304348         0.4       0.737704918
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_4833          "Poa p 2 (""Grasses, Group 2"")"        3         70550     436       1
         70.8626   172       9.42E-15  29        118       202       293       36        52        2         92        0.391304348         0.4       0.737704918
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_4832          "Tri a 2 (""Grasses, Group 2"")"        3         70550     436       1
         70.8626   172       9.42E-15  29        118       202       293       36        52        2         92        0.391304348         0.4       0.737704918
Unigene1403         20120710_JGPPBS_1_8.6880.6965.2         S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_05g001956 [Sorghum bicolor] >gi|241934780|gb|EES07925.1| hypothetical
protein SORBIDRAFT_05g001956 [Sorghum bicolor]    Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1           Query_1757          Cyn d 23 (Not given)
         4         24831     253       1         55.4546   132       5.73E-10  31        114       63        146       33        54        0         84        0.392857143         0.392857143
         0.711864407
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2184          "Cyn d 15 (""Grasses, Group 15;Expansin"")"       7
         48366     255       1         47.3654   111       3.96E-07  44        105       110       175       26        44        4         66        0.393939394         0.419354839
         0.553571429
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2727          "Ory s 2 (""Grasses, Group 2"")"        4
         35050     252       1         67.0106   162       1.58E-14  1         88        77        167       36        55        3         91        0.395604396         0.409090909
         0.977777778
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_1775          "Ory s 2 (""Grasses, Group 2"")"        3
         87282     246       1         41.2022   95        0.000102381       19        75        49        106       23        38        1         58        0.396551724         0.403508772
         0.407142857
CL1122.Contig2      20120710_JGPPBS_1_8.4202.4311.3         S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2575          "Ory s 2 (""Grasses, Group 2"")"        4
         35050     252       1         68.1662   165       1.37E-14  22        111       75        167       37        56        3         93        0.397849462         0.411111111
         0.796460177
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                Query_1286          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"       5         91018     470       1         112.079   279       1.32E-28  38        193       76        230       64        92        9         160
         0.4       0.42384106          0.762626263
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2184          "Cyn d 15 (""Grasses, Group 15;Expansin"")"      3         70550     436
         1         54.6842   130       2.47E-09  21        108       202       296       38        54        7         95        0.4       0.431818182         0.785714286
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_4829          "Dac g 2 (""Grasses, Group 2"")"        1         47854     201       1
         68.9366   167       7.09E-15  29        121       12        100       38        55        8         95        0.4       0.436781609         0.713114754
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_4834          "Hol l 2 (""Grasses, Group 2"")"        2         47854     201       1
         68.9366   167       7.23E-15  29        121       12        100       38        55        8         95        0.4       0.436781609         0.713114754
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_4830          "Lol m 2 (""Grasses, Group 2"")"        2         47854     201       1
         68.9366   167       7.23E-15  29        121       12        100       38        55        8         95        0.4       0.436781609         0.713114754
```

CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2053 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 73.559 179 1.73E-16 19 115 68 167 40 59 3 100 0.4 0.412371134 0.829059829
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2038 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 76.6406 187 1.51E-17 19 115 68 167 40 60 3 100 0.4 0.412371134 0.829059829
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_4831 "Phl p 2 (""Grasses, Group 2"")" 2 47854 201 1
68.9366 167 7.23E-15 29 121 12 100 38 55 8 95 0.4 0.436781609 0.713114754
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_4833 "Poa p 2 (""Grasses, Group 2"")" 2 47854 201 1
68.9366 167 7.23E-15 29 121 12 100 38 55 8 95 0.4 0.436781609 0.713114754
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_4832 "Tri a 2 (""Grasses, Group 2"")" 2 47854 201 1
68.9366 167 7.23E-15 29 121 12 100 38 55 8 95 0.4 0.436781609 0.713114754
Unigene1403 20120710_JGPPBS_1_8.6880.6965.2 S.halepenseFrame1Rev hypothetical protein SORBIDRAFT_05g001956 [Sorghum bicolor] >gi|241934780|gb|EES07925.1| hypothetical protein SORBIDRAFT_05g001956 [Sorghum bicolor] Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1 Query_1581 Ory s 23 (Not given)
6 24831 253 1 51.2174 121 3.34E-08 43 125 60 144 34 49 2 85 0.4 0.409638554
0.619402985
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1127 Bra di 7 (Polcalcin;CBP) 10 1167 415 2
46.2098 108 7.92E-07 5 63 180 239 24 37 1 60 0.4 0.406779661 0.7375
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1376 Zea m 7 (Polcalcin;CBP) 11 1167 415 2
45.8246 107 1.29E-06 5 63 180 239 24 36 1 60 0.4 0.406779661 0.7375
CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_4828 "Cyn d 2 (""Grasses, Group 2"")" 3 70550 436 1
72.0182 175 3.54E-15 29 118 202 293 37 52 2 92 0.402173913 0.411111111 0.737704918
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1352 Cyn d 7 (Polcalcin;CBP) 6 1167 415 1
53.5286 127 3.19E-09 5 65 107 168 25 38 1 62 0.403225806 0.409836066 0.7625
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_1926 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 66.2402 160 4.99E-14 12 97 79 167 36 54 3 89 0.404494382 0.418604651
0.868686869
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1375 Sor b 7 (Polcalcin;CBP) 7 1167 415 1
54.6842 130 1.08E-09 3 65 105 168 26 38 1 64 0.40625 0.412698413 0.7875
CL962.Contig1 20120710_JGPPBS_1_8.7811.7897.2 S.halepenseFrame1 hypothetical protein SORBIDRAFT_05g001953 [Sorghum bicolor] >gi|241934779|gb|EES07924.1| hypothetical protein SORBIDRAFT_05g001953 [Sorghum bicolor] Vegetative cell wall protein gp1 OS=Chlamydomonas reinhardtii GN=GP1 PE=2 SV=1 Query_1581 Ory s 23 (Not given) 8
3929 436 1 44.2838 103 8.64E-06 52 120 96 166 29 42 2 71 0.408450704 0.420289855
0.514925373
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1288 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")" 5 91018 470 1 119.783 299 2.38E-31 38 197 76 234 67 98 9 164
0.408536585 0.432258065 0.78680203
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2574 "Ory s 2 (""Grasses, Group 2"")" 2
48366 255 1 76.2554 186 1.09E-16 22 113 89 181 38 59 1 93 0.408602151 0.413043478
0.474226804
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1126 Bra di 7 (Polcalcin;CBP) 8 1167 415 1
53.1434 126 4.01E-09 6 65 108 168 25 38 1 61 0.409836066 0.416666667 0.75
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1338 Phl p 7 (Polcalcin;CBP) 7 1167 415 1
53.1434 126 3.08E-09 4 63 108 168 25 38 1 61 0.409836066 0.416666667 0.769230769
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2051 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 79.337 194 1.50E-18 19 115 68 167 41 61 3 100 0.41 0.422680412 0.829059829
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2046 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 75.8702 185 3.16E-17 19 115 68 167 41 58 3 100 0.41 0.422680412 0.829059829
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_1189 "Ory s 3 (""Grasses, Group 3"")" 4
35050 252 1 73.9442 180 1.02E-16 7 103 68 167 41 59 3 100 0.41 0.422680412 0.91509434

CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2037 "Ory s 3 (""Grasses, Group 3"")" 4
35050 252 1 74.3294 181 8.76E-17 19 115 68 167 41 59 3 100 0.41 0.422680412 0.822033898
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_4828 "Cyn d 2 (""Grasses, Group 2"")" 2 47854 201 1
69.707 169 3.29E-15 29 121 12 100 39 55 8 95 0.410526316 0.448275862 0.713114754
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2184 "Cyn d 15 (""Grasses, Group 15;Expansin"")"
5 88192 280 1 51.2174 121 2.33E-08 44 107 82 149 28 45 4 68 0.411764706 0.4375
0.571428571
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_1376 Zea m 7 (Polcalcin;CBP)
7 68206 407 1 53.5286 127 2.87E-09 3 62 170 232 26 39 3 63 0.412698413 0.433333333
0.75
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2573 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 67.3958 163 2.36E-14 21 104 74 160 36 53 3 87 0.413793103 0.428571429
0.743362832
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2042 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 2 68.5514 166 1.00E-13 137 220 75 161 36 54 3 87 0.413793103 0.428571429
0.368421053
CL200.Contig1 20120710_JGPPBS_1_7.10909.10996.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_0067s002010 [Sorghum bicolor] >gi|241947385|gb|EES20530.1| hypothetical protein SORBIDRAFT_0067s002010 [Sorghum bicolor] "Beta-fructofuranosidase, insoluble isoenzyme 3 OS=Oryza sativa subsp. japonica GN=CIN3 PE=2 SV=1" Query_2719 Lol p FT (Fructosyltransferase) 5 36418 653 1 396.741 1018 5.26E-128 124 635 32 562 223 308 33 538 0.414498141
0.441584158 0.779320988
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_4450 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 58.151 139 2.90E-11 3 81 79 160 34 47 3 82 0.414634146 0.430379747
0.877777778
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1352 Cyn d 7 (Polcalcin;CBP) 6 1167 415 2
48.9062 115 1.21E-07 1 63 173 239 28 38 4 67 0.417910448 0.444444444 0.7875
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2337 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 73.559 179 1.05E-16 5 94 75 167 39 58 3 93 0.419354839 0.433333333
0.9375
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1137 Ory s 7 (Polcalcin;CBP) 5 1167 415 1
54.6842 130 1.25E-09 7 67 107 168 26 39 1 62 0.419354839 0.426229508 0.743902439
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_1246 Zea m 7 (Polcalcin;CBP) 8 1167 415 1
52.7582 125 4.91E-09 5 65 107 168 26 38 1 62 0.419354839 0.426229508 0.7625
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2039 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 80.1073 196 8.32E-19 19 115 68 167 42 61 3 100 0.42 0.432989691 0.829059829
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2040 "Ory s 2 (""Grasses, Group 2"")" 4
35050 252 1 79.7221 195 1.09E-18 19 115 68 167 42 61 3 100 0.42 0.432989691 0.829059829
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2036 "Ory s 3 (""Grasses, Group 3"")" 4
35050 252 1 77.7962 190 6.09E-18 19 115 68 167 42 61 3 100 0.42 0.432989691 0.829059829
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1291 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")" 5 91018 470 1 286.189 731 1.41E-90 38 416 76 436 161 221 26 383
0.420365535 0.450980392 0.841981132
CL2052.Contig1 20120710_JGPPBS_1_8.3818.3823.2 S.halepenseFrame1 hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1 Query_2161 Zea m Zm13 (Ole e 1-like) 4 1675 380 1
120.553 301 3.90E-32 12 169 74 227 67 89 6 159 0.421383648 0.437908497 0.9
Unigene681 20120710_JGPPBS_1_8.7556.7561.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1 Query_1375 Sor b 7 (Polcalcin;CBP) 33
84312 325 1 37.3502 85 0.000766254 3 47 51 95 19 24 0 45 0.422222222 0.422222222
0.5625
CL1754.Contig1 20120710_JGPPBS_1_8.6580.6583.2 S.halepenseFrame1 hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2 Query_1917 Aeg ta 11

(Ole e 1-like) 4 1224 596 1 116.701 291 4.08E-30 30 159 80 208 55 79 1 130 0.423076923
0.426356589 0.77245509
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_1126 Bra di 7
(Polcalcin;CBP) 7 68206 407 1 53.5286 127 2.82E-09 5 62 172 232 26 39 3 61 0.426229508
0.448275862 0.725
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_1127 Bra di 7
(Polcalcin;CBP) 7 68206 407 1 52.7582 125 5.56E-09 5 62 172 232 26 37 3 61 0.426229508
0.448275862 0.725
CL1754.Contig1 20120710_JGPPBS_1_8.6580.6583.2 S.halepenseFrame1 hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein
SORBIDRAFT_06g014730 [Sorghum bicolor] Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2 Query_5342 Sor b 11 (Ole
e 1-like) 4 1224 596 1 117.857 294 1.69E-30 29 164 80 214 58 82 1 136 0.426470588 0.42962963
0.813253012
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2574 "Ory s 2 (""Grasses, Group 2"")" 3
87282 246 2 64.6994 156 1.45E-12 22 95 56 130 32 49 1 75 0.426666667 0.432432432
0.381443299
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_6313 "Ory s 2 (""Grasses, Group 2"")" 3
87282 246 1 74.7146 182 4.92E-17 8 104 50 152 44 60 6 103 0.427184466 0.453608247
0.923809524
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1285 "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")" 5 91018 470 1 166.392 420 1.13E-46 38 250 76 287 92 126 5 215
0.427906977 0.438095238 0.681818182
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_1775 "Ory s 2 (""Grasses, Group 2"")" 2
48366 255 1 45.0542 105 5.39E-06 26 73 89 137 21 32 1 49 0.428571429 0.4375 0.342857143
CL2015.Contig1 20120710_JGPPBS_1_8.6546.6551.3 S.halepenseFrame1Rev hypothetical protein SORBIDRAFT_06g018320 [Sorghum bicolor] >gi|241937758|gb|EES10903.1| hypothetical
protein SORBIDRAFT_06g018320 [Sorghum bicolor] Uncharacterized protein OsI_031781 OS=Oryza sativa subsp. indica GN=OsI_031781 PE=1 SV=1 Query_1581 Ory s 23 (Not given)
1 19028 415 1 65.0846 157 1.03E-12 27 128 153 263 48 62 11 112 0.428571429 0.475247525
0.753731343
CL1754.Contig1 20120710_JGPPBS_1_8.6580.6583.2 S.halepenseFrame1 hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein
SORBIDRAFT_06g014730 [Sorghum bicolor] Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2 Query_1939 Ory s 11 (Ole
e 1-like) 4 1224 596 1 122.094 305 5.45E-32 38 167 80 208 56 84 1 130 0.430769231 0.434108527
0.737142857
CL1754.Contig1 20120710_JGPPBS_1_8.6580.6583.2 S.halepenseFrame1 hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein
SORBIDRAFT_06g014730 [Sorghum bicolor] Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2 Query_4242 Sor b 11 (Ole
e 1-like) 4 1224 596 1 123.25 308 1.66E-32 31 164 80 212 58 84 1 134 0.432835821 0.436090226
0.786982249
CL1754.Contig1 20120710_JGPPBS_1_8.6580.6583.2 S.halepenseFrame1 hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein
SORBIDRAFT_06g014730 [Sorghum bicolor] Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2 Query_4243 Zea m 11 (Ole
e 1-like) 4 1224 596 1 120.939 302 1.17E-31 26 159 80 212 58 82 1 134 0.432835821 0.436090226
0.81097561
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2573 "Ory s 2 (""Grasses, Group 2"")" 3
87282 246 1 76.6406 187 1.47E-17 22 112 56 152 42 60 6 97 0.432989691 0.461538462
0.805309735
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_1774 "Ory s 2 (""Grasses, Group 2"")" 3
48366 255 1 87.4261 215 2.07E-21 20 113 81 177 42 62 3 97 0.432989691 0.446808511
0.803418803
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_1137 Ory s 7 (Polcalcin;CBP)
9 68206 407 1 51.9878 123 9.10E-09 8 64 173 232 26 37 3 60 0.433333333 0.456140351
0.695121951
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_1338 Phl p 7 (Polcalcin;CBP)
9 68206 407 1 52.373 124 6.07E-09 4 60 173 232 26 37 3 60 0.433333333 0.456140351
0.730769231
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_1375 Sor b 7 (Polcalcin;CBP)
8 68206 407 1 52.7582 125 4.50E-09 6 62 173 232 26 38 3 60 0.433333333 0.456140351
0.7125

Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_1246 Zea m 7 (Polcalcin;CBP)
9 68206 407 1 52.373 124 7.69E-09 6 62 173 232 26 37 3 60 0.433333333 0.456140351
0.7125
CL200.Contig1 20120710_JGPPBS_1_7.10909.10996.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_0067s002010 [Sorghum bicolor] >gi|241947385|gb|EES20530.1| hypothetical protein SORBIDRAFT_0067s002010 [Sorghum bicolor] "Beta-fructofuranosidase, insoluble isoenzyme 3 OS=Oryza sativa subsp. japonica GN=CIN3 PE=2 SV=1" Query_4425 Lol p FT (Fructosyltransferase)
5 36418 653 1 424.476 1090 2.49E-138 125 640 32 547 230 327 28 530 0.433962264
0.458167331 0.749253731
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2574 "Ory s 2 (""Grasses, Group 2"")"
4
35050 252 2 63.929 154 2.19E-12 21 95 74 151 34 50 3 78 0.435897436 0.453333333
0.386597938
Unigene9701 20120710_JGPPBS_1_7.3821.3832.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor] >gi|241929664|gb|EES02809.1| hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor] Chitinase 10 OS=Oryza sativa subsp. japonica GN=Cht10 PE=2 SV=1 Query_1842 Zea m Chitinase (Chitinase)
3
104214 206 1 154.836 390 4.63E-45 65 222 29 200 75 109 14 172 0.436046512 0.474683544
0.570397112
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2041 "Ory s 2 (""Grasses, Group 2"")"
4
35050 252 1 77.411 189 9.35E-18 19 109 68 161 41 57 3 94 0.436170213 0.450549451
0.777777778
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2043 "Ory s 2 (""Grasses, Group 2"")"
4
35050 252 1 77.411 189 7.48E-18 19 109 68 161 41 57 3 94 0.436170213 0.450549451
0.777777778
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2042 "Ory s 2 (""Grasses, Group 2"")"
4
35050 252 1 77.0258 188 1.02E-16 19 109 68 161 41 57 3 94 0.436170213 0.450549451
0.399122807
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_788 Cyn d 7 (Polcalcin;CBP)
5 1167 415 2 47.3654 111
3.00E-07 3 56 185 239 24 34 1 55 0.436363636 0.444444444 0.739726027
Unigene681 20120710_JGPPBS_1_8.7556.7561.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1 Query_1376 Zea m 7 (Polcalcin;CBP)
34
84312 325 2 36.5798 83 0.00109563 4 47 48 95 21 26 4 48 0.4375 0.477272727
0.55
CL1715.Contig1 20120710_JGPPBS_1_8.6904.6909.3 S.halepenseFrame1 hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2 Query_788 Cyn d 7 (Polcalcin;CBP)
5 1167 415 1 53.5286 127
2.49E-09 3 58 112 168 25 37 1 57 0.438596491 0.446428571 0.767123288
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1454 "Bra di 13 (""Polygalacturonase;Grasses, Group 13""")"
5 91018 470 1 307.76 787 5.07E-99 40 403 76 436 161 226 7 366
0.43989071 0.448467967 0.871359223
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2044 "Ory s 3 (""Grasses, Group 3"")"
4
35050 252 1 82.4185 202 1.32E-19 19 115 68 167 44 62 3 100 0.44 0.453608247 0.822033898
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_4450 "Ory s 2 (""Grasses, Group 2"")"
3
87282 246 1 67.0106 162 1.54E-14 3 85 60 143 37 50 1 84 0.44047619 0.445783133
0.922222222
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_1774 "Ory s 2 (""Grasses, Group 2"")"
4
35050 252 1 77.0258 188 1.16E-17 19 108 68 160 41 56 3 93 0.440860215 0.455555556
0.769230769
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_6150 "Hor v 13 (""Grasses, Group 13;Polygalacturonase"")"
5 91018 470 1 321.627 823 4.48E-104 63 430 80 443 163 230 6 369 0.441734417
0.449035813 0.840277778
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_741 "Phl p 13 (""Grasses, Group 13;Polygalacturonase"")"
5 91018 470 1 315.464 807 3.05E-102 25 392 80 443 163 228 6 369 0.441734417
0.449035813 0.921319797
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2563 "Ory s 2 (""Grasses, Group 2"")"
2
48366 255 1 75.485 184 2.36E-17 20 101 92 177 38 55 4 86 0.441860465 0.463414634
0.780952381

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Unigene681	20120710_JGPPBS_1_8.7556.7561.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor] >gi|241941286|gb|EES14431.1| hypothetical protein SORBIDRAFT_07g001680 [Sorghum bicolor]	Probable calcium-binding protein CML7 OS=Oryza sativa subsp. japonica GN=CML7 PE=2 SV=1	Query_1246	Zea m 7 (Polcalcin;CBP)	28	84312	325	1	37.7354	86	0.0005456	5	47	53	95	19	24	0	43	0.441860465	0.441860465	0.5375
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2575	"Ory s 2 (""Grasses, Group 2"")"	3	87282	246	1	79.337	194	1.57E-18	22	112	56	152	43	61	6	97	0.443298969	0.472527473	0.805309735
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2042	"Ory s 2 (""Grasses, Group 2"")"	3	87282	246	2	79.7221	195	1.28E-17	137	227	56	152	43	61	6	97	0.443298969	0.472527473	0.399122807
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_1781	"Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"	5	91018	470	1	309.686	792	1.58E-99	55	419	75	436	163	226	7	367	0.444141689	0.452777778	0.843091335
Unigene832	20120710_JGPPBS_1_8.10249.10249.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor]	Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1	Query_1352	Cyn d 7 (Polcalcin;CBP)	5	68206	407	1	54.299	129	1.34E-09	3	62	170	232	28	37	3	63	0.444444444	0.466666667	0.75
Unigene578	20120710_JGPPBS_1_8.7307.7384.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor]	Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1	Query_350 Lol p 11 (Ole e 1-like)	5	83429	417	1	116.701	291	4.12E-31	2	134	76	212	61	80	4	137	0.445255474	0.458646617	0.992537313
Unigene578	20120710_JGPPBS_1_8.7307.7384.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor]	Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1	Query_351 Phl p 11 (Ole e 1-like)	5	83429	417	1	112.464	280	1.77E-29	6	140	80	218	62	81	4	139	0.446043165	0.459259259	0.944055944
CL1754.Contig1	20120710_JGPPBS_1_8.6580.6583.2	S.halepenseFrame1	hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor]	Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2	Query_5493	Zea m 11 (Ole e 1-like)	3	1224	596	1	133.265	334	3.03E-36	25	163	78	215	62	89	1	139	0.446043165	0.449275362	0.836363636
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_2275	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	5	91018	470	1	306.605	784	6.08E-99	49	391	76	417	154	216	5	345	0.446376812	0.452941176	0.869565217
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_2279	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	5	91018	470	1	306.99	785	5.60E-99	53	395	76	417	154	216	5	345	0.446376812	0.452941176	0.860759494
CL1715.Contig1	20120710_JGPPBS_1_8.6904.6909.3	S.halepenseFrame1	hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor]	Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2	Query_1339	Hor v 7 (Polcalcin;CBP)	10	1167	415	1	51.6026	122	1.29E-08	9	63	113	168	25	36	1	56	0.446428571	0.454545455	0.705128205
CL1715.Contig1	20120710_JGPPBS_1_8.6904.6909.3	S.halepenseFrame1	hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor]	Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2	Query_1376	Zea m 7 (Polcalcin;CBP)	11	1167	415	1	50.8322	120	2.37E-08	11	65	113	168	25	35	1	56	0.446428571	0.454545455	0.6875
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_1287	"Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"	5	91018	470	1	322.783	826	5.82E-105	40	402	76	436	163	229	6	365	0.446575342	0.454038997	0.875609756
CL1754.Contig1	20120710_JGPPBS_1_8.6580.6583.2	S.halepenseFrame1	hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor]	Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2	Query_351 Phl p 11 (Ole e 1-like)	3	1224	596	1	124.405	311	2.85E-33	4	135	78	208	59	81	1	132	0.446969697	0.450381679	0.916083916
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_2276	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	5	91018	470	1	307.375	786	4.18E-99	51	393	76	417	155	215	5	345	0.449275362	0.455882353	0.865139949
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_2277	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	5	91018	470	1	307.375	786	4.18E-99	51	393	76	417	155	215	5	345	0.449275362	0.455882353	0.865139949
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_2278	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	5	91018	470	1	307.375	786	4.09E-99	51	393	76	417	155	215	5	345	0.449275362	0.455882353	0.865139949
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_6050	"Pas n 13 (""Grasses, Group
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13;Polygalacturonase"")"      5         91018     470       1         142.895   359       7.10E-40  4         161       282       436       71        100       3         158       0.449367089
          0.458064516         0.917159763
Unigene832          20120710_JGPPBS_1_8.10249.10249.2       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]    Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1           Query_1339          Hor v 7 (Polcalcin;CBP)
          7         68206     407       1         53.5286   127       2.77E-09  4         60        173       232       27        37        3         60        0.45      0.473684211
          0.730769231
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                 Query_2323          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"       5         91018     470       1         251.136   640       1.94E-78  14        315       135       431       138       189       11        305
          0.452459016         0.469387755         0.896341463
CL1715.Contig1      20120710_JGPPBS_1_8.6904.6909.3         S.halepenseFrame1   hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein
SORBIDRAFT_02g043510 [Sorghum bicolor]  Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2              Query_786 Cyn d 7 (Polcalcin;CBP)       5         1167      415       1         51.2174   121
          1.28E-08  5         56        116       168       24        35        1         53        0.452830189         0.461538462         0.732394366
CL1715.Contig1      20120710_JGPPBS_1_8.6904.6909.3         S.halepenseFrame1   hypothetical protein SORBIDRAFT_02g043510 [Sorghum bicolor] >gi|241924624|gb|EER97768.1| hypothetical protein
SORBIDRAFT_02g043510 [Sorghum bicolor]  Calmodulin OS=Hordeum vulgare GN=CAM PE=2 SV=2              Query_786 Cyn d 7 (Polcalcin;CBP)       5         1167      415       2         45.8246   107
          1.09E-06  3         54        187       239       24        32        1         53        0.452830189         0.461538462         0.732394366
Unigene578          20120710_JGPPBS_1_8.7307.7384.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein
SORBIDRAFT_02g012930 [Sorghum bicolor]  Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1            Query_1917          Aeg ta 11 (Ole e 1-like)      3         83429     417       1
          115.931   289       2.19E-30  30        164       80        218       63        80        4         139       0.45323741          0.466666667         0.808383234
CL1754.Contig1      20120710_JGPPBS_1_8.6580.6583.2         S.halepenseFrame1   hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein
SORBIDRAFT_06g014730 [Sorghum bicolor]  Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2               Query_5494          Zea m 11 (Ole
e 1-like) 3         1224      596       1         135.191   339       7.54E-37  25        163       78        215       63        89        1         139       0.45323741          0.456521739
          0.836363636
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2562          "Ory s 2 (""Grasses, Group 2"")"        2
          48366     255       1         78.1814   191       3.41E-18  20        101       92        177       39        56        4         86        0.453488372         0.475609756
          0.780952381
Unigene578          20120710_JGPPBS_1_8.7307.7384.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein
SORBIDRAFT_02g012930 [Sorghum bicolor]  Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1            Query_5342          Sor b 11 (Ole e 1-like)       3         83429     417       1
          119.783   299       8.31E-32  12        159       67        214       69        89        8         152       0.453947368         0.479166667         0.86746988
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_6313          "Ory s 2 (""Grasses, Group 2"")"        2
          48366     255       1         81.2629   199       2.67E-19  14        100       89        176       40        56        1         88        0.454545455         0.459770115
          0.828571429
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                 Query_217 "Zea m 13 (""Polygalacturonase;Grasses,
Group 13"")"      5         91018     470       1         310.457   794       3.82E-100 39        403       76        436       168       226       12        369       0.455284553
          0.470588235         0.868613139
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                 Query_6051          "Pas n 13 (""Grasses, Group
13;Polygalacturonase"")"      5         91018     470       1         144.436   363       2.24E-40  4         161       282       436       72        100       3         158       0.455696203
          0.464516129         0.917159763
CL1754.Contig1      20120710_JGPPBS_1_8.6580.6583.2         S.halepenseFrame1   hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein
SORBIDRAFT_06g014730 [Sorghum bicolor]  Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2               Query_350 Lol p 11 (Ole e 1-like)
          3         1224      596       1         126.331   316       4.03E-34  4         132       78        205       59        81        1         129       0.457364341         0.4609375
          0.955223881
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2563          "Ory s 2 (""Grasses, Group 2"")"        3
          87282     246       1         71.2478   173       7.35E-16  20        104       59        152       43        55        9         94        0.457446809         0.505882353
          0.80952381
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                 Query_221 "Zea m 13 (""Polygalacturonase;Grasses,
Group 13"")"      5         91018     470       1         317.39    812       6.98E-103 32        396       76        436       169       233       12        369       0.45799458
          0.473389356         0.883663366
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                 Query_1271          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"       5         91018     470       1         318.161   814       4.37E-103 38        402       76        436       169       232       12        369
          0.45799458          0.473389356         0.870731707
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                 Query_1272          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"       5         91018     470       1         318.931   816       1.83E-103 38        402       76        436       169       233       12        369
          0.45799458          0.473389356         0.870731707
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1                 Query_1273          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"       5         91018     470       1         318.546   815       3.31E-103 38        402       76        436       169       233       12        369
          0.45799458          0.473389356         0.870731707
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CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1289 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")" 5 91018 470 1 312.383 799 7.32E-101 38 402 76 436 169 228 12 369
0.45799458 0.473389356 0.870731707
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1290 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")" 5 91018 470 1 312.383 799 7.32E-101 38 402 76 436 169 228 12 369
0.45799458 0.473389356 0.870731707
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1282 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")" 5 91018 470 1 313.538 802 2.82E-101 38 402 76 436 169 227 12 369
0.45799458 0.473389356 0.870731707
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1283 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")" 5 91018 470 1 312.383 799 6.72E-101 38 402 76 436 169 226 12 369
0.45799458 0.473389356 0.870731707
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1284 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")" 5 91018 470 1 313.153 801 3.49E-101 38 402 76 436 169 227 12 369
0.45799458 0.473389356 0.870731707
Unigene578 20120710_JGPPBS_1_8.7307.7384.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1 Query_5362 Zea m 11 (Ole e 1-like) 4 83429 417 1
121.709 304 2.41E-32 32 171 71 214 66 88 4 144 0.458333333 0.471428571 0.786516854
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2073 "Zea m 2 (""Grasses, Group 2"")" 4
35050 252 1 87.0409 214 3.97E-21 1 118 49 167 55 72 3 120 0.458333333 0.47008547
0.975
Unigene578 20120710_JGPPBS_1_8.7307.7384.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1 Query_1939 Ory s 11 (Ole e 1-like) 3 83429 417 1
123.25 308 5.93E-33 38 172 80 218 64 82 4 139 0.460431655 0.474074074 0.771428571
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2337 "Ory s 2 (""Grasses, Group 2"")" 2
48366 255 1 89.3521 220 2.37E-22 5 92 89 177 41 62 1 89 0.460674157 0.465909091
0.916666667
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2039 "Ory s 2 (""Grasses, Group 2"")" 3
48366 255 1 89.7373 221 3.27E-22 26 113 89 177 41 62 1 89 0.460674157 0.465909091
0.752136752
Unigene551 20120710_JGPPBS_1_8.8266.8340.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2046 "Ory s 2 (""Grasses, Group 2"")" 3
48366 255 1 87.4261 215 1.99E-21 26 113 89 177 41 59 1 89 0.460674157 0.465909091
0.752136752
Unigene578 20120710_JGPPBS_1_8.7307.7384.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1 Query_4243 Zea m 11 (Ole e 1-like) 3 83429 417 1
124.405 311 1.93E-33 18 156 72 214 66 86 4 143 0.461538462 0.474820144 0.847560976
CL1754.Contig1 20120710_JGPPBS_1_8.6580.6583.2 S.halepenseFrame1 hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2 Query_5362 Zea m 11 (Ole e 1-like) 3 1224 596 1 127.487 319 6.99E-34 41 170 80 208 60 83 1 130 0.461538462 0.465116279
0.724719101
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2046 "Ory s 2 (""Grasses, Group 2"")" 2
87282 246 1 88.9669 219 5.89E-22 19 116 49 152 48 65 6 104 0.461538462 0.489795918
0.837606838
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_1774 "Ory s 2 (""Grasses, Group 2"")" 2
87282 246 1 88.9669 219 5.95E-22 19 116 49 152 48 66 6 104 0.461538462 0.489795918
0.837606838
Unigene832 20120710_JGPPBS_1_8.10249.10249.2 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1 Query_786 Cyn d 7 (Polcalcin;CBP) 10
68206 407 1 47.3654 111 3.17E-07 5 53 181 232 24 32 3 52 0.461538462 0.489795918
0.690140845
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_1769 "Sor b 13 (""Grasses, Group 13;Polygalacturonase"")" 5 91018 470 1 330.102 845 1.34E-107 56 414 80 436 167 227 6 361 0.462603878
0.470422535 0.841232227

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CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2337          "Ory s 2 (""Grasses, Group 2"")"        3
          87282     246       1         84.3445   207       1.37E-20  3         96        54        148       44        63        1         95        0.463157895         0.468085106
          0.979166667
Unigene540          20120710_JGPPBS_1_8.4018.4126.2         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical
protein SORBIDRAFT_09g007260 [Sorghum bicolor]    Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1                Query_2161          Zea m Zm13 (Ole e 1-like)     5         30861     181
          1         110.153   274       1.18E-29  39        147       72        181       51        70        1         110       0.463636364         0.467889908         0.641176471
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2073          "Zea m 2 (""Grasses, Group 2"")"        3
          48366     255       1         88.1965   217       1.49E-21  21        115       81        176       45        63        3         97        0.463917526         0.478723404
          0.783333333
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_4450          "Ory s 2 (""Grasses, Group 2"")"        1
          48366     255       1         78.9518   193       9.35E-19  3         85        93        176       39        54        1         84        0.464285714         0.469879518
          0.922222222
Unigene832          20120710_JGPPBS_1_8.10249.10249.2        S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]    Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_788 Cyn d 7 (Polcalcin;CBP)       8
          68206     407       1         51.2174   121       1.48E-08  3         55        177       232       26        35        3         56        0.464285714         0.490566038
          0.726027397
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2052          "Ory s 2 (""Grasses, Group 2"")"        2
          87282     246       1         39.2762   90        7.35E-05  1         59        30        89        28        41        1         60        0.466666667         0.474576271         1
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2042          "Ory s 2 (""Grasses, Group 2"")"        2
          48366     255       2         89.7373   221       5.72E-21  26        114       89        178       42        61        1         90        0.466666667         0.471910112
          0.390350877
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2562          "Ory s 2 (""Grasses, Group 2"")"        3
          87282     246       1         73.9442   180       1.00E-16  20        104       59        152       44        56        9         94        0.468085106         0.517647059
          0.80952381
CL1754.Contig1      20120710_JGPPBS_1_8.6580.6583.2         S.halepenseFrame1   hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein
SORBIDRAFT_06g014730 [Sorghum bicolor]  Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2                Query_4594          Bra di 11
(Ole e 1-like)      3         1224      596       1         136.732   343       1.99E-37  29        160       78        208       62        89        1         132       0.46969697
          0.473282443         0.775147929
CL986.Contig1       20120710_JGPPBS_1_6.8403.8498.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1               Query_2555          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"        5         91018     470       1         211.075   536       3.29E-64  3         232       203       431       109       147       5         232
          0.469827586         0.480176211         0.926530612
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2052          "Ory s 2 (""Grasses, Group 2"")"        3
          48366     255       1         36.5798   83        0.000642747         26        59        89        122       16        24        0         34        0.470588235         0.470588235
          0.576271186
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2727          "Ory s 2 (""Grasses, Group 2"")"        3
          87282     246       1         80.4925   197       2.59E-19  3         90        60        148       42        58        1         89        0.471910112         0.477272727
          0.977777778
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_1926          "Ory s 2 (""Grasses, Group 2"")"        3
          87282     246       1         80.4925   197       3.64E-19  12        99        60        148       42        58        1         89        0.471910112         0.477272727
          0.888888889
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2573          "Ory s 2 (""Grasses, Group 2"")"        2
          48366     255       1         88.1965   217       1.24E-21  22        109       89        177       42        61        1         89        0.471910112         0.477272727
          0.778761062
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2040          "Ory s 2 (""Grasses, Group 2"")"        3
          48366     255       1         90.5077   223       1.98E-22  26        113       89        177       42        62        1         89        0.471910112         0.477272727
          0.752136752
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2041          "Ory s 2 (""Grasses, Group 2"")"        3
          48366     255       1         89.3521   220       4.32E-22  26        113       89        177       42        60        1         89        0.471910112         0.477272727
          0.752136752
Unigene551          20120710_JGPPBS_1_8.8266.8340.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                  Query_2043          "Ory s 2 (""Grasses, Group 2"")"        3
          48366     255       1         89.7373   221       3.80E-22  26        113       89        177       42        60        1         89        0.471910112         0.477272727
          0.752136752
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CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_2821	"Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"	5	91018	470	1	330.102	845	1.25E-107 41	404	75	436	173	229	6	366	0.472677596	0.480555556	0.873786408
CL986.Contig1	20120710_JGPPBS_1_6.8403.8498.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor]	Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1	Query_2820	"Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"	5	91018	470	1	329.717	844	1.76E-107 42	405	75	436	173	229	6	366	0.472677596	0.480555556	0.871670702
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2574	"Ory s 2 (""Grasses, Group 2"")"	2	48366	255	2	76.2554	186	1.14E-16	116	190	102	177	36	52	1	76	0.473684211	0.48	0.386597938
Unigene9701	20120710_JGPPBS_1_7.3821.3832.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor] >gi|241929664|gb|EES02809.1| hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor]	Chitinase 10 OS=Oryza sativa subsp. japonica GN=Cht10 PE=2 SV=1	Query_1918	Tri a Chitinase (Chitinase)	1	104214	206	1	158.303	399	1.20E-46	23	178	36	206	81	109	15	171	0.473684211	0.519230769	0.609375
Unigene578	20120710_JGPPBS_1_8.7307.7384.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor]	Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1	Query_4242	Sor b 11 (Ole e 1-like)	3	83429	417	1	127.872	320	1.19E-34	31	161	80	214	64	84	4	135	0.474074074	0.488549618	0.775147929
Unigene578	20120710_JGPPBS_1_8.7307.7384.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor]	Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1	Query_5493	Zea m 11 (Ole e 1-like)	4	83429	417	1	124.405	311	1.70E-33	27	157	80	214	64	84	4	135	0.474074074	0.488549618	0.793939394
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2563	"Ory s 2 (""Grasses, Group 2"")"	4	35050	252	1	66.2402	160	5.26E-14	26	97	89	161	35	45	1	73	0.479452055	0.486111111	0.685714286
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2043	"Ory s 2 (""Grasses, Group 2"")"	2	87282	246	1	91.2781	225	7.38E-23	1	116	30	152	59	79	7	123	0.479674797	0.50862069	0.991452991
Unigene578	20120710_JGPPBS_1_8.7307.7384.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor]	Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1	Query_4594	Bra di 11 (Ole e 1-like)	4	83429	417	1	128.257	321	8.63E-35	31	161	80	214	65	86	4	135	0.481481481	0.496183206	0.775147929
Unigene578	20120710_JGPPBS_1_8.7307.7384.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor]	Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1	Query_5494	Zea m 11 (Ole e 1-like)	4	83429	417	1	126.331	316	3.41E-34	27	157	80	214	65	84	4	135	0.481481481	0.496183206	0.793939394
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_1775	"Ory s 2 (""Grasses, Group 2"")"	1	88192	280	1	52.373	124	1.51E-08	19	73	54	109	27	38	1	56	0.482142857	0.490909091	0.392857143
Unigene832	20120710_JGPPBS_1_8.10249.10249.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor]	Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1	Query_1352	Cyn d 7 (Polcalcin;CBP)	5	68206	407	2	33.113	74	0.0206007 7	35	81	109	14	19	0	29	0.482758621	0.482758621	0.3625
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2575	"Ory s 2 (""Grasses, Group 2"")"	2	48366	255	1	90.8929	224	1.02E-22	22	109	89	177	43	62	1	89	0.483146067	0.488636364	0.778761062
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2042	"Ory s 2 (""Grasses, Group 2"")"	2	48366	255	1	91.2781	225	1.63E-21	137	224	89	177	43	62	1	89	0.483146067	0.488636364	0.385964912
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2044	"Ory s 3 (""Grasses, Group 3"")"	3	48366	255	1	95.5153	236	3.22E-24	26	113	89	177	43	63	1	89	0.483146067	0.488636364	0.745762712
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_1455	"Zea m 2 (""Grasses, Group 2"")"	4	35050	252	1	84.7297	208	2.44E-20	1	118	49	167	58	72	3	120	0.483333333	0.495726496	0.975
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2078	"Zea m 2 (""Grasses, Group 2"")"	4	35050	252	1	87.8113	216	2.00E-21	1	118	49	167	58	72	3	120	0.483333333	0.495726496	0.975
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2080	"Zea m 2 (""Grasses, Group 2"")"	4
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        35050   252     1       89.7373 221     3.83E-22  1       118     49      167     58      74      3       120     0.483333333     0.495726496
        0.975
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3       S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2082          "Zea m 2 (""Grasses, Group 2"")"        4
        35050   252     1       85.1149 209     1.63E-20  1       118     49      167     58      72      3       120     0.483333333     0.495726496
        0.975
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3       S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2081          "Zea m 3 (""Grasses, Group 3"")"        4
        35050   252     1       85.1149 209     1.63E-20  1       118     49      167     58      72      3       120     0.483333333     0.495726496
        0.975
CL986.Contig1   20120710_JGPPBS_1_6.8403.8498.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1               Query_4436          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"       5       91018   470     1       248.054 632     2.64E-77  38      304     165     431     131     173     8       271
        0.483394834     0.498098859     0.829652997
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2076          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       88.9669 219     6.56E-22  23      115     83      176     46      63      3       95      0.484210526     0.5     0.766666667
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2054          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       89.3521 220     5.93E-22  23      115     83      176     46      63      3       95      0.484210526     0.5     0.766666667
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2082          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       94.7449 234     5.71E-24  21      115     81      176     47      65      3       97      0.484536082     0.5     0.783333333
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_1455          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       92.4337 228     3.46E-23  21      115     81      176     47      65      3       97      0.484536082     0.5     0.783333333
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2078          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       92.8189 229     2.58E-23  21      115     81      176     47      65      3       97      0.484536082     0.5     0.783333333
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2081          "Zea m 3 (""Grasses, Group 3"")"        3
        48366   255     1       94.7449 234     5.71E-24  21      115     81      176     47      65      3       97      0.484536082     0.5     0.783333333
Unigene492      20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_1587          "Tri ur 1 (""Grasses, Group 1;Expansin;CCD-bearing Protein (XF)"")"   3
        47854   201     1       114.005 284     1.65E-31  19      125     1       105     52      73      2       107     0.485981308     0.495238095
        0.813953488
Unigene492      20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2130          "Tri ur 1 (""Grasses, Group 1;Expansin;CCD-bearing Protein (XF)"")"   3
        47854   201     1       112.464 280     5.91E-30  96      202     1       105     52      73      2       107     0.485981308     0.495238095
