CREATION OF A TRANSCRIPTOME OF *S. ETUBEROSUM* WITH SEQUENCING OF A SEGREGATING POTATO POPULATION TO EVALUATE DIFFERENTIAL GENE EXPRESSION ASSOCIATED WITH POTATO LEAFROLL VIRUS RESISTANCE

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by
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AUTHORIZATION TO SUBMIT THESIS

This thesis of Mikeal Dan Wall, submitted for the degree of Master of Science with a major in Plant Science and titled "**CREATION OF A TRANSCRIPTOME OF *S. ETUBEROSUM* WITH SEQUENCING OF A SEGREGATING POTATO POPULATION TO EVALUATE DIFFERENTIAL GENE EXPRESSION ASSOCIATED WITH POTATO LEAFROLL VIRUS RESISTANCE**," has been reviewed in final form. Permission, as indicated by the signatures and dates given below, is now granted to submit final copies to the college of graduate studies for approval.

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ABSTRACT

Wild species of potato (*Solanum tuberosum sp*.) can provide a rich source of disease resistance for the modern day breeder. A unique breeding population designated A05379 segregates for potato leafroll virus resistance derived from *S. etuberosum;* resistance being conferred by gene *Rlr*$_{etb}$. RNA was extracted from *Solanum etuberosum* and two backcross 4 (BC$_4$) subsets of the A05379 population. These two BC$_4$ subsets represented a pool of plants immune and susceptible to potato leafroll virus (PLRV). The RNA of *Solanum etuberosum* and the BC$_4$ pools were sequenced using Pacific Biosciences and Illumina methodologies, respectively. The two BC$_4$ pools allowed the comparison of transcripts from immune and susceptible plants to determine variations in gene expression that might be associated with resistance to PLRV. The Pacific Biosciences sequences from *Solanum etuberosum* served as a reference sequence for the Illumina reads, since the whole genome sequence to *S. etuberosum* has not been reported. Comparison of susceptible and immune sequence data identified transcripts unique to one pool or the other, and identified putative candidate genes candidates for *Rlr*$_{etb}$.

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DEDICATION

A very special thanks goes out to my beautiful wife Jaclyn and our two sons, Liam and Kade. These three blessings helped me get through this wonderful but trying time. I love you three.

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positions for each ORF are shown. Solid lines represent the gRNA, sgRNA1, sgRNA2 and sgRNA3 of PLRV (Ashoub et al. 1998; Hwang et al. 2012; Kawchuck et al. 1990; Mayo and Ziegler-Graff 1996; Smith and Harris 1990).

Figure 2.1 40

TapeStation 2200 gel image and electropherograms for *S. etuberosum*, 16-1, samples. Electropherograms are presented in the right column while the gel image is shown in the left column. Each electropherogram is labeled with an individual letter corresponding to a lane visible in the gel image. Peak intensity in each electropherogram is represented in fluorescent units (FU) to the 10^3 magnitude. “Lower” indicates a control peak provided with the TapeStation reagents and should be visible in all TapeStation 2200 electropherogram images. Number of nucleotides are shown in the far-left lane in the gel image with a description of “nt”. Each band in the gel ladder corresponds with a number of nucleotides seen in the nt lane. Sample loaded in lane A represents extracted RNA samples from five pooled 16-1 *Solanum etuberosum* plants used for Pac Bio sequencing (see table 2.2 first row). Electropherogram B (see also lane B on gel image) is a duplicate of electropherogram A and contains the same five pooled 16-1 RNA samples. Electropherogram E is a 1:1 (5µl Millipore purified H_20 + 5µl Sample) dilution of electropherogram B. Electropherogram F is a 1:1 (5µl Millipore purified H_20 + 5µl Sample) dilution of electropherogram A.