        0.509708738
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2041          "Ory s 2 (""Grasses, Group 2"")"        2
        87282   246     1       91.2781 225     7.45E-23  1       116     30      152     60      79      7       123     0.487804878     0.517241379
        0.991452991
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2574          "Ory s 2 (""Grasses, Group 2"")"        1
        88192   280     2       80.4925 197     5.10E-18  22      102     61      142     40      58      1       82      0.487804878     0.49382716
        0.417525773
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2574          "Ory s 2 (""Grasses, Group 2"")"        3
        87282   246     1       73.1738 178     1.54E-15  116     193     69      152     41      52      6       84      0.488095238     0.525641026
        0.402061856
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2       S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_1536          "Tri a 1 (""Grasses, Group 1;Expansin"")"        2       70550   436
        1       257.684 657     4.22E-82  6       264     39      293     128     167     10      262     0.488549618     0.507936508     0.929889299
CL986.Contig1   20120710_JGPPBS_1_6.8403.8498.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical
protein SORBIDRAFT_07g016970 [Sorghum bicolor]    Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1               Query_2556          "Zea m 13
(""Polygalacturonase;Grasses, Group 13"")"       5       91018   470     1       219.935 559     1.29E-67  3       237     203     436     116     150     5       237
        0.489451477     0.5     0.946938776
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_1189          "Ory s 3 (""Grasses, Group 3"")"        2
        87282   246     1       92.8189 229     1.50E-23  7       105     49      148     49      68      1       100     0.49    0.494949495     0.933962264
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3       S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                Query_2076          "Zea m 2 (""Grasses, Group 2"")"        4
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        35050   252     1       88.5817 218     1.04E-21  1       118     49      167     59      74      3       120     0.491666667     0.504273504
        0.975
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3       S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2079          "Zea m 2 (""Grasses, Group 2"")"        4
        35050   252     1       91.2781 225     1.11E-22  1       118     49      167     59      75      3       120     0.491666667     0.504273504
        0.975
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2       S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_1538          "Tri a 1 (""Grasses, Group 1;Expansin"")"        2       70550   436
        1       259.225 661     1.05E-82  6       264     39      293     129     168     10      262     0.492366412     0.511904762     0.929889299
CL1122.Contig2  20120710_JGPPBS_1_8.4202.4311.3       S.halepenseFrame2   hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2562          "Ory s 2 (""Grasses, Group 2"")"        4
        35050   252     1       68.9366 167     6.06E-15  26      97      89      161     36      46      1       73      0.493150685     0.5     0.685714286
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2727          "Ory s 2 (""Grasses, Group 2"")"        2
        48366   255     1       83.5741 205     2.61E-20  3       86      93      177     42      57      1       85      0.494117647     0.5     0.933333333
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_1926          "Ory s 2 (""Grasses, Group 2"")"        2
        48366   255     1       83.1889 204     4.07E-20  12      95      93      177     42      57      1       85      0.494117647     0.5     0.848484848
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2038          "Ory s 2 (""Grasses, Group 2"")"        3
        48366   255     1       92.4337 228     3.68E-23  26      113     89      177     44      61      1       89      0.494382022     0.5     0.752136752
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2075          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       92.4337 228     3.49E-23  23      115     83      176     47      64      3       95      0.494736842     0.510869565
        0.766666667
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2077          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       92.4337 228     3.64E-23  23      115     83      176     47      64      3       95      0.494736842     0.510869565
        0.766666667
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2079          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       92.4337 228     4.14E-23  23      115     83      176     47      64      3       95      0.494736842     0.510869565
        0.766666667
Unigene551      20120710_JGPPBS_1_8.8266.8340.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2080          "Zea m 2 (""Grasses, Group 2"")"        3
        48366   255     1       92.4337 228     4.49E-23  23      115     83      176     47      64      3       95      0.494736842     0.510869565
        0.766666667
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2073          "Zea m 2 (""Grasses, Group 2"")"        2
        88192   280     1       94.3597 233     8.53E-24  20      120     54      153     50      65      1       101     0.495049505     0.5     0.833333333
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2076          "Zea m 2 (""Grasses, Group 2"")"        2
        88192   280     1       93.9745 232     1.20E-23  20      120     54      153     50      64      1       101     0.495049505     0.5     0.833333333
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2054          "Zea m 2 (""Grasses, Group 2"")"        2
        88192   280     1       93.5893 231     2.09E-23  20      120     54      153     50      64      1       101     0.495049505     0.5     0.833333333
Unigene492      20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2129          "Tri a 1 (""Grasses, Group 1;Expansin"")"        4       47854   201
        1       114.775 286     5.03E-30  160     266     1       105     53      74      2       107     0.495327103     0.504761905     0.388888889
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2042          "Ory s 2 (""Grasses, Group 2"")"        3
        87282   246     1       90.1225 222     3.85E-21  1       113     30      144     57      76      2       115     0.495652174     0.504424779
        0.495614035
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2039          "Ory s 2 (""Grasses, Group 2"")"        2
        87282   246     1       95.5153 236     2.08E-24  1       117     30      148     59      81      2       119     0.495798319     0.504273504     1
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2040          "Ory s 2 (""Grasses, Group 2"")"        2
        87282   246     1       95.9005 237     1.58E-24  1       117     30      148     59      81      2       119     0.495798319     0.504273504     1
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2053          "Ory s 2 (""Grasses, Group 2"")"        3
        87282   246     1       92.4337 228     3.05E-23  1       117     30      148     59      79      2       119     0.495798319     0.504273504     1
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CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2036 "Ory s 3 (""Grasses, Group 3"")" 2 87282 246 1 97.8265 242 3.46E-25 1 117 30 148 59 81 2 119 0.495798319 0.504273504 1
CL153.Contig1 20120710_JGPPBS_1_7.4269.4371.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1 Query_1537 "Tri a 1 (""Grasses, Group 1;Expansin"")" 1 70550 436 1 254.218 648 7.62E-81 6 264 39 293 130 176 10 262 0.496183206 0.515873016 0.929889299
Unigene578 20120710_JGPPBS_1_8.7307.7384.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] >gi|241923256|gb|EER96400.1| hypothetical protein SORBIDRAFT_02g012930 [Sorghum bicolor] Pollen-specific protein C13 OS=Zea mays GN=MGS1 PE=2 SV=1 Query_2161 Zea m Zm13 (Ole e 1-like) 3 83429 417 1 130.954 328 8.24E-36 21 160 70 210 72 94 9 145 0.496551724 0.529411765 0.8
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_955 "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")" 5 91018 470 1 157.147 396 4.75E-45 4 161 282 436 79 104 3 158 0.5 0.509677419 0.917159763
CL986.Contig1 20120710_JGPPBS_1_6.8403.8498.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] >gi|241940587|gb|EES13732.1| hypothetical protein SORBIDRAFT_07g016970 [Sorghum bicolor] Exopolygalacturonase (Fragment) OS=Platanus acerifolia GN=plaa2 PE=1 SV=1 Query_6048 "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")" 5 91018 470 1 157.147 396 4.52E-45 4 161 282 436 79 104 3 158 0.5 0.509677419 0.917159763
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_4450 "Ory s 2 (""Grasses, Group 2"")" 2 88192 280 1 78.1814 191 1.91E-18 3 85 65 148 42 53 1 84 0.5 0.506024096 0.922222222
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_6313 "Ory s 2 (""Grasses, Group 2"")" 1 88192 280 1 87.0409 214 2.68E-21 8 100 55 148 47 59 1 94 0.5 0.505376344 0.885714286
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_1774 "Ory s 2 (""Grasses, Group 2"")" 1 88192 280 1 99.3673 246 1.33E-25 19 113 54 149 48 66 1 96 0.5 0.505263158 0.811965812
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2574 "Ory s 2 (""Grasses, Group 2"")" 4 35050 252 1 68.5514 166 5.08E-14 116 186 90 161 36 45 1 72 0.5 0.507042254 0.365979381
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2054 "Zea m 2 (""Grasses, Group 2"")" 4 35050 252 1 87.8113 216 1.62E-21 1 118 49 167 60 75 3 120 0.5 0.512820513 0.975
CL1122.Contig2 20120710_JGPPBS_1_8.4202.4311.3 S.halepenseFrame2 hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2077 "Zea m 2 (""Grasses, Group 2"")" 4 35050 252 1 90.8929 224 1.35E-22 1 118 49 167 60 75 3 120 0.5 0.512820513 0.975
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2073 "Zea m 2 (""Grasses, Group 2"")" 1 87282 246 1 100.908 250 2.86E-26 1 116 30 144 58 77 1 116 0.5 0.504347826 0.958333333
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2038 "Ory s 2 (""Grasses, Group 2"")" 2 87282 246 1 96.2857 238 1.10E-24 1 117 30 148 60 80 2 119 0.504201681 0.512820513 1
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2135 "Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")" 4 47854 201 1 114.005 284 6.41E-30 156 262 1 105 54 74 2 107 0.504672897 0.514285714 0.399239544
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2136 "Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")" 4 47854 201 1 114.005 284 6.41E-30 156 262 1 105 54 74 2 107 0.504672897 0.514285714 0.399239544
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2080 "Zea m 2 (""Grasses, Group 2"")" 2 88192 280 1 96.2857 238 1.84E-24 20 120 54 153 51 65 1 101 0.504950495 0.51 0.833333333
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2075 "Zea m 2 (""Grasses, Group 2"")" 2 88192 280 1 97.0561 240 1.07E-24 20 120 54 153 51 65 1 101 0.504950495 0.51 0.833333333
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2077 "Zea m 2 (""Grasses, Group 2"")" 2 88192 280 1 96.6709 239 1.23E-24 20 120 54 153 51 65 1 101 0.504950495 0.51 0.833333333
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical

protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2079	"Zea m 2 (""Grasses, Group 2"")"	2
88192	280	1	96.6709	239	1.46E-24	20	120	54	153	51	65	1	101	0.504950495	0.51	0.833333333
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_1455	"Zea m 2 (""Grasses, Group 2"")"	2
88192	280	1	97.8265	242	5.62E-25	20	120	54	153	51	66	1	101	0.504950495	0.51	0.833333333
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2078	"Zea m 2 (""Grasses, Group 2"")"	2
88192	280	1	98.2117	243	4.20E-25	20	120	54	153	51	66	1	101	0.504950495	0.51	0.833333333
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2337	"Ory s 2 (""Grasses, Group 2"")"	1
88192	280	1	96.2857	238	7.54E-25	3	96	59	153	48	66	1	95	0.505263158	0.510638298
0.979166667
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2053	"Ory s 2 (""Grasses, Group 2"")"	2
48366	255	1	92.8189	229	2.25E-23	26	113	89	177	45	61	1	89	0.505617978	0.511363636
0.752136752
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2051	"Ory s 2 (""Grasses, Group 2"")"	3
48366	255	1	94.3597	233	8.00E-24	26	113	89	177	45	62	1	89	0.505617978	0.511363636
0.752136752
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_1189	"Ory s 3 (""Grasses, Group 3"")"	3
48366	255	1	92.4337	228	2.22E-23	14	101	89	177	45	62	1	89	0.505617978	0.511363636
0.830188679
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2036	"Ory s 3 (""Grasses, Group 3"")"	3
48366	255	1	95.5153	236	3.05E-24	26	113	89	177	45	63	1	89	0.505617978	0.511363636
0.752136752
Unigene551	20120710_JGPPBS_1_8.8266.8340.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_08g002500 [Sorghum bicolor] >gi|241943461|gb|EES16606.1| hypothetical protein
SORBIDRAFT_08g002500 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2037	"Ory s 3 (""Grasses, Group 3"")"	3
48366	255	1	93.2041	230	2.04E-23	26	113	89	177	45	62	1	89	0.505617978	0.511363636
0.745762712
Unigene832	20120710_JGPPBS_1_8.10249.10249.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]	Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1	Query_4104	Zea m 7 (Polcalcin;CBP)
2	68206	407	1	69.707	169	1.32E-13	149	219	168	237	36	49	1	71	0.507042254	0.514285714
0.315315315
CL1122.Contig2	20120710_JGPPBS_1_8.4202.4311.3	S.halepenseFrame2	hypothetical protein SORBIDRAFT_05g027110 [Sorghum bicolor] >gi|241937137|gb|EES10282.1| hypothetical protein
SORBIDRAFT_05g027110 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2075	"Zea m 2 (""Grasses, Group 2"")"	4
35050	252	1	90.8929	224	1.22E-22	1	118	49	167	61	76	3	120	0.508333333	0.521367521
0.975
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2039	"Ory s 2 (""Grasses, Group 2"")"	1
88192	280	1	105.916	263	5.83E-28	19	117	54	153	51	70	1	100	0.51	0.515151515	0.846153846
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2082	"Zea m 2 (""Grasses, Group 2"")"	2
88192	280	1	98.5969	244	2.75E-25	21	120	55	153	51	65	1	100	0.51	0.515151515	0.825
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2081	"Zea m 3 (""Grasses, Group 3"")"	2
88192	280	1	98.5969	244	2.75E-25	21	120	55	153	51	65	1	100	0.51	0.515151515	0.825
CL1695.Contig1	20120710_JGPPBS_1_8.8109.8184.3	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2046	"Ory s 2 (""Grasses, Group 2"")"	1
88192	280	1	100.138	248	7.54E-26	19	113	54	149	49	65	1	96	0.510416667	0.515789474
0.811965812
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2051	"Ory s 2 (""Grasses, Group 2"")"	2
87282	246	1	98.2117	243	2.32E-25	1	117	30	148	61	82	2	119	0.512605042	0.521367521	1
CL1122.Contig1	20120710_JGPPBS_1_8.7949.8025.2	S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]	Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1	Query_2037	"Ory s 3 (""Grasses, Group 3"")"	2

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        87282   246     1       95.5153 236     2.77E-24        1       117     30      148     61      81      2       119     0.512605042     0.521367521
        0.991525424
CL1152.Contig1  20120710_JGPPBS_1_8.5697.5850.3       S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_02g004850 [Sorghum bicolor] >gi|241924945|gb|EER98089.1| hypothetical
protein SORBIDRAFT_02g004850 [Sorghum bicolor]  Thioredoxin H-type OS=Oryza sativa subsp. indica GN=TRXH PE=1 SV=1          Query_1240      Zea m 25 (Thioredoxin)      2
        17690   256     1       127.872 320     2.51E-36        12      128     33      149     60      82      0       117     0.512820513     0.512820513
        0.9140625
Unigene492      20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2133      "Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"    4
        47854   201     1       117.857 294     2.83E-31        156     262     1       105     55      75      2       107     0.514018692     0.523809524
        0.399239544
Unigene492      20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_929 "Dac g 1 (""Grasses, Group 1;Expansin"")"      4       47854   201     1
        119.783 299     3.06E-32        133     239     1       105     55      76      2       107     0.514018692     0.523809524     0.4375
Unigene492      20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2131      "Dac g 1 (""Grasses, Group 1;Expansin"")"      4       47854   201
        1       120.939 302     1.91E-32        157     263     1       105     55      76      2       107     0.514018692     0.523809524     0.397727273
Unigene492      20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2139      "Poa p 1 (""Grasses, Group 1;Expansin"")"      4       47854   201
        1       120.939 302     1.63E-32        156     262     1       105     55      77      2       107     0.514018692     0.523809524     0.399239544
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1          Query_2573      "Ory s 2 (""Grasses, Group 2"")"      1
        88192   280     1       91.6633 226     8.09E-23        22      109     61      149     46      63      1       89      0.516853933     0.522727273
        0.778761062
CL1152.Contig1  20120710_JGPPBS_1_8.5697.5850.3       S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_02g004850 [Sorghum bicolor] >gi|241924945|gb|EER98089.1| hypothetical
protein SORBIDRAFT_02g004850 [Sorghum bicolor]  Thioredoxin H-type OS=Oryza sativa subsp. indica GN=TRXH PE=1 SV=1          Query_1234      Tri a 25 (Thioredoxin)      2
        17690   256     1       123.635 309     9.81E-35        9       124     33      148     60      80      0       116     0.517241379     0.517241379
        0.928
Unigene832      20120710_JGPPBS_1_8.10249.10249.2      S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]  Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_1126      Bra di 7
(Polcalcin;CBP)     7       68206   407     2       36.5798 83      0.00125936      7       35      81      109     15      21      0       29      0.517241379
        0.517241379     0.3625
Unigene832      20120710_JGPPBS_1_8.10249.10249.2      S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]  Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_1127      Bra di 7
(Polcalcin;CBP)     7       68206   407     2       35.8094 81      0.00250259      7       35      81      109     15      20      0       29      0.517241379
        0.517241379     0.3625
Unigene832      20120710_JGPPBS_1_8.10249.10249.2      S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]  Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_1339      Hor v 7 (Polcalcin;CBP)
        7       68206   407     2       35.8094 81      0.00253238      5       33      81      109     15      20      0       29      0.517241379
        0.517241379     0.371794872
Unigene832      20120710_JGPPBS_1_8.10249.10249.2      S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]  Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_1137      Ory s 7 (Polcalcin;CBP)
        9       68206   407     2       35.8094 81      0.00273101      9       37      81      109     15      20      0       29      0.517241379
        0.517241379     0.353658537
Unigene832      20120710_JGPPBS_1_8.10249.10249.2      S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]  Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_1338      Phl p 7 (Polcalcin;CBP)
        9       68206   407     2       35.8094 81      0.0021719 5     33      81      109     15      20      0       29      0.517241379     0.517241379
        0.371794872
Unigene832      20120710_JGPPBS_1_8.10249.10249.2      S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]  Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_1375      Sor b 7 (Polcalcin;CBP)
        8       68206   407     2       35.4242 80      0.00294436      7       35      81      109     15      20      0       29      0.517241379
        0.517241379     0.3625
Unigene832      20120710_JGPPBS_1_8.10249.10249.2      S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]  Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_1246      Zea m 7 (Polcalcin;CBP)
        9       68206   407     2       36.965  84      0.00115048      7       35      81      109     15      21      0       29      0.517241379
        0.517241379     0.3625
Unigene832      20120710_JGPPBS_1_8.10249.10249.2      S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]  Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1          Query_1376      Zea m 7 (Polcalcin;CBP)
        7       68206   407     2       36.965  84      0.00104152      7       35      81      109     15      21      0       29      0.517241379
        0.517241379     0.3625
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2        S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1              Query_1539      "Hor v 1 (""Grasses, Group 1;Expansin"")"      2       70550   436
        1       251.136 640     1.51E-79        35      264     71      293     119     164     7       230     0.517391304     0.533632287     0.822878229
Unigene492      20120710_JGPPBS_1_7.8636.8708.2       S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2113      "Hor v 1 (""Grasses, Group 1;Expansin"")"      4       47854   201
        1       121.709 304     1.02E-32        155     262     1       106     56      78      2       108     0.518518519     0.528301887     0.404580153
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Unigene11756 20120710_JGPPBS_1_7.4020.4020.2 S.halepenseFrame3 hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor] >gi|241929664|gb|EES02809.1| hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor] Chitinase 10 OS=Oryza sativa subsp. japonica GN=Cht10 PE=2 SV=1 Query_1918 Tri a Chitinase (Chitinase) 2 75131 107
1 76.2554 186 4.00E-17 177 254 4 81 41 53 2 79 0.518987342 0.532467532 0.30078125
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2040 "Ory s 2 (""Grasses, Group 2"")" 1
88192 280 1 106.301 264 3.46E-28 19 117 54 153 52 70 1 100 0.52 0.525252525 0.846153846
CL1122.Contig1 20120710_JGPPBS_1_8.7949.8025.2 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2044 "Ory s 3 (""Grasses, Group 3"")" 2
87282 246 1 100.908 250 2.88E-26 19 117 49 148 52 69 1 100 0.52 0.525252525 0.838983051
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2041 "Ory s 2 (""Grasses, Group 2"")" 1
88192 280 1 101.679 252 1.99E-26 19 113 54 149 50 66 1 96 0.520833333 0.526315789
0.811965812
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2043 "Ory s 2 (""Grasses, Group 2"")" 1
88192 280 1 101.679 252 2.28E-26 19 113 54 149 50 66 1 96 0.520833333 0.526315789
0.811965812
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2042 "Ory s 2 (""Grasses, Group 2"")" 1
88192 280 1 100.908 250 7.84E-25 19 113 54 149 50 66 1 96 0.520833333 0.526315789
0.416666667
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2132 "Fes p 1 (""Grasses, Group 1;Expansin"")" 4 47854 201
1 120.553 301 2.60E-32 156 262 1 105 56 76 2 107 0.523364486 0.533333333 0.399239544
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2134 "Fes p 1 (""Grasses, Group 1;Expansin"")" 4 47854 201
1 120.168 300 3.10E-32 156 262 1 105 56 76 2 107 0.523364486 0.533333333 0.399239544
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2137 "Fes p 1 (""Grasses, Group 1;Expansin"")" 4 47854 201
1 120.553 301 2.98E-32 156 262 1 105 56 76 2 107 0.523364486 0.533333333 0.399239544
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2122 "Hol l 1 (""Grasses, Group 1;Expansin"")" 4 47854 201
1 119.783 299 5.24E-32 158 264 1 105 56 76 2 107 0.523364486 0.533333333 0.396226415
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2123 "Hol l 1 (""Grasses, Group 1;Expansin"")" 4 47854 201
1 119.783 299 5.24E-32 158 264 1 105 56 76 2 107 0.523364486 0.533333333 0.396226415
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_4204 "Pha a 1 (""Grasses, Group 1;Expansin"")" 4 47854 201
1 115.546 288 1.91E-30 162 264 1 101 54 73 2 103 0.524271845 0.534653465 0.375464684
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_1536 "Tri a 1 (""Grasses, Group 1;Expansin"")" 5 47854 201
1 127.872 320 5.16E-35 157 270 1 109 60 83 5 114 0.526315789 0.550458716 0.402214022
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_1538 "Tri a 1 (""Grasses, Group 1;Expansin"")" 5 47854 201
1 127.872 320 4.69E-35 157 270 1 109 60 83 5 114 0.526315789 0.550458716 0.402214022
Unigene2745 20120710_JGPPBS_1_8.8767.8854.2 S.halepenseFrame1Rev hypothetical protein SORBIDRAFT_09g024960 [Sorghum bicolor] >gi|241945326|gb|EES18471.1| hypothetical protein SORBIDRAFT_09g024960 [Sorghum bicolor] Thioredoxin H-type OS=Triticum aestivum PE=1 SV=3 Query_1140 Tri a Trx (Thioredoxin) 2 28525 179 1
127.872 320 3.01E-37 6 115 35 144 58 77 0 110 0.527272727 0.527272727 0.93220339
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2727 "Ory s 2 (""Grasses, Group 2"")" 1
88192 280 1 95.5153 236 1.42E-24 1 90 63 153 48 62 1 91 0.527472527 0.533333333 1
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_2119 "Hol l 1 (""Grasses, Group 1;Expansin"")" 4 47854 201
1 124.02 310 1.35E-33 156 263 1 106 57 78 2 108 0.527777778 0.537735849 0.403041825
Unigene492 20120710_JGPPBS_1_7.8636.8708.2 S.halepenseFrame2 hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2 Query_5701 "Hor v 1 (""Grasses, Group 1;Expansin"")" 3 47854 201
1 122.479 306 6.74E-35 14 121 1 106 57 78 2 108 0.527777778 0.537735849 0.876033058
CL1695.Contig1 20120710_JGPPBS_1_8.8109.8184.3 S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1 Query_2575 "Ory s 2 (""Grasses, Group 2"")" 1

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        88192   280     1       94.7449 234     6.24E-24        22      109     61      149     47      64      1       89      0.528089888     0.534090909
        0.778761062
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1  Query_2042  "Ory s 2 (""Grasses, Group 2"")"  1
        88192   280     2       95.1301 235     9.02E-23        137     224     61      149     47      64      1       89      0.528089888     0.534090909
        0.385964912
Unigene332      20120710_JGPPBS_1_5.3902.4020.2  S.halepenseFrame2Rev  hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1  Query_5492  "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       63860   679     1       201.06  510     1.76E-58        50      230     160     335     96      129     5       181     0.53038674      0.545454545
        0.611111111
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3  S.halepenseFrame1Rev  hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1  Query_1286  "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       182.185 461     9.60E-53        34      193     52      209     85      107     2       160     0.53125 0.537974684
        0.797979798
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2  hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2  Query_2140  "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"  4
        47854   201     1       123.635 309     1.55E-33        156     262     1       105     57      77      2       107     0.53271028      0.542857143
        0.399239544
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2  hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2  Query_2128  "Bra di 1 (""Grasses, Group 1;Expansin"")"  4  47854  201
        1       128.642 322     2.59E-35        158     264     1       105     57      80      2       107     0.53271028      0.542857143     0.396226415
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2  hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2  Query_2248  "Zea m 1 (""Grasses, Group 1;Expansin"")"  4  47854  201
        1       128.257 321     3.53E-35        165     269     1       105     56      79      0       105     0.533333333     0.533333333     0.388888889
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1  Query_1926  "Ory s 2 (""Grasses, Group 2"")"  1
        88192   280     1       92.0485 227     3.77E-23        11      99      64      153     48      61      1       90      0.533333333     0.539325843
        0.898989899
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2  hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2  Query_5801  "Sec c 1 (""Grasses, Group 1;Expansin"")"  4  47854  201
        1       116.701 291     3.51E-31        137     239     1       101     55      73      2       103     0.533980583     0.544554455     0.422594142
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1  Query_2076  "Zea m 2 (""Grasses, Group 2"")"  1
        87282   246     1       100.908 250     2.40E-26        1       116     30      144     62      78      1       116     0.534482759     0.539130435
        0.958333333
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1  Query_2079  "Zea m 2 (""Grasses, Group 2"")"  1
        87282   246     1       103.99  258     1.99E-27        1       116     30      144     62      79      1       116     0.534482759     0.539130435
        0.958333333
CL1122.Contig1  20120710_JGPPBS_1_8.7949.8025.2  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1  Query_2080  "Zea m 2 (""Grasses, Group 2"")"  1
        87282   246     1       103.99  258     2.01E-27        1       116     30      144     62      79      1       116     0.534482759     0.539130435
        0.958333333
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3  S.halepenseFrame1Rev  hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1  Query_1291  "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       426.787 1096    2.68E-141       34      424     52      426     209     266     16      391     0.534526854     0.557333333
        0.884433962
Unigene332      20120710_JGPPBS_1_5.3902.4020.2  S.halepenseFrame2Rev  hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1  Query_1285  "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3       63860   679     1       263.462 672     2.00E-81        1       250     86      335     137     179     10      255     0.537254902     0.559183673
        0.795454545
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2  hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2  Query_2117  "Ory s 1 (""Grasses, Group 1;Expansin"")"  4  47854  201
        1       105.145 261     6.49E-27        147     226     29      108     43      65      0       80      0.5375  0.5375  0.350877193
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1  Query_2038  "Ory s 2 (""Grasses, Group 2"")"  1
        88192   280     1       107.457 267     1.25E-28        19      117     54      153     54      69      1       100     0.54    0.545454545     0.846153846
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3  S.halepenseFrame1Rev  hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1  Query_1288  "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       193.741 491     6.00E-57        34      197     52      213     89      116     2       164     0.542682927     0.549382716
        0.822335025
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Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_5535          "Zea m 1 (""Grasses, Group 1;Expansin"")"         4         47854     201
        1       131.339   329       2.47E-36  158       262       1         105       57        80        0         105       0.542857143         0.542857143         0.399239544
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_1455          "Zea m 2 (""Grasses, Group 2"")"         1
        87282     246       1         102.834   255       5.59E-27  1         116       30        144       63        79        1         116       0.543103448         0.547826087
        0.958333333
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2054          "Zea m 2 (""Grasses, Group 2"")"         1
        87282     246       1         100.523   249       3.55E-26  1         116       30        144       63        79        1         116       0.543103448         0.547826087
        0.958333333
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2077          "Zea m 2 (""Grasses, Group 2"")"         1
        87282     246       1         103.99    258       1.77E-27  1         116       30        144       63        79        1         116       0.543103448         0.547826087
        0.958333333
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2078          "Zea m 2 (""Grasses, Group 2"")"         1
        87282     246       1         104.76    260       8.22E-28  1         116       30        144       63        79        1         116       0.543103448         0.547826087
        0.958333333
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2082          "Zea m 2 (""Grasses, Group 2"")"         1
        87282     246       1         102.834   255       4.94E-27  1         116       30        144       63        78        1         116       0.543103448         0.547826087
        0.958333333
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2081          "Zea m 3 (""Grasses, Group 3"")"         1
        87282     246       1         102.834   255       4.94E-27  1         116       30        144       63        78        1         116       0.543103448         0.547826087
        0.958333333
Unigene492          20120710_JGPPBS_1_7.8636.8708.2          S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_1539          "Hor v 1 (""Grasses, Group 1;Expansin"")"         4         47854     201
        1       126.716   317       1.33E-34  157       270       1         109       62        83        5         114       0.543859649         0.568807339         0.402214022
Unigene332          20120710_JGPPBS_1_5.3902.4020.2          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1288          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3         63860     679       1         206.453   524       9.45E-62  1         197       86        282       110       143       10        202       0.544554455         0.572916667
        0.974619289
Unigene332          20120710_JGPPBS_1_5.3902.4020.2          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_6150          "Hor v 13 (""Grasses, Group 13;Polygalacturonase"")"
        4         63860     679       1         460.299   1183      2.08E-155 11        432       83        498       231       307       8         423       0.546099291         0.556626506
        0.960648148
Unigene492          20120710_JGPPBS_1_7.8636.8708.2          S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2138          "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    4
        47854     201       1         127.872   320       3.99E-35  156       263       1         106       59        80        2         108       0.546296296         0.556603774
        0.403041825
Unigene332          20120710_JGPPBS_1_5.3902.4020.2          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1286          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3         63860     679       1         195.282   495       1.30E-57  1         187       86        272       105       134       10        192       0.546875  0.576923077
        0.919191919
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_1540          "Tri a 1 (""Grasses, Group 1;Expansin"")"         2         70550     436
        1       263.462   672       2.57E-84  37        266       71        293       127       172       9         231       0.54978355          0.572072072         0.813186813
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2053          "Ory s 2 (""Grasses, Group 2"")"         1
        88192     280       1         103.605   257       3.91E-27  19        117       54        153       55        68        1         100       0.55      0.555555556         0.846153846
CL1695.Contig1      20120710_JGPPBS_1_8.8109.8184.3          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2044          "Ory s 3 (""Grasses, Group 3"")"         1
        88192     280       1         112.464   280       2.15E-30  19        117       54        153       55        73        1         100       0.55      0.555555556         0.838983051
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2117          "Ory s 1 (""Grasses, Group 1;Expansin"")"         1         70550     436
        1       259.996   663       9.06E-84  1         223       35        295       144       172       38        261       0.551724138         0.64573991          0.978070175
CL1122.Contig1      20120710_JGPPBS_1_8.7949.8025.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g032080 [Sorghum bicolor] >gi|241921529|gb|EER94673.1| hypothetical
protein SORBIDRAFT_01g032080 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1                 Query_2075          "Zea m 2 (""Grasses, Group 2"")"         1
        87282     246       1         104.375   259       1.53E-27  1         116       30        144       64        80        1         116       0.551724138         0.556521739
        0.958333333
Unigene332          20120710_JGPPBS_1_5.3902.4020.2          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1291          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
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        3       63860   679     1       456.447 1173    6.66E-154 1       424     86      497     238     304     26      431     0.552204176     0.587654321
        0.955188679
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_5365          "Zea m 1 (""Grasses, Group 1;Expansin"")"        4       47854   201
        1       136.346 342     3.48E-38  164   268     1       105     58      82      0       105     0.552380952     0.552380952     0.390334572
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_1537          "Tri a 1 (""Grasses, Group 1;Expansin"")"        5       47854   201
        1       128.257 321     4.27E-35  157   270     1       109     63      83      5       114     0.552631579     0.577981651     0.402214022
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2563          "Ory s 2 (""Grasses, Group 2"")"        1
        88192   280     1       84.7297   208   1.89E-20  27      101     74      149     42      52      1       76      0.552631579     0.56    0.714285714
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2949          "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       302.368 773     1.42E-99  1     265     35      296     148     194     3       265     0.558490566     0.564885496     0.973977695
Unigene332      20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev        hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1               Query_2323          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       63860   679     1       365.155   936     5.32E-120 13      328     185     497     178     235     7       318     0.559748428     0.572347267
        0.948170732
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2051          "Ory s 2 (""Grasses, Group 2"")"        1
        88192   280     1       108.997   271   3.42E-29  19      117     54      153     56      70      1       100     0.56    0.565656566     0.846153846
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2036          "Ory s 3 (""Grasses, Group 3"")"        1
        88192   280     1       110.153   274   1.68E-29  19      117     54      153     56      72      1       100     0.56    0.565656566     0.846153846
Unigene832      20120710_JGPPBS_1_8.10249.10249.2        S.halepenseFrame2Rev        hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]    Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1           Query_788 Cyn d 7 (Polcalcin;CBP)       8
        68206   407     2       31.187    69    0.074663  4       28      85      109     14      17      0       25      0.56    0.56    0.342465753
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_1540          "Tri a 1 (""Grasses, Group 1;Expansin"")"        4       47854   201
        1       139.043 349     3.46E-39  159   272     1       109     64      86      5       114     0.561403509     0.587155963     0.399267399
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2948          "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       303.908 777     4.32E-100 1     265     35      296     149     194     3       265     0.562264151     0.56870229      0.973977695
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_1634          "Ory s 1 (""Grasses, Group 1;Expansin"")"        3       47854   201
        1       144.436 363     3.59E-43  19    128     1       108     62      87      2       110     0.563636364     0.574074074     0.830769231
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2944          "Sor b 1 (""Grasses, Group 1;Expansin"")"        2       70550   436
        1       307.76  787     9.63E-102 9     263     42      296     144     185     0       255     0.564705882     0.564705882     0.958646617
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2562          "Ory s 2 (""Grasses, Group 2"")"        1
        88192   280     1       87.0409   214   2.16E-21  27      101     74      149     43      53      1       76      0.565789474     0.573333333
        0.714285714
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]    Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1               Query_2574          "Ory s 2 (""Grasses, Group 2"")"        1
        88192   280     1       86.6557   213   3.75E-20  116     190     74      149     43      53      1       76      0.565789474     0.573333333
        0.386597938
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2945          "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       306.605 784     3.68E-101 1     265     35      296     150     195     3       265     0.566037736     0.572519084     0.973977695
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2946          "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       306.605 784     3.68E-101 1     265     35      296     150     195     3       265     0.566037736     0.572519084     0.973977695
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2947          "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       306.605 784     4.06E-101 1     265     35      296     150     195     3       265     0.566037736     0.572519084     0.973977695
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1             Query_2951          "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       307.76  787     1.31E-101 1     265     35      296     150     195     3       265     0.566037736     0.572519084     0.973977695
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1               Query_1271          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
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        4       19725   778     1       467.618 1202    2.72E-157 1       410     23      426     236     290     16      415     0.568674699     0.591478697
        0.973170732
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_5492      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3       19725   778     1       219.935 559     7.09E-65  50      230     88      266     103     127     2       181     0.569060773     0.575418994
        0.621527778
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1285      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       258.84  660     6.05E-79  35      250     53      266     123     155     2       216     0.569444444     0.574766355
        0.694805195
Unigene2745     20120710_JGPPBS_1_8.8767.8854.2  S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_09g024960 [Sorghum bicolor] >gi|241945326|gb|EES18471.1| hypothetical
protein SORBIDRAFT_09g024960 [Sorghum bicolor]  Thioredoxin H-type OS=Triticum aestivum PE=1 SV=3          Query_1998      Zea m 25 (Thioredoxin)  2       28525   179     1
        115.161 287     3.36E-32  6       105     35      134     57      68      0       100     0.57    0.57    0.819672131
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1          Query_1189      "Ory s 3 (""Grasses, Group 3"")"         1
        88192   280     1       105.531 262     4.77E-28  7       105     54      153     57      70      1       100     0.57    0.575757576     0.933962264
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1          Query_2037      "Ory s 3 (""Grasses, Group 3"")"         1
        88192   280     1       106.301 264     4.00E-28  19      117     54      153     57      70      1       100     0.57    0.575757576     0.838983051
Unigene332      20120710_JGPPBS_1_5.3902.4020.2  S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_2279      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        4       63860   679     1       443.736 1140    1.76E-149 4       395     80      469     229     295     18      400     0.5725  0.59947644
        0.967088608
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2114      "Ory s 1 (""Grasses, Group 1;Expansin"")"        4       47854   201
        1       143.665 361     4.96E-41  156     265     1       108     63      88      2       110     0.572727273     0.583333333     0.404494382
Unigene492      20120710_JGPPBS_1_7.8636.8708.2  S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2115      "Ory s 1 (""Grasses, Group 1;Expansin"")"        4       47854   201
        1       143.665 361     4.96E-41  156     265     1       108     63      88      2       110     0.572727273     0.583333333     0.404494382
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1272      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       472.241 1214    3.74E-159 1       410     23      426     238     292     16      415     0.573493976     0.596491228
        0.973170732
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1273      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       472.241 1214    4.90E-159 1       410     23      426     238     291     16      415     0.573493976     0.596491228
        0.973170732
Unigene493      20120710_JGPPBS_1_7.4502.4597.3  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                 Query_4235      "Ory s 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       163.696 413     2.42E-48  88      209     55      176     70      91      0       122     0.573770492     0.573770492
        0.382445141
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1454      "Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       471.855 1213    6.97E-159 14      410     30      425     229     284     1       397     0.576826196     0.578282828
        0.961165049
CL1737.Contig1  20120710_JGPPBS_1_6.10573.10640.2  S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1286      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        2       88260   613     1       232.646 592     6.55E-72  1       194     27      232     120     141     16      208     0.576923077     0.625
        0.96969697
Unigene332      20120710_JGPPBS_1_5.3902.4020.2  S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_2278      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        4       63860   679     1       443.351 1139    2.14E-149 4       393     80      469     230     294     16      398     0.577889447     0.602094241
        0.972010178
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_2323      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3       19725   778     1       386.726 992     2.45E-127 8       328     108     426     186     234     2       321     0.579439252     0.5830721
        0.972560976
Unigene332      20120710_JGPPBS_1_5.3902.4020.2  S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_2276      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        4       63860   679     1       445.662 1145    2.61E-150 4       393     80      469     231     294     16      398     0.58040201      0.604712042
        0.972010178
Unigene332      20120710_JGPPBS_1_5.3902.4020.2  S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_2277      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
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        4       63860   679     1       445.662 1145    2.61E-150 4       393     80      469     231     294     16      398     0.58040201      0.604712042
        0.972010178
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_1244          "Bra di 1 (""Grasses, Group 1;Expansin"")"       4       47854   201
        1       136.732 343     2.03E-38  158   262     1       103     61      82      2       105     0.580952381     0.59223301      0.387218045
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_2102          "Bra sy 1 (""Grasses, Group 1;Expansin"")"       4       47854   201
        1       136.732 343     2.07E-38  156   260     1       103     61      82      2       105     0.580952381     0.59223301      0.390151515
Unigene493      20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2               Query_4099          "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"  3       100096  176     1       175.252 443     1.41E-53  13      153     37      176     82      100     1       141     0.581560284
        0.585714286     0.534351145
Unigene493      20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2               Query_4100          "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"  3       100096  176     1       174.866 442     1.78E-53  13      153     37      176     82      100     1       141     0.581560284
        0.585714286     0.534351145
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1              Query_2953          "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       305.834 782     6.82E-101 15    265     48      296     146     188     2       251     0.581673307     0.586345382     0.925650558
Unigene492      20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2               Query_4235          "Ory s 1 (""Grasses, Group 1;Expansin"")"        4       47854   201
        1       147.132 370     9.92E-42  208   317     1       108     64      89      2       110     0.581818182     0.592592593     0.338557994
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1              Query_4436          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       357.451 916     4.07E-116 23      317     128     426     174     213     4       299     0.581939799     0.589830508
        0.930599369
Unigene493      20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2               Query_1539          "Hor v 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       165.622 418     1.22E-49  32      158     52      176     74      93      2       127     0.582677165     0.592     0.461254613
Unigene493      20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2               Query_2117          "Ory s 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       166.777 421     1.06E-50  21      147     40      166     74      92      0       127     0.582677165     0.582677165
        0.557017544
Unigene332      20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev        hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1              Query_2275          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        4       63860   679     1       442.58  1137    4.28E-149 9       391     93      469     226     291     14      387     0.583979328     0.605898123
        0.953964194
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1              Query_1289          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       464.922 1195    3.31E-156 35      410     53      426     220     277     2       376     0.585106383     0.588235294
        0.912195122
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1              Query_1290          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       464.922 1195    3.31E-156 35      410     53      426     220     277     2       376     0.585106383     0.588235294
        0.912195122
CL1695.Contig1  20120710_JGPPBS_1_8.8109.8184.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|242084680|ref|XP_002442765.1|
hypothetical protein SORBIDRAFT_08g002460 [Sorghum bicolor] >gi|241943457|gb|EES16602.1| hypothetical protein SORBIDRAFT_08g002450 [Sorghum bicolor] >gi|241943458|gb|EES16603.1| hypothetical
protein SORBIDRAFT_08g002460 [Sorghum bicolor]  Pollen allergen Phl p 2 OS=Phleum pratense GN=PHLPII PE=1 SV=1              Query_2052          "Ory s 2 (""Grasses, Group 2"")"        1
        88192   280     1       48.521  114     5.32E-08  19      59      54      94      24      29      0       41      0.585365854     0.585365854
        0.694915254
CL2052.Contig1  20120710_JGPPBS_1_8.3818.3823.2         S.halepenseFrame1   hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein
SORBIDRAFT_03g001020 [Sorghum bicolor]  Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1          Query_4243          Zea m 11 (Ole e 1-like)         2       1675    380     1
        191.815 486     4.59E-59  6     160     67      226     94      116     5       160     0.5875  0.606451613     0.945121951
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1              Query_1283          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       466.848 1200    4.92E-157 35      410     53      426     221     276     2       376     0.587765957     0.590909091
        0.912195122
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1              Query_2950          "Zea m 1 (""Grasses, Group 1;Expansin"")"        2       70550   436
        1       219.935 559     1.79E-68  1     182     35      213     107     131     3       182     0.587912088     0.597765363     0.85645933
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3        S.halepenseFrame1Rev        hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1              Query_2820          "Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"
        4       19725   778     1       477.633 1228    3.93E-161 34      413     45      426     225     284     2       382     0.589005236     0.592105263
        0.920096852
Unigene9701     20120710_JGPPBS_1_7.3821.3832.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor] >gi|241929664|gb|EES02809.1| hypothetical
protein SORBIDRAFT_03g011710 [Sorghum bicolor]  Chitinase 10 OS=Oryza sativa subsp. japonica GN=Cht10 PE=2 SV=1              Query_4572          Tri a Endochitinase (Chitinase)         1
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        104214    206       1         218.009   554       5.41E-69  78        242       41        206       98        125       1         166       0.590361446         0.593939394
        0.517241379
Unigene9701         20120710_JGPPBS_1_7.3821.3832.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor] >gi|241929664|gb|EES02809.1| hypothetical
protein SORBIDRAFT_03g011710 [Sorghum bicolor]    Chitinase 10 OS=Oryza sativa subsp. japonica GN=Cht10 PE=2 SV=1                Query_4573          Tri a Endochitinase (Chitinase)         1
        104214    206       1         218.009   554       5.01E-69  78        242       41        206       98        125       1         166       0.590361446         0.593939394
        0.517241379
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1282          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4         19725     778       1         468.003   1203      1.66E-157 35        410       53        426       222       277       2         376       0.590425532         0.593582888
        0.912195122
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1284          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4         19725     778       1         468.389   1204      1.49E-157 35        410       53        426       222       277       2         376       0.590425532         0.593582888
        0.912195122
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_217 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"       4
        19725     778       1         466.463   1199      8.75E-157 36        411       53        426       222       277       2         376       0.590425532         0.593582888
        0.909975669
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                           Query_2128          "Bra di 1 (""Grasses, Group 1;Expansin"")"       3
        100096    176       1         181.8     460       4.06E-56  28        159       45        176       78        99        0         132       0.590909091         0.590909091
        0.498113208
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                           Query_2113          "Hor v 1 (""Grasses, Group 1;Expansin"")"       3
        100096    176       1         173.326   438       7.04E-53  25        156       45        176       78        94        0         132       0.590909091         0.590909091
        0.503816794
Unigene832          20120710_JGPPBS_1_8.10249.10249.2        S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_02g043140 [Sorghum bicolor] >gi|241924599|gb|EER97743.1| hypothetical
protein SORBIDRAFT_02g043140 [Sorghum bicolor]    Probable calcium-binding protein CML24 OS=Oryza sativa subsp. japonica GN=CML24 PE=2 SV=1           Query_786 Cyn d 7 (Polcalcin;CBP)       10
        68206     407       2         29.6462   65        0.204774  5         26        88        109       13        16        0         22        0.590909091         0.590909091
        0.309859155
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_2821          "Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"
        4         19725     778       1         478.404   1230      1.63E-161 35        412       45        426       226       284       4         382       0.591623037         0.597883598
        0.917475728
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_2555          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4         19725     778       1         306.99    785       4.49E-98  1         245       182       426       145       184       0         245       0.591836735         0.591836735
        1
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1289          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3         63860     679       1         492.656   1267      2.85E-168 1         410       86        497       247       314       12        417       0.592326139         0.609876543
        0.987804878
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1290          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3         63860     679       1         492.656   1267      2.85E-168 1         410       86        497       247       314       12        417       0.592326139         0.609876543
        0.987804878
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1769          "Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"
        4         19725     778       1         501.516   1290      2.34E-170 1         422       23        426       252       302       24        425       0.592941176         0.628428928
        0.950236967
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_217 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"       3
        63860     679       1         488.419   1256      1.16E-166 3         411       87        497       247       310       12        416       0.59375   0.611386139         0.98296837
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1283          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3         63860     679       1         493.041   1268      1.59E-168 1         410       86        497       248       312       12        417       0.594724221         0.612345679
        0.987804878
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_2555          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3         63860     679       1         311.227   796       1.24E-100 1         245       251       497       147       190       2         247       0.5951417 0.6       1
Unigene9701         20120710_JGPPBS_1_7.3821.3832.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_03g011710 [Sorghum bicolor] >gi|241929664|gb|EES02809.1| hypothetical
protein SORBIDRAFT_03g011710 [Sorghum bicolor]    Chitinase 10 OS=Oryza sativa subsp. japonica GN=Cht10 PE=2 SV=1                Query_4571          Tri a Endochitinase (Chitinase)         1
        104214    206       1         221.09    562       4.30E-70  79        243       41        206       99        127       1         166       0.596385542         0.6       0.515625
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1282          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
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        3       63860   679     1       494.582 1272    4.23E-169 1       410     86      497     249     313     12      417     0.597122302     0.614814815
        0.987804878
Unigene332      20120710_JGPPBS_1_5.3902.4020.2     S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_1284      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        3       63860   679     1       494.582 1272    3.80E-169 1       410     86      497     249     313     12      417     0.597122302     0.614814815
        0.987804878
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3    S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_741 "Phl p 13 (""Grasses, Group 13;Polygalacturonase"")"      4
        19725   778     1       461.455 1186    3.15E-155 13      392     48      425     227     276     2       380     0.597368421     0.600529101
        0.959390863
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2        Query_2138      "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"      3       100096  176     1       180.259 456     1.85E-55  26      157     45      176     79      97      0       132     0.598484848
        0.598484848     0.501901141
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2        Query_2139      "Poa p 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       181.415 459     7.43E-56  26      157     45      176     79      98      0       132     0.598484848     0.598484848
        0.501901141
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2        Query_2114      "Ory s 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       186.422 472     7.82E-58  21      157     40      176     82      103     0       137     0.598540146     0.598540146
        0.513108614
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2        Query_2115      "Ory s 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       186.422 472     7.82E-58  21      157     40      176     82      103     0       137     0.598540146     0.598540146
        0.513108614
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2        Query_5365      "Zea m 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       198.749 504     1.57E-62  4       165     15      176     97      116     0       162     0.598765432     0.598765432
        0.602230483
Unigene332      20120710_JGPPBS_1_5.3902.4020.2     S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_1781      "Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"
        3       63860   679     1       512.686 1319    7.81E-176 1       427     86      497     257     318     19      429     0.599067599     0.626829268
        0.960187354
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3    S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_2556      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        4       19725   778     1       313.923 803     9.82E-101 1       245     182     426     147     187     0       245     0.6     0.6     1
Unigene332      20120710_JGPPBS_1_5.3902.4020.2     S.halepenseFrame2Rev    hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_221 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"      3
        63860   679     1       486.878 1252    4.07E-166 1       404     92      497     247     311     12      411     0.600973236     0.619047619
        0.987623762
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3    S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_221 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"      4
        19725   778     1       469.159 1206    4.63E-158 29      404     53      426     226     278     2       376     0.60106383      0.604278075
        0.925742574
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3    S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_2275      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        3       19725   778     1       451.055 1159    4.22E-151 41      391     48      398     211     259     0       351     0.601139601     0.601139601
        0.89769821
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3    S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_2276      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        3       19725   778     1       451.055 1159    4.30E-151 43      393     48      398     211     258     0       351     0.601139601     0.601139601
        0.893129771
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3    S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_2277      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        3       19725   778     1       451.055 1159    4.30E-151 43      393     48      398     211     258     0       351     0.601139601     0.601139601
        0.893129771
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3    S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_2278      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        3       19725   778     1       451.055 1159    4.49E-151 43      393     48      398     211     258     0       351     0.601139601     0.601139601
        0.893129771
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3    S.halepenseFrame1Rev    hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1        Query_2279      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        3       19725   778     1       451.44  1160    2.79E-151 45      395     48      398     211     259     0       351     0.601139601     0.601139601
        0.888607595
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Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1273          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          3         63860     679       1         499.204   1284      6.84E-171 1         410       86        497       251       317       12        417       0.601918465         0.619753086
          0.987804878
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_6150          "Hor v 13 (""Grasses, Group 13;Polygalacturonase"")"
          3         19725     778       1         471.085   1211      3.05E-158 49        430       46        425       230       277       2         382       0.602094241         0.605263158
          0.87962963
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2130          "Tri ur 1 (""Grasses, Group 1;Expansin;CCD-bearing Protein (XF)"")"   2
          70550     436       1         165.236   417       8.95E-48  53        203       148       296       91        115       2         151       0.602649007         0.610738255
          0.723300971
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                   Query_5535          "Zea m 1 (""Grasses, Group 1;Expansin"")"          3
          100096    176       1         197.978   502       2.34E-62  1         159       18        176       96        116       0         159       0.603773585         0.603773585
          0.604562738
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1272          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          3         63860     679       1         500.36    1287      2.10E-171 1         410       86        497       252       317       12        417       0.604316547         0.622222222
          0.987804878
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                   Query_2140          "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group
1;Expansin"")"      3         100096    176       1         183.726   465       7.52E-57  26        157       45        176       80        99        0         132       0.606060606
          0.606060606         0.501901141
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                   Query_2119          "Hol l 1 (""Grasses, Group 1;Expansin"")"          3
          100096    176       1         182.57    462       1.92E-56  26        157       45        176       80        98        0         132       0.606060606         0.606060606
          0.501901141
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                   Query_1536          "Tri a 1 (""Grasses, Group 1;Expansin"")"          3
          100096    176       1         169.474   428       3.42E-51  32        158       52        176       77        93        2         127       0.606299213         0.616     0.461254613
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                   Query_1538          "Tri a 1 (""Grasses, Group 1;Expansin"")"          3
          100096    176       1         169.474   428       2.92E-51  32        158       52        176       77        93        2         127       0.606299213         0.616     0.461254613
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                   Query_1537          "Tri a 1 (""Grasses, Group 1;Expansin"")"          3
          100096    176       1         169.474   428       3.57E-51  32        158       52        176       77        93        2         127       0.606299213         0.616     0.461254613
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                   Query_2129          "Tri a 1 (""Grasses, Group 1;Expansin"")"          3
          100096    176       1         180.259   456       2.07E-55  27        161       45        176       82        100       3         135       0.607407407         0.621212121
          0.488888889
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1781          "Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"
          4         19725     778       1         477.248   1227      8.51E-161 48        427       48        426       231       283       1         380       0.607894737         0.609498681
          0.887587822
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1271          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          3         63860     679       1         501.901   1291      6.81E-172 1         410       86        497       254       317       12        417       0.60911271          0.627160494
          0.987804878
CL248.Contig1       20120710_JGPPBS_1_5.10377.10489.3       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_6050          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
          4         19725     778       1         216.083   549       2.54E-65  1         169       258       426       103       127       0         169       0.609467456         0.609467456
          1
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1769          "Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"
          3         63860     679       1         509.99    1312      5.73E-175 1         422       86        497       259       318       14        424       0.610849057         0.631707317
          0.971563981
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_1288          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         248.825   634       4.64E-78  1         197       27        235       129       155       16        211       0.611374408         0.661538462
          0.989847716
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                   Query_4436          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          3         63860     679       1         360.533   924       2.30E-118 28        317       205       497       181       224       9         296       0.611486486         0.630662021
          0.905362776
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Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_5509	"Ory s 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	190.274	482	1.36E-59	6	142	40	176	84	104	0	137	0.613138686	0.613138686	0.543650794
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_5510	"Ory s 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	188.348	477	1.01E-58	6	142	40	176	84	103	0	137	0.613138686	0.613138686	0.543650794
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2092	"Ory s 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	190.66	483	1.61E-59	21	157	40	176	84	104	0	137	0.613138686	0.613138686	0.513108614
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2135	"Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"	3	100096	176	1	183.726	465	7.12E-57	26	157	45	176	81	98	0	132	0.613636364	0.613636364	0.501901141
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2136	"Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"	3	100096	176	1	183.726	465	7.12E-57	26	157	45	176	81	98	0	132	0.613636364	0.613636364	0.501901141
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2132	"Fes p 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	183.726	465	7.52E-57	26	157	45	176	81	98	0	132	0.613636364	0.613636364	0.501901141
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2942	"Pas n 1 (""Grasses, Group 1;Expansin"")"	2	70550	436	1	321.627	823	4.18E-107	1	262	35	296	162	196	4	264	0.613636364	0.623076923	0.981132075
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_5801	"Sec c 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	183.341	464	4.81E-57	7	138	45	176	81	98	0	132	0.613636364	0.613636364	0.552301255
Unigene332	20120710_JGPPBS_1_5.3902.4020.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_2820	"Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"	3	63860	679	1	511.916	1317	8.79E-176	4	413	93	497	253	317	9	412	0.61407767	0.627791563	0.975786925
CL248.Contig1	20120710_JGPPBS_1_5.10377.10489.3	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_1287	"Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"	4	19725	778	1	486.878	1252	9.82E-165	35	410	51	426	231	279	0	376	0.614361702	0.614361702	0.917073171
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_192 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	3	100096	176	1	174.481	441	1.96E-53	6	135	48	176	80	97	1	130	0.615384615	0.620155039	0.528688525
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_193 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	3	100096	176	1	174.096	440	2.09E-53	6	135	48	176	80	97	1	130	0.615384615	0.620155039	0.528688525
CL248.Contig1	20120710_JGPPBS_1_5.10377.10489.3	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_6051	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	4	19725	778	1	217.238	552	9.23E-66	1	169	258	426	104	127	0	169	0.615384615	0.615384615	1
CL2052.Contig1	20120710_JGPPBS_1_8.3818.3823.2	S.halepenseFrame1	hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_4594	Bra di 11 (Ole e 1-like)	1	1675	380	1	203.371	516	2.13E-63	7	165	69	226	98	116	1	159	0.616352201	0.620253165	0.934911243
Unigene332	20120710_JGPPBS_1_5.3902.4020.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_2821	"Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"	3	63860	679	1	508.064	1307	2.66E-174	4	412	93	497	254	318	10	412	0.616504854	0.631840796	0.975728155
Unigene332	20120710_JGPPBS_1_5.3902.4020.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_1287	"Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"	3	63860	679	1	514.227	1323	1.04E-176	1	410	86	497	256	320	8	415	0.61686747	0.628992629	0.992682927
Unigene332	20120710_JGPPBS_1_5.3902.4020.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_2556	"Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"	3	63860	679	1	322.783	826	4.95E-105	3	245	253	497	152	194	2	245	0.620408163	0.625514403	0.991836735
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Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2133	"Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"	3	100096	176	1	186.422	472	6.97E-58	26	157	45	176	82	99	0	132	0.621212121	0.621212121	0.501901141
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_929	"Dac g 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	185.652	470	6.84E-58	3	134	45	176	82	99	0	132	0.621212121	0.621212121	0.55
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2131	"Dac g 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	186.808	473	6.06E-58	27	158	45	176	82	99	0	132	0.621212121	0.621212121	0.501901141
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2134	"Fes p 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	186.037	471	8.65E-58	26	157	45	176	82	99	0	132	0.621212121	0.621212121	0.501901141
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2137	"Fes p 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	186.808	473	4.34E-58	26	157	45	176	82	100	0	132	0.621212121	0.621212121	0.501901141
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_4204	"Pha a 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	186.037	471	1.38E-57	32	163	45	176	82	100	0	132	0.621212121	0.621212121	0.49070632
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_164	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	4	47854	201	1	144.05	362	2.29E-41	134	244	1	109	69	84	2	111	0.621621622	0.633027523	0.443089431
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_4098	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	4	47854	201	1	142.51	358	1.11E-40	152	262	1	109	69	84	2	111	0.621621622	0.633027523	0.416030534
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2116	"Ory s 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	115.161	287	2.31E-32	21	102	40	121	51	61	0	82	0.62195122	0.62195122	0.700854701
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_4098	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	3	100096	176	1	176.022	445	6.85E-54	24	153	48	176	81	98	1	130	0.623076923	0.627906977	0.492366412
Unigene332	20120710_JGPPBS_1_5.3902.4020.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_6050	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	3	63860	679	1	226.868	577	8.60E-70	4	169	330	497	105	134	2	168	0.625	0.63253012	0.982248521
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2248	"Zea m 1 (""Grasses, Group 1;Expansin"")"	3	100096	176	1	197.978	502	3.31E-62	28	166	38	176	87	105	0	139	0.625899281	0.625899281	0.514814815
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_5510	"Ory s 1 (""Grasses, Group 1;Expansin"")"	4	47854	201	1	148.288	373	5.63E-43	141	250	1	108	69	87	2	110	0.627272727	0.638888889	0.428571429
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_5509	"Ory s 1 (""Grasses, Group 1;Expansin"")"	4	47854	201	1	146.747	369	2.49E-42	141	250	1	108	69	87	2	110	0.627272727	0.638888889	0.428571429
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2092	"Ory s 1 (""Grasses, Group 1;Expansin"")"	4	47854	201	1	147.517	371	1.98E-42	156	265	1	108	69	87	2	110	0.627272727	0.638888889	0.404494382
CL2052.Contig1	20120710_JGPPBS_1_8.3818.3823.2	S.halepenseFrame1	hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_4242	Sor b 11 (Ole e 1-like)	2	1675	380	1	206.068	523	2.14E-64	6	161	67	222	98	117	0	156	0.628205128	0.628205128	0.923076923
CL2052.Contig1	20120710_JGPPBS_1_8.3818.3823.2	S.halepenseFrame1	hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_5493	Zea m 11 (Ole e 1-like)	2	1675	380	1	203.756	517	1.21E-63	3	157	67	222	98	119	1	156	0.628205128	0.632258065	0.939393939
CL2052.Contig1	20120710_JGPPBS_1_8.3818.3823.2	S.halepenseFrame1	hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_5494	Zea m 11 (Ole e 1-like)	2	1675	380	1	201.83	512	6.98E-63	3	157	67	222	98	118	1	156	0.628205128	0.632258065	0.939393939
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2122	"Hol l 1 (""Grasses, Group 1;Expansin"")"	3
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        100096  176     1       189.889 481     3.10E-59  28      159     45      176     83      101     0       132     0.628787879     0.628787879
        0.498113208
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                Query_2123      "Hol l 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       189.889 481     3.10E-59  28      159     45      176     83      101     0       132     0.628787879     0.628787879
        0.498113208
CL1737.Contig1  20120710_JGPPBS_1_6.10573.10640.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                Query_1285      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        2       88260   613     1       320.087 819     9.86E-104 1       251     27      289     167     198     16      265     0.630188679     0.670682731
        0.808441558
Unigene492      20120710_JGPPBS_1_7.8636.8708.2      S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_192 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    4
        47854   201     1       146.362 368     2.75E-42  134     244     1       109     70      85      2       111     0.630630631     0.642201835
        0.446721311
Unigene492      20120710_JGPPBS_1_7.8636.8708.2      S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_193 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    4
        47854   201     1       146.362 368     2.47E-42  134     244     1       109     70      85      2       111     0.630630631     0.642201835
        0.446721311
Unigene332      20120710_JGPPBS_1_5.3902.4020.2      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                Query_6051      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        3       63860   679     1       228.409 581     2.67E-70  4       169     330     497     106     134     2       168     0.630952381     0.638554217
        0.982248521
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3      S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                Query_6048      "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        4       19725   778     1       223.787 569     4.47E-68  1       169     258     426     107     129     0       169     0.633136095     0.633136095
        1
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2      S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_1587      "Tri ur 1 (""Grasses, Group 1;Expansin;CCD-bearing Protein (XF)"")"   2
        70550   436     1       144.05  362     4.09E-41  1       126     173     296     80      98      2       126     0.634920635     0.64516129
        0.96124031
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                Query_1540      "Tri a 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       172.555 436     2.22E-52  37      160     55      176     79      94      2       124     0.637096774     0.647540984
        0.446886447
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                Query_164 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    3
        100096  176     1       179.874 455     1.49E-55  6       135     48      176     83      99      1       130     0.638461538     0.643410853
        0.524390244
CL248.Contig1   20120710_JGPPBS_1_5.10377.10489.3      S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_04g006610 [Sorghum bicolor] >gi|241931553|gb|EES04698.1| hypothetical
protein SORBIDRAFT_04g006610 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                Query_955 "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"        4
        19725   778     1       223.402 568     4.95E-68  4       169     261     426     106     128     0       166     0.638554217     0.638554217
        0.982248521
Unigene332      20120710_JGPPBS_1_5.3902.4020.2      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                Query_1454      "Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"
        3       63860   679     1       525.013 1351    0         1       412     86      498     266     323     7       416     0.639423077     0.650366748
        0.992718447
Unigene808      20120710_JGPPBS_1_2.8068.8144.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]  Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_6363      "Phl p 4 (""CCD-bearing Protein
(XF);Grasses, Group 4"")"       1       102811  637     1       667.922 1722    0       8       498     45      533     314     398     2       491     0.639511202
        0.642126789     0.978
Unigene492      20120710_JGPPBS_1_7.8636.8708.2      S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_4099      "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    4
        47854   201     1       149.828 377     2.09E-43  152     262     1       109     71      85      2       111     0.63963964      0.651376147
        0.416030534
Unigene492      20120710_JGPPBS_1_7.8636.8708.2      S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_4100      "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    4
        47854   201     1       149.828 377     2.11E-43  152     262     1       109     71      85      2       111     0.63963964      0.651376147
        0.416030534
Unigene540      20120710_JGPPBS_1_8.4018.4126.2      S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical
protein SORBIDRAFT_09g007260 [Sorghum bicolor]  Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1                Query_1939      Ory s 11 (Ole e 1-like)       2       30861   181
        1       156.762 395     1.40E-47  41      151     71      181     71      88      0       111     0.63963964      0.63963964      0.634285714
Unigene808      20120710_JGPPBS_1_2.8068.8144.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]  Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_6037      "Phl p 4 (""CCD-bearing Protein
(XF);Grasses, Group 4"")"       1       102811  637     1       672.929 1735    0       16      506     45      533     315     400     2       491     0.641547862
        0.644171779     0.962598425
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CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_5701          "Hor v 1 (""Grasses, Group 1;Expansin"")"         2         70550     436
         1         140.969   354       5.49E-40  1         121       178       296       78        94        2         121       0.644628099         0.655462185         0.983471074
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                 Query_1244          "Bra di 1 (""Grasses, Group 1;Expansin"")"        3
         100096    176       1         192.586   488       3.26E-60  27        159       45        176       86        105       1         133       0.646616541         0.651515152
         0.496240602
Unigene808          20120710_JGPPBS_1_2.8068.8144.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2            Query_349 "Dac g 4 (""CCD-bearing Protein
(XF);Grasses, Group 4"")"     1         102811    637       1         31.5722   70        0.0423348 23        42        154       173       13        17        0         20        0.65
         0.65      0.363636364
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2113          "Hor v 1 (""Grasses, Group 1;Expansin"")"         1         70550     436
         1         320.087   819       1.76E-106 1         262       36        296       171       201       3         263       0.650190114         0.657692308         0.992366412
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2102          "Bra sy 1 (""Grasses, Group 1;Expansin"")"         1         70550     436
         1         331.257   848       7.65E-111 1         263       35        296       173       206       5         265       0.652830189         0.665384615         0.984848485
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2129          "Tri a 1 (""Grasses, Group 1;Expansin"")"         1         70550     436
         1         319.701   818       2.84E-106 1         267       35        296       175       206       7         268       0.652985075         0.670498084         0.966666667
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                 Query_2102          "Bra sy 1 (""Grasses, Group 1;Expansin"")"        3
         100096    176       1         193.741   491       1.21E-60  25        157       45        176       87        106       1         133       0.654135338         0.659090909         0.5
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev         hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_741 "Phl p 13 (""Grasses, Group 13;Polygalacturonase"")"        3
         63860     679       1         500.745   1288      1.12E-171 23        394       130       498       244       299       5         373       0.654155496         0.663043478
         0.934010152
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev         hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_6048          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         3         63860     679       1         236.884   603       1.41E-73  1         169       327       497       112       140       2         171       0.65497076          0.662721893
         1
CL830.Contig1       20120710_JGPPBS_1_6.3009.3022.2         S.halepenseFrame2Rev         hypothetical protein SORBIDRAFT_08g022830 [Sorghum bicolor] >gi|241944341|gb|EES17486.1| hypothetical
protein SORBIDRAFT_08g022830 [Sorghum bicolor]    Pathogenesis-related protein 1A OS=Nicotiana tabacum PE=1 SV=1               Query_6052          Cyn d 24 (PR-1 Protein)       2
         55903     899       1         221.09    562       4.66E-67  5         153       124       272       99        123       4         151       0.655629139         0.673469388
         0.960784314
Unigene808          20120710_JGPPBS_1_2.8068.8144.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2            Query_6329          "Phl p 4 (""CCD-bearing Protein
(XF);Grasses, Group 4"")"     1         102811    637       1         672.929   1735      0         8         498       45        533       322       395       2         491       0.655804481
         0.658486708         0.978
Unigene808          20120710_JGPPBS_1_2.8068.8144.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2            Query_6331          "Phl p 4 (""CCD-bearing Protein
(XF);Grasses, Group 4"")"     1         102811    637       1         672.544   1734      0         8         498       45        533       322       395       2         491       0.655804481
         0.658486708         0.978
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_1634          "Ory s 1 (""Grasses, Group 1;Expansin"")"         2         70550     436
         1         154.066   388       9.40E-45  1         125       173       295       82        100       2         125       0.656     0.666666667         0.946153846
Unigene332          20120710_JGPPBS_1_5.3902.4020.2         S.halepenseFrame2Rev         hypothetical protein SORBIDRAFT_03g021050 [Sorghum bicolor] >gi|241927668|gb|EES00813.1| hypothetical
protein SORBIDRAFT_03g021050 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_955 "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"        3
         63860     679       1         235.728   600       3.82E-73  3         169       329       497       111       139       2         169       0.656804734         0.664670659
         0.98816568
Unigene808          20120710_JGPPBS_1_2.8068.8144.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2            Query_6044          "Hor v 4 (""Grasses, Group 4"")"
         1         102811    637       1         700.279   1806      0         18        516       28        532       332       411       6         505       0.657425743         0.665330661
         0.963320463
Unigene808          20120710_JGPPBS_1_2.8068.8144.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2            Query_2111          "Hor v 4 (""Grasses, Group 4"")"
         1         102811    637       1         700.664   1807      0         20        518       28        532       332       411       6         505       0.657425743         0.665330661
         0.959615385
Unigene540          20120710_JGPPBS_1_8.4018.4126.2         S.halepenseFrame1Rev         hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical
protein SORBIDRAFT_09g007260 [Sorghum bicolor]    Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1               Query_1917          Aeg ta 11 (Ole e 1-like)      2         30861     181
         1         159.073   401       1.29E-48  33        143       71        181       73        86        0         111       0.657657658         0.657657658         0.664670659
Unigene540          20120710_JGPPBS_1_8.4018.4126.2         S.halepenseFrame1Rev         hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical
protein SORBIDRAFT_09g007260 [Sorghum bicolor]    Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1               Query_350 Lol p 11 (Ole e 1-like)       2         30861     181       1
         159.458   402       2.90E-49  9         119       71        181       73        88        0         111       0.657657658         0.657657658         0.828358209
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_4099          "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    1
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        70550   436     1       332.413 851     2.38E-111 1       259     40      296     171     199     4       260     0.657692308     0.66796875
        0.977099237
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_6150          "Hor v 13 (""Grasses, Group 13;Polygalacturonase"")"
        2       88260   613     1       548.895 1413    0       13      430     26      447     279     333     8       424     0.658018868     0.670673077
        0.962962963
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_295 "Lol p 4 (""Grasses, Group 4;CCD-bearing
Protein (XF)"")"    1       102811  637     1       590.497 1521    0       2       423     106     525     278     347     2       422     0.658767773
        0.661904762     0.992907801
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_6330          "Phl p 4 (""CCD-bearing Protein
(XF);Grasses, Group 4"")"    1      102811  637     1       678.707 1750    0       8       498     45      533     324     397     2       491     0.6598778
        0.662576687     0.978
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_6038          "Phl p 4 (""CCD-bearing Protein
(XF);Grasses, Group 4"")"    1      102811  637     1       679.478 1752    0       16      506     45      533     324     397     2       491     0.6598778
        0.662576687     0.962598425
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_1859          "Phl p 4 (""CCD-bearing Protein
(XF);Grasses, Group 4"")"    1      102811  637     1       679.478 1752    0       33      523     45      533     324     397     2       491     0.6598778
        0.662576687     0.931428571
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_1244          "Bra di 1 (""Grasses, Group 1;Expansin"")"       1       70550   436
        1       335.109 858     2.42E-112 1       265     35      296     175     207     3       265     0.660377358     0.667938931     0.984962406
CL1152.Contig1      20120710_JGPPBS_1_8.5697.5850.3         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_02g004850 [Sorghum bicolor] >gi|241924945|gb|EER98089.1| hypothetical
protein SORBIDRAFT_02g004850 [Sorghum bicolor]    Thioredoxin H-type OS=Oryza sativa subsp. indica GN=TRXH PE=1 SV=1              Query_1140          Tri a Trx (Thioredoxin)     1
        17690   256     1       166.392 420     2.33E-51  1       118     35      152     78      91      0       118     0.661016949     0.661016949     1
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2092          "Ory s 1 (""Grasses, Group 1;Expansin"")"       1       70550   436
        1       344.354 882     5.87E-116 1       263     35      296     175     209     3       264     0.662878788     0.670498084     0.97752809
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_4100          "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    1
        70550   436     1       336.265 861     6.75E-113 1       259     40      296     173     201     4       260     0.665384615     0.67578125
        0.977099237