Figure 2.2 41

TapeStation 2200 gel image and electropherograms for immune (BC_4I) samples. Each electropherogram is labeled with an individual letter (A-F) corresponding to a lane visible in the gel image (top left). Peak intensity in each electropherogram is represented in fluorescent units (FU) to the 10^3 magnitude. “Lower” indicates a control peak provided with the TapeStation reagents and should be visible in all TapeStation 2200 electropherogram images. Number of nucleotides are shown in the far-left lane in the gel image with a description of “nt”. Each band in the gel ladder correlates with a number of nucleotides seen in the nt lane. Electropherogram A represents extracted RNA from three separate immune plants, each individually numbered 16, 34 and 61 then pooled to make one sample (see Table 2.2 row 2). Electropherogram B represents extracted RNA from a different set of immune plants. Each plant individually numbered 63, 90 and 100 respectively (see Table 2.2 row 3). Electropherogram C represents yet another set of three immune plants numbered 112, 214 and 219 respectively (see Table 2.2 row 4). Samples producing electropherogram F are a 1:1 dilution (5µl Millipore purified H_20 + 5µl Sample) of the samples seen in electropherogram B. Samples producing electropherogram E are a 1:1 dilution (5µl Millipore purified H_20 + 5µl Sample) of the samples seen in electropherogram A. Samples producing electropherogram D are a 1:1 dilution (5µl Millipore purified H_20 + 5µl Sample) of the samples seen in electropherogram C.

CHAPTER 1

LITERATURE REVIEW

Breeding for Resistance

Major obstacles affecting quality and yield in today's crops are insects and pathogens, including bacteria, fungi, nematodes and viruses (Brown and Caligari 2008). For this reason, breeding for resistance is still a primary objective of plant breeding. Insects and diseases often evolve to overcome resistance control measures. Thus, the length and durability of the plant's resistance to such diseases can be as important as the disease for which it carries resistance. Before one starts to breed for resistance there are some questions that should be asked. Such as "What diseases effect this crop?" and "What is the effect of these diseases on yield and quality?" Once you have answered these questions you can focus efforts to identify disease resistance genes and begin breeding for resistance.

Breeding for resistance is a primary objective of plant breeding (Brown and Caligari 2008). Before one starts to breed or select for resistance one must determine which genotypes are resistant and which are susceptible. The most common way to answer these questions is to grow a series of genotypes under conditions where the disease can be evaluated in a controlled setting.

There are two forms of resistance to be considered. Qualitative resistance is a case where a single gene or locus confers resistance to a given disease. This form of resistance is also known as specific or vertical resistance. On the other hand, quantitative resistance is controlled by several genes or loci and shows continually variable degrees of resistance and is also referred to as non-specific, field, general or horizontal resistance. There are positive and negative aspects to each form of resistance. For example, vertical resistance can be easier to breed/select for while horizontal resistance, which tends to be controlled by many genes, is generally more durable.

New methods of plant breeding have emerged of the past several decades that can speed up the entire process from initial crosses to creating a new cultivar. Cisgenesis and transgenesis use artificial gene transfer, which can result in less extensive change to an organism's genome than mutagenesis, which was widely used before genetic engineering was developed (Schouten et al. 2006). Transgenesis entails inserting a gene or DNA fragment from another organism that is not a relative or even closely related into your crop of choice. Typically done with stable transformation and the use of *Agrobacterium tumefaciens* or particle bombardment. Cisgenesis uses foreign genes from the same species or a close relative of the plant to create a new cultivar. Both techniques create what is termed a genetically modified organism (GMO). Ideally these techniques can create new cultivars within 5 years compared to conventional breeding which can take as many as 10 to 15 years for potato cultivars.

In the early 1990's zinc fingers were being used to create new mutations and modify crops for beneficial purposes. The zinc finger is a self-contained domain stabilized by a zinc ion ligated to a pair of cysteines and a pair of histidines, and by an inner hydrophobic core. This discovery showed not only a new protein fold but also a novel principle of DNA recognition. This modular design offers a large number of possibilities for the specific recognition of DNA (or RNA). An example of a zinc finger application is the ability to inhibit expression of human immunodeficiency virus (Perez et al. 2008).