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1454          "Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"
        2       88260   613     1       569.696 1467    0       1       410     27      447     281     330     13      422     0.665876777     0.687041565
        0.992718447
Unigene540          20120710_JGPPBS_1_8.4018.4126.2         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical
protein SORBIDRAFT_09g007260 [Sorghum bicolor]    Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1               Query_351 Phl p 11 (Ole e 1-like)       2       30861   181     1
        161.384 407     6.81E-50  9       119     71      181     74      88      0       111     0.666666667     0.666666667     0.776223776
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_5652          "Tri a 4 (""Grasses, Group 4"")"
        1       102811  637     1       694.115 1790    0       28      516     45      533     326     400     0       489     0.666666667     0.666666667
        0.944015444
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_164 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    2
        70550   436     1       315.079 806     7.22E-105 6       241     64      296     158     189     3       236     0.669491525     0.678111588
        0.947154472
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_1944          "Bra di 4 (""Grasses, Group
4;CCD-bearing Protein (XF)"")"          1       102811  637     1       707.212 1824    0       1       519     8       532     352     427     6       525
        0.67047619      0.67822736      0.994252874
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_5638          "Sec c 4 (""Grasses, Group 4"")"
        1       102811  637     1       711.835 1836    0       18      518     28      532     339     414     4       505     0.671287129     0.676646707
        0.963461538
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_5651          "Sec c 4 (""Grasses, Group 4"")"
        1       102811  637     1       697.197 1798    0       29      516     45      533     329     401     1       489     0.672801636     0.674180328
        0.942084942
Unigene808          20120710_JGPPBS_1_2.8068.8144.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2           Query_5566          "Tri a 4 (""Grasses, Group 4"")"
        1       102811  637     1       697.582 1799    0       28      516     45      533     329     401     0       489     0.672801636     0.672801636
        0.944015444
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CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2114	"Ory s 1 (""Grasses, Group 1;Expansin"")"	1	70550	436	1	348.591	893	1.47E-117	1	262	35	295	177	207	3	263	0.673003802	0.680769231	0.973782772
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2115	"Ory s 1 (""Grasses, Group 1;Expansin"")"	1	70550	436	1	348.591	893	1.47E-117	1	262	35	295	177	207	3	263	0.673003802	0.680769231	0.973782772
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_4098	"Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	1	70550	436	1	337.806	865	2.14E-113	1	259	40	296	175	204	4	260	0.673076923	0.68359375	0.977099237
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2116	"Ory s 1 (""Grasses, Group 1;Expansin"")"	1	70550	436	1	138.272	347	3.39E-39	1	100	35	135	68	77	1	101	0.673267327	0.68	0.854700855
CL1737.Contig1	20120710_JGPPBS_1_6.10573.10640.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_1291	"Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"	2	88260	613	1	573.548	1477	0	1	424	27	448	295	336	30	438	0.673515982	0.723039216	0.962264151
Unigene540	20120710_JGPPBS_1_8.4018.4126.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_5342	Sor b 11 (Ole e 1-like)	2	30861	181	1	163.696	413	2.55E-50	32	142	71	181	75	88	0	111	0.675675676	0.675675676	0.668674699
Unigene540	20120710_JGPPBS_1_8.4018.4126.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_5362	Zea m 11 (Ole e 1-like)	2	30861	181	1	164.851	416	1.10E-50	44	154	71	181	75	89	0	111	0.675675676	0.675675676	0.623595506
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2128	"Bra di 1 (""Grasses, Group 1;Expansin"")"	1	70550	436	1	339.732	870	4.15E-114	1	265	35	296	180	208	5	266	0.676691729	0.689655172	0.98490566
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_5509	"Ory s 1 (""Grasses, Group 1;Expansin"")"	1	70550	436	1	338.576	867	7.02E-114	1	248	51	296	168	200	2	248	0.677419355	0.682926829	0.976190476
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_5510	"Ory s 1 (""Grasses, Group 1;Expansin"")"	1	70550	436	1	337.035	863	2.78E-113	1	248	51	296	168	198	2	248	0.677419355	0.682926829	0.976190476
Unigene808	20120710_JGPPBS_1_2.8068.8144.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor]	Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2	Query_2110	"Hor v 4 (""Grasses, Group 4"")"	1	102811	637	1	722.62	1864	0	20	519	28	533	343	417	6	506	0.677865613	0.686	0.959692898
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_192 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	1	70550	436	1	317.005	811	1.06E-105	6	241	64	296	161	189	3	236	0.68220339	0.690987124	0.954918033
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_193 "Cyn d 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"	1	70550	436	1	317.775	813	7.06E-106	6	241	64	296	161	189	3	236	0.68220339	0.690987124	0.954918033
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2135	"Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"	1	70550	436	1	341.658	875	6.23E-115	1	263	36	296	181	207	2	263	0.688212928	0.69348659	0.992395437
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_2136	"Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"	1	70550	436	1	341.658	875	6.23E-115	1	263	36	296	181	207	2	263	0.688212928	0.69348659	0.992395437
CL2052.Contig1	20120710_JGPPBS_1_8.3818.3823.2	S.halepenseFrame1	hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_1939	Ory s 11 (Ole e 1-like)	1	1675	380	1	244.202	622	4.67E-79	8	175	65	229	116	136	3	168	0.69047619	0.703030303	0.942857143
CL1737.Contig2	20120710_JGPPBS_1_5.4032.4130.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_6150	"Hor v 13 (""Grasses, Group 13;Polygalacturonase"")"	1	88261	593	1	585.489	1508	0	13	430	18	427	291	341	12	420	0.692857143	0.713235294	0.944444444
CL153.Contig1	20120710_JGPPBS_1_7.4269.4371.2	S.halepenseFrame3	hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor]	Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1	Query_4204	"Pha a 1 (""Grasses, Group 1;Expansin"")"	1	70550	436	1	338.191	866	1.60E-113	5	269	35	296	185	204	5	266	0.695488722	0.708812261	0.970260223
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2949	"Zea m 1 (""Grasses, Group 1;Expansin"")"	4	47854	201	1	167.162	422	4.63E-50	158	268	1	109	78	94	2	111	0.702702703	0.71559633	0.405204461
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CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2138          "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    1
          70550     436       1         348.206   892       1.59E-117 1         263       36        296       185       208       2         263       0.703422053         0.708812261
          0.992395437
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2133          "Lol p 1 (""Grasses, Group 1;CCD-bearing Protein (XF);Expansin"")"    1
          70550     436       1         346.665   888       7.49E-117 1         263       36        296       185       207       2         263       0.703422053         0.708812261
          0.992395437
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2132          "Fes p 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
          1         345.125   884       2.39E-116 1         263       36        296       185       207       2         263       0.703422053         0.708812261         0.992395437
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2137          "Fes p 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
          1         346.665   888       6.30E-117 1         263       36        296       185       207       2         263       0.703422053         0.708812261         0.992395437
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_4235          "Ory s 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
          1         321.242   822       4.71E-106 89        314       72        295       159       184       2         226       0.703539823         0.709821429         0.702194357
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2122          "Hol l 1 (""Grasses, Group 1;Expansin"")"          2         70550     436
          1         345.51    885       2.05E-116 1         265       35        296       187       206       3         265       0.705660377         0.713740458         0.988679245
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2123          "Hol l 1 (""Grasses, Group 1;Expansin"")"          2         70550     436
          1         345.51    885       2.05E-116 1         265       35        296       187       206       3         265       0.705660377         0.713740458         0.988679245
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2134          "Fes p 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
          1         348.591   893       1.24E-117 1         263       36        296       186       208       2         263       0.707224335         0.712643678         0.992395437
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2119          "Hol l 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
          1         347.051   889       4.55E-117 1         263       36        296       186       205       2         263       0.707224335         0.712643678         0.992395437
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2140          "Phl p 1 (""CCD-bearing Protein (XF);Grasses, Group 1;Expansin"")"    1
          70550     436       1         351.288   900       9.80E-119 1         263       36        296       187       208       2         263       0.711026616         0.716475096
          0.992395437
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2139          "Poa p 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
          1         350.517   898       2.21E-118 1         263       36        296       187       206       2         263       0.711026616         0.716475096         0.992395437
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2948          "Zea m 1 (""Grasses, Group 1;Expansin"")"          4         47854     201
          1         168.703   426       1.51E-50  158       268       1         109       79        94        2         111       0.711711712         0.724770642         0.405204461
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2947          "Zea m 1 (""Grasses, Group 1;Expansin"")"          4         47854     201
          1         167.162   422       4.99E-50  158       268       1         109       79        93        2         111       0.711711712         0.724770642         0.405204461
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2951          "Zea m 1 (""Grasses, Group 1;Expansin"")"          4         47854     201
          1         167.162   422       5.05E-50  158       268       1         109       79        93        2         111       0.711711712         0.724770642         0.405204461
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_2820          "Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"
          2         88260     613       1         616.305   1588      0         4         413       34        448       301       354       17        421       0.714964371         0.745049505
          0.978208232
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_2821          "Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"
          2         88260     613       1         616.69    1589      0         4         412       34        448       301       354       16        420       0.716666667         0.745049505
          0.980582524
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1283          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         614.379   1583      0         1         410       27        448       305       347       16        424       0.719339623         0.74754902
          0.995121951
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2945          "Zea m 1 (""Grasses, Group 1;Expansin"")"          4         47854     201
          1         169.474   428       6.76E-51  158       268       1         109       80        94        2         111       0.720720721         0.733944954         0.405204461
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2946          "Zea m 1 (""Grasses, Group 1;Expansin"")"          4         47854     201
          1         169.474   428       6.76E-51  158       268       1         109       80        94        2         111       0.720720721         0.733944954         0.405204461
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                 Query_2953          "Zea m 1 (""Grasses, Group 1;Expansin"")"          4         47854     201
          1         169.474   428       7.06E-51  158       268       1         109       80        94        2         111       0.720720721         0.733944954         0.405204461
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CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1271          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         611.683   1576      0         1         410       27        448       306       346       16        424       0.721698113         0.75
          0.995121951
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1282          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         615.535   1586      0         1         410       27        448       306       348       16        424       0.721698113         0.75
          0.995121951
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1284          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         615.92    1587      0         1         410       27        448       306       348       16        424       0.721698113         0.75
          0.995121951
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1289          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         613.994   1582      0         1         410       27        448       306       349       16        424       0.721698113         0.75
          0.995121951
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1290          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         613.994   1582      0         1         410       27        448       306       349       16        424       0.721698113         0.75
          0.995121951
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_5492          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         268.085   684       4.72E-84  59        231       119       289       125       144       2         173       0.722543353         0.730994152
          0.59375
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_217 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"       2
          88260     613       1         608.601   1568      0         7         411       32        448       303       345       16        419       0.723150358         0.751861042
          0.98053528
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1273          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         613.994   1582      0         1         410       27        448       307       348       16        424       0.724056604         0.75245098
          0.995121951
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2275          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
          2         88260     613       1         569.311   1466      0         1         391       27        420       287       327       7         396       0.724747475         0.737789203
          0.99488491
Unigene808          20120710_JGPPBS_1_2.8068.8144.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical
protein SORBIDRAFT_10g021680 [Sorghum bicolor]    Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2      Query_1943          "Cyn d 4 (""Grasses, Group 4"")"
          1         102811    637       1         763.837   1971      0         1         522       8         532       381       444       3         525       0.725714286         0.729885057
          1
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1272          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         615.15    1585      0         1         410       27        448       308       348       16        424       0.726415094         0.754901961
          0.995121951
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2276          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
          2         88260     613       1         568.926   1465      0         13        393       34        420       282       323       8         388       0.726804124         0.742105263
          0.96692112
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2277          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
          2         88260     613       1         568.926   1465      0         13        393       34        420       282       323       8         388       0.726804124         0.742105263
          0.96692112
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2278          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
          2         88260     613       1         570.466   1469      0         13        393       34        420       282       323       8         388       0.726804124         0.742105263
          0.96692112
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2279          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
          2         88260     613       1         568.926   1465      0         13        395       34        420       283       323       6         388       0.729381443         0.740837696
          0.967088608
CL2052.Contig1      20120710_JGPPBS_1_8.3818.3823.2         S.halepenseFrame1   hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein
SORBIDRAFT_03g001020 [Sorghum bicolor]  Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1                Query_1917          Aeg ta 11 (Ole e 1-like)      1         1675      380       1
          243.432   620       5.76E-79  5         167       69        229       119       135       2         163       0.73006135          0.739130435         0.964071856
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2          S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_2131          "Dac g 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
          1         361.688   927       8.67E-123 1         264       35        296       193       211       2         264       0.731060606         0.736641221         0.992424242
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CL1444.Contig1      20120710_JGPPBS_1_8.10665.10670.2       S.halepenseFrame1   soluble acid invertase [Sorghum bicolor]          Beta-fructofuranosidase 1 OS=Zea mays GN=IVR1 PE=3 SV=1
          Query_2719          Lol p FT (Fructosyltransferase)         1         768       730       1         863.988   2231      0         76        648       15        610       438       484
          25        597       0.733668342         0.765734266         0.882716049
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1781          "Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         626.706   1615      0         1         427       27        448       315       359       7         428       0.735981308         0.748218527
          0.985948478
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_741 "Phl p 13 (""Grasses, Group 13;Polygalacturonase"")"       2
          88260     613       1         571.622   1472      0         14        392       71        447       279       324       2         379       0.736147757         0.74005305
          0.956852792
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1454          "Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"
          1         88261     593       1         623.239   1606      0         1         410       19        427       302       346       1         410       0.736585366         0.738386308
          0.992718447
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_5801          "Sec c 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
          1         328.176   840       4.31E-110 7         239       61        291       172       189       2         233       0.738197425         0.744588745         0.966527197
Unigene492          20120710_JGPPBS_1_7.8636.8708.2         S.halepenseFrame2   hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein
SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2                Query_2942          "Pas n 1 (""Grasses, Group 1;Expansin"")"          4         47854     201
          1         164.851   416       3.48E-49  156       265       1         109       82        96        3         111       0.738738739         0.759259259         0.40754717
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4998          Zea m 12 (Profilin) 3         56585     203
          1         121.709   304       5.96E-35  14        87        1         74        55        64        0         74        0.743243243         0.743243243         0.74
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1781          "Bra di 13 (""Polygalacturonase;Grasses, Group 13"")"
          1         88261     593       1         649.818   1675      0         1         427       19        428       318       358       17        427       0.744730679         0.775609756
          0.960187354
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_741 "Phl p 13 (""Grasses, Group 13;Polygalacturonase"")"       1
          88261     593       1         590.882   1522      0         7         392       42        427       289       335       4         388       0.744845361         0.752604167
          0.974619289
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4998          Zea m 12 (Profilin) 1         63644     330
          1         152.91    385       1.18E-45  1         87        64        150       65        77        0         87        0.747126437         0.747126437         0.87
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2323          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
          2         88260     613       1         494.197   1271      3.76E-171 13        328       135       448       237       270       2         316       0.75      0.75477707
          0.957317073
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5087          Bra di 12 (Profilin)          2
          56585     203       1         192.586   488       5.93E-62  14        130       1         117       88        104       0         117       0.752136752         0.752136752
          0.893129771
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2820          "Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"
          1         88261     593       1         645.966   1665      0         4         413       26        428       309       360       7         410       0.753658537         0.76674938
          0.975786925
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2821          "Ory s 13 (""Grasses, Group 13;Polygalacturonase"")"
          1         88261     593       1         645.966   1665      0         4         412       26        428       309       360       6         409       0.755501222         0.76674938
          0.97815534
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_929 "Dac g 1 (""Grasses, Group 1;Expansin"")"          1         70550     436       1
          347.436   890       1.32E-117 2         240       60        296       181       198       2         239       0.757322176         0.76371308          0.9875
Unigene2745         20120710_JGPPBS_1_8.8767.8854.2         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_09g024960 [Sorghum bicolor] >gi|241945326|gb|EES18471.1| hypothetical
protein SORBIDRAFT_09g024960 [Sorghum bicolor]    Thioredoxin H-type OS=Triticum aestivum PE=1 SV=3           Query_1234          Tri a 25 (Thioredoxin)        1         28525     179       1
          184.882   468       2.20E-59  16        125       35        144       84        100       0         110       0.763636364         0.763636364         0.88
CL1444.Contig1      20120710_JGPPBS_1_8.10665.10670.2        S.halepenseFrame1   soluble acid invertase [Sorghum bicolor]          Beta-fructofuranosidase 1 OS=Zea mays GN=IVR1 PE=3 SV=1
          Query_4425          Lol p FT (Fructosyltransferase)         1         768       730       1         908.286   2346      0         81        663       18        604       453       499
          14        592       0.765202703         0.783737024         0.862686567
Unigene540          20120710_JGPPBS_1_8.4018.4126.2         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical
protein SORBIDRAFT_09g007260 [Sorghum bicolor]    Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1               Query_4594          Bra di 11 (Ole e 1-like)      2         30861     181
          1         192.586   488       1.21E-61  34        144       71        181       85        98        0         111       0.765765766         0.765765766         0.656804734
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1291          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
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        1       88261   593     1       649.432 1674    0       1       424     19      428     327     356     18      426     0.767605634     0.801470588
        0.962264151
CL2052.Contig1      20120710_JGPPBS_1_8.3818.3823.2      S.halepenseFrame1   hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein
SORBIDRAFT_03g001020 [Sorghum bicolor]  Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1              Query_350 Lol p 11 (Ole e 1-like)      1       1675    380     1
        215.312 547     1.41E-68    1       134     87      220     103     112     0       134     0.768656716     0.768656716     1
CL2052.Contig1      20120710_JGPPBS_1_8.3818.3823.2      S.halepenseFrame1   hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein
SORBIDRAFT_03g001020 [Sorghum bicolor]  Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1              Query_351 Phl p 11 (Ole e 1-like)      1       1675    380     1
        231.491 589     1.01E-74    1       143     87      229     110     119     0       143     0.769230769     0.769230769     1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5087          Bra di 12 (Profilin)        1
        63644   330     1       221.861 564     9.94E-72    1       130     64      193     100     117     0       130     0.769230769     0.769230769
        0.992366412
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2     S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1287          "Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"
        2       88260   613     1       654.055 1686    0       1       410     27      448     326     353     12      422     0.772511848     0.795121951
        1
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2555          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        1       88261   593     1       403.29  1035    3.09E-137 1       245     184     428     190     218     0       245     0.775510204     0.775510204
        1
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2     S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2555          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        2       88260   613     1       403.675 1036    3.64E-137 1       245     204     448     190     218     0       245     0.775510204     0.775510204
        1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5260          Hor v 12 (Profilin) 1       63644   330
        1       222.246 565     5.73E-72    1       130     64      193     101     116     0       130     0.776923077     0.776923077     0.992366412
Unigene308          20120710_JGPPBS_1_8.8195.8201.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_4996          Zea m 12 (Profilin) 1       63644   330
        1       229.95  585     6.43E-75    1       131     64      194     102     119     0       131     0.778625954     0.778625954     1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_4997          Zea m 12 (Profilin) 1       63644   330
        1       229.95  585     6.43E-75    1       131     64      194     102     119     0       131     0.778625954     0.778625954     1
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2     S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_221 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"       2
        88260   613     1       606.675 1563    0       29      404     75      448     294     331     2       376     0.781914894     0.786096257
        0.925742574
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2275          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        1       88261   593     1       615.15  1585    0       9       391     26      400     301     334     8       383     0.785900783     0.802666667
        0.959079284
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2279          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
        1       88261   593     1       615.535 1586    0       13      395     26      400     301     334     8       383     0.785900783     0.802666667
        0.949367089
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5260          Hor v 12 (Profilin) 2       56585   203
        1       197.978 502     4.91E-64    14      130     1       117     92      104     0       117     0.786324786     0.786324786     0.893129771
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1285          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        1       88261   593     1       396.356 1017    1.60E-133 1       251     19      269     199     218     4       253     0.786561265     0.799196787
        0.808441558
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_5492          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        1       88261   593     1       299.286 765     3.90E-96  52        231     92      269     142     158     2       180     0.788888889     0.797752809
        0.618055556
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2       S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_1286          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        1       88261   593     1       310.457 794     5.59E-102 1       194     19      212     155     167     4       196     0.790816327     0.807291667
        0.96969697
Unigene308          20120710_JGPPBS_1_8.8195.8201.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5145          Tri a 12 (Profilin) 1       63644   330
        1       226.868 577     1.17E-73    1       130     64      193     103     119     0       130     0.792307692     0.792307692     0.942028986
Unigene308          20120710_JGPPBS_1_8.8195.8201.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_4986          Tri a 12 (Profilin) 1       63644   330
        1       224.942 572     9.85E-73    1       130     64      193     103     118     0       130     0.792307692     0.792307692     0.928571429
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Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4990          Tri a 12 (Profilin) 1         63644     330
         1         227.254   578       9.63E-74  1         130       64        193       103       119       0         130       0.792307692         0.792307692         0.921985816
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2276          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         1         88261     593       1         617.461   1591      0         13        393       26        400       302       335       6         381       0.792650919         0.805333333
         0.954198473
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2277          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         1         88261     593       1         617.461   1591      0         13        393       26        400       302       335       6         381       0.792650919         0.805333333
         0.954198473
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2278          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         1         88261     593       1         617.076   1590      0         13        393       26        400       302       335       6         381       0.792650919         0.805333333
         0.954198473
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5122          Zea m 12 (Profilin) 1         63644     330
         1         234.572   597       1.09E-76  1         131       64        194       104       119       0         131       0.79389313          0.79389313          1
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5145          Tri a 12 (Profilin) 2         56585     203
         1         203.371   516       5.44E-66  14        130       1         117       93        107       0         117       0.794871795         0.794871795         0.847826087
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4996          Zea m 12 (Profilin) 2         56585     203
         1         202.986   515       5.26E-66  14        130       1         117       93        106       0         117       0.794871795         0.794871795         0.893129771
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4997          Zea m 12 (Profilin) 2         56585     203
         1         202.986   515       5.26E-66  14        130       1         117       93        106       0         117       0.794871795         0.794871795         0.893129771
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5122          Zea m 12 (Profilin) 2         56585     203
         1         203.756   517       2.93E-66  14        130       1         117       93        106       0         117       0.794871795         0.794871795         0.893129771
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_6051          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         1         88261     593       1         285.034   728       1.33E-92  1         169       260       428       135       153       0         169       0.798816568         0.798816568
         1
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_6051          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         2         88260     613       1         285.034   728       1.93E-92  1         169       280       448       135       153       0         169       0.798816568         0.798816568
         1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4985          Tri a 12 (Profilin) 1         63644     330
         1         228.409   581       2.33E-74  1         130       64        193       104       119       0         130       0.8       0.8       0.992366412
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                  Query_2323          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
         1         88261     593       1         516.538   1329      3.26E-180 19        328       121       428       248       276       2         310       0.8       0.805194805
         0.93902439
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5142          Tri a 12 (Profilin) 1         63644     330
         1         226.868   577       1.16E-73  1         131       64        194       105       119       0         131       0.801526718         0.801526718         1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5123          Zea m 12 (Profilin) 1         63644     330
         1         236.113   601       3.05E-77  1         131       64        194       105       120       0         131       0.801526718         0.801526718         1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5124          Zea m 12 (Profilin) 1         63644     330
         1         236.113   601       3.05E-77  1         131       64        194       105       120       0         131       0.801526718         0.801526718         1
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5188          Sor b 12 (Profilin) 2         56585     203
         1         198.749   504       2.13E-64  14        130       1         117       94        105       0         117       0.803418803         0.803418803         0.893129771
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4986          Tri a 12 (Profilin) 2         56585     203
         1         202.601   514       1.20E-65  14        130       1         117       94        107       0         117       0.803418803         0.803418803         0.835714286
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4990          Tri a 12 (Profilin) 2         56585     203
         1         204.142   518       2.59E-66  14        130       1         117       94        108       0         117       0.803418803         0.803418803         0.829787234
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3          S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5123          Zea m 12 (Profilin) 2         56585     203
         1         205.682   522       4.63E-67  14        130       1         117       94        107       0         117       0.803418803         0.803418803         0.893129771
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Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5124	Zea m 12 (Profilin) 2	56585	203	1	205.682	522	4.63E-67	14	130	1	117	94	107	0	117	0.803418803	0.803418803	0.893129771
CL1737.Contig2	20120710_JGPPBS_1_5.4032.4130.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_6050	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	1	88261	593	1	286.189	731	4.52E-93	1	169	260	428	136	153	0	169	0.804733728	0.804733728	1
CL1737.Contig1	20120710_JGPPBS_1_6.10573.10640.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_6050	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	2	88260	613	1	286.189	731	6.02E-93	1	169	280	448	136	153	0	169	0.804733728	0.804733728	1
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5142	Tri a 12 (Profilin) 2	56585	203	1	202.986	515	4.99E-66	14	131	1	118	95	107	0	118	0.805084746	0.805084746	0.900763359
CL1737.Contig2	20120710_JGPPBS_1_5.4032.4130.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_2556	"Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"	1	88261	593	1	418.313	1074	4.27E-143	1	245	184	428	198	224	0	245	0.808163265	0.808163265	1
CL1737.Contig1	20120710_JGPPBS_1_6.10573.10640.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_2556	"Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"	2	88260	613	1	418.313	1074	7.58E-143	1	245	204	448	198	224	0	245	0.808163265	0.808163265	1
Unigene808	20120710_JGPPBS_1_2.8068.8144.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor] >gi|241916763|gb|EER89907.1| hypothetical protein SORBIDRAFT_10g021680 [Sorghum bicolor]	Reticuline oxidase-like protein OS=Arabidopsis thaliana GN=At4g20830 PE=1 SV=2	Query_2199	"Zea m 4 (""Grasses, Group 4"")"	1	102811	637	1	832.017	2148	0	1	526	8	533	427	473	0	526	0.811787072	0.811787072	1
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5061	Ory s 12 (Profilin) 2	56585	203	1	206.453	524	2.72E-67	14	130	1	117	95	108	0	117	0.811965812	0.811965812	0.893129771
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_4985	Tri a 12 (Profilin) 2	56585	203	1	206.068	523	2.78E-67	14	130	1	117	95	108	0	117	0.811965812	0.811965812	0.893129771
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5121	Bra di 12 (Profilin)	2	56585	203	1	207.223	526	1.08E-67	14	131	1	118	96	107	0	118	0.813559322	0.813559322	0.900763359
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5141	Hor v 12 (Profilin) 2	56585	203	1	205.297	521	6.34E-67	14	131	1	118	96	105	0	118	0.813559322	0.813559322	0.900763359
CL1737.Contig2	20120710_JGPPBS_1_5.4032.4130.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_1288	"Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"	1	88261	593	1	327.02	837	1.95E-108	1	197	19	215	162	176	4	199	0.814070352	0.830769231	0.989847716
CL1737.Contig2	20120710_JGPPBS_1_5.4032.4130.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_217	"Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"	1	88261	593	1	683.33	1762	0	3	411	20	428	335	366	4	411	0.815085158	0.823095823	0.99026764
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5141	Hor v 12 (Profilin) 1	63644	330	1	229.18	583	1.19E-74	1	131	64	194	107	117	0	131	0.816793893	0.816793893	1
Unigene540	20120710_JGPPBS_1_8.4018.4126.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_4243	Zea m 11 (Ole e 1-like)	1	30861	181	1	219.55	558	3.25E-72	1	139	38	181	118	127	5	144	0.819444444	0.848920863	0.847560976
CL1737.Contig2	20120710_JGPPBS_1_5.4032.4130.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_1283	"Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"	1	88261	593	1	691.419	1783	0	1	410	19	428	338	369	4	412	0.82038835	0.828431373	0.995121951
CL110.Contig1	20120710_JGPPBS_1_3.3239.3321.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_10g024000 [Sorghum bicolor] >gi|241916892|gb|EER90036.1| hypothetical protein SORBIDRAFT_10g024000 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_6050	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	6	52423	204	1	102.834	255	1.13E-26	114	169	1	56	46	52	0	56	0.821428571	0.821428571	0.331360947
CL110.Contig1	20120710_JGPPBS_1_3.3239.3321.2	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_10g024000 [Sorghum bicolor] >gi|241916892|gb|EER90036.1| hypothetical protein SORBIDRAFT_10g024000 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_6051	"Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"	6	52423	204	1	102.834	255	1.11E-26	114	169	1	56	46	52	0	56	0.821428571	0.821428571	0.331360947
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CL110.Contig1       20120710_JGPPBS_1_3.3239.3321.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_10g024000 [Sorghum bicolor] >gi|241916892|gb|EER90036.1| hypothetical
protein SORBIDRAFT_10g024000 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                    Query_955 "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"        6
         52423     204       1         105.531   262       1.08E-27  114       169       1         56        46        52        0         56        0.821428571         0.821428571
         0.331360947
CL110.Contig1       20120710_JGPPBS_1_3.3239.3321.2         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_10g024000 [Sorghum bicolor] >gi|241916892|gb|EER90036.1| hypothetical
protein SORBIDRAFT_10g024000 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                    Query_6048          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         6         52423     204       1         105.531   262       1.14E-27  114       169       1         56        46        52        0         56        0.821428571         0.821428571
         0.331360947
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5219          Hor v 12 (Profilin) 2         56585     203
         1         211.46    537       2.75E-69  14        131       1         118       97        108       0         118       0.822033898         0.822033898         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5144          Tri a 12 (Profilin) 2         56585     203
         1         208.379   529       4.48E-68  14        131       1         118       97        108       0         118       0.822033898         0.822033898         0.900763359
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                    Query_1282          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
         1         88261     593       1         692.96    1787      0         1         410       19        428       339       370       4         412       0.822815534         0.830882353
         0.995121951
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                    Query_1284          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
         1         88261     593       1         692.575   1786      0         1         410       19        428       339       370       4         412       0.822815534         0.830882353
         0.995121951
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                    Query_1289          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
         1         88261     593       1         691.034   1782      0         1         410       19        428       339       370       4         412       0.822815534         0.830882353
         0.995121951
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                    Query_1290          "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
         1         88261     593       1         691.034   1782      0         1         410       19        428       339       370       4         412       0.822815534         0.830882353
         0.995121951
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5061          Ory s 12 (Profilin) 1         63644     330
         1         235.343   599       5.84E-77  1         130       64        193       107       121       0         130       0.823076923         0.823076923         0.992366412
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5121          Bra di 12 (Profilin)          1
         63644     330       1         236.884   603       1.46E-77  1         131       64        194       108       120       0         131       0.824427481         0.824427481         1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5188          Sor b 12 (Profilin) 1         63644     330
         1         234.187   596       1.27E-76  1         131       64        194       108       119       0         131       0.824427481         0.824427481         1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5144          Tri a 12 (Profilin) 1         63644     330
         1         233.802   595       2.11E-76  1         131       64        194       108       120       0         131       0.824427481         0.824427481         1
CL153.Contig1       20120710_JGPPBS_1_7.4269.4371.2         S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1               Query_2248          "Zea m 1 (""Grasses, Group 1;Expansin"")"          1         70550     436
         1         445.662   1145      1.22E-155 1         270       31        296       224       242       4         270       0.82962963          0.842105263         0.985185185
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5143          Hor v 12 (Profilin) 2         56585     203
         1         209.92    533       1.02E-68  14        131       1         118       98        108       0         118       0.830508475         0.830508475         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5108          Phl p 12 (Profilin) 2         56585     203
         1         214.927   546       9.27E-71  14        131       1         118       98        110       0         118       0.830508475         0.830508475         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5243          Phl p 12 (Profilin) 2         56585     203
         1         214.927   546       1.23E-70  14        131       1         118       98        110       0         118       0.830508475         0.830508475         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5112          Phl p 12 (Profilin) 2         56585     203
         1         214.157   544       2.52E-70  14        131       1         118       98        110       0         118       0.830508475         0.830508475         0.900763359
CL1152.Contig1      20120710_JGPPBS_1_8.5697.5850.3         S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_02g004850 [Sorghum bicolor] >gi|241924945|gb|EER98089.1| hypothetical
protein SORBIDRAFT_02g004850 [Sorghum bicolor]    Thioredoxin H-type OS=Oryza sativa subsp. indica GN=TRXH PE=1 SV=1            Query_1998          Zea m 25 (Thioredoxin)        1
         17690     256       1         209.92    533       3.18E-68  1         118       35        152       98        110       0         118       0.830508475         0.830508475
         0.967213115
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5143          Hor v 12 (Profilin) 1         63644     330
         1         235.343   599       5.24E-77  1         131       64        194       109       120       0         131       0.832061069         0.832061069         1
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                    Query_221 "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"        1
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        88261   593     1       682.945 1761    0       1       404     25      428     338     369     4       406     0.832512315     0.84079602
        0.995049505
CL1737.Contig2  20120710_JGPPBS_1_5.4032.4130.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1271      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        1       88261   593     1       698.738 1802    0       1       410     19      428     343     375     4       412     0.832524272     0.840686275
        0.995121951
CL1737.Contig2  20120710_JGPPBS_1_5.4032.4130.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1273      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        1       88261   593     1       701.049 1808    0       1       410     19      428     344     377     4       412     0.834951456     0.843137255
        0.995121951
CL1754.Contig1  20120710_JGPPBS_1_8.6580.6583.2      S.halepenseFrame1   hypothetical protein SORBIDRAFT_06g014730 [Sorghum bicolor] >gi|241937546|gb|EES10691.1| hypothetical protein
SORBIDRAFT_06g014730 [Sorghum bicolor]  Probable glucuronosyltransferase Os04g0398600 OS=Oryza sativa subsp. japonica GN=Os04g0398600 PE=2 SV=2        Query_2161      Zea m Zm13
(Ole e 1-like)  1       1224    596     1       288.5   737     6.02E-94  1       170     43      215     147     156     9       176     0.835227273
        0.880239521     0.982352941
CL1737.Contig2  20120710_JGPPBS_1_5.4032.4130.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1272      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        1       88261   593     1       701.819 1810    0       1       410     19      428     345     377     4       412     0.837378641     0.845588235
        0.995121951
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5103      Phl p 12 (Profilin) 2   56585   203
        1       216.853 551     2.05E-71  14      131     1       118     99      111     0       118     0.838983051     0.838983051     0.900763359
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5240      Phl p 12 (Profilin) 2   56585   203
        1       216.853 551     2.18E-71  14      131     1       118     99      111     0       118     0.838983051     0.838983051     0.900763359
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5105      Phl p 12 (Profilin) 2   56585   203
        1       216.083 549     4.29E-71  14      131     1       118     99      110     0       118     0.838983051     0.838983051     0.900763359
CL1737.Contig2  20120710_JGPPBS_1_5.4032.4130.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_1769      "Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"
        2       88261   593     1       707.212 1824    0       1       422     19      428     357     370     12      422     0.845971564     0.870731707
        0.971563981
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2      S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_5535      "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       446.817 1148    3.40E-156 2       263     38      296     222     240     3       262     0.847328244     0.857142857     0.984790875
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5104      Phl p 12 (Profilin) 2   56585   203
        1       218.009 554     8.04E-72  14      131     1       118     100     111     0       118     0.847457627     0.847457627     0.900763359
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5242      Phl p 12 (Profilin) 2   56585   203
        1       216.468 550     2.33E-71  14      131     1       118     100     109     0       118     0.847457627     0.847457627     0.900763359
Unigene308      20120710_JGPPBS_1_8.8195.8201.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5219      Hor v 12 (Profilin) 1   63644   330
        1       246.899 629     1.43E-81  1       131     64      194     112     122     0       131     0.854961832     0.854961832     1
CL153.Contig1   20120710_JGPPBS_1_7.4269.4371.2      S.halepenseFrame3   hypothetical protein SORBIDRAFT_01g050210 [Sorghum bicolor] >gi|241919875|gb|EER93019.1| hypothetical protein
SORBIDRAFT_01g050210 [Sorghum bicolor]  Expansin-B11 OS=Zea mays GN=EXPB11 PE=1 SV=1                Query_5365      "Zea m 1 (""Grasses, Group 1;Expansin"")"        1       70550   436
        1       457.603 1176    2.32E-160 1       269     31      296     230     245     3       269     0.855018587     0.864661654     0.988847584
CL1737.Contig1  20120710_JGPPBS_1_6.10573.10640.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_4436      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
        1       88260   613     1       519.235 1336    0       25      317     152     448     254     273     4       297     0.855218855     0.866894198
        0.924290221
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]  Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                 Query_2942      "Pas n 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       262.307 669     1.85E-87  1       157     18      176     136     146     2       159     0.855345912     0.866242038
        0.59245283
Unigene540      20120710_JGPPBS_1_8.4018.4126.2      S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical
protein SORBIDRAFT_09g007260 [Sorghum bicolor]  Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1          Query_5493      Zea m 11 (Ole e 1-like)         1       30861   181
        1       216.468 550     5.39E-71  30      140     71      181     95      107     0       111     0.855855856     0.855855856     0.672727273
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5239      Phl p 12 (Profilin) 2   56585   203
        1       218.009 554     7.06E-72  14      131     1       118     101     110     0       118     0.855932203     0.855932203     0.900763359
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3      S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]  Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1          Query_5241      Phl p 12 (Profilin) 2   56585   203
        1       218.779 556     3.84E-72  14      131     1       118     101     110     0       118     0.855932203     0.855932203     0.900763359
CL1737.Contig2  20120710_JGPPBS_1_5.4032.4130.2      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]  Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_4436      "Zea m 13 (""Polygalacturonase;Grasses, Group 13"")"
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        2       88261   593     1       506.138 1302    2.24E-176 33      317     140     428     249     265     4       289     0.861591696     0.873684211
        0.899053628
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2              Query_2951      "Zea m 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       279.256 713     5.23E-94  1       159     18      176     137     146     0       159     0.86163522      0.86163522
        0.591078067
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2              Query_2953      "Zea m 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       278.1   710     1.47E-93  1       159     18      176     137     146     0       159     0.86163522      0.86163522
        0.591078067
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5103      Phl p 12 (Profilin) 1   63644   330
        1       247.669 631     7.65E-82  1       131     64      194     113     122     0       131     0.86259542      0.86259542      1
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5105      Phl p 12 (Profilin) 1   63644   330
        1       247.284 630     1.15E-81  1       131     64      194     113     121     0       131     0.86259542      0.86259542      1
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5108      Phl p 12 (Profilin) 1   63644   330
        1       247.284 630     1.11E-81  1       131     64      194     113     122     0       131     0.86259542      0.86259542      1
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5112      Phl p 12 (Profilin) 1   63644   330
        1       246.514 628     2.16E-81  1       131     64      194     113     122     0       131     0.86259542      0.86259542      1
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5220      Aeg ta 12 (Profilin)    2
        56585   203     1       217.624 553     9.78E-72  14      131     1       118     102     109     0       118     0.86440678      0.86440678
        0.900763359
Unigene540      20120710_JGPPBS_1_8.4018.4126.2       S.halepenseFrame1Rev          hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical
protein SORBIDRAFT_09g007260 [Sorghum bicolor]    Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1            Query_5494      Zea m 11 (Ole e 1-like)         1       30861   181
        1       217.624 553     1.78E-71  30      140     71      181     96      107     0       111     0.864864865     0.864864865     0.672727273
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2              Query_2945      "Zea m 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       279.256 713     5.35E-94  1       159     18      176     138     147     0       159     0.867924528     0.867924528
        0.591078067
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2              Query_2946      "Zea m 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       279.256 713     5.35E-94  1       159     18      176     138     147     0       159     0.867924528     0.867924528
        0.591078067
Unigene493      20120710_JGPPBS_1_7.4502.4597.3      S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2              Query_2947      "Zea m 1 (""Grasses, Group 1;Expansin"")"        3
        100096  176     1       278.87  712     5.83E-94  1       159     18      176     138     147     0       159     0.867924528     0.867924528
        0.591078067
CL2052.Contig1  20120710_JGPPBS_1_8.3818.3823.2      S.halepenseFrame1   hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein
SORBIDRAFT_03g001020 [Sorghum bicolor]  Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1            Query_5362      Zea m 11 (Ole e 1-like)         1       1675    380     1
        290.041 741     7.09E-97  19      178     70      229     139     145     0       160     0.86875 0.86875 0.898876404
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5104      Phl p 12 (Profilin) 1   63644   330
        1       249.21  635     2.33E-82  1       131     64      194     114     122     0       131     0.870229008     0.870229008     1
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5239      Phl p 12 (Profilin) 1   63644   330
        1       248.44  633     4.60E-82  1       131     64      194     114     121     0       131     0.870229008     0.870229008     1
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5240      Phl p 12 (Profilin) 1   63644   330
        1       249.21  635     1.87E-82  1       131     64      194     114     123     0       131     0.870229008     0.870229008     1
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5242      Phl p 12 (Profilin) 1   63644   330
        1       248.054 632     5.59E-82  1       131     64      194     114     122     0       131     0.870229008     0.870229008     1
Unigene308      20120710_JGPPBS_1_8.8195.8201.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5243      Phl p 12 (Profilin) 1   63644   330
        1       248.825 634     2.77E-82  1       131     64      194     114     123     0       131     0.870229008     0.870229008     1
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5244      Bra di 12 (Profilin)    2
        56585   203     1       219.164 557     2.80E-72  14      131     1       118     103     110     0       118     0.872881356     0.872881356
        0.900763359
Unigene1043     20120710_JGPPBS_1_2.7234.7317.3       S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5259      Zea m 12 (Profilin) 2   56585   203
        1       216.853 551     2.02E-71  14      132     1       118     104     111     1       119     0.87394958      0.881355932     0.893939394
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protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5241          Phl p 12 (Profilin) 1         63644     330
         1         250.366   638       6.27E-83  1         131       64        194       115       123       0         131       0.877862595         0.877862595         1
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5119          Zea m 12 (Profilin) 2         56585     203
         1         217.624   553       8.61E-72  14        129       1         116       102       109       0         116       0.879310345         0.879310345         0.892307692
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                Query_2950          "Zea m 1 (""Grasses, Group 1;Expansin"")"         1
         100096    176       1         278.87    712       7.48E-95  1         159       18        176       140       147       0         159       0.880503145         0.880503145
         0.76076555
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                Query_2948          "Zea m 1 (""Grasses, Group 1;Expansin"")"         3
         100096    176       1         281.182   718       7.63E-95  1         159       18        176       140       147       0         159       0.880503145         0.880503145
         0.591078067
Unigene493          20120710_JGPPBS_1_7.4502.4597.3         S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical
protein SORBIDRAFT_01g029840 [Sorghum bicolor]    Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2                Query_2949          "Zea m 1 (""Grasses, Group 1;Expansin"")"         3
         100096    176       1         281.182   718       6.99E-95  1         159       18        176       140       147       0         159       0.880503145         0.880503145
         0.591078067
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5222          Bra di 12 (Profilin)          2
         56585     203       1         221.476   563       3.33E-73  14        131       1         118       104       110       0         118       0.881355932         0.881355932
         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5249          Zea m 12 (Profilin) 2         56585     203
         1         222.246   565       1.49E-73  14        131       1         118       104       112       0         118       0.881355932         0.881355932         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5120          Zea m 12 (Profilin) 2         56585     203
         1         220.32    560       8.94E-73  14        131       1         118       104       111       0         118       0.881355932         0.881355932         0.900763359
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5220          Aeg ta 12 (Profilin)          1
         63644     330       1         252.292   643       1.22E-83  1         131       64        194       116       123       0         131       0.885496183         0.885496183         1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5253          Zea m 12 (Profilin) 1         63644     330
         1         252.292   643       1.20E-83  1         131       64        194       116       123       0         131       0.885496183         0.885496183         1
Unigene308          20120710_JGPPBS_1_8.8195.8201.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical
protein SORBIDRAFT_03g034110 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_4706          Zea m 12 (Profilin) 1         63644     330
         1         258.07    658       8.56E-86  6         137       63        194       117       125       0         132       0.886363636         0.886363636         0.96350365
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_955 "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"         1
         88261     593       1         310.071   793       2.86E-102 2         169       261       428       149       160       0         168       0.886904762         0.886904762
         0.99408284
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_955 "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"         2
         88260     613       1         310.071   793       4.14E-102 2         169       281       448       149       160       0         168       0.886904762         0.886904762
         0.99408284
CL1737.Contig2      20120710_JGPPBS_1_5.4032.4130.2          S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical
protein SORBIDRAFT_10g024010 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_6048          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         1         88261     593       1         311.612   797       5.53E-103 1         169       260       428       150       161       0         169       0.887573964         0.887573964
         1
CL1737.Contig1      20120710_JGPPBS_1_6.10573.10640.2        S.halepenseFrame3RevFrame3Rev hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical
protein SORBIDRAFT_10g021590 [Sorghum bicolor]    Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1                 Query_6048          "Pas n 13 (""Grasses, Group 13;Polygalacturonase"")"
         2         88260     613       1         311.612   797       9.14E-103 1         169       280       448       150       161       0         169       0.887573964         0.887573964
         1
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5067          Cyn d 12 (Profilin) 2         56585     203
         1         223.402   568       5.41E-74  14        131       1         118       105       111       0         118       0.889830508         0.889830508         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5221          Hor v 12 (Profilin) 2         56585     203
         1         221.476   563       3.15E-73  14        131       1         118       105       110       0         118       0.889830508         0.889830508         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5248          Zea m 12 (Profilin) 2         56585     203
         1         222.246   565       1.68E-73  14        131       1         118       105       112       0         118       0.889830508         0.889830508         0.900763359
Unigene1043         20120710_JGPPBS_1_2.7234.7317.3         S.halepenseFrame2Rev          hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical
protein SORBIDRAFT_09g026120 [Sorghum bicolor]    Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1            Query_5253          Zea m 12 (Profilin) 2         56585     203
         1         220.705   561       5.31E-73  14        131       1         118       105       109       0         118       0.889830508         0.889830508         0.900763359
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Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5117 Zea m 12 (Profilin) 2 56585 203
1 223.402 568 5.02E-74 14 131 1 118 105 112 0 118 0.889830508 0.889830508 0.900763359
Unigene308 20120710_JGPPBS_1_8.8195.8201.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5244 Bra di 12 (Profilin) 1
63644 330 1 251.906 642 1.60E-83 1 131 64 194 117 124 0 131 0.893129771 0.893129771 1
Unigene308 20120710_JGPPBS_1_8.8195.8201.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5102 Zea m 12 (Profilin) 1 63644 330
1 256.144 653 4.58E-85 1 131 64 194 117 124 0 131 0.893129771 0.893129771 1
Unigene308 20120710_JGPPBS_1_8.8195.8201.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5254 Zea m 12 (Profilin) 1 63644 330
1 253.832 647 3.51E-84 1 131 64 194 117 124 0 131 0.893129771 0.893129771 1
CL70.Contig1 20120710_JGPPBS_1_5.5536.5637.2 S.halepenseFrame2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays] Enolase 1 OS=Zea mays GN=ENO1 PE=2 SV=1 Query_1247 Cyn d 22 (Enolase) 1 38236 562 1 836.639 2160 0 1 446 26 471 399 425 0 446 0.894618834
0.894618834 1
CL70.Contig1 20120710_JGPPBS_1_5.5536.5637.2 S.halepenseFrame2 enolase 1 [Zea mays] >gi|119355|sp|P26301.1|ENO1_MAIZE RecName: Full=Enolase 1; AltName: Full=2-phospho-D-glycerate hydro-lyase 1; AltName: Full=2-phosphoglycerate dehydratase 1 >gi|22273|emb|CAA39454.1| enolase [Zea mays] Enolase 1 OS=Zea mays GN=ENO1 PE=2 SV=1 Query_1248 Zea m 22 (Enolase) 1 38236 562 1 836.639 2160 0 1 446 26 471 399 425 0 446 0.894618834
0.894618834 1
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5102 Zea m 12 (Profilin) 2 56585 203
1 225.713 574 6.56E-75 14 131 1 118 106 110 0 118 0.898305085 0.898305085 0.900763359
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5245 Zea m 12 (Profilin) 2 56585 203
1 223.402 568 4.40E-74 14 131 1 118 106 112 0 118 0.898305085 0.898305085 0.900763359
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5246 Zea m 12 (Profilin) 2 56585 203
1 223.402 568 4.40E-74 14 131 1 118 106 112 0 118 0.898305085 0.898305085 0.900763359
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5254 Zea m 12 (Profilin) 2 56585 203
1 223.016 567 6.44E-74 14 131 1 118 106 110 0 118 0.898305085 0.898305085 0.900763359
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5255 Zea m 12 (Profilin) 2 56585 203
1 224.942 572 1.37E-74 14 131 1 118 106 112 0 118 0.898305085 0.898305085 0.900763359
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5264 Zea m 12 (Profilin) 2 56585 203
1 224.942 572 1.16E-74 14 131 1 118 106 112 0 118 0.898305085 0.898305085 0.900763359
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_4706 Zea m 12 (Profilin) 2 56585 203
1 226.098 575 5.27E-75 20 137 1 118 106 110 0 118 0.898305085 0.898305085 0.861313869
Unigene2745 20120710_JGPPBS_1_8.8767.8854.2 S.halepenseFrame1Rev hypothetical protein SORBIDRAFT_09g024960 [Sorghum bicolor] >gi|241945326|gb|EES18471.1| hypothetical protein SORBIDRAFT_09g024960 [Sorghum bicolor] Thioredoxin H-type OS=Triticum aestivum PE=1 SV=3 Query_1240 Zea m 25 (Thioredoxin) 1 28525 179 1
208.379 529 1.71E-68 19 127 35 143 98 105 0 109 0.899082569 0.899082569 0.8515625
Unigene451 20120710_JGPPBS_1_1.8204.8279.2 S.halepenseFrame1Rev hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2 Query_1126 Bra di 7 (Polcalcin;CBP) 1 30083 314 1
148.673 374 1.64E-44 1 80 75 154 72 74 0 80 0.9 0.9 1
Unigene451 20120710_JGPPBS_1_1.8204.8279.2 S.halepenseFrame1Rev hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2 Query_1352 Cyn d 7 (Polcalcin;CBP) 1 30083 314 1
150.214 378 5.10E-45 1 80 75 154 72 76 0 80 0.9 0.9 1
Unigene308 20120710_JGPPBS_1_8.8195.8201.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5222 Bra di 12 (Profilin) 1
63644 330 1 254.218 648 2.16E-84 1 131 64 194 118 123 0 131 0.900763359 0.900763359 1
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5247 Zea m 12 (Profilin) 2 56585 203
1 221.861 564 4.05E-73 14 129 1 116 105 110 0 116 0.905172414 0.905172414 0.794520548
Unigene1043 20120710_JGPPBS_1_2.7234.7317.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5114 Zea m 12 (Profilin) 2 56585 203
1 224.942 572 1.41E-74 14 130 1 117 106 110 0 117 0.905982906 0.905982906 0.9
Unigene308 20120710_JGPPBS_1_8.8195.8201.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5114 Zea m 12 (Profilin) 1 63644 330
1 256.144 653 3.82E-85 1 130 64 193 118 124 0 130 0.907692308 0.907692308 1
Unigene308 20120710_JGPPBS_1_8.8195.8201.3 S.halepenseFrame2Rev hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1 Query_5221 Hor v 12 (Profilin) 1 63644 330
1 255.373 651 6.92E-85 1 131 64 194 119 123 0 131 0.908396947 0.908396947 1

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Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_1127	Bra di 7 (Polcalcin;CBP)	1	30083	314	1
150.599	379	3.34E-45	1	80	75	154	73	75	0	80	0.9125	0.9125	1
Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_786 Cyn d 7 (Polcalcin;CBP)	1	30083	314	1
132.494	332	1.53E-38	3	71	86	154	63	67	0	69	0.913043478	0.913043478	0.971830986
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5115	Zea m 12 (Profilin) 2	56585	203
1	223.787	569	3.26E-74	14	130	1	117	107	111	0	117	0.914529915	0.914529915	0.9
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5256	Ory s 12 (Profilin) 2	56585	203
1	228.024	580	7.87E-76	14	131	1	118	108	113	0	118	0.915254237	0.915254237	0.900763359
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5257	Ory s 12 (Profilin) 2	56585	203
1	228.024	580	7.87E-76	14	131	1	118	108	113	0	118	0.915254237	0.915254237	0.900763359
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5252	Sor b 12 (Profilin) 2	56585	203
1	226.483	576	3.81E-75	14	131	1	118	108	112	0	118	0.915254237	0.915254237	0.900763359
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5116	Zea m 12 (Profilin) 2	56585	203
1	226.098	575	4.89E-75	14	131	1	118	108	112	0	118	0.915254237	0.915254237	0.900763359
CL1737.Contig2	20120710_JGPPBS_1_5.4032.4130.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor] >gi|241915498|gb|EER88642.1| hypothetical protein SORBIDRAFT_10g024010 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_1287	"Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"
1	88261	593	1	778.474	2009	0	1	410	19	428	378	396	0	410	0.92195122	0.92195122
1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5067	Cyn d 12 (Profilin) 1	63644	330
1	263.077	671	6.57E-88	1	131	64	194	121	127	0	131	0.923664122	0.923664122	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5251	Sor b 12 (Profilin) 1	63644	330
1	259.996	663	1.20E-86	1	131	64	194	121	125	0	131	0.923664122	0.923664122	1
Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_788 Cyn d 7 (Polcalcin;CBP)	1	30083	314	1
136.346	342	7.52E-40	4	73	85	154	65	68	0	70	0.928571429	0.928571429	0.95890411
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5119	Zea m 12 (Profilin) 1	63644	330
1	259.61	662	1.53E-86	1	129	64	192	120	125	0	129	0.930232558	0.930232558	0.992307692
Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_1339	Hor v 7 (Polcalcin;CBP)	1	30083	314	1
145.591	366	2.27E-43	4	78	80	154	70	72	0	75	0.933333333	0.933333333	0.961538462
Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_1137	Ory s 7 (Polcalcin;CBP)	1	30083	314	1
154.066	388	1.67E-46	4	82	76	154	74	76	0	79	0.936708861	0.936708861	0.963414634
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5120	Zea m 12 (Profilin) 1	63644	330
1	264.618	675	2.10E-88	1	131	64	194	123	127	0	131	0.938931298	0.938931298	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5259	Zea m 12 (Profilin) 1	63644	330
1	261.151	666	4.71E-87	1	132	64	194	124	128	1	132	0.939393939	0.946564885	0.992424242
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5117	Zea m 12 (Profilin) 1	63644	330
1	266.929	681	2.56E-89	1	131	64	194	124	128	0	131	0.946564885	0.946564885	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5249	Zea m 12 (Profilin) 1	63644	330
1	266.929	681	2.38E-89	1	131	64	194	124	129	0	131	0.946564885	0.946564885	1
Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_1246	Zea m 7 (Polcalcin;CBP)	1	30083	314	1
157.532	397	6.39E-48	1	80	75	154	76	77	0	80	0.95	0.95	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5116	Zea m 12 (Profilin) 1	63644	330
1	267.314	682	1.47E-89	1	131	64	194	125	128	0	131	0.954198473	0.954198473	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5248	Zea m 12 (Profilin) 1	63644	330
1	266.544	680	2.89E-89	1	131	64	194	125	129	0	131	0.954198473	0.954198473	1
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Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5264	Zea m 12 (Profilin) 1	63644	330
1	268.085	684	6.97E-90	1	131	64	194	125	129	0	131	0.954198473	0.954198473	1
Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_1338	Phl p 7 (Polcalcin;CBP)	1	30083	314	1
149.443	376	8.81E-45	4	78	80	154	72	73	0	75	0.96	0.96	0.961538462
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5247	Zea m 12 (Profilin) 1	63644	330
1	265.003	676	2.60E-88	1	129	64	192	124	127	0	129	0.96124031	0.96124031	0.883561644
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5115	Zea m 12 (Profilin) 1	63644	330
1	266.544	680	2.74E-89	1	130	64	193	125	127	0	130	0.961538462	0.961538462	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5245	Zea m 12 (Profilin) 1	63644	330
1	268.085	684	7.44E-90	1	131	64	194	126	129	0	131	0.961832061	0.961832061	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5246	Zea m 12 (Profilin) 1	63644	330
1	268.085	684	7.44E-90	1	131	64	194	126	129	0	131	0.961832061	0.961832061	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5255	Zea m 12 (Profilin) 1	63644	330
1	270.011	689	1.56E-90	1	131	64	194	126	129	0	131	0.961832061	0.961832061	1
Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_1376	Zea m 7 (Polcalcin;CBP)	1	30083	314	1
160.614	405	4.03E-49	1	80	75	154	77	78	0	80	0.9625	0.9625	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5256	Ory s 12 (Profilin) 1	63644	330
1	272.322	695	1.55E-91	1	131	64	194	128	130	0	131	0.977099237	0.977099237	1
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5257	Ory s 12 (Profilin) 1	63644	330
1	272.322	695	1.55E-91	1	131	64	194	128	130	0	131	0.977099237	0.977099237	1
Unigene492	20120710_JGPPBS_1_7.8636.8708.2	S.halepenseFrame2	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B1 OS=Zea mays GN=EXPB1 PE=1 SV=2	Query_2944	"Sor b 1 (""Grasses, Group 1;Expansin"")"	4	47854	201
1	228.024	580	1.08E-73	158	266	1	109	107	109	0	109	0.981651376	0.981651376	0.409774436
CL1737.Contig1	20120710_JGPPBS_1_6.10573.10640.2	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor] >gi|241916751|gb|EER89895.1| hypothetical protein SORBIDRAFT_10g021590 [Sorghum bicolor]	Exopolygalacturonase OS=Zea mays GN=PG2C PE=2 SV=1	Query_1769	"Sor b 13 (""Grasses, Group 13;Polygalacturonase"")"
1	88260	613	1	842.032	2174	0	1	422	27	448	415	418	0	422	0.983412322	0.983412322
1
Unigene493	20120710_JGPPBS_1_7.4502.4597.3	S.halepenseFrame3RevFrame3Rev	hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor] >gi|241921393|gb|EER94537.1| hypothetical protein SORBIDRAFT_01g029840 [Sorghum bicolor]	Expansin-B9 OS=Zea mays GN=EXPB9 PE=1 SV=2	Query_2944	"Sor b 1 (""Grasses, Group 1;Expansin"")"	1
100096	176	1	331.257	848	1.63E-114	1	159	18	176	158	158	0	159	0.993710692	0.993710692
0.597744361
CL2052.Contig1	20120710_JGPPBS_1_8.3818.3823.2	S.halepenseFrame1	hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor] >gi|241926874|gb|EES00019.1| hypothetical protein SORBIDRAFT_03g001020 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_5342	Sor b 11 (Ole e 1-like)	1	1675	380	1
342.043	876	1.46E-117	1	166	64	229	165	165	0	166	0.993975904	0.993975904	1
Unigene540	20120710_JGPPBS_1_8.4018.4126.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor] >gi|241946096|gb|EES19241.1| hypothetical protein SORBIDRAFT_09g007260 [Sorghum bicolor]	Pollen allergen Phl p 11 OS=Phleum pratense PE=1 SV=1	Query_4242	Sor b 11 (Ole e 1-like)	1	30861	181
1	300.442	768	5.63E-104	1	144	38	181	144	144	0	144	1	1	0.852071006
Unigene308	20120710_JGPPBS_1_8.8195.8201.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor] >gi|241928307|gb|EES01452.1| hypothetical protein SORBIDRAFT_03g034110 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5252	Sor b 12 (Profilin) 1	63644	330
1	275.404	703	1.19E-92	1	131	64	194	131	131	0	131	1	1	1
Unigene1043	20120710_JGPPBS_1_2.7234.7317.3	S.halepenseFrame2Rev	hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor] >gi|241946693|gb|EES19838.1| hypothetical protein SORBIDRAFT_09g026120 [Sorghum bicolor]	Profilin-A OS=Oryza sativa subsp. japonica GN=Os10g0323600 PE=2 SV=1	Query_5251	Sor b 12 (Profilin) 2	56585	203
1	244.202	622	4.07E-82	14	131	1	118	118	118	0	118	1	1	0.900763359
Unigene451	20120710_JGPPBS_1_1.8204.8279.2	S.halepenseFrame1Rev	hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor] >gi|241942023|gb|EES15168.1| hypothetical protein SORBIDRAFT_07g023990 [Sorghum bicolor]	Polcalcin Cyn d 7 OS=Cynodon dactylon PE=1 SV=2	Query_1375	Sor b 7 (Polcalcin;CBP)	1	30083	314	1
167.162	422	1.39E-51	1	80	75	154	80	80	0	80	1	1	1
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Table E8 Mass spectra data for IgE-reactive allergen spots excised from 2D gels of JGP analysed against the JGP transcriptome.

number	filename	parent_charge	score	Local FDR (%)	Global FDR (%)	FDR Search #	percent_scored_peak_intensity	totalIntensity	sequence	modifications	accession_number
434	JGP2Dspots_1.2345.2412.2	2	14.51	<0.1%	<0.1%	JGP2Dspots_1/1	74	1.38E+06	(K)EKGGDAYQPLK(H)		CL153.Contig1_S.halepenseFrame3
290	JGP2Dspots_1.2533.2682.2	2	16.95	<0.1%	<0.1%	JGP2Dspots_1/1	90.4	3.05E+07	(K)GGDAYQPLK(H)		CL153.Contig1_S.halepenseFrame3
111	JGP2Dspots_1.2573.2647.2	2	20.41	<0.1%	<0.1%	JGP2Dspots_1/1	93.5	4.48E+06	(K)VTFHVEK(G)		CL153.Contig1_S.halepenseFrame3
143	JGP2Dspots_1.2717.2792.2	2	19.58	<0.1%	<0.1%	JGP2Dspots_1/1	93	8.51E+06	(K)VTFHVEK(G)		CL153.Contig1_S.halepenseFrame3
366	JGP2Dspots_1.2748.2838.2	2	15.69	<0.1%	<0.1%	JGP2Dspots_1/1	84.5	1.86E+05	(K)GGDAYQPLK(H)		CL153.Contig1_S.halepenseFrame3
114	JGP2Dspots_1.2857.2932.2	2	20.28	<0.1%	<0.1%	JGP2Dspots_1/1	94.6	3.80E+06	(K)VTFHVEK(G)		CL153.Contig1_S.halepenseFrame3
204	JGP2Dspots_1.3449.3527.4	4	18.37	<0.1%	<0.1%	JGP2Dspots_1/1	78.3	4.93E+06	(K)ATWYGKPTGAGPDDNGGACGYKDVNK(A)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
57	JGP2Dspots_1.3459.3463.3	3	21.59	<0.1%	<0.1%	JGP2Dspots_1/1	89.7	7.76E+05	(K)ATWYGKPTGAGPDDNGGACGYKDVNK(A)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
42	JGP2Dspots_1.3483.3612.3	3	21.89	<0.1%	<0.1%	JGP2Dspots_1/1	73.2	3.10E+07	(K)ATWYGKPTGAGPDDNGGACGYK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
11	JGP2Dspots_1.3495.3613.2	2	23.56	<0.1%	<0.1%	JGP2Dspots_1/1	97.7	2.61E+06	(K)ATWYGKPTGAGPDDNGGACGYK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
350	JGP2Dspots_1.3508.3617.4	4	15.93	<0.1%	<0.1%	JGP2Dspots_1/1	73.2	1.43E+06	(K)ATWYGKPTGAGPDDNGGACGYK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
385	JGP2Dspots_1.3944.4013.3	3	15.31	<0.1%	<0.1%	JGP2Dspots_1/1	80.3	2.31E+05	(K)YVDGDGDVVGVDIKEK(G)		CL153.Contig1_S.halepenseFrame3
187	JGP2Dspots_1.4110.4177.3	3	18.6	<0.1%	<0.1%	JGP2Dspots_1/1	89.3	1.57E+06	(K)YVDGDGDVVGVDIKEK(G)		CL153.Contig1_S.halepenseFrame3
135	JGP2Dspots_1.4199.4203.2	2	19.74	<0.1%	<0.1%	JGP2Dspots_1/1	79.8	1.34E+05	(K)YVDGDGDVVGVDIKEK(G)		CL153.Contig1_S.halepenseFrame3
396	JGP2Dspots_1.4243.4249.3	3	15.17	<0.1%	<0.1%	JGP2Dspots_1/1	75.6	1.81E+04	(K)YVDGDGDVVGVDIKEK(G)		CL153.Contig1_S.halepenseFrame3
72	JGP2Dspots_1.4278.4347.2	2	21.26	<0.1%	<0.1%	JGP2Dspots_1/1	92.1	3.41E+06	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
399	JGP2Dspots_1.4314.4384.3	3	15.14	<0.1%	<0.1%	JGP2Dspots_1/1	80.2	5.27E+05	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
13	JGP2Dspots_1.4412.4512.2	2	23.38	<0.1%	<0.1%	JGP2Dspots_1/1	95.9	3.35E+07	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
246	JGP2Dspots_1.4495.4572.3	3	17.61	<0.1%	<0.1%	JGP2Dspots_1/1	94.8	5.17E+06	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
181	JGP2Dspots_1.4523.4528.2	2	18.72	<0.1%	<0.1%	JGP2Dspots_1/1	91.6	6.81E+03	(K)VIDVVVSAAPPAK(Q)		CL2015.Contig1_S.halepenseFrame1Rev
424	JGP2Dspots_1.4533.4548.2	2	14.67	<0.1%	<0.1%	JGP2Dspots_1/1	67.4	1.29E+05	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
62	JGP2Dspots_1.4542.4673.2	2	21.34	<0.1%	<0.1%	JGP2Dspots_1/1	92.4	4.95E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
16	JGP2Dspots_1.4577.4652.2	2	23.2	<0.1%	<0.1%	JGP2Dspots_1/1	98.2	7.36E+07	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
234	JGP2Dspots_1.4632.4707.3	3	17.82	<0.1%	<0.1%	JGP2Dspots_1/1	93.2	4.55E+06	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
63	JGP2Dspots_1.4677.4763.2	2	21.34	<0.1%	<0.1%	JGP2Dspots_1/1	92.5	6.99E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
28	JGP2Dspots_1.4717.4792.2	2	22.57	<0.1%	<0.1%	JGP2Dspots_1/1	94.1	1.43E+07	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
58	JGP2Dspots_1.4817.4947.2	2	21.57	<0.1%	<0.1%	JGP2Dspots_1/1	92.2	2.55E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
61	JGP2Dspots_1.4857.4934.2	2	21.35	<0.1%	<0.1%	JGP2Dspots_1/1	90.5	8.85E+05	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
328	JGP2Dspots_1.5058.5152.4	4	16.39	<0.1%	<0.1%	JGP2Dspots_1/1	89.4	1.70E+07	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
3	JGP2Dspots_1.5073.5168.3	3	25.75	<0.1%	<0.1%	JGP2Dspots_1/1	100	5.88E+06	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
19	JGP2Dspots_1.5080.5172.2	2	22.95	<0.1%	<0.1%	JGP2Dspots_1/1	100	1.51E+07	(K)FPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
325	JGP2Dspots_1.5098.5102.2	2	16.46	<0.1%	<0.1%	JGP2Dspots_1/1	71.5	5.75E+05	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
249	JGP2Dspots_1.5228.5338.2	2	17.51	<0.1%	<0.1%	JGP2Dspots_1/1	88.1	4.52E+05	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
67	JGP2Dspots_1.5253.5395.2	2	21.29	<0.1%	<0.1%	JGP2Dspots_1/1	98.1	5.85E+06	(K)FPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
343	JGP2Dspots_1.5343.5343.3	3	16.08	<0.1%	<0.1%	JGP2Dspots_1/1	85.5	6.02E+05	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
78	JGP2Dspots_1.5413.5492.2	2	21.1	<0.1%	<0.1%	JGP2Dspots_1/1	95.7	5.33E+06	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
55	JGP2Dspots_1.5557.5652.2	2	21.64	<0.1%	<0.1%	JGP2Dspots_1/1	96.8	1.81E+07	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
301	JGP2Dspots_1.5582.5678.3	3	16.79	<0.1%	<0.1%	JGP2Dspots_1/1	84.5	4.15E+06	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
360	JGP2Dspots_1.5630.5719.3	3	15.79	<0.1%	<0.1%	JGP2Dspots_1/1	80	3.49E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
255	JGP2Dspots_1.5634.5787.3	3	17.42	<0.1%	<0.1%	JGP2Dspots_1/1	81.1	4.87E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
231	JGP2Dspots_1.5665.5749.2	2	17.85	<0.1%	<0.1%	JGP2Dspots_1/1	90.3	5.66E+05	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
88	JGP2Dspots_1.5732.5812.2	2	20.91	<0.1%	<0.1%	JGP2Dspots_1/1	97.6	6.01E+07	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
241	JGP2Dspots_1.5752.5832.3	3	17.72	<0.1%	<0.1%	JGP2Dspots_1/1	90.7	1.00E+07	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
425	JGP2Dspots_1.5772.5854.4	4	14.64	<0.1%	<0.1%	JGP2Dspots_1/1	73	1.44E+07	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
239	JGP2Dspots_1.5795.5930.3	3	17.75	<0.1%	<0.1%	JGP2Dspots_1/1	84.5	4.58E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
112	JGP2Dspots_1.5882.5957.2	2	20.32	<0.1%	<0.1%	JGP2Dspots_1/1	95.5	1.99E+07	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
302	JGP2Dspots_1.5902.5989.3	3	16.79	<0.1%	<0.1%	JGP2Dspots_1/1	79.2	2.71E+06	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
433	JGP2Dspots_1.5922.6007.4	4	14.52	<0.1%	<0.1%	JGP2Dspots_1/1	74.8	6.63E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
430	JGP2Dspots_1.6129.6219.3	3	14.54	<0.1%	<0.1%	JGP2Dspots_1/1	76.6	4.80E+05	(K)DVNKAPFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
182	JGP2Dspots_1.6193.6277.3	3	18.72	<0.1%	<0.1%	JGP2Dspots_1/1	93.1	1.23E+07	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
36	JGP2Dspots_1.6194.6332.2	2	22.05	<0.1%	<0.1%	JGP2Dspots_1/1	92.5	1.45E+07	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
368	JGP2Dspots_1.6338.6463.2	2	15.67	<0.1%	<0.1%	JGP2Dspots_1/1	68.1	8.07E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
223	JGP2Dspots_1.6342.6467.3	3	17.95	<0.1%	<0.1%	JGP2Dspots_1/1	89.2	6.92E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
7	JGP2Dspots_1.6772.6844.2	2	24.3	<0.1%	<0.1%	JGP2Dspots_1/1	97.2	2.32E+06	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
148	JGP2Dspots_1.6779.6892.2	2	19.49	<0.1%	<0.1%	JGP2Dspots_1/1	88.2	7.77E+07	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
280	JGP2Dspots_1.6784.6913.3	3	17.12	<0.1%	<0.1%	JGP2Dspots_1/1	92.8	1.26E+07	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
25	JGP2Dspots_1.6902.6978.2	2	22.65	<0.1%	<0.1%	JGP2Dspots_1/1	91.7	3.32E+06	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
124	JGP2Dspots_1.6907.7032.2	2	19.98	<0.1%	<0.1%	JGP2Dspots_1/1	88	7.78E+07	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
421	JGP2Dspots_1.6910.6979.3	3	14.68	<0.1%	<0.1%	JGP2Dspots_1/1	72.9	1.53E+06	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
318	JGP2Dspots_1.6980.7048.3	3	16.52	<0.1%	<0.1%	JGP2Dspots_1/1	90.9	7.24E+06	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
149	JGP2Dspots_1.7042.7137.2	2	19.49	<0.1%	<0.1%	JGP2Dspots_1/1	88	2.30E+07	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
392	JGP2Dspots_1.7044.7122.2	2	15.2	<0.1%	<0.1%	JGP2Dspots_1/1	72.3	1.21E+05	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
391	JGP2Dspots_1.7113.7208.3	3	15.21	<0.1%	<0.1%	JGP2Dspots_1/1	84.5	1.13E+06	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
365	JGP2Dspots_1.7657.7730.5	5	15.7	<0.1%	<0.1%	JGP2Dspots_1/1	76.6	2.80E+04	(K)CDKPAECSGEAVVVHITDmNYEQIAAYHFDLAGTAFGAmAK(K)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
384	JGP2Dspots_2.2531.2606.2	2	15.35	<0.1%	<0.1%	JGP2Dspots_2/1	84	3.51E+07	(K)GGDAYQPLK(H)		CL153.Contig1_S.halepenseFrame3

420	JGP2Dspots_2.2549.2559.2	2	14.69	<0.1%	<0.1%	JGP2Dspots_2/1	87.9	2.61E+04	(R)SPLVVK(T)		UG7484_S.halepenseFrame2Rev
205	JGP2Dspots_2.2574.2701.2	2	18.37	<0.1%	<0.1%	JGP2Dspots_2/1	86.8	6.74E+06	(K)VTFHVEK(G)		CL153.Contig1_S.halepenseFrame3
299	JGP2Dspots_2.2671.2793.2	2	16.84	<0.1%	<0.1%	JGP2Dspots_2/1	89.3	1.73E+07	(K)GGDAYQPLK(H)		CL153.Contig1_S.halepenseFrame3
172	JGP2Dspots_2.2707.2831.2	2	18.93	<0.1%	<0.1%	JGP2Dspots_2/1	91.2	8.92E+06	(K)VTFHVEK(G)		CL153.Contig1_S.halepenseFrame3
176	JGP2Dspots_2.2836.2901.2	2	18.89	<0.1%	<0.1%	JGP2Dspots_2/1	86.9	3.32E+06	(K)VTFHVEK(G)		CL153.Contig1_S.halepenseFrame3
15	JGP2Dspots_2.3434.3546.3	3	23.24	<0.1%	<0.1%	JGP2Dspots_2/1	78.5	2.75E+07	(K)ATWYGKPTGAGPDDNGGACGYK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
56	JGP2Dspots_2.3448.3526.2	2	21.63	<0.1%	<0.1%	JGP2Dspots_2/1	90.2	2.10E+06	(K)ATWYGKPTGAGPDDNGGACGYK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
340	JGP2Dspots_2.3453.3548.4	4	16.16	<0.1%	<0.1%	JGP2Dspots_2/1	71.7	1.23E+06	(K)ATWYGKPTGAGPDDNGGACGYK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
378	JGP2Dspots_2.3564.3641.2	2	15.41	<0.1%	<0.1%	JGP2Dspots_2/1	90.6	1.13E+07	(K)AGIIDMK(F)		CL153.Contig1_S.halepenseFrame3
431	JGP2Dspots_2.3701.3706.2	2	14.54	<0.1%	<0.1%	JGP2Dspots_2/1	84.5	1.85E+05	(K)AGIIDMK(F)		CL153.Contig1_S.halepenseFrame3
372	JGP2Dspots_2.3888.3956.3	3	15.57	<0.1%	<0.1%	JGP2Dspots_2/1	76.4	1.72E+05	(K)YVDGDGDVVGVDIKEK(G)		CL153.Contig1_S.halepenseFrame3
235	JGP2Dspots_2.4058.4126.3	3	17.8	<0.1%	<0.1%	JGP2Dspots_2/1	84.9	6.27E+05	(K)YVDGDGDVVGVDIKEK(G)		CL153.Contig1_S.halepenseFrame3
46	JGP2Dspots_2.4214.4281.2	2	21.81	<0.1%	<0.1%	JGP2Dspots_2/1	93.7	3.20E+06	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
26	JGP2Dspots_2.4392.4466.2	2	22.64	<0.1%	<0.1%	JGP2Dspots_2/1	96.3	4.25E+07	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
225	JGP2Dspots_2.4404.4532.3	3	17.91	<0.1%	<0.1%	JGP2Dspots_2/1	94.4	5.23E+06	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
68	JGP2Dspots_2.4458.4521.2	2	21.29	<0.1%	<0.1%	JGP2Dspots_2/1	91.2	2.32E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
27	JGP2Dspots_2.4526.4596.2	2	22.64	<0.1%	<0.1%	JGP2Dspots_2/1	96.3	5.95E+07	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
285	JGP2Dspots_2.4536.4601.3	3	17.08	<0.1%	<0.1%	JGP2Dspots_2/1	93.6	4.61E+06	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
65	JGP2Dspots_2.4586.4674.2	2	21.32	<0.1%	<0.1%	JGP2Dspots_2/1	92.2	6.24E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
38	JGP2Dspots_2.4657.4727.2	2	21.99	<0.1%	<0.1%	JGP2Dspots_2/1	91.8	7.55E+06	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
84	JGP2Dspots_2.4722.4856.2	2	20.98	<0.1%	<0.1%	JGP2Dspots_2/1	89.5	2.19E+07	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
413	JGP2Dspots_2.4794.4929.2	2	14.84	<0.1%	<0.1%	JGP2Dspots_2/1	74	5.86E+05	(K)YVDGDGDVVGVDIK(E)		CL153.Contig1_S.halepenseFrame3
439	JGP2Dspots_2.4949.5046.4	4	14.43	<0.1%	<0.1%	JGP2Dspots_2/1	88.9	1.78E+07	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
35	JGP2Dspots_2.4963.5056.3	3	22.2	<0.1%	<0.1%	JGP2Dspots_2/1	100	7.05E+06	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
8	JGP2Dspots_2.4977.5066.2	2	23.7	<0.1%	<0.1%	JGP2Dspots_2/1	100	1.91E+07	(K)FPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
208	JGP2Dspots_2.5097.5187.2	2	18.23	<0.1%	<0.1%	JGP2Dspots_2/1	87.9	3.32E+05	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
130	JGP2Dspots_2.5134.5221.3	3	19.82	<0.1%	<0.1%	JGP2Dspots_2/1	91.1	3.10E+06	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
17	JGP2Dspots_2.5141.5247.2	2	23.2	<0.1%	<0.1%	JGP2Dspots_2/1	100	1.05E+07	(K)FPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
91	JGP2Dspots_2.5283.5362.2	2	20.78	<0.1%	<0.1%	JGP2Dspots_2/1	94.3	3.62E+06	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
309	JGP2Dspots_2.5299.5372.3	3	16.7	<0.1%	<0.1%	JGP2Dspots_2/1	88.5	6.52E+05	(R)KDSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
352	JGP2Dspots_2.5318.5406.3	3	15.9	<0.1%	<0.1%	JGP2Dspots_2/1	79.7	1.45E+06	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
77	JGP2Dspots_2.5432.5588.2	2	21.17	<0.1%	<0.1%	JGP2Dspots_2/1	97.7	4.14E+07	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
444	JGP2Dspots_2.5449.5464.2	2	14.26	<0.1%	<0.1%	JGP2Dspots_2/1	76.9	4.19E+03	(K)FPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
258	JGP2Dspots_2.5471.5571.3	3	17.34	<0.1%	<0.1%	JGP2Dspots_2/1	89.4	5.24E+06	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
320	JGP2Dspots_2.5514.5602.4	4	16.51	<0.1%	<0.1%	JGP2Dspots_2/1	83.3	9.21E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
50	JGP2Dspots_2.5533.5617.3	3	21.71	<0.1%	<0.1%	JGP2Dspots_2/1	93.8	4.02E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
259	JGP2Dspots_2.5568.5647.2	2	17.34	<0.1%	<0.1%	JGP2Dspots_2/1	86.5	6.70E+05	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
103	JGP2Dspots_2.5596.5671.2	2	20.61	<0.1%	<0.1%	JGP2Dspots_2/1	96.5	5.79E+07	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
201	JGP2Dspots_2.5641.5716.3	3	18.41	<0.1%	<0.1%	JGP2Dspots_2/1	91	8.38E+06	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
432	JGP2Dspots_2.5667.5742.4	4	14.53	<0.1%	<0.1%	JGP2Dspots_2/1	81.1	1.95E+07	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
214	JGP2Dspots_2.5682.5757.3	3	18.12	<0.1%	<0.1%	JGP2Dspots_2/1	88.1	5.95E+06	(K)DSDKPIKFPVTVQITTEGGTK(T)		CL153.Contig1_S.halepenseFrame3
102	JGP2Dspots_2.5737.5812.2	2	20.63	<0.1%	<0.1%	JGP2Dspots_2/1	97	1.65E+07	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
349	JGP2Dspots_2.5781.5786.3	3	15.97	<0.1%	<0.1%	JGP2Dspots_2/1	83.8	1.04E+06	(K)TAYEDVIPEGWK(A)		CL153.Contig1_S.halepenseFrame3
219	JGP2Dspots_2.6063.6137.3	3	18.05	<0.1%	<0.1%	JGP2Dspots_2/1	97.2	1.02E+07	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
105	JGP2Dspots_2.6064.6136.2	2	20.56	<0.1%	<0.1%	JGP2Dspots_2/1	92.6	1.07E+07	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
329	JGP2Dspots_2.6196.6316.3	3	16.38	<0.1%	<0.1%	JGP2Dspots_2/1	87.4	7.23E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
66	JGP2Dspots_2.6198.6256.2	2	21.3	<0.1%	<0.1%	JGP2Dspots_2/1	97.9	6.97E+06	(K)APFNSmGACGNLPIFK(D)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
261	JGP2Dspots_2.6496.6611.2	2	17.3	<0.1%	<0.1%	JGP2Dspots_2/1	79.7	1.42E+05	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
29	JGP2Dspots_2.6587.6656.2	2	22.49	<0.1%	<0.1%	JGP2Dspots_2/1	92.1	1.20E+07	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
338	JGP2Dspots_2.6612.6677.3	3	16.18	<0.1%	<0.1%	JGP2Dspots_2/1	89.4	7.76E+06	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
100	JGP2Dspots_2.6671.6741.2	2	20.64	<0.1%	<0.1%	JGP2Dspots_2/1	90.2	7.43E+07	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
18	JGP2Dspots_2.6716.6786.2	2	23.17	<0.1%	<0.1%	JGP2Dspots_2/1	94.8	1.39E+07	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
253	JGP2Dspots_2.6722.6791.3	3	17.46	<0.1%	<0.1%	JGP2Dspots_2/1	84.2	7.25E+06	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
351	JGP2Dspots_2.6737.6808.3	3	15.92	<0.1%	<0.1%	JGP2Dspots_2/1	87.7	8.75E+06	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
162	JGP2Dspots_2.6801.6881.2	2	19.15	<0.1%	<0.1%	JGP2Dspots_2/1	87.3	3.48E+07	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
206	JGP2Dspots_2.6846.6931.2	2	18.33	<0.1%	<0.1%	JGP2Dspots_2/1	74.2	1.21E+06	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
427	JGP2Dspots_2.6852.6932.3	3	14.62	<0.1%	<0.1%	JGP2Dspots_2/1	75.6	6.03E+05	(K)APFNSMGACGNLPIFK(D)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
357	JGP2Dspots_2.6872.6947.3	3	15.83	<0.1%	<0.1%	JGP2Dspots_2/1	86.5	2.79E+06	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
286	JGP2Dspots_2.6937.7011.2	2	17.05	<0.1%	<0.1%	JGP2Dspots_2/1	69.4	3.74E+06	(K)GSNPNYLALLVK(Y)		CL153.Contig1_S.halepenseFrame3
237	JGP2Dspots_2.7508.7508.5	5	17.78	<0.1%	<0.1%	JGP2Dspots_2/1	77	1.84E+05	(K)CDKPAECSGEAVVVHITDmNYEQIAAYHFDLAGTAFGAmAK(K)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
287	JGP2Dspots_2.7806.7867.5	5	17.05	<0.1%	<0.1%	JGP2Dspots_2/1	86.3	1.42E+06	(K)CDKPAECSGEAVVVHITDMNYEQIAAYHFDLAGTAFGAmAK(K)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
273	JGP2Dspots_2.7921.7921.5	5	17.21	<0.1%	<0.1%	JGP2Dspots_2/1	76.1	7.19E+05	(K)CDKPAECSGEAVVVHITDmNYEQIAAYHFDLAGTAFGAMAK(K)	C:Carbamidomethylation m:Oxidized methionine	CL153.Contig1_S.halepenseFrame3
54	JGP2Dspots_2.8186.8196.5	5	21.66	<0.1%	<0.1%	JGP2Dspots_2/1	88.3	6.60E+05	(K)CDKPAECSGEAVVVHITDMNYEQIAAYHFDLAGTAFGAMAK(K)	C:Carbamidomethylation	CL153.Contig1_S.halepenseFrame3
400	JGP2Dspots_3.2555.2620.2	2	15.13	<0.1%	<0.1%	JGP2Dspots_3/1	62.6	2.87E+06	(K)GCGSCYEVR(C)	C:Carbamidomethylation	UG493_S.halepenseFrame3RevFrame3Rev
315	JGP2Dspots_3.3122.3184.3	3	16.59	<0.1%	<0.1%	JGP2Dspots_3/1	81.7	3.19E+06	(R)FDTPKPVK(G)		UG492_S.halepenseFrame2
310	JGP2Dspots_3.3189.3254.2	2	16.67	<0.1%	<0.1%	JGP2Dspots_3/1	84.4	4.88E+05	(R)FDTPKPVK(G)		UG492_S.halepenseFrame2
394	JGP2Dspots_3.3618.3680.2	2	15.18	<0.1%	<0.1%	JGP2Dspots_3/1	70.9	1.60E+05	(K)ImFHVEK(G)	m:Oxidized methionine	UG492_S.halepenseFrame2
198	JGP2Dspots_3.4059.4165.3	3	18.44	<0.1%	<0.1%	JGP2Dspots_3/1	87.6	1.37E+06	(K)AFGSLAKPGLNDK(L)		UG493_S.halepenseFrame3RevFrame3Rev

222	JGP2Dspots_3.4141.4209.2	2	17.98	<0.1%	<0.1%	JGP2Dspots_3/1	83.6	2.65E+05	(K)AFGSLAKPGLNDK(L)	UG493_S.halepenseFrame3RevFrame3Rev
164	JGP2Dspots_3.4810.4922.2	2	19.14	<0.1%	<0.1%	JGP2Dspots_3/1	86.2	3.55E+05	(K)YVDGDGDVVGVDIK(E)	CL153.Contig1_S.halepenseFrame3
380	JGP2Dspots_3.4927.4993.2	2	15.38	<0.1%	<0.1%	JGP2Dspots_3/1	78.3	1.56E+05	(K)DGLGCGSCFEIK(C)	C:Carbamidomethylation CL153.Contig1_S.halepenseFrame3
440	JGP2Dspots_3.5071.5135.2	2	14.35	<0.1%	<0.1%	JGP2Dspots_3/1	77.2	1.07E+06	(K)QSWGAVWR(F)	UG492_S.halepenseFrame2
266	JGP2Dspots_3.5125.5192.2	2	17.25	<0.1%	<0.1%	JGP2Dspots_3/1	88	2.43E+05	(R)AATLLVVPDK(L)	UG384_S.halepenseFrame2Rev
274	JGP2Dspots_3.5356.5361.2	2	17.19	<0.1%	<0.1%	JGP2Dspots_3/1	86.7	6.65E+04	(K)FPVTVQITTEGGTK(T)	CL153.Contig1_S.halepenseFrame3
139	JGP2Dspots_3.5362.5366.2	2	19.68	<0.1%	<0.1%	JGP2Dspots_3/1	88.5	3.82E+04	(R)IYSPSQSALNALR(N)	UG6817_S.halepenseFrame1Rev
215	JGP2Dspots_3.5683.5742.2	2	18.09	<0.1%	<0.1%	JGP2Dspots_3/1	87.1	1.64E+05	(K)TAYEDVIPEGWK(A)	CL153.Contig1_S.halepenseFrame3
442	JGP2Dspots_3.5889.5957.3	3	14.34	<0.1%	<0.1%	JGP2Dspots_3/1	80.2	2.81E+05	(R)TAILPTLLSNTDKK(L)	UG384_S.halepenseFrame2Rev
86	JGP2Dspots_3.6099.6216.2	2	20.96	<0.1%	<0.1%	JGP2Dspots_3/1	85.9	2.79E+06	(K)GSNPNYLAVLVK(N)	UG492_S.halepenseFrame2
212	JGP2Dspots_3.6221.6291.2	2	18.19	<0.1%	<0.1%	JGP2Dspots_3/1	85.3	2.33E+06	(K)GSNPNYLAVLVK(N)	UG492_S.halepenseFrame2
402	JGP2Dspots_3.6242.6246.3	3	15.11	<0.1%	<0.1%	JGP2Dspots_3/1	81.8	3.12E+05	(K)GSNPNYLAVLVK(N)	UG492_S.halepenseFrame2
171	JGP2Dspots_3.6542.6621.2	2	18.96	<0.1%	<0.1%	JGP2Dspots_3/1	85.9	3.16E+05	(K)NVADDGNIVLmELEDK(A)	m:Oxidized methionine UG492_S.halepenseFrame2
251	JGP2Dspots_3.6662.6776.2	2	17.48	<0.1%	<0.1%	JGP2Dspots_3/1	77.7	2.11E+05	(K)GSNPNYLALLVK(Y)	CL153.Contig1_S.halepenseFrame3
95	JGP2Dspots_3.6677.6791.2	2	20.69	<0.1%	<0.1%	JGP2Dspots_3/1	84.4	4.26E+05	(K)NVADDGNIVLMELEDK(A)	UG492_S.halepenseFrame2
403	JGP2Dspots_3.6747.6861.3	3	15.1	<0.1%	<0.1%	JGP2Dspots_3/1	81.4	3.63E+05	(K)NVADDGNIVLMELEDK(A)	UG492_S.halepenseFrame2
107	JGP2Dspots_3.6796.6856.2	2	20.54	<0.1%	<0.1%	JGP2Dspots_3/1	88.6	5.46E+05	(K)NVADDGNIVLMELEDK(A)	UG492_S.halepenseFrame2
393	JGP2Dspots_3.7501.7517.3	3	15.19	<0.1%	<0.1%	JGP2Dspots_3/1	79.6	1.04E+05	(K)LQPAVANHVLLSYFDPIK(L)	UG384_S.halepenseFrame2Rev
121	JGP2Dspots_4.0971.1073.2	2	20.08	<0.1%	<0.1%	JGP2Dspots_4/1	88	4.26E+05	(K)AYCETDSK(I)	C:Carbamidomethylation CL2015.Contig1_S.halepenseFrame1Rev
361	JGP2Dspots_4.2894.3008.2	2	15.79	<0.1%	<0.1%	JGP2Dspots_4/1	75.1	1.65E+06	(K)TMYTAGSTINK(A)	CL2015.Contig1_S.halepenseFrame1Rev
220	JGP2Dspots_4.3046.3114.2	2	18.04	<0.1%	<0.1%	JGP2Dspots_4/1	87.9	3.83E+05	(K)AADEVIAAAPADK(L)	CL2015.Contig1_S.halepenseFrame1Rev
260	JGP2Dspots_4.3054.3174.2	2	17.31	<0.1%	<0.1%	JGP2Dspots_4/1	80.8	3.97E+05	(K)AADEVIAAAPADK(L)	CL2015.Contig1_S.halepenseFrame1Rev
228	JGP2Dspots_4.3095.3213.2	2	17.88	<0.1%	<0.1%	JGP2Dspots_4/1	84.3	3.59E+05	(K)AADAVIAAAPADK(L)	UG7877_S.halepenseFrame3
189	JGP2Dspots_4.3180.3296.2	2	18.57	<0.1%	<0.1%	JGP2Dspots_4/1	93	4.68E+06	(K)AADEVIAAAPADK(L)	CL2015.Contig1_S.halepenseFrame1Rev
94	JGP2Dspots_4.3219.3341.2	2	20.73	<0.1%	<0.1%	JGP2Dspots_4/1	96.7	3.08E+06	(K)AADAVIAAAPADK(L)	UG7877_S.halepenseFrame3
281	JGP2Dspots_4.3248.3368.3	3	17.11	<0.1%	<0.1%	JGP2Dspots_4/1	86.5	6.50E+05	(K)AADEVIAAAPADK(L)	CL2015.Contig1_S.halepenseFrame1Rev
157	JGP2Dspots_4.3301.3371.2	2	19.37	<0.1%	<0.1%	JGP2Dspots_4/1	95.1	5.70E+06	(K)AADEVIAAAPADK(L)	CL2015.Contig1_S.halepenseFrame1Rev
221	JGP2Dspots_4.3316.3390.3	3	17.99	<0.1%	<0.1%	JGP2Dspots_4/1	93.5	3.34E+05	(K)AADAVIAAAPADK(L)	UG7877_S.halepenseFrame3
300	JGP2Dspots_4.3321.3326.2	2	16.81	<0.1%	<0.1%	JGP2Dspots_4/1	82.8	8.78E+04	(K)CAEQAAEFEPGPGK(K)	C:Carbamidomethylation CL994.Contig1_S.halepenseFrame2
331	JGP2Dspots_4.3405.3410.2	2	16.35	<0.1%	<0.1%	JGP2Dspots_4/1	85.4	1.69E+06	(K)AADAVIAAAPADK(L)	UG7877_S.halepenseFrame3
429	JGP2Dspots_4.4199.4270.2	2	14.59	<0.1%	<0.1%	JGP2Dspots_4/1	83.6	1.44E+05	(K)VIDVVVSAAPPDK(Q)	CL2015.Contig2_S.halepenseFrame1Rev
209	JGP2Dspots_4.4203.4273.2	2	18.21	<0.1%	<0.1%	JGP2Dspots_4/1	88.1	8.55E+06	(K)IAQVLAAYSK(A)	CL2015.Contig1_S.halepenseFrame1Rev
319	JGP2Dspots_4.4205.4274.2	2	16.52	<0.1%	<0.1%	JGP2Dspots_4/1	72.6	3.58E+05	(K)AFDGVVAAAPVEK(R)	CL2015.Contig1_S.halepenseFrame1Rev
326	JGP2Dspots_4.4333.4448.2	2	16.44	<0.1%	<0.1%	JGP2Dspots_4/1	84.6	3.42E+04	(K)IAQVLAAYSK(A)	CL2015.Contig1_S.halepenseFrame1Rev
306	JGP2Dspots_4.4453.4523.2	2	16.73	<0.1%	<0.1%	JGP2Dspots_4/1	84.6	7.34E+06	(K)AFDGVVAAAPVEK(R)	CL2015.Contig1_S.halepenseFrame1Rev
207	JGP2Dspots_4.4509.4593.2	2	18.28	<0.1%	<0.1%	JGP2Dspots_4/1	96	1.77E+06	(K)VIDVVVSAAPPDK(Q)	CL2015.Contig2_S.halepenseFrame1Rev
161	JGP2Dspots_4.4511.4578.2	2	19.16	<0.1%	<0.1%	JGP2Dspots_4/1	92.7	3.96E+06	(K)VIDVVVSAAPPAK(Q)	CL2015.Contig1_S.halepenseFrame1Rev
154	JGP2Dspots_4.4515.4638.2	2	19.43	<0.1%	<0.1%	JGP2Dspots_4/1	94.5	4.65E+06	(K)VIDVVVSAAPPAK(Q)	CL2015.Contig1_S.halepenseFrame1Rev
435	JGP2Dspots_4.4521.4644.3	3	14.48	<0.1%	<0.1%	JGP2Dspots_4/1	87.4	4.93E+05	(K)VIDVVVSAAPPDK(Q)	CL2015.Contig2_S.halepenseFrame1Rev
196	JGP2Dspots_4.4643.4708.2	2	18.46	<0.1%	<0.1%	JGP2Dspots_4/1	93.4	3.60E+06	(K)VIDVVVSAAPPAK(Q)	CL2015.Contig1_S.halepenseFrame1Rev
173	JGP2Dspots_4.4656.4660.2	2	18.92	<0.1%	<0.1%	JGP2Dspots_4/1	94.5	8.74E+05	(K)VIDVVVSAAPPDK(Q)	CL2015.Contig2_S.halepenseFrame1Rev
363	JGP2Dspots_4.4786.4848.2	2	15.75	<0.1%	<0.1%	JGP2Dspots_4/1	84.3	3.36E+05	(K)SIGDLNLEVEK(V)	CL2015.Contig1_S.halepenseFrame1Rev
336	JGP2Dspots_4.4813.4879.3 CL2015.Contig1_S.halepenseFrame1Rev	3	16.21	<0.1%	<0.1%	JGP2Dspots_4/1	85.8	1.98E+05	(K)AADEVIAAAPADKLTImEK(T)	m:Oxidized methionine
283	JGP2Dspots_4.4904.4973.2	2	17.1	<0.1%	<0.1%	JGP2Dspots_4/1	87.5	2.16E+06	(K)SIGDLNLEVEK(V)	CL2015.Contig1_S.halepenseFrame1Rev
247	JGP2Dspots_4.5015.5084.3 CL2015.Contig1_S.halepenseFrame1Rev	3	17.53	<0.1%	<0.1%	JGP2Dspots_4/1	80.8	2.34E+05	(K)KLmmmEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine
32	JGP2Dspots_4.5033.5134.2	2	22.25	<0.1%	<0.1%	JGP2Dspots_4/1	97.5	4.04E+06	(K)SIGDLNLEVEK(V)	CL2015.Contig1_S.halepenseFrame1Rev
33	JGP2Dspots_4.5156.5273.3 CL2015.Contig1_S.halepenseFrame1Rev	3	22.24	<0.1%	<0.1%	JGP2Dspots_4/1	97.2	4.63E+04	(K)LmmmEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine
159	JGP2Dspots_4.5244.5363.3	3	19.26	<0.1%	<0.1%	JGP2Dspots_4/1	92.7	2.40E+06	(R)VEIAAAIINAAPADKK(L)	CL2015.Contig1_S.halepenseFrame1Rev
24	JGP2Dspots_4.5281.5343.2	2	22.67	<0.1%	<0.1%	JGP2Dspots_4/1	95	1.34E+05	(R)VEIAAAIINAAPADKK(L)	CL2015.Contig1_S.halepenseFrame1Rev
170	JGP2Dspots_4.5378.5444.3 CL2015.Contig1_S.halepenseFrame1Rev	3	18.97	<0.1%	<0.1%	JGP2Dspots_4/1	88	9.02E+04	(K)KLmMmEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine
186	JGP2Dspots_4.5439.5439.3 CL2015.Contig1_S.halepenseFrame1Rev	3	18.63	<0.1%	<0.1%	JGP2Dspots_4/1	86.4	9.02E+04	(K)KLmMmEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine
37	JGP2Dspots_4.5505.5575.3 CL2015.Contig1_S.halepenseFrame1Rev	3	22.02	<0.1%	<0.1%	JGP2Dspots_4/1	94.9	6.49E+03	(K)LmmMEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine
74	JGP2Dspots_4.5616.5688.2	2	21.19	<0.1%	<0.1%	JGP2Dspots_4/1	93	1.23E+06	(R)VEIAAAIINAAPADK(K)	CL2015.Contig1_S.halepenseFrame1Rev
108	JGP2Dspots_4.5748.5753.2	2	20.54	<0.1%	<0.1%	JGP2Dspots_4/1	92.7	9.85E+05	(R)VEIAAAIINAAPADK(K)	CL2015.Contig1_S.halepenseFrame1Rev
416	JGP2Dspots_4.5754.5758.3	3	14.75	<0.1%	<0.1%	JGP2Dspots_4/1	85.5	5.20E+05	(R)VEIAAAIINAAPADK(K)	CL2015.Contig1_S.halepenseFrame1Rev
254	JGP2Dspots_4.5976.6049.3 CL2015.Contig1_S.halepenseFrame1Rev	3	17.46	<0.1%	<0.1%	JGP2Dspots_4/1	86.9	6.75E+03	(K)LmMMEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine
150	JGP2Dspots_4.6115.6228.3 CL2015.Contig1_S.halepenseFrame1Rev	3	19.48	<0.1%	<0.1%	JGP2Dspots_4/1	90.2	1.23E+05	(K)LmMMEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine
202	JGP2Dspots_4.6168.6233.3 CL2015.Contig1_S.halepenseFrame1Rev	3	18.41	<0.1%	<0.1%	JGP2Dspots_4/1	87	1.23E+05	(K)LmMMEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine
141	JGP2Dspots_4.6356.6438.2	2	19.61	<0.1%	<0.1%	JGP2Dspots_4/1	94.6	2.32E+05	(R)VIGAATELMVANFR(S)	CL994.Contig1_S.halepenseFrame2
59	JGP2Dspots_4.6494.6563.3 CL2015.Contig1_S.halepenseFrame1Rev	3	21.49	<0.1%	<0.1%	JGP2Dspots_4/1	92.5	4.52E+04	(K)LMMMEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation
375	JGP2Dspots_4.7258.7346.3	3	15.51	<0.1%	<0.1%	JGP2Dspots_4/1	89.4	9.86E+04	(K)LVFRVEIAAAIINAAPADK(K)	CL2015.Contig1_S.halepenseFrame1Rev
193	JGP2Dspots_4.7662.7724.3	3	18.51	<0.1%	<0.1%	JGP2Dspots_4/1	85.2	2.94E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine CL994.Contig1_S.halepenseFrame2
117	JGP2Dspots_4.7666.7779.3	3	20.19	<0.1%	<0.1%	JGP2Dspots_4/1	92.1	3.29E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine CL994.Contig1_S.halepenseFrame2
125	JGP2Dspots_4.7784.7784.3	3	19.97	<0.1%	<0.1%	JGP2Dspots_4/1	89.3	2.20E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine CL994.Contig1_S.halepenseFrame2
73	JGP2Dspots_4.8172.8249.3	3	21.23	<0.1%	<0.1%	JGP2Dspots_4/1	91.4	1.94E+05	(K)AVMYPSILVVQGLVSGYTPPR(S)	CL994.Contig1_S.halepenseFrame2
245	JGP2Dspots_4.9168.9314.3	3	17.64	<0.1%	<0.1%	JGP2Dspots_4/1	84.3	1.07E+06	(K)SIGDLNLEVEKVIDVVVSAAPPAK(Q)	CL2015.Contig1_S.halepenseFrame1Rev

373	JGP2Dspots_5.0864.0869.3	3	15.57	<0.1%	<0.1%	JGP2Dspots_5/1	80.9	4.14E+04	(K)AYAEGDKDK(I)	CL962.Contig1_S.halepenseFrame1	
382	JGP2Dspots_5.1072.1154.2	2	15.37	<0.1%	<0.1%	JGP2Dspots_5/1	93.3	9.33E+05	(K)AVPDADK(L)	CL994.Contig1_S.halepenseFrame2	
379	JGP2Dspots_5.1201.1268.2	2	15.41	<0.1%	<0.1%	JGP2Dspots_5/1	78.1	2.33E+05	(R)ALAAmGDDNK(V)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
292	JGP2Dspots_5.2224.2316.2	2	16.94	<0.1%	<0.1%	JGP2Dspots_5/1	85.8	4.99E+05	(R)LATDAAINK(A)	CL962.Contig1_S.halepenseFrame1	
389	JGP2Dspots_5.2282.2346.2	2	15.25	<0.1%	<0.1%	JGP2Dspots_5/1	86	1.55E+06	(R)ALAAMGDDNK(V)	CL994.Contig1_S.halepenseFrame2	
145	JGP2Dspots_5.2382.2446.2	2	19.56	<0.1%	<0.1%	JGP2Dspots_5/1	95.4	8.03E+06	(R)LATDAAINK(A)	CL962.Contig1_S.halepenseFrame1	
405	JGP2Dspots_5.2406.2438.2	2	15.09	<0.1%	<0.1%	JGP2Dspots_5/1	87.6	1.56E+06	(R)ALAAMGDDNK(V)	CL994.Contig1_S.halepenseFrame2	
256	JGP2Dspots_5.2488.2606.2	2	17.4	<0.1%	<0.1%	JGP2Dspots_5/1	80.5	2.64E+06	(R)CSPSVMPK(V)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
147	JGP2Dspots_5.2501.2617.2	2	19.53	<0.1%	<0.1%	JGP2Dspots_5/1	94.2	7.50E+06	(R)LATDAAINK(A)	CL962.Contig1_S.halepenseFrame1	
257	JGP2Dspots_5.2795.2910.2	2	17.35	<0.1%	<0.1%	JGP2Dspots_5/1	86.4	6.65E+05	(K)AADAVIAASPANK(L)	CL962.Contig1_S.halepenseFrame1	
270	JGP2Dspots_5.2849.2914.2	2	17.23	<0.1%	<0.1%	JGP2Dspots_5/1	88.4	6.65E+05	(K)AADAVIAASPANK(L)	CL962.Contig1_S.halepenseFrame1	
232	JGP2Dspots_5.2870.2989.3	3	17.84	<0.1%	<0.1%	JGP2Dspots_5/1	94.1	1.44E+06	(K)CAEQAAEFEPGPGKK(E)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
282	JGP2Dspots_5.2887.2949.2	2	17.11	<0.1%	<0.1%	JGP2Dspots_5/1	81.1	3.10E+05	(K)CAEQAAEFEPGPGKK(E)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
410	JGP2Dspots_5.2890.2954.2	2	14.95	<0.1%	<0.1%	JGP2Dspots_5/1	76	3.10E+05	(K)CAEQAAEFEPGPGKK(E)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
250	JGP2Dspots_5.2974.3044.2	2	17.49	<0.1%	<0.1%	JGP2Dspots_5/1	93.1	6.89E+06	(K)AADAVIAASPANK(L)	CL962.Contig1_S.halepenseFrame1	
216	JGP2Dspots_5.3006.3069.2	2	18.08	<0.1%	<0.1%	JGP2Dspots_5/1	89.5	1.24E+05	(K)AADEVIAAAPADK(L)	CL2015.Contig1_S.halepenseFrame1Rev	
364	JGP2Dspots_5.3070.3074.3	3	15.72	<0.1%	<0.1%	JGP2Dspots_5/1	84	1.05E+06	(K)AADAVIAASPANK(L)	CL962.Contig1_S.halepenseFrame1	
426	JGP2Dspots_5.3104.3124.2	2	14.63	<0.1%	<0.1%	JGP2Dspots_5/1	86.3	3.83E+04	(K)AADAVIAASPANK(L)	CL962.Contig1_S.halepenseFrame1	
52	JGP2Dspots_5.3159.3284.2	2	21.69	<0.1%	<0.1%	JGP2Dspots_5/1	88.4	3.23E+06	(K)CAEQAAEFEPGPGK(K)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
293	JGP2Dspots_5.3172.3300.3	3	16.92	<0.1%	<0.1%	JGP2Dspots_5/1	90.1	1.81E+06	(K)CAEQAAEFEPGPGK(K)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
422	JGP2Dspots_5.3205.3279.3	3	14.68	<0.1%	<0.1%	JGP2Dspots_5/1	80.9	2.10E+05	(K)AADEVIAAAPADK(L)	CL2015.Contig1_S.halepenseFrame1Rev	
213	JGP2Dspots_5.3224.3304.2	2	18.19	<0.1%	<0.1%	JGP2Dspots_5/1	92	1.90E+06	(K)AADEVIAAAPADK(L)	CL2015.Contig1_S.halepenseFrame1Rev	
271	JGP2Dspots_5.3289.3409.2	2	17.22	<0.1%	<0.1%	JGP2Dspots_5/1	84.8	2.69E+06	(K)CAEQAAEFEPGPGK(K)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
353	JGP2Dspots_5.3305.3419.3	3	15.9	<0.1%	<0.1%	JGP2Dspots_5/1	77.3	1.09E+06	(K)CAEQAAEFEPGPGK(K)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
262	JGP2Dspots_5.3312.3429.3	3	17.3	<0.1%	<0.1%	JGP2Dspots_5/1	79.3	9.45E+04	(R)CTAAAAADKPFCETYAK(T)	C:Carbamidomethylation	CL962.Contig1_S.halepenseFrame1
437	JGP2Dspots_5.3356.3414.3	3	14.44	<0.1%	<0.1%	JGP2Dspots_5/1	71.6	1.35E+05	(K)CAEQAAEFEPGPGK(K)	C:Carbamidomethylation	CL994.Contig1_S.halepenseFrame2
119	JGP2Dspots_5.3436.3554.3	3	20.17	<0.1%	<0.1%	JGP2Dspots_5/1	85.8	6.20E+06	(R)CTAAAAADKPFCETYAK(T)	C:Carbamidomethylation	CL962.Contig1_S.halepenseFrame1
53	JGP2Dspots_5.3457.3519.2	2	21.67	<0.1%	<0.1%	JGP2Dspots_5/1	88.6	1.04E+06	(R)CTAAAAADKPFCETYAK(T)	C:Carbamidomethylation	CL962.Contig1_S.halepenseFrame1
80	JGP2Dspots_5.4080.4144.2	2	21.01	<0.1%	<0.1%	JGP2Dspots_5/1	91.1	4.14E+06	(R)QAFDGVVAAAPAEK(R)	CL962.Contig1_S.halepenseFrame1	
417	JGP2Dspots_5.4091.4154.2	2	14.75	<0.1%	<0.1%	JGP2Dspots_5/1	69.3	1.48E+06	(K)IAQVLAAYSK(A)	CL2015.Contig1_S.halepenseFrame1Rev	
370	JGP2Dspots_5.4095.4156.3	3	15.58	<0.1%	<0.1%	JGP2Dspots_5/1	84	9.08E+05	(R)QAFDGVVAAAPAEK(R)	CL962.Contig1_S.halepenseFrame1	
441	JGP2Dspots_5.4149.4149.2	2	14.35	<0.1%	<0.1%	JGP2Dspots_5/1	77.5	1.48E+06	(K)IAQVLAAYSK(A)	CL2015.Contig1_S.halepenseFrame1Rev	
289	JGP2Dspots_5.4160.4285.2	2	17	<0.1%	<0.1%	JGP2Dspots_5/1	90.9	1.29E+07	(K)AFAGVIATGDSPR(T)	CL962.Contig1_S.halepenseFrame1	
408	JGP2Dspots_5.4171.4239.3	3	15.03	<0.1%	<0.1%	JGP2Dspots_5/1	80.9	1.59E+06	(K)AFAGVIATGDSPR(T)	CL962.Contig1_S.halepenseFrame1	
194	JGP2Dspots_5.4289.4316.2	2	18.51	<0.1%	<0.1%	JGP2Dspots_5/1	91.2	9.85E+06	(K)AFAGVIATGDSPR(T)	CL962.Contig1_S.halepenseFrame1	
230	JGP2Dspots_5.4299.4369.3	3	17.86	<0.1%	<0.1%	JGP2Dspots_5/1	92.6	1.74E+07	(K)AVPDADKLLPTK(A)	CL994.Contig1_S.halepenseFrame2	
21	JGP2Dspots_5.4324.4395.2	2	22.84	<0.1%	<0.1%	JGP2Dspots_5/1	74.8	3.54E+05	(R)VmEQTFSAVAAAAHQPAAAAK(A)	m:Oxidized methionine	CL962.Contig1_S.halepenseFrame1
82	JGP2Dspots_5.4329.4394.2	2	20.99	<0.1%	<0.1%	JGP2Dspots_5/1	93.9	2.12E+06	(K)AVPDADKLLPTK(A)	CL994.Contig1_S.halepenseFrame2	
83	JGP2Dspots_5.4370.4444.3	3	20.99	<0.1%	<0.1%	JGP2Dspots_5/1	65	5.36E+06	(R)VmEQTFSAVAAAAHQPAAAAK(A)	m:Oxidized methionine	CL962.Contig1_S.halepenseFrame1
243	JGP2Dspots_5.4424.4499.2	2	17.69	<0.1%	<0.1%	JGP2Dspots_5/1	88.1	2.37E+06	(K)AFDGVVAAAPVEK(R)	CL2015.Contig1_S.halepenseFrame1Rev	
419	JGP2Dspots_5.4449.4455.3	3	14.72	<0.1%	<0.1%	JGP2Dspots_5/1	78.1	4.27E+05	(K)AFDGVVAAAPVEK(R)	CL2015.Contig1_S.halepenseFrame1Rev	
304	JGP2Dspots_5.4464.4534.2	2	16.75	<0.1%	<0.1%	JGP2Dspots_5/1	91.2	1.64E+06	(K)VIDVVVSAAPPAK(Q)	CL2015.Contig1_S.halepenseFrame1Rev	
90	JGP2Dspots_5.4556.4624.3	3	20.83	<0.1%	<0.1%	JGP2Dspots_5/1	95.9	8.71E+05	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.Contig1_S.halepenseFrame1	
190	JGP2Dspots_5.4571.4651.2	2	18.57	<0.1%	<0.1%	JGP2Dspots_5/1	85	1.82E+05	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.Contig1_S.halepenseFrame1	
307	JGP2Dspots_5.4594.4600.2	2	16.73	<0.1%	<0.1%	JGP2Dspots_5/1	89.9	1.42E+06	(K)VIDVVVSAAPPAK(Q)	CL2015.Contig1_S.halepenseFrame1Rev	
226	JGP2Dspots_5.4769.4845.3	3	17.91	<0.1%	<0.1%	JGP2Dspots_5/1	91	1.18E+06	(K)ATASGDENNFVSVAGAYEK(A)	CL962.Contig1_S.halepenseFrame1	
6	JGP2Dspots_5.4770.4885.2	2	24.61	<0.1%	<0.1%	JGP2Dspots_5/1	97.8	9.61E+05	(K)ATASGDENNFVSVAGAYEK(A)	CL962.Contig1_S.halepenseFrame1	
341	JGP2Dspots_5.4847.4914.2	2	16.15	<0.1%	<0.1%	JGP2Dspots_5/1	96.6	1.35E+07	(R)SLLAELR(K)	CL994.Contig1_S.halepenseFrame2	
330	JGP2Dspots_5.4860.4865.3	3	16.36	<0.1%	<0.1%	JGP2Dspots_5/1	83.9	1.26E+05	(K)AADEVIAAAPADKLTImEK(T)	m:Oxidized methionine	
	CL2015.Contig1_S.halepenseFrame1Rev										
10	JGP2Dspots_5.4887.4954.3	3	23.57	<0.1%	<0.1%	JGP2Dspots_5/1	81	6.46E+06	(R)VMEQTFSAVAAAAHQPAAAAK(A)	CL962.Contig1_S.halepenseFrame1	
69	JGP2Dspots_5.4912.4984.2	2	21.28	<0.1%	<0.1%	JGP2Dspots_5/1	84.8	3.27E+05	(R)VMEQTFSAVAAAAHQPAAAAK(A)	CL962.Contig1_S.halepenseFrame1	
445	JGP2Dspots_5.4916.4985.4	4	14.24	<0.1%	<0.1%	JGP2Dspots_5/1	70	5.33E+05	(R)VMEQTFSAVAAAAHQPAAAAK(A)	CL962.Contig1_S.halepenseFrame1	
297	JGP2Dspots_5.4924.4994.2	2	16.85	<0.1%	<0.1%	JGP2Dspots_5/1	91.4	8.84E+05	(K)SIGDLNLEVEK(V)	CL2015.Contig1_S.halepenseFrame1Rev	
398	JGP2Dspots_5.4974.5049.2	2	15.16	<0.1%	<0.1%	JGP2Dspots_5/1	96.7	2.25E+07	(R)SLLAELR(K)	CL994.Contig1_S.halepenseFrame2	
167	JGP2Dspots_5.5014.5129.3	3	19.02	<0.1%	<0.1%	JGP2Dspots_5/1	71.3	4.92E+06	(R)VMEQTFSAVAAAAHQPAAAAK(A)	CL962.Contig1_S.halepenseFrame1	
127	JGP2Dspots_5.5054.5059.2	2	19.9	<0.1%	<0.1%	JGP2Dspots_5/1	95.2	9.20E+05	(K)SIGDLNLEVEK(V)	CL2015.Contig1_S.halepenseFrame1Rev	
199	JGP2Dspots_5.5250.5254.3	3	18.43	<0.1%	<0.1%	JGP2Dspots_5/1	83.7	3.28E+04	(K)LmmmEDSFNSVAAPSPLDCPTVDK(A)	C:Carbamidomethylation m:Oxidized methionine	
	CL2015.Contig1_S.halepenseFrame1Rev										
180	JGP2Dspots_5.5324.5329.3	3	18.74	<0.1%	<0.1%	JGP2Dspots_5/1	93.5	7.65E+05	(R)VEIAAAIINAAPADKK(L)	CL2015.Contig1_S.halepenseFrame1Rev	
305	JGP2Dspots_5.5507.5609.2	2	16.74	<0.1%	<0.1%	JGP2Dspots_5/1	81.2	4.81E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
303	JGP2Dspots_5.5517.5596.2	2	16.76	<0.1%	<0.1%	JGP2Dspots_5/1	86.1	6.81E+05	(R)LGFTDVVLK(Q)	CL962.Contig1_S.halepenseFrame1	
136	JGP2Dspots_5.5532.5664.2	2	19.73	<0.1%	<0.1%	JGP2Dspots_5/1	95.9	1.10E+07	(R)ALPAEWATAIK(Y)	CL962.Contig1_S.halepenseFrame1	
438	JGP2Dspots_5.5542.5616.3	3	14.44	<0.1%	<0.1%	JGP2Dspots_5/1	77.3	3.58E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
374	JGP2Dspots_5.5554.5631.3	3	15.55	<0.1%	<0.1%	JGP2Dspots_5/1	82.6	6.50E+05	(R)ALPAEWATAIK(Y)	CL962.Contig1_S.halepenseFrame1	
116	JGP2Dspots_5.5660.5736.2	2	20.21	<0.1%	<0.1%	JGP2Dspots_5/1	91.5	4.06E+05	(R)LGFTDVVLK(Q)	CL962.Contig1_S.halepenseFrame1	
75	JGP2Dspots_5.5662.5734.2	2	21.18	<0.1%	<0.1%	JGP2Dspots_5/1	92.5	4.16E+05	(R)VEIAAAIINAAPADK(K)	CL2015.Contig1_S.halepenseFrame1Rev	
109	JGP2Dspots_5.5669.5742.2	2	20.48	<0.1%	<0.1%	JGP2Dspots_5/1	94.9	7.14E+06	(R)ALPAEWATAIK(Y)	CL962.Contig1_S.halepenseFrame1	
272	JGP2Dspots_5.5674.5679.2	2	17.22	<0.1%	<0.1%	JGP2Dspots_5/1	81	3.24E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
358	JGP2Dspots_5.5680.5790.3	3	15.82	<0.1%	<0.1%	JGP2Dspots_5/1	76.7	2.17E+06	(R)VIGAATELmVANFR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
386	JGP2Dspots_5.5681.5755.3	3	15.29	<0.1%	<0.1%	JGP2Dspots_5/1	80.7	2.22E+05	(R)VEIAAAIINAAPADK(K)	CL2015.Contig1_S.halepenseFrame1Rev	
45	JGP2Dspots_5.5794.5866.2	2	21.86	<0.1%	<0.1%	JGP2Dspots_5/1	96.3	1.49E+07	(R)LGFTDVVLK(Q)	CL962.Contig1_S.halepenseFrame1	
312	JGP2Dspots_5.5797.5801.2	2	16.65	<0.1%	<0.1%	JGP2Dspots_5/1	82.8	2.36E+05	(R)VEIAAAIINAAPADK(K)	CL2015.Contig1_S.halepenseFrame1Rev	
138	JGP2Dspots_5.5871.5939.3	3	19.69	<0.1%	<0.1%	JGP2Dspots_5/1	98.4	1.10E+07	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.Contig1_S.halepenseFrame1	
1	JGP2Dspots_5.5887.6014.2	2	26	<0.1%	<0.1%	JGP2Dspots_5/1	100	1.94E+06	(K)ILAAYAQAADAVAAAAPPEK(L)	CL962.Contig1_S.halepenseFrame1	
30	JGP2Dspots_5.5924.5929.2	2	22.39	<0.1%	<0.1%	JGP2Dspots_5/1	96.5	1.60E+05	(R)LGFTDVVLK(Q)	CL962.Contig1_S.halepenseFrame1	

155	JGP2Dspots_5.5999.6069.3	3	19.39	<0.1%	<0.1%	JGP2Dspots_5/1	98.3	1.03E+07	(K)ILAAYAQAADAVAAAAPPEK(L)		CL962.Contig1_S.halepenseFrame1
22	JGP2Dspots_5.6020.6020.2	2	22.81	<0.1%	<0.1%	JGP2Dspots_5/1	95.5	1.04E+06	(K)ILAAYAQAADAVAAAAPPEK(L)		CL962.Contig1_S.halepenseFrame1
177	JGP2Dspots_5.6196.6260.3	3	18.88	<0.1%	<0.1%	JGP2Dspots_5/1	94.9	5.74E+05	(K)RSEAVEAVLQQQLNmDVSLGK(A)	m:Oxidized methionine	CL962.Contig1_S.halepenseFrame1
284	JGP2Dspots_5.6274.6341.3 CL994.Contig1_S.halepenseFrame2	3	17.09	<0.1%	<0.1%	JGP2Dspots_5/1	84.8	2.76E+04	(R)ALAAMGDDNKVEYVYDISSWmDEmDmK(F)	m:Oxidized methionine	
333	JGP2Dspots_5.6296.6325.4 CL994.Contig1_S.halepenseFrame2	4	16.28	<0.1%	<0.1%	JGP2Dspots_5/1	78	9.31E+03	(R)ALAAMGDDNKVEYVYDISSWmDEmDmK(F)	m:Oxidized methionine	
140	JGP2Dspots_5.6412.6529.2	2	19.65	<0.1%	<0.1%	JGP2Dspots_5/1	88.1	8.13E+06	(R)VIGAATELMVANFR(S)		CL994.Contig1_S.halepenseFrame2
414	JGP2Dspots_5.6419.6484.3	3	14.83	<0.1%	<0.1%	JGP2Dspots_5/1	80.3	5.72E+06	(R)VIGAATELMVANFR(S)		CL994.Contig1_S.halepenseFrame2
165	JGP2Dspots_5.6534.6655.2	2	19.08	<0.1%	<0.1%	JGP2Dspots_5/1	94.1	7.41E+06	(R)VIGAATELMVANFR(S)		CL994.Contig1_S.halepenseFrame2
316	JGP2Dspots_5.6659.6766.2	2	16.58	<0.1%	<0.1%	JGP2Dspots_5/1	87.9	1.23E+04	(R)VIGAATELMVANFR(S)		CL994.Contig1_S.halepenseFrame2
423	JGP2Dspots_5.6896.6896.3 CL994.Contig1_S.halepenseFrame2	3	14.68	<0.1%	<0.1%	JGP2Dspots_5/1	78.6	3.65E+04	(R)ALAAmGDDNKVEYVYDISSWmDEMDMK(F)	m:Oxidized methionine	
404	JGP2Dspots_5.7321.7386.3	3	15.1	<0.1%	<0.1%	JGP2Dspots_5/1	90.9	1.02E+05	(K)LVFRVEIAAAIINAAPADK(K)		CL2015.Contig1_S.halepenseFrame1Rev
92	JGP2Dspots_5.7757.7824.3	3	20.78	<0.1%	<0.1%	JGP2Dspots_5/1	96.6	7.09E+06	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
14	JGP2Dspots_5.7782.7879.2	2	23.25	<0.1%	<0.1%	JGP2Dspots_5/1	96.5	1.44E+06	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
334	JGP2Dspots_5.7786.7854.4	4	16.24	<0.1%	<0.1%	JGP2Dspots_5/1	84.5	5.41E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
60	JGP2Dspots_5.7884.7949.3	3	21.47	<0.1%	<0.1%	JGP2Dspots_5/1	100	9.09E+06	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
311	JGP2Dspots_5.7914.7919.4	4	16.66	<0.1%	<0.1%	JGP2Dspots_5/1	85.5	3.66E+05	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
295	JGP2Dspots_5.7934.7950.2	2	16.89	<0.1%	<0.1%	JGP2Dspots_5/1	80.7	1.11E+04	(K)AVmYPSILVVQGLVSGYTPPR(S)	m:Oxidized methionine	CL994.Contig1_S.halepenseFrame2
153	JGP2Dspots_5.8024.8052.3	3	19.44	<0.1%	<0.1%	JGP2Dspots_5/1	88.3	1.50E+05	(R)ALAAMGDDNKVEYVYDISSWMDEMDMK(F)		CL994.Contig1_S.halepenseFrame2
118	JGP2Dspots_5.8226.8294.3	3	20.19	<0.1%	<0.1%	JGP2Dspots_5/1	87.9	6.55E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.Contig1_S.halepenseFrame2
156	JGP2Dspots_5.8231.8304.2	2	19.38	<0.1%	<0.1%	JGP2Dspots_5/1	83.7	2.72E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.Contig1_S.halepenseFrame2
115	JGP2Dspots_5.8236.8364.2	2	20.27	<0.1%	<0.1%	JGP2Dspots_5/1	85.8	2.81E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.Contig1_S.halepenseFrame2
412	JGP2Dspots_5.8252.8379.4	4	14.86	<0.1%	<0.1%	JGP2Dspots_5/1	82.6	6.83E+05	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.Contig1_S.halepenseFrame2
89	JGP2Dspots_5.8354.8425.3	3	20.91	<0.1%	<0.1%	JGP2Dspots_5/1	88.5	6.38E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.Contig1_S.halepenseFrame2
168	JGP2Dspots_5.8369.8369.2	2	19	<0.1%	<0.1%	JGP2Dspots_5/1	80.5	1.57E+06	(K)AVMYPSILVVQGLVSGYTPPR(S)		CL994.Contig1_S.halepenseFrame2
40	JGP2Dspots_5.9221.9259.3	3	21.92	<0.1%	<0.1%	JGP2Dspots_5/1	89	2.61E+05	(K)SIGDLNLEVEKVIDVVVSAAPPAK(Q)		CL2015.Contig1_S.halepenseFrame1Rev
377	JGP2Dspots_6.2183.2213.2	2	15.46	<0.1%	<0.1%	JGP2Dspots_6/1	82.9	1.80E+05	(R)VASDSPSCIK(V)	C:Carbamidomethylation	UG1499_S.halepenseFrame1Rev
122	JGP2Dspots_6.2770.2843.2	2	20.07	<0.1%	<0.1%	JGP2Dspots_6/1	87.1	3.77E+06	(K)TSSSSSSAADIVDK(F)		UG388_S.halepenseFrame2
362	JGP2Dspots_6.2971.3030.2	2	15.77	<0.1%	<0.1%	JGP2Dspots_6/1	82.7	1.14E+05	(R)EEFYGQPR(W)		CL623.Contig2_S.halepenseFrame1Rev
203	JGP2Dspots_6.3297.3364.2	2	18.39	<0.1%	<0.1%	JGP2Dspots_6/1	87.5	1.50E+06	(K)WCQVASDSPSCVK(V)	C:Carbamidomethylation	UG388_S.halepenseFrame2
183	JGP2Dspots_6.3321.3398.3	3	18.71	<0.1%	<0.1%	JGP2Dspots_6/1	77.8	6.15E+05	(K)WCQVASDSPSCVK(V)	C:Carbamidomethylation	UG388_S.halepenseFrame2
278	JGP2Dspots_6.3420.3524.2	2	17.16	<0.1%	<0.1%	JGP2Dspots_6/1	85.1	1.31E+06	(K)WCQVASDSPSCVK(V)	C:Carbamidomethylation	UG388_S.halepenseFrame2
418	JGP2Dspots_6.3680.3685.2	2	14.74	<0.1%	<0.1%	JGP2Dspots_6/1	80.5	7.52E+04	(K)STDPVSGIDYK(R)		CL623.Contig2_S.halepenseFrame1Rev
137	JGP2Dspots_6.3827.3893.2	2	19.73	<0.1%	<0.1%	JGP2Dspots_6/1	90.2	3.87E+06	(K)GAADTLLAAEK(G)		UG388_S.halepenseFrame2
335	JGP2Dspots_6.3954.3960.2	2	16.22	<0.1%	<0.1%	JGP2Dspots_6/1	85.1	5.16E+06	(K)GAADTLLAAEK(G)		UG388_S.halepenseFrame2
344	JGP2Dspots_6.4595.4709.2	2	16.03	<0.1%	<0.1%	JGP2Dspots_6/1	80.5	4.69E+05	(K)FHDIWNVAK(V)		UG388_S.halepenseFrame2
376	JGP2Dspots_6.4665.4741.3	3	15.49	<0.1%	<0.1%	JGP2Dspots_6/1	79	2.29E+05	(K)ATASGDENNFVSVAGAYEK(A)		CL962.Contig1_S.halepenseFrame1
120	JGP2Dspots_6.4670.4730.2	2	20.14	<0.1%	<0.1%	JGP2Dspots_6/1	89.2	1.93E+05	(K)ATASGDENNFVSVAGAYEK(A)		CL962.Contig1_S.halepenseFrame1
288	JGP2Dspots_6.5200.5271.3	3	17.05	<0.1%	<0.1%	JGP2Dspots_6/1	97	7.46E+05	(K)VIESIPGIQEVDYNNAGK(V)		UG388_S.halepenseFrame2
267	JGP2Dspots_6.5208.5273.2	2	17.25	<0.1%	<0.1%	JGP2Dspots_6/1	91.4	1.50E+05	(K)LLLIGDSGVGK(S)		UG2123_S.halepenseFrame1Rev
409	JGP2Dspots_6.5229.5293.2	2	15.03	<0.1%	<0.1%	JGP2Dspots_6/1	85.6	5.38E+05	(K)VIESIPGIQEVDYNNAGK(V)		UG388_S.halepenseFrame2
233	JGP2Dspots_6.5323.5388.3	3	17.83	<0.1%	<0.1%	JGP2Dspots_6/1	92.8	5.33E+06	(K)VIESIPGIQEVDYNNAGK(V)		UG388_S.halepenseFrame2
371	JGP2Dspots_6.5448.5560.3	3	15.58	<0.1%	<0.1%	JGP2Dspots_6/1	80.6	1.95E+06	(K)VIESIPGIQEVDYNNAGK(V)		UG388_S.halepenseFrame2
195	JGP2Dspots_6.5668.5673.3	3	18.5	<0.1%	<0.1%	JGP2Dspots_6/1	78.2	3.69E+05	(K)SmAEVLVNLPAGQDDMNAYQTYK(E)	m:Oxidized methionine	UG388_S.halepenseFrame2
345	JGP2Dspots_6.5715.5779.4	4	16.03	<0.1%	<0.1%	JGP2Dspots_6/1	72.9	1.21E+05	(K)TSSSSSSAADIVDKFHDIWNVAK(V)		UG388_S.halepenseFrame2
354	JGP2Dspots_6.5893.5958.3	3	15.89	<0.1%	<0.1%	JGP2Dspots_6/1	71.7	1.08E+06	(K)SMAEVLVNLPAGQDDmNAYQTYK(E)	m:Oxidized methionine	UG388_S.halepenseFrame2
200	JGP2Dspots_6.6244.6323.3	3	18.43	<0.1%	<0.1%	JGP2Dspots_6/1	85.3	4.53E+05	(K)SMAEVLVNLPAGQDDMNAYQTYK(E)		UG388_S.halepenseFrame2
327	JGP2Dspots_6.6670.6764.4	4	16.41	<0.1%	<0.1%	JGP2Dspots_6/1	80.1	4.93E+06	(K)TSSSSSSAADIVDKFHDIWNVAK(V)		UG388_S.halepenseFrame2
64	JGP2Dspots_6.6769.6834.3	3	21.33	<0.1%	<0.1%	JGP2Dspots_6/1	88.2	7.81E+05	(K)TSSSSSSAADIVDKFHDIWNVAK(V)		UG388_S.halepenseFrame2
317	JGP2Dspots_6.7593.7602.3	3	16.53	<0.1%	<0.1%	JGP2Dspots_6/1	81.2	5.38E+04	(R)FADDSYLDSYISTIGVDFK(I)		UG993_S.halepenseFrame1Rev
348	JGP2Dspots_7.3256.3374.2	2	15.98	<0.1%	<0.1%	JGP2Dspots_7/1	94.1	4.98E+07	(K)TFTLDSK(D)		UG551_S.halepenseFrame2
321	JGP2Dspots_7.3379.3439.2	2	16.51	<0.1%	<0.1%	JGP2Dspots_7/1	95.2	5.88E+07	(K)TFTLDSK(D)		UG551_S.halepenseFrame2
347	JGP2Dspots_7.3499.3569.2	2	16	<0.1%	<0.1%	JGP2Dspots_7/1	94.5	2.63E+07	(K)TFTLDSK(D)		UG551_S.halepenseFrame2
128	JGP2Dspots_7.3559.3685.3	3	19.85	<0.1%	<0.1%	JGP2Dspots_7/1	75.6	5.50E+06	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
264	JGP2Dspots_7.3565.3634.2	2	17.28	<0.1%	<0.1%	JGP2Dspots_7/1	81.5	5.61E+06	(K)GATDFTDDLK(E)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
2	JGP2Dspots_7.3580.3644.2	2	25.99	<0.1%	<0.1%	JGP2Dspots_7/1	94.4	7.74E+05	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
210	JGP2Dspots_7.3619.3690.3	3	18.21	<0.1%	<0.1%	JGP2Dspots_7/1	69.6	5.50E+06	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
381	JGP2Dspots_7.3630.3706.2	2	15.38	<0.1%	<0.1%	JGP2Dspots_7/1	91.1	1.68E+05	(K)TFTLDSK(D)		UG551_S.halepenseFrame2
355	JGP2Dspots_7.3699.3769.2	2	15.89	<0.1%	<0.1%	JGP2Dspots_7/1	78.8	6.02E+05	(K)GATDFTDDLK(E)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
43	JGP2Dspots_7.3749.3819.3	3	21.89	<0.1%	<0.1%	JGP2Dspots_7/1	73.7	6.05E+05	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
31	JGP2Dspots_7.3835.3914.2	2	22.29	<0.1%	<0.1%	JGP2Dspots_7/1	94.1	1.16E+06	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
324	JGP2Dspots_7.3889.3969.3	3	16.47	<0.1%	<0.1%	JGP2Dspots_7/1	67.2	7.07E+06	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
185	JGP2Dspots_7.3996.4124.2	2	18.69	<0.1%	<0.1%	JGP2Dspots_7/1	80.8	3.50E+05	(K)GATDFTDDLK(E)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
163	JGP2Dspots_7.4074.4080.2	2	19.15	<0.1%	<0.1%	JGP2Dspots_7/1	86.7	3.40E+04	(K)INENVQQVVVDR(L)		CL939.Contig1_S.halepenseFrame3
175	JGP2Dspots_7.4129.4256.2	2	18.9	<0.1%	<0.1%	JGP2Dspots_7/1	86.7	4.21E+07	(K)GATDFTDDLK(E)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
48	JGP2Dspots_7.4171.4254.2	2	21.72	<0.1%	<0.1%	JGP2Dspots_7/1	88.8	1.42E+05	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
160	JGP2Dspots_7.4269.4354.3	3	19.17	<0.1%	<0.1%	JGP2Dspots_7/1	75.3	6.19E+07	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
383	JGP2Dspots_7.4320.4405.3	3	15.36	<0.1%	<0.1%	JGP2Dspots_7/1	91.7	2.66E+06	(R)VVDNAIPADFK(A)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
41	JGP2Dspots_7.4324.4404.2	2	21.91	<0.1%	<0.1%	JGP2Dspots_7/1	89.2	2.09E+07	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
132	JGP2Dspots_7.4370.4449.2	2	19.8	<0.1%	<0.1%	JGP2Dspots_7/1	97.5	8.56E+07	(R)VVDNAIPADFK(A)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
126	JGP2Dspots_7.4424.4499.3	3	19.95	<0.1%	<0.1%	JGP2Dspots_7/1	76.8	3.97E+07	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
104	JGP2Dspots_7.4474.4550.2	2	20.57	<0.1%	<0.1%	JGP2Dspots_7/1	89.3	8.00E+06	(K)GATDFTDDLKESEPK(T)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
346	JGP2Dspots_7.4475.4549.3	3	16.01	<0.1%	<0.1%	JGP2Dspots_7/1	91.1	4.85E+06	(R)VVDNAIPADFK(A)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
146	JGP2Dspots_7.4519.4594.2	2	19.54	<0.1%	<0.1%	JGP2Dspots_7/1	97.3	1.02E+08	(R)VVDNAIPADFK(A)		CL1695.Contig1_S.halepenseFrame3RevFrame3Rev

131	JGP2Dspots_7.4564.4635.3	3	19.82	<0.1%	<0.1%	JGP2Dspots_7/1	71.4	9.40E+06	(K)GATDFTDDLKESEPK(T)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
277	JGP2Dspots_7.4614.4684.3	3	17.17	<0.1%	<0.1%	JGP2Dspots_7/1	97	3.54E+06	(R)VVDNAIPADFK(A)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
49	JGP2Dspots_7.4615.4680.2	2	21.72	<0.1%	<0.1%	JGP2Dspots_7/1	84	5.76E+04	(K)GATDFTDDLKESEPK(T)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
129	JGP2Dspots_7.4654.4724.2	2	19.85	<0.1%	<0.1%	JGP2Dspots_7/1	98.6	5.21E+07	(R)VVDNAIPADFK(A)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
39	JGP2Dspots_7.4695.4766.3	3	21.96	<0.1%	<0.1%	JGP2Dspots_7/1	76.2	9.76E+05	(K)GATDFTDDLKESEPK(T)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
367	JGP2Dspots_7.4744.4819.3	3	15.68	<0.1%	<0.1%	JGP2Dspots_7/1	87.2	1.04E+06	(R)VVDNAIPADFK(A)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
252	JGP2Dspots_7.4784.4859.2	2	17.47	<0.1%	<0.1%	JGP2Dspots_7/1	95.3	3.58E+06	(R)VVDNAIPADFK(A)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
192	JGP2Dspots_7.5104.5110.3	3	18.52	<0.1%	<0.1%	JGP2Dspots_7/1	92.5	1.93E+05	(R)AIAPLFVEHAK(K)	CL1152.Contig1_S.halepenseFrame1Rev
188	JGP2Dspots_7.5121.5189.2	2	18.6	<0.1%	<0.1%	JGP2Dspots_7/1	86.1	6.54E+06	(K)EPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
87	JGP2Dspots_7.5127.5244.2	2	20.92	<0.1%	<0.1%	JGP2Dspots_7/1	86.5	7.00E+06	(K)EPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
134	JGP2Dspots_7.5249.5314.2	2	19.77	<0.1%	<0.1%	JGP2Dspots_7/1	85.3	3.99E+07	(K)EPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
142	JGP2Dspots_7.5374.5439.2	2	19.6	<0.1%	<0.1%	JGP2Dspots_7/1	87	4.05E+07	(K)EPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
406	JGP2Dspots_7.5406.5474.3	3	15.05	<0.1%	<0.1%	JGP2Dspots_7/1	84.4	1.14E+06	(K)EPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
401	JGP2Dspots_7.5455.5519.3	3	15.13	<0.1%	<0.1%	JGP2Dspots_7/1	94.3	4.12E+05	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
227	JGP2Dspots_7.5494.5559.2	2	17.91	<0.1%	<0.1%	JGP2Dspots_7/1	82.8	6.31E+06	(K)EPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
369	JGP2Dspots_7.5521.5589.2	2	15.63	<0.1%	<0.1%	JGP2Dspots_7/1	86	9.82E+04	(K)GNVTPDAVLQTVSK(T)	UG2170_S.halepenseFrame1
390	JGP2Dspots_7.5689.5694.2	2	15.23	<0.1%	<0.1%	JGP2Dspots_7/1	87.8	7.00E+04	(R)LDVSLALAR(V)	UG1403_S.halepenseFrame1Rev
291	JGP2Dspots_7.5921.5989.2	2	16.95	<0.1%	<0.1%	JGP2Dspots_7/1	85.7	1.75E+05	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
81	JGP2Dspots_7.6135.6204.3	3	21.01	<0.1%	<0.1%	JGP2Dspots_7/1	90.4	2.62E+07	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
279	JGP2Dspots_7.6137.6254.3	3	17.13	<0.1%	<0.1%	JGP2Dspots_7/1	87.5	3.13E+05	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
158	JGP2Dspots_7.6157.6229.2	2	19.35	<0.1%	<0.1%	JGP2Dspots_7/1	83.5	6.04E+05	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
5	JGP2Dspots_7.6160.6299.2	2	24.63	<0.1%	<0.1%	JGP2Dspots_7/1	98.6	7.71E+06	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
174	JGP2Dspots_7.6265.6339.2	2	18.92	<0.1%	<0.1%	JGP2Dspots_7/1	85	2.35E+07	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
356	JGP2Dspots_7.6266.6340.4	4	15.89	<0.1%	<0.1%	JGP2Dspots_7/1	77.7	1.44E+06	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
98	JGP2Dspots_7.6274.6354.3	3	20.66	<0.1%	<0.1%	JGP2Dspots_7/1	94.4	7.09E+07	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
314	JGP2Dspots_7.6294.6377.4	4	16.6	<0.1%	<0.1%	JGP2Dspots_7/1	81.6	2.59E+06	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
20	JGP2Dspots_7.6304.6374.2	2	22.87	<0.1%	<0.1%	JGP2Dspots_7/1	93.7	1.06E+07	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
166	JGP2Dspots_7.6324.6404.3	3	19.08	<0.1%	<0.1%	JGP2Dspots_7/1	86.4	3.90E+07	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
106	JGP2Dspots_7.6409.6484.2	2	20.55	<0.1%	<0.1%	JGP2Dspots_7/1	89.8	1.55E+07	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
342	JGP2Dspots_7.6410.6489.4	4	16.15	<0.1%	<0.1%	JGP2Dspots_7/1	81.7	1.30E+06	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
97	JGP2Dspots_7.6424.6499.3	3	20.67	<0.1%	<0.1%	JGP2Dspots_7/1	94.4	4.12E+07	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
47	JGP2Dspots_7.6444.6520.2	2	21.73	<0.1%	<0.1%	JGP2Dspots_7/1	96.1	3.80E+06	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
339	JGP2Dspots_7.6446.6522.4	4	16.18	<0.1%	<0.1%	JGP2Dspots_7/1	83.4	1.11E+06	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
99	JGP2Dspots_7.6469.6544.3	3	20.66	<0.1%	<0.1%	JGP2Dspots_7/1	89	1.67E+07	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
44	JGP2Dspots_7.6559.6629.3	3	21.88	<0.1%	<0.1%	JGP2Dspots_7/1	94.5	6.43E+06	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
152	JGP2Dspots_7.6604.6674.3	3	19.46	<0.1%	<0.1%	JGP2Dspots_7/1	83.7	4.69E+06	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
244	JGP2Dspots_7.6689.6762.3	3	17.66	<0.1%	<0.1%	JGP2Dspots_7/1	83.8	3.45E+05	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
269	JGP2Dspots_7.6734.6854.3	3	17.24	<0.1%	<0.1%	JGP2Dspots_7/1	84.7	4.64E+05	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
218	JGP2Dspots_7.6864.6979.3	3	18.06	<0.1%	<0.1%	JGP2Dspots_7/1	86.9	4.77E+04	(K)LSLITNVAISEVSVKPK(G)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
395	JGP2Dspots_8.11133.11231.2	2	15.18	<0.1%	<0.1%	JGP2Dspots_8/1	78.9	2.92E+03	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
242	JGP2Dspots_8.14560.14645.2	2	17.7	<0.1%	<0.1%	JGP2Dspots_8/1	84.7	4.50E+05	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
263	JGP2Dspots_8.3109.3172.2	2	17.3	<0.1%	<0.1%	JGP2Dspots_8/1	94.9	1.48E+07	(K)TFTYESK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
308	JGP2Dspots_8.3228.3297.2	2	16.73	<0.1%	<0.1%	JGP2Dspots_8/1	93	1.87E+07	(K)TFTYESK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
323	JGP2Dspots_8.3738.3808.4	4	16.49	<0.1%	<0.1%	JGP2Dspots_8/1	72.5	4.83E+05	(K)DKGATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
428	JGP2Dspots_8.3822.3822.3	3	14.62	<0.1%	<0.1%	JGP2Dspots_8/1	72.1	1.20E+05	(K)DKGATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
191	JGP2Dspots_8.3901.3970.2	2	18.53	<0.1%	<0.1%	JGP2Dspots_8/1	91.8	3.28E+05	(K)GATDFSDDLK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
9	JGP2Dspots_8.3919.3952.3	3	23.58	<0.1%	<0.1%	JGP2Dspots_8/1	84.5	3.28E+05	(K)GATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
4	JGP2Dspots_8.3996.4000.3	3	24.75	<0.1%	<0.1%	JGP2Dspots_8/1	90.9	2.69E+05	(K)DKGATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
387	JGP2Dspots_8.4031.4128.2	2	15.26	<0.1%	<0.1%	JGP2Dspots_8/1	74.8	4.39E+05	(K)GATDFSDDLK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
197	JGP2Dspots_8.4033.4126.3	3	18.46	<0.1%	<0.1%	JGP2Dspots_8/1	91	3.13E+06	(K)TFTYESKEPIK(G)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
96	JGP2Dspots_8.4047.4106.2	2	20.69	<0.1%	<0.1%	JGP2Dspots_8/1	96	6.33E+05	(K)TFTYESKEPIK(G)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
12	JGP2Dspots_8.4087.4151.3	3	23.39	<0.1%	<0.1%	JGP2Dspots_8/1	82.7	5.83E+05	(K)GATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
110	JGP2Dspots_8.4124.4192.2	2	20.48	<0.1%	<0.1%	JGP2Dspots_8/1	92.9	3.24E+06	(K)DKGATDFSDDLK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
397	JGP2Dspots_8.4131.4251.3	3	15.17	<0.1%	<0.1%	JGP2Dspots_8/1	86.6	7.64E+06	(K)DKGATDFSDDLK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
332	JGP2Dspots_8.4141.4266.4	4	16.35	<0.1%	<0.1%	JGP2Dspots_8/1	76.4	1.08E+07	(K)DKGATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
298	JGP2Dspots_8.4159.4163.2	2	16.85	<0.1%	<0.1%	JGP2Dspots_8/1	79.4	2.17E+05	(K)GATDFSDDLK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
184	JGP2Dspots_8.4252.4257.2	2	18.7	<0.1%	<0.1%	JGP2Dspots_8/1	83.2	5.18E+04	(K)DKGATDFSDDLK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
407	JGP2Dspots_8.4268.4347.2	2	15.04	<0.1%	<0.1%	JGP2Dspots_8/1	79.1	3.89E+06	(K)EPIKGPLSVR(F)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
236	JGP2Dspots_8.4271.4346.4	4	17.79	<0.1%	<0.1%	JGP2Dspots_8/1	83.5	1.67E+07	(K)DKGATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
93	JGP2Dspots_8.4281.4361.3	3	20.76	<0.1%	<0.1%	JGP2Dspots_8/1	83.1	1.05E+07	(K)DKGATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
113	JGP2Dspots_8.4306.4386.2	2	20.3	<0.1%	<0.1%	JGP2Dspots_8/1	84	1.12E+06	(K)DKGATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
169	JGP2Dspots_8.4319.4391.2	2	19	<0.1%	<0.1%	JGP2Dspots_8/1	84.2	3.90E+06	(K)GATDFSDDLK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
313	JGP2Dspots_8.4431.4438.3	3	16.62	<0.1%	<0.1%	JGP2Dspots_8/1	79.5	8.07E+04	(K)DKGATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
34	JGP2Dspots_8.4446.4511.3	3	22.24	<0.1%	<0.1%	JGP2Dspots_8/1	86.2	1.04E+07	(K)GATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
211	JGP2Dspots_8.4456.4527.2	2	18.21	<0.1%	<0.1%	JGP2Dspots_8/1	85.6	5.39E+06	(K)GATDFSDDLK(E)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
51	JGP2Dspots_8.4467.4536.2	2	21.7	<0.1%	<0.1%	JGP2Dspots_8/1	83.5	2.30E+06	(K)GATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
71	JGP2Dspots_8.4576.4581.3	3	21.27	<0.1%	<0.1%	JGP2Dspots_8/1	87.2	1.30E+07	(K)GATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
23	JGP2Dspots_8.4601.4606.2	2	22.8	<0.1%	<0.1%	JGP2Dspots_8/1	89.1	1.81E+06	(K)GATDFSDDLKESPAK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
265	JGP2Dspots_8.4962.5020.3	3	17.28	<0.1%	<0.1%	JGP2Dspots_8/1	69.8	3.42E+05	(K)GATDFTDDLKESEPK(T)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
76	JGP2Dspots_8.5297.5361.3	3	21.18	<0.1%	<0.1%	JGP2Dspots_8/1	90.1	2.48E+06	(K)TFTYESKEPIKGPLSVR(F)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
101	JGP2Dspots_8.5355.5425.4	4	20.64	<0.1%	<0.1%	JGP2Dspots_8/1	90.8	9.49E+06	(K)TFTYESKEPIKGPLSVR(F)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
238	JGP2Dspots_8.5421.5426.3	3	17.76	<0.1%	<0.1%	JGP2Dspots_8/1	79.6	4.27E+04	(K)TFTYESKEPIKGPLSVR(F)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
224	JGP2Dspots_8.5641.5760.3	3	17.92	<0.1%	<0.1%	JGP2Dspots_8/1	94.9	1.92E+07	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
240	JGP2Dspots_8.5730.5800.2	2	17.74	<0.1%	<0.1%	JGP2Dspots_8/1	93.2	3.97E+06	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
436	JGP2Dspots_8.5743.5810.4	4	14.46	<0.1%	<0.1%	JGP2Dspots_8/1	84.3	4.42E+05	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
296	JGP2Dspots_8.5766.5890.3	3	16.89	<0.1%	<0.1%	JGP2Dspots_8/1	94.3	6.27E+07	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev

294	JGP2Dspots_8.5783.5851.2	2	16.9	<0.1%	<0.1%	JGP2Dspots_8/1	82.8	7.74E+04	(K)EPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
123	JGP2Dspots_8.5802.5870.3	3	20.02	<0.1%	<0.1%	JGP2Dspots_8/1	87.7	7.73E+05	(R)LVLVASADVSEVAVKDK(G)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
337	JGP2Dspots_8.5860.5930.2	2	16.2	<0.1%	<0.1%	JGP2Dspots_8/1	92.1	5.87E+06	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
415	JGP2Dspots_8.5875.5966.4	4	14.78	<0.1%	<0.1%	JGP2Dspots_8/1	90.7	5.19E+05	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
275	JGP2Dspots_8.5895.5960.3	3	17.19	<0.1%	<0.1%	JGP2Dspots_8/1	94.7	4.29E+07	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
85	JGP2Dspots_8.5931.6001.3	3	20.97	<0.1%	<0.1%	JGP2Dspots_8/1	86.3	1.58E+06	(R)LVLVASADVSEVAVKDK(G)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
443	JGP2Dspots_8.5990.5997.2	2	14.34	<0.1%	<0.1%	JGP2Dspots_8/1	91.3	1.86E+04	(R)TTDDVIPADFKPGSVYK(T)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
151	JGP2Dspots_8.6055.6120.3	3	19.47	<0.1%	<0.1%	JGP2Dspots_8/1	90.2	5.60E+05	(R)LVLVASADVSEVAVKDK(G)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
133	JGP2Dspots_8.6227.6300.2	2	19.8	<0.1%	<0.1%	JGP2Dspots_8/1	84	1.94E+06	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
388	JGP2Dspots_8.6238.6301.3	3	15.26	<0.1%	<0.1%	JGP2Dspots_8/1	84.2	1.60E+06	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
70	JGP2Dspots_8.6360.6430.2	2	21.28	<0.1%	<0.1%	JGP2Dspots_8/1	95.7	5.06E+06	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
276	JGP2Dspots_8.6361.6431.3	3	17.18	<0.1%	<0.1%	JGP2Dspots_8/1	87.2	3.94E+06	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
79	JGP2Dspots_8.6490.6561.2	2	21.06	<0.1%	<0.1%	JGP2Dspots_8/1	96.8	2.02E+06	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
322	JGP2Dspots_8.6491.6562.3	3	16.5	<0.1%	<0.1%	JGP2Dspots_8/1	88.6	1.68E+06	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
178	JGP2Dspots_8.6620.6687.2	2	18.84	<0.1%	<0.1%	JGP2Dspots_8/1	89.7	8.07E+05	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
359	JGP2Dspots_8.6622.6686.3	3	15.82	<0.1%	<0.1%	JGP2Dspots_8/1	84.8	7.04E+05	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
248	JGP2Dspots_8.6740.6806.2	2	17.52	<0.1%	<0.1%	JGP2Dspots_8/1	88.1	3.83E+05	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
179	JGP2Dspots_8.6808.6925.3	3	18.81	<0.1%	<0.1%	JGP2Dspots_8/1	85.4	4.57E+05	(K)TFTLDSKEPIEGPIAFR(F)	CL1695.Contig1_S.halepenseFrame3RevFrame3Rev
217	JGP2Dspots_8.6866.6931.2	2	18.08	<0.1%	<0.1%	JGP2Dspots_8/1	89.4	2.03E+05	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
229	JGP2Dspots_8.6985.7051.2	2	17.87	<0.1%	<0.1%	JGP2Dspots_8/1	85.4	1.55E+05	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
144	JGP2Dspots_8.7106.7201.2	2	19.57	<0.1%	<0.1%	JGP2Dspots_8/1	92.1	1.30E+05	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
268	JGP2Dspots_8.7255.7320.2	2	17.25	<0.1%	<0.1%	JGP2Dspots_8/1	81.5	9.00E+04	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev
411	JGP2Dspots_8.7373.7433.2	2	14.9	<0.1%	<0.1%	JGP2Dspots_8/1	85.7	8.01E+04	(R)LVLVASADVSEVAVK(D)	CL1122.Contig1_S.halepenseFrame3RevFrame3Rev

Supplementary TABLE E9. Percentage identity and similarity between Sor h 2 isoforms and other closest subtropical and temperate grass pollen allergen[a].

	CL1122.1	**CL1122.2**	**CL1695**
CL1122.1			
CL1122.2	63%/76% over 118[b]		
CL1695	61%/74% over 121	48%/64% over 120	
Zea m 2	75%/89% over 93 (B6TRH9)	50%/63% over 120 (AFW61602.1)	75%/85% over 96 (B6TRH9)
Phl p 2/3	24%/53% over 98 (Phl p 2; P43214.1)	31%/ 44% over 90 (Phl p 3; AAR31142.1)	29%/51% over 98 (Phl p 2; P43214.1)

[a] closest match with an allergen identified by BLASTP search of the NCBI database.

[b] Alignment and matches discovered by BLASTP searches using the BLOSSOM62 amino acid substitution matrix. Data expressed as the percentage identity/similarity over given number of amino acids.

Supplementary TABLE E10. Percentage identity and similarity between Sor h 13 isoforms and other Panicoideae sequences encoding polygalacturonase proteins.

	Sor h 13.0101A (422) (CL1737.1)	**Sor h 13.0201B (410) (CL1737.2)**
Sor h 13.0201B (411)	86%/88% over 422[b]	
XP_002437275.1 *S bicolor* [a]		92%/97% over 410
XP_002438528.1 *S. bicolor* [a]	98%/99% over 422	
CBM42661.1 (Pas n 13A58)	73%/84% over 396	77%/ 86% over 383
CBM42660.1 (Pas n 13A511)	73%/84% over 396	77%/ 86% over 383
CBM42662.1 (Pas n 13B54)	74%/ 83% over 376	79%/ 88% over 370
CBM42663.1 (Pas n 13B561)	74%/ 83% over 376	79%/ 88% over 370
Phl p 13	38.3%/ over 426	68.8% over 445

[a] closest match identified by BLASTP search of the NCBI database.

[b] Alignment and matches discovered by BLASTP searches using the BLOSSOM62 amino acid substitution matrix. Data expressed as the percentage identity/similarity over given number of amino acids.

A

Output statistics of sequencing

Sample	Total raw reads	Total clean reads	Total clean nucleotides	Q20 percentage	N percentage	GC percentage
S. halepense	44,686,994	39,503,924	3,555,353,160	96.54%	0.00%	57.04%

B

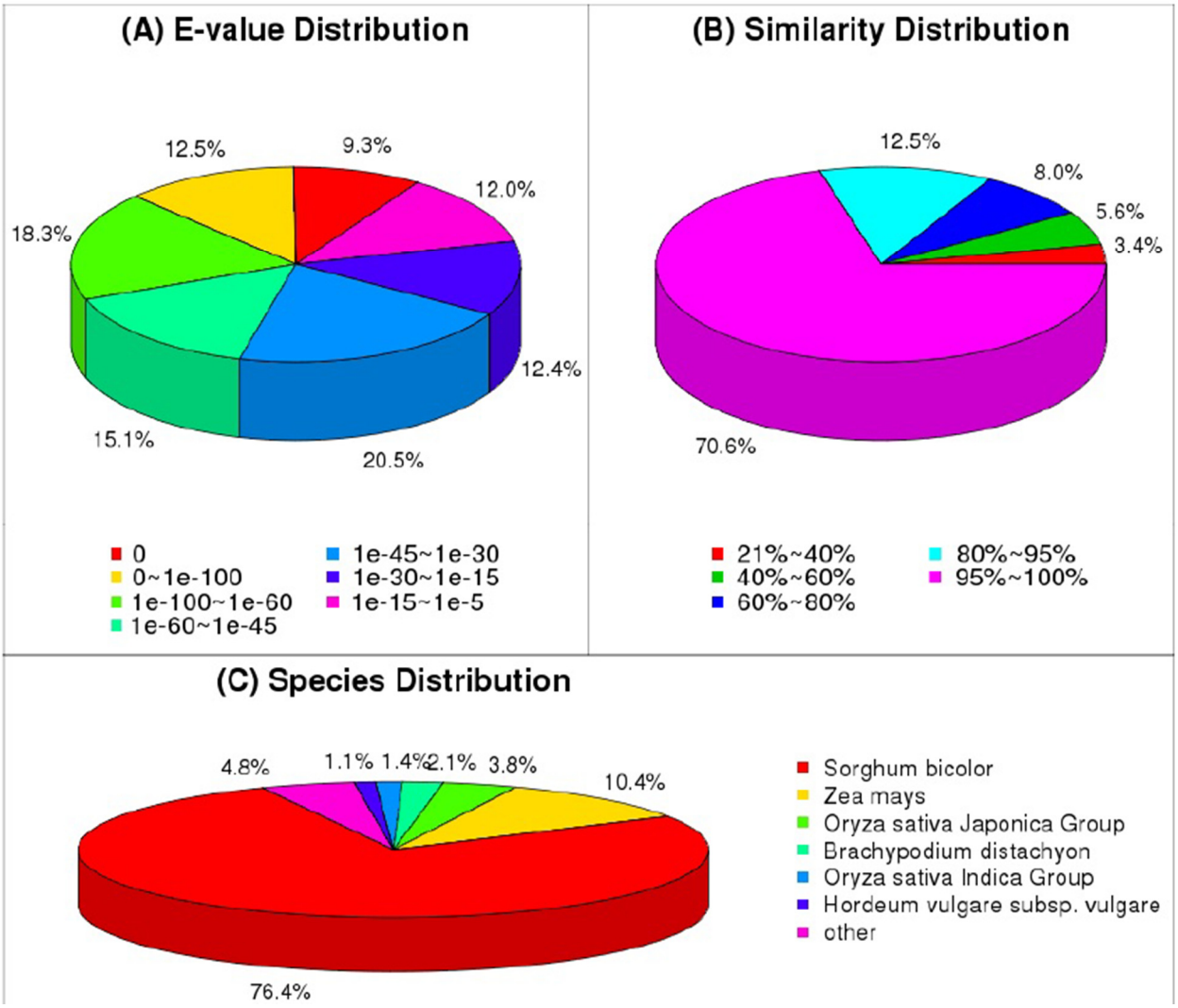
Statistics of assembly quality

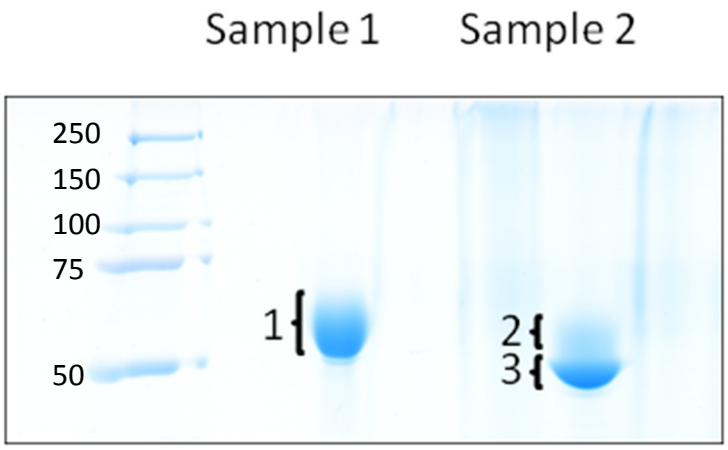
	Sample	Total number	Total length (nt)	Mean length (nt)	Total consensus sequences	Distinct clusters	Distinct singletons
Contig	*S. halepense*	56,319	15,143,474	269	-	-	-
Unigene	*S. halepense*	22,223	13,158,821	592	22,223	4,867	17,356

C

Statistics of annotation results

Sample	Non-Redundant NCBI	NT	SwissProt	Kyoto Encyclopedia of Genes and Genomes	Cluster of Orthologous Groups	Gene Ontology
S. halepense	16,700	18,447	9,391	9,500	5.636	12,524


(A) E-value Distribution
12.5%
9.3%
12.0%
18.3%
12.4%
15.1%
20.5%
0
0~1e-100
1e-100~1e-60
1e-60~1e-45
1e-45~1e-30
1e-30~1e-15
1e-15~1e-5
(B) Similarity Distribution
12.5%
8.0%
5.6%
3.4%
70.6%
21%~40%
40%~60%
60%~80%
80%~95%
95%~100%
(C) Species Distribution
4.8%
1.1%
1.4%
2.1%
3.8%
10.4%
76.4%
Sorghum bicolor
Zea mays
Oryza sativa Japonica Group
Brachypodium distachyon
Oryza sativa Indica Group
Hordeum vulgare subsp. vulgare
other


Sample 1
Sample 2
250
150
100
75
50
1
2
3

A

```
UG493   1    MGSLANKIVAMAAVLAALVTGGSCAPKKFPPGPNITTNYNGQWLSARATWYGQPNGAGPD  60
             MGSLANKIVAMAAVLAALVTGGSCAPKKFPPGPNITTNYNGQWL ARATWYGQPNGAGPD
Sbjct   1    MGSLANKIVAMAAVLAALVTGGSCAPKKFPPGPNITTNYNGQWLVARATWYGQPNGAGPD  60

UG493   61   DNGGACGIKNVNLPPYNGFTACGNVPIFKDGKGCGSCYEVRCKEMPECSGNPITVFITDM  120
             DNGGACGIKNVNLPPYNGFTACGNVPIFKDGKGCGSCYEVRCKEMPECSGNPITVFITDM
Sbjct   61   DNGGACGIKNVNLPPYNGFTACGNVPIFKDGKGCGSCYEVRCKEMPECSGNPITVFITDM  120

UG493   121  NYEPIAPYHFDFSGKAFGSLAKPGLNDKLRHCGIMNVEF  159
             NYEPIAPYHFDFSGKAFGSLAKPGLNDKLRHCGIMNVEF
Sbjct   121  NYEPIAPYHFDFSGKAFGSLAKPGLNDKLRHCGIMNVEF  159
```

B

```
UG492-1 1    EFRRVRCKLGGKIMFHVEKGSNPNYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWG  60
             EFRRVRCKLGGKIMFHVEKGSNPNYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWG
Sbjct   158  EFRRVRCKLGGKIMFHVEKGSNPNYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWG  217

UG492-1 61   AVWRFDTPKPVKGPFSIRLTSESGKKLVAPNVIPATWKPDTLYNSNIQF  109
             AVWRFDTPKP+KGPFSIRLTSESGKKLVAPNVIPA+WKPDTLYNSNIQF
Sbjct   218  AVWRFDTPKPIKGPFSIRLTSESGKKLVAPNVIPASWKPDTLYNSNIQF  266
```

C

```
Sor h 1.02B 1   MGSLANKIVAMAAVLAALVTGGSCAPKKFPPGPNITTNYNGQWLSARATWYGQPNGAGPD  60
                MGSLANKIVAMAAVLAALVTGGSCAPKKFPPGPNITTNYNGQWL ARATWYGQPNGAGPD
Subject         1   MGSLANKIVAMAAVLAALVTGGSCAPKKFPPGPNITTNYNGQWLVARATWYGQPNGAGPD  60

Sor h 1.02B 61  DNGGACGIKNVNLPPYNGFTACGNVPIFKDGKGCGSCYEVRCKEMPECSGNPITVFITDM  120
                DNGGACGIKNVNLPPYNGFTACGNVPIFKDGKGCGSCYEVRCKEMPECSGNPITVFITDM
Subject         61  DNGGACGIKNVNLPPYNGFTACGNVPIFKDGKGCGSCYEVRCKEMPECSGNPITVFITDM  120

Sor h 1.02B 121 NYEPIAPYHFDFSGKAFGSLAKPGLNDKLRHCGIMNVEFRRVRCKLGGKIMFHVEKGSNP  180
                NYEPIAPYHFDFSGKAFGSLAKPGLNDKLRHCGIMNVEFRRVRCKLGGKIMFHVEKGSNP
Subject         121 NYEPIAPYHFDFSGKAFGSLAKPGLNDKLRHCGIMNVEFRRVRCKLGGKIMFHVEKGSNP  180

Sor h 1.02B 181 NYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWGAVWRFDTPKPVKGPFSIRLTSES  240
                NYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWGAVWRFDTPKP+KGPFSIRLTSES
Subject         181 NYLAVLVKNVADDGNIVLMELEDKASPGFKPMKQSWGAVWRFDTPKPIKGPFSIRLTSES  240

Sor h 1.02B 241 GKKLVAPNVIPATWKPDTLYNSNIQF  266
                GKKLVAPNVIPA+WKPDTLYNSNIQF
Subject         241 GKKLVAPNVIPASWKPDTLYNSNIQF  266
```

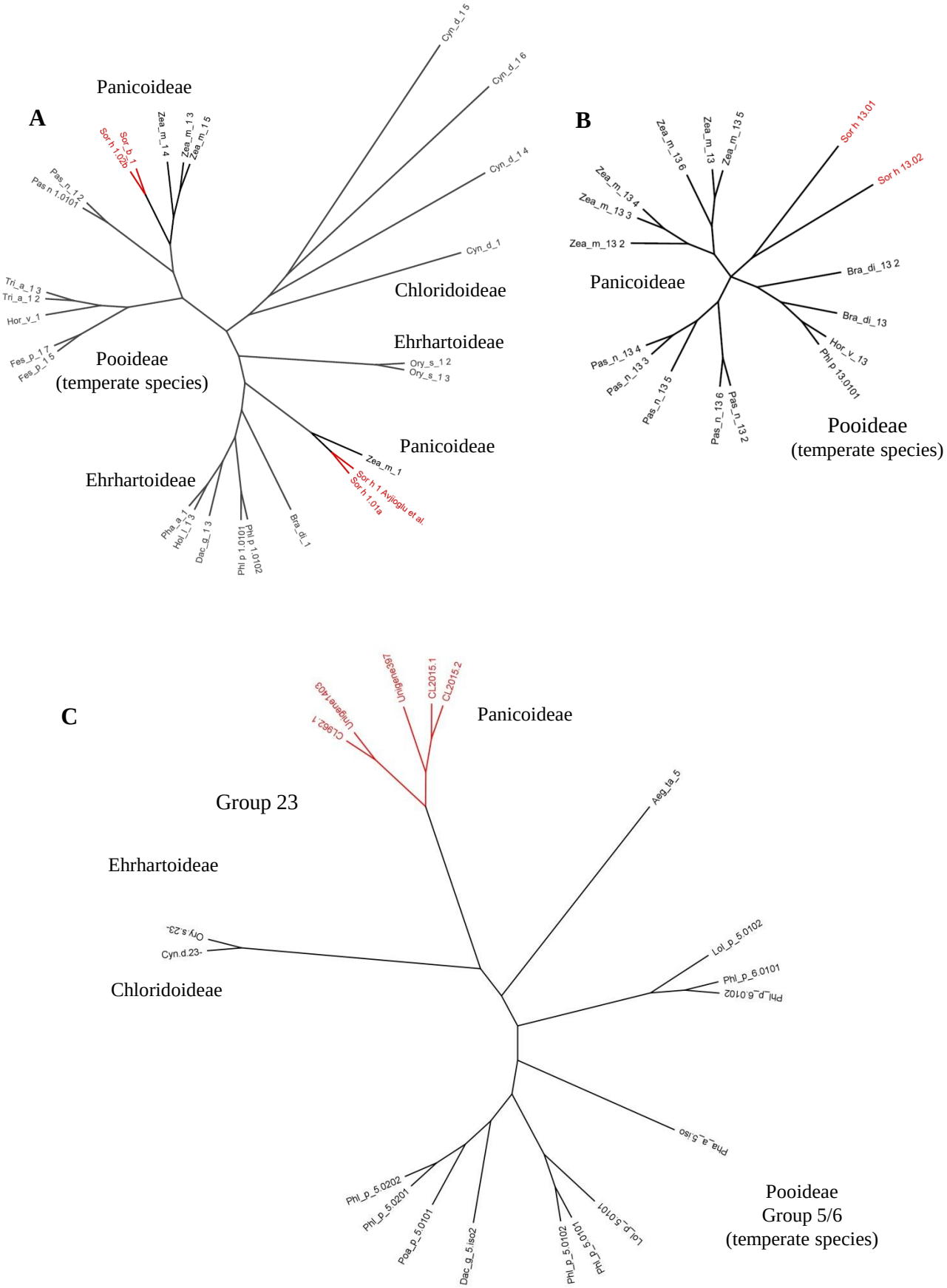
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Sor h 1.01A  GAWCGPPKVAPGKNITATYGSDWLEAKATWYGKPTGAGPDDNGGACGYKDVNKAPFNSMG  83
             G  C P K  PG NIT  Y   WL A+ATWYG+P GAGPDDNGGACG K+VN  P+N
Sor h 1.02B  GGSCAPKKFPPGPNITTNYNGQWLSARATWYGQPNGAGPDDNGGACGIKNVNLPPYNGFT  80

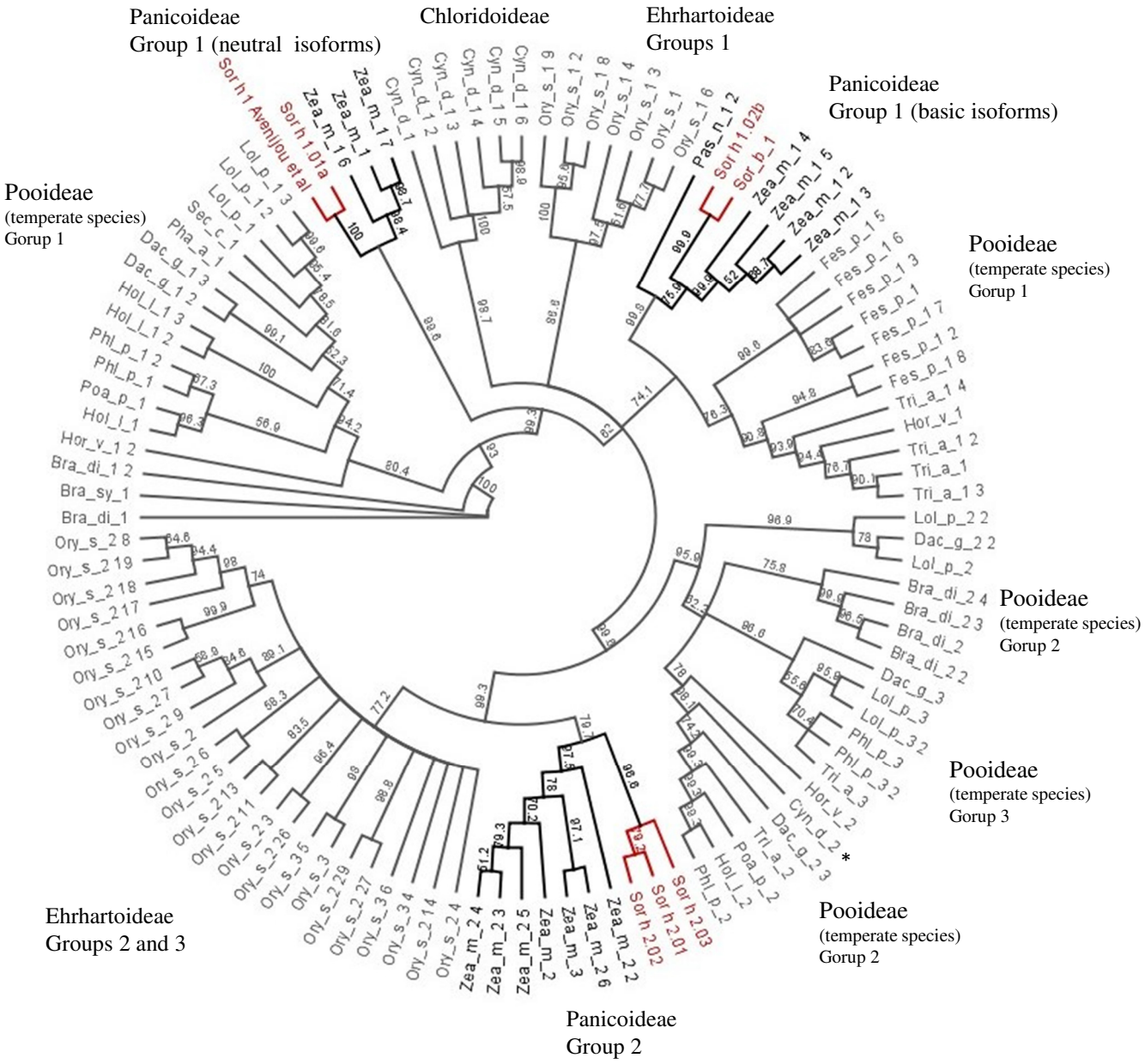
Sor h 1.01A  ACGNLPIFKDGLGCGSCFEIKCDKPAECSGEAVVVHITDMNYEQIAAYHFDLAGTAFGAM  143
             ACGN+PIFKDG GCGSC+E++C +  ECSG  + V ITDMNYE IA YHFD +G AFG++
Sor h 1.02B  ACGNVPIFKDGKGCGSCYEVRCKEMPECSGNPITVFITDMNYEPIAPYHFDFSGKAFGSL  140

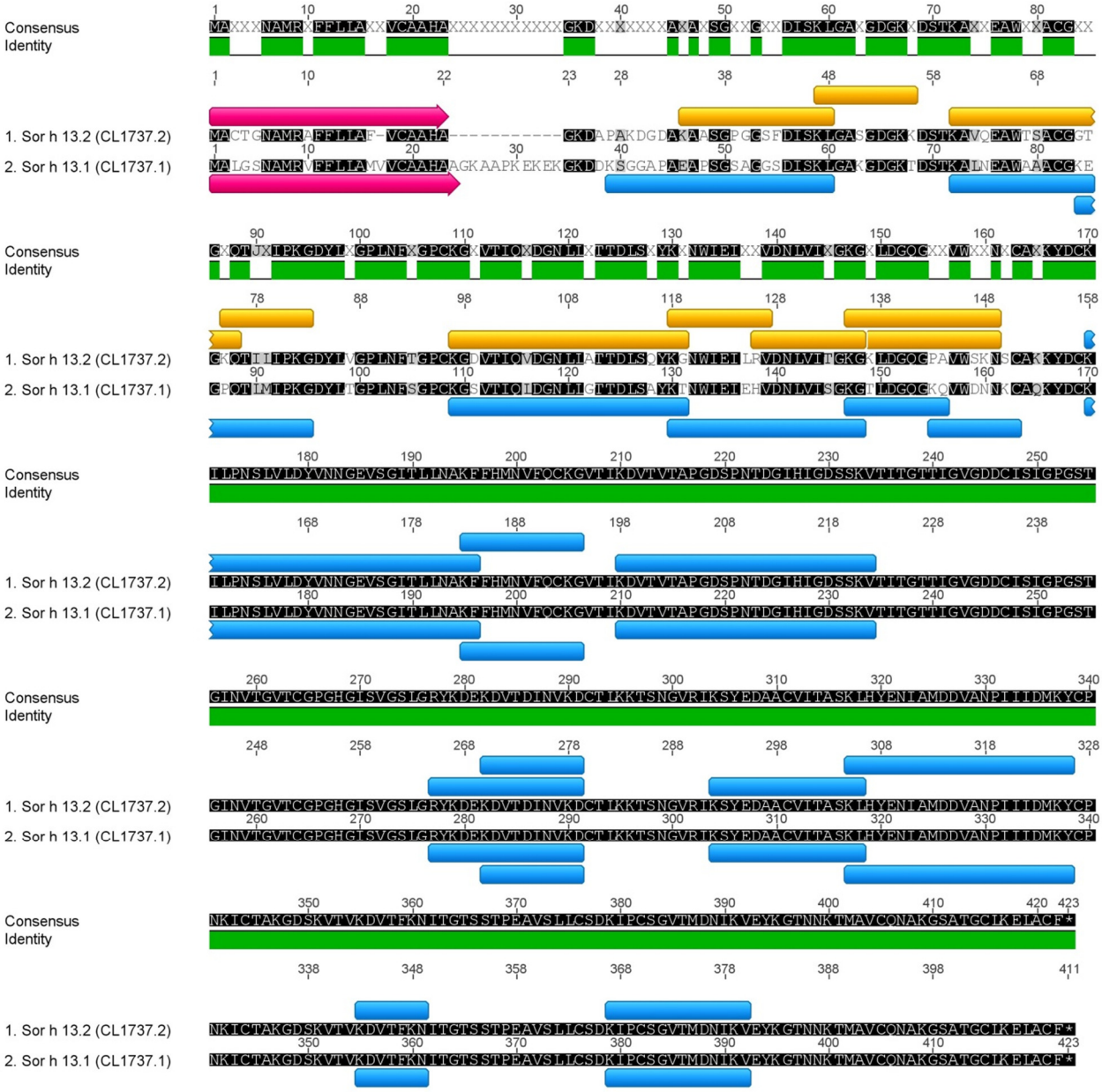
Sor h 1.01A  AKKGEEEKLRKAGIIDMKFRRVKCKYGEKVTFHVEKGSNPNYLALLVKYVDGDGDVVGVD  203
             AK G  +KLR  GI++++FRRV+CK G K+ FHVEKGSNPNYLA+LVK V  DG++V ++
Sor h 1.02B  AKPGLNDKLRHCGIMNVEFRRVRCKLGGKIMFHVEKGSNPNYLAVLVKNVADDGNIVLME  200

Sor h 1.01A  IKEKGGDAYQPLKHSWGAIWRKDSDKPIKFPVTVQITTEGGTKTAYEDVIPEGWKADTTY  263
             +++K    ++P+K SWGA+WR D+ KP+K P ++++T+E G K    +VIP  WK DT Y
Sor h 1.02B  LEDKASPGFKPMKQSWGAVWRFDTPKPVKGPFSIRLTSESGKKLVAPNVIPATWKPDTLY  260

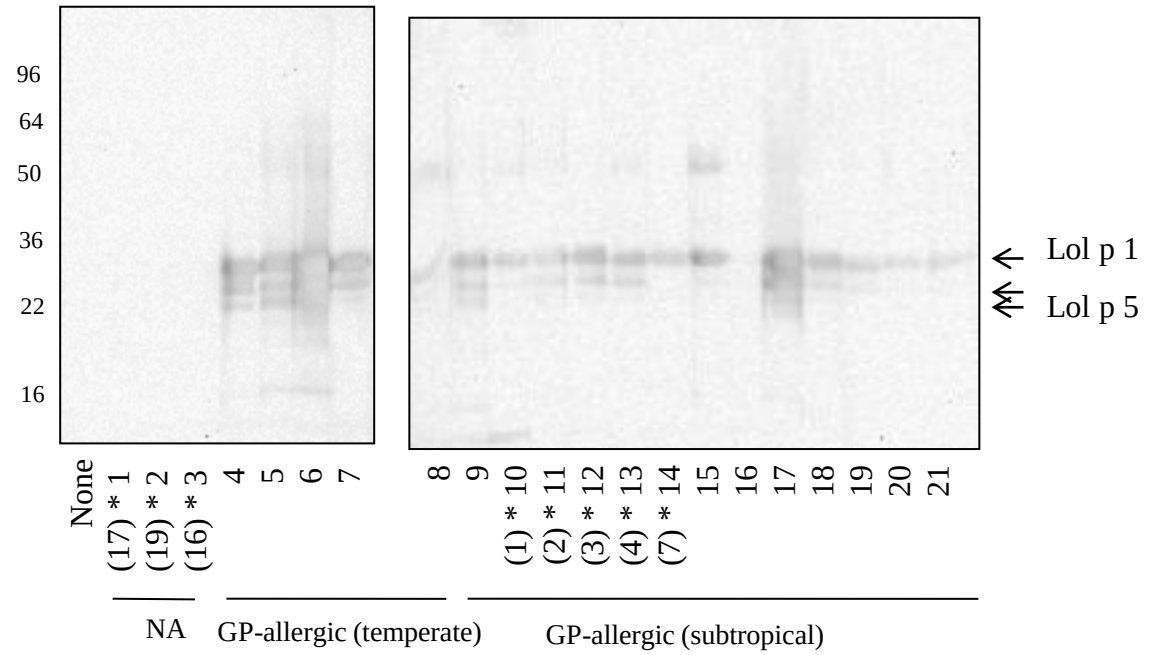
Sor h 1.01A  TA  265
              +
Sor h 1.02B  NS  262
```


A
Panicoideae
Sor_h_1.02b
Sor_b_1
Zea_m_1.4
Zea_m_1.3
Zea_m_1.5
Pas_n_1.2
Pas n 1.0101
Cyn_d_1.5
Cyn_d_1.6
Cyn_d_1.4
Cyn_d_1
Chloridoideae
Tri_a_1.3
Tri_a_1.2
Hor_v_1
Fes_p_1.7
Fes_p_1.5
Ehrhartoideae
Pooideae
(temperate species)
Ory_s_1.2
Ory_s_1.3
Panicoideae
Zea_m_1
Sor h 1 Avlioglu et al.
Sor.h.1.01a
Ehrhartoideae
Pha_a_1
Hol_l_1.3
Dac_g_1.3
Phl p 1.0101
Phl p 1.0102
Bra_di_1
B
Zea_m_13.6
Zea_m_13
Zea_m_13.5
Sor h 13.01
Sor h 13.02
Zea_m_13.4
Zea_m_13.3
Zea_m_13.2
Panicoideae
Bra_di_13.2
Bra_di_13
Hor_v_13
Phl p 13.0101
Pas_n_13.4
Pas_n_13.3
Pas_n_13.5
Pas_n_13.6
Pas_n_13.2
Pooideae
(temperate species)
C
CL962.1
Unigene1403
Unigene7937
CL2015.1
CL2015.2
Panicoideae
Group 23
Ehrhartoideae
Aeg_ta_5
Lol_p_5.0102
Phl_p_6.0101
Phl_p_6.0102
Ory.s.23-
Cyn.d.23-
Chloridoideae
Pha_a_5.iso
Phl_p_5.0202
Phl_p_5.0201
Poa_p_5.0101
Dac_g_5.iso2
Phl_p_5.0102
Phl_p_5.0101
Lol_p_5.0101
Pooideae
Group 5/6
(temperate species)

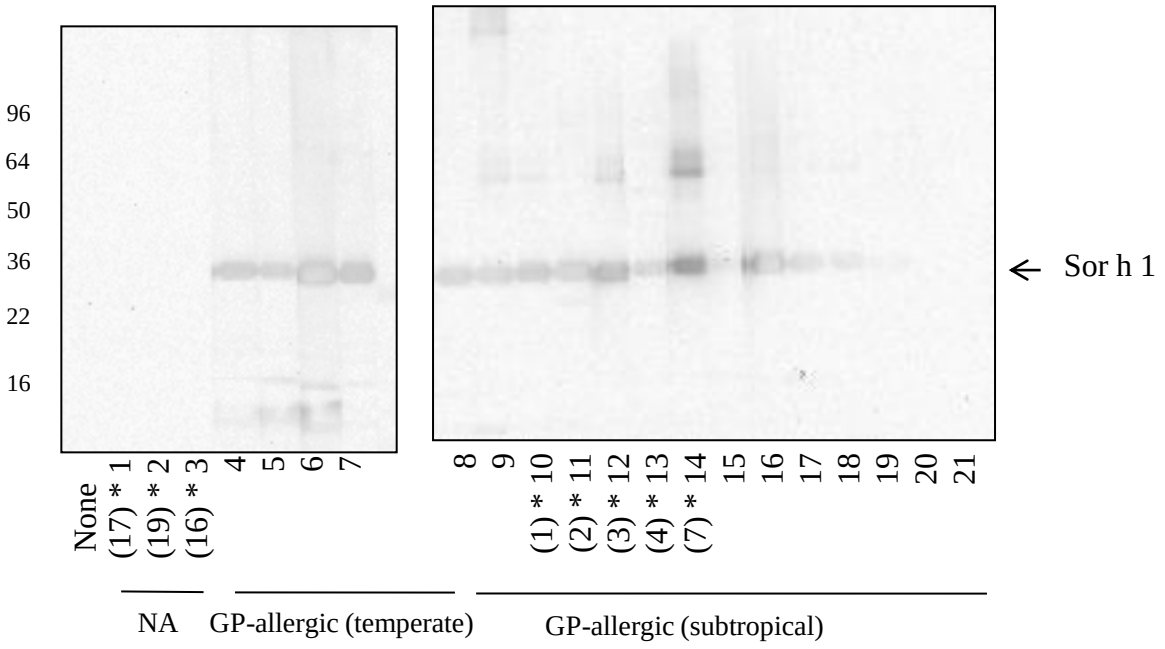

Panicoideae
Group 1 (neutral isoforms)
Chloridoideae
Ehrhartoideae
Groups 1
Panicoideae
Group 1 (basic isoforms)
Pooideae
(temperate species)
Gorup 1
Pooideae
(temperate species)
Gorup 1
Pooideae
(temperate species)
Gorup 2
Pooideae
(temperate species)
Gorup 3
Pooideae
(temperate species)
Gorup 2
Panicoideae
Group 2
Ehrhartoideae
Groups 2 and 3
Sor h 1 Avenjou et al
Sor h 1.01a
Sor h 1.02b
Sor_b_1
Sor h 2.01
Sor h 2.02
Sor h 2.03
*

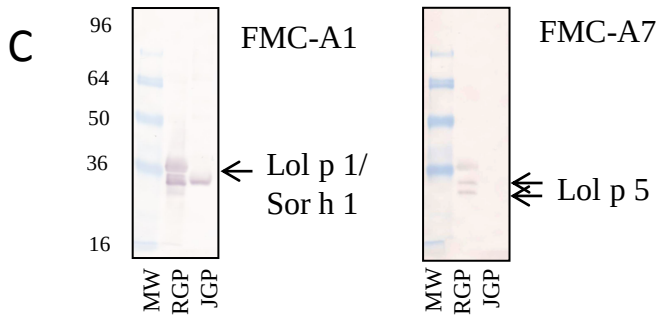

Consensus
Identity
1. Sor h 13.2 (CL1737.2)
2. Sor h 13.1 (CL1737.1)

A. Ryegrass pollen extract (*L. perenne*)



B. Johnson grass pollen extract (*S. halepense*)





Supplementary Figure legends

FIGURE E1. **Transcriptome library quality**. **A**. Output statistics showing results for raw and clean reads of *S. halepense* pollen mRNA transcriptome sequences. **B** Statistics of assembly quality for alignment and assembly of raw reads into transcripts. **C**. Statistics of annotation results. Two classes of sequences are present in the data, Unigene sequences represent the best fit transcript from any single locus, and contigs that represent all the transcripts arising from any single locus. The Unigenes determined for S. halepense were annotated with matches to similar sequences known within a series of sequence databases.

FIGURE E2. **Distribution of matches with known sequences of the non-redundant plant database with the Johnson grass pollen transcriptome. A** E-value distribution from BLAST results. **B**. Similarity distribution **C**. Species distribution of homologous sequence matches. NR database (http://www.ncbi.nlm.nih.gov/).

FIGURE E3. **Purified samples of Sor h 13 stained with Coomassie blue.** Sample 1, fraction 1 (marked by bracket) shows the Sor h 13 fraction A (Sor h 13.0101) used in the ELISA and mass spectrometry. Sample 2, fraction 3 (marked by bracket) was used in the mass spectrometry analysis for Sor h 13 B (Sor h 13.0201). Molecular weight markers are shown on the left with sized in kDa.

FIGURE E4. **Concatenation of the sequence of UG493 and UG492 matches the sequence of a related *S. bicolor* gene transcript. A**. Match identified between UG493 to an unidentified sequence XP_002467539.1 (sbjct). There were 158/159 identical (99%) and 158/159 similar (99%) amino acids. **B**. Match identified between UG492-1 to the same hypothetical protein XP_002467539.1 (sbjct). There were 107/109 identical (98%) and 109/109 similar (100%) amino acids. **C**. Alignment of Sor h 1.02B, deduced by concatenation of amino acids 1 to 158 of UG493 to amino acids 3 to109 of UG 492.1, with

the *S. bicolor* sequence XP_002467539 (Subject). There were 263/266 identical (99%) and 265/266 similar (100%) amino acids. Sequences were aligned using BLASTP with the BLOSSOM62 amino acid substitution matrix. In A and B the two overlapping amino acids encoded by an 8 base pair overlap between UG 493 and UG 492 are shown in yellow. Amino acid differences are highlighted in green.

FIGURE E5. **The relationship between Sor h 1.01A (CL153.1) and Sor h 1.02B (UG493/492.1).** The predicted mature peptide sequences encoded by CL153.1 and the UG493-492.1 transcripts were paired using BLASTP with the BLOSSOM62 amino acid substitution matrix. There were 57% identical and 73% similar amino acids. MW standards shown on left with sizes in kDa.

FIG E6 Alignment of group 1 (**A**), 13 (**B**) and 23 (**C**) grass pollen allergen sequences identified for JGP (red) with similar allergens identified in the Allergome.org database. Related Allergome.org entries were appended with numbers to denote separate sequences. Dendrograms were assembled as unrooted neighbour-joining trees.

FIGURE E7 **Alignment of beta-expansin allergen sequences from groups 1, 2 and 3 grass pollen allergen families.** Newly identified JGP sequences (red) and similar allergens from the Allergome.org database were included. Due to limited annotation of Allergome.org, sequences from the same allergen family and species were appended with numbers to show uniqueness in this dendrogram assembled as an unrooted neighbour-joining tree. Branches containing allergen sequences from particular subfamilies are labelled. Panicoideae allergens are in bold.

FIGURE E8. **Coverage of peptide spectra observed in mass spectrometry of purified Sor h 13 samples A and B (shown in FIGURE E2) aligned with sequences of the polygalacturonase encoding transcripts CL1737.1 (Sor h 13.0101) and CL1737.2 (Sor h**

13.0201). The presence of peptides unique to each sequence confirmed that both were present in the transcriptome and proteome of JGP. There was 56.3% and 56.5% coverage of the peptide sequence for CL1737.1 and CL1737.2 respectively. Coloured bars represent annotations, where magenta highlights the signal peptide predicted by SignalP, blue highlights the peptide fragments mapping uniquely to Sor h 13.0101 or are shared with the Sor h 13.0201 C-terminal, and gold highlights the peptide fragments uniquely mapping to Sor h 13.2.

FIGURE E9. **Spectrum Mill proteomic data of mass spectra identified in purified Sor h 13 fractions 1, 2 and 3 (FIGURE E3).** Fraction 1 contained peptides uniquely detected in CL1737.1 (Sor h 13.01A; Sor h 13.0101) whilst Fraction 3 contained peptides uniquely detected in CL1737.2 (Sor h 13.02B; Sor h 13.0201).FIGURE E10. **Comparative IgE immunoblotting with Ryegrass pollen extract and Johnson grass pollen extract.** IgE immunoblotting of three non-atopic subjects (1-3), grass pollen (GP)-allergic patients from a temperate region (4-9), four of whom show IgE with bands consistent with Lol p 5), and GP-allergic patients from a subtropical region (10-21, eight of whom showed IgE reactivity with bands consistent with Lol p 5. Numbers in brackets indicate the serum number in Figure 1. A. Ryegrass pollen B. Johnson grass pollen. C. Immunoblotting of both pollen extracts with monoclonal antibodies[E21] to group 1 allergen (FMC-A1) and group 5 allergen (FMC-A7) showing band pattern for Lol p 1 and Sor h 1 (left panel) and Lol p 5 (right panel).