In the mid to late 2000s transcription activator-like effector nucleases (TALENs) were being used for the purpose of recognizing specific DNA sequences but with much higher specificity than zinc fingers. Developed around 2009, TALENs are restriction enzymes that can be engineered to cut specific sequences of DNA. They're created by combining a TAL effector DNA-binding domain with a DNA cleavage domain. These quickly gained popularity over zinc fingers due to their flexibility and specificity. TALEN's have been used to improve soybean oil quality (Haun 2014), engineer diatoms (microalgae) for enhanced biofuel production (Daboussi et al. 2014) and TALEN constructs are believed to have the greatest precision of the currently available technologies (Boglioli and Richard 2015).

CRISPR/Cas9 or simply "CRISPR" (**C**lustered **r**egularly **i**nterspaced **s**hort **p**alindromic **r**epeats/ **C**RISPR **a**ssociated protein **9**) was unveiled around 2012 and quickly became a favorite of researchers everywhere because it is user friendly and perhaps more importantly it is cost effective. CRISPR acts as a “database” of sorts and retains sequences from previous infections that can be “passed” to Cas9. Cas9, with sequence from CRISPR, operates as a nuclease and cleaves dsDNA at the recognition site guided by the sequence it gained from CRISPR. Work has been done using CRISPR which involves inactivating genes in human cell lines (Shalem et al. 2014) or modifying yeasts used to make biofuels (Ledford 2015).

Molecular Markers

First hypothesized in the early 1920’s (Brown and Caligari 2008), molecular markers are used as a point of reference for the chromosomal segment in the vicinity of the gene that is of interest. The aim is to obtain markers that are closely associated with the locus determining the desirable phenotypic expression of characters such as yield or quality. There are three general systems of markers that can and have been used in plant breeding: morphological, biochemical and molecular (Collard et al. 2005). Morphological markers are those that can be observed simply by looking at the plants phenotype such as pigmentation or dwarfism. Biochemical markers exploit biochemical differences such as protein mobility during electrophoresis as observed in isozyme markers. Isozyme markers are variant forms of enzymes that are functionally identical but can be classified by migration using electrophoresis. Molecular markers can be partitioned as non-PCR (polymerase chain reaction) - based and PCR-based. The main characteristics of molecular markers is that they are a ubiquitous form of variation, are free from environmental influence, show high levels of polymorphism, have no discernable effect on phenotype and only pieces of tissue are required from any stage of development (Brown and Caligari 2008). A list of molecular markers can be seen in Table 1.1.

Some positive aspects of plant molecular markers are that they can help identify cultivars, assist with backcrossing, and aid in building a genetic map of genomes. These are often called genetic linkage maps. The more detailed the linkage map the simpler it is to associate quantitative traits with existing markers. A linkage map created for the chromosomal region surrounding Rlr_{etb} can be seen in Figure 1.1.

Table 1.1 Marker systems, genetic properties, strengths, and limitations derived from Collard et al. (2005). Davierwala et al. (2000); Huettel et al. (1999); Mohapatra et al. (2003) and Winter et al. (1999) all refer to SSR's as sequence tagged microsatellite site (STMS) markers.

Molecular Marker	**Type of Inheritance**	**PCR-Based**	**Strengths**	**Limitations**
RFLP (Random Amplified Length Polymorphism)	Co-dominant	No	Large number of loci	Pre-screen for single copy sequence to be used as probes
				Slower than isozymes
				Assumption that when samples share a fragment, they share flanking cleavage sites
RAPD (Random Amplified Polymorphic DNA)	Dominant	Yes	Fast	Sensitive to reaction conditions (reproducibility issues)
			Measures phenotype in outcrossing species	Assumption that when two samples share a fragment, it is the same locus
			Multiple loci can be scored in single reaction	
AFLP (Amplified Fragment Length Polymorphism)	Dominant	Yes	Detects large number of bands and therefore polymorphism	Multi-step, therefore high technical requirements
SSR* (Simple Sequence Repeat)	Co-dominant	Yes	Fast	Requires sequence data, therefore expensive to develop primers
			Commercially available for some crops	
			Detect multiple alleles	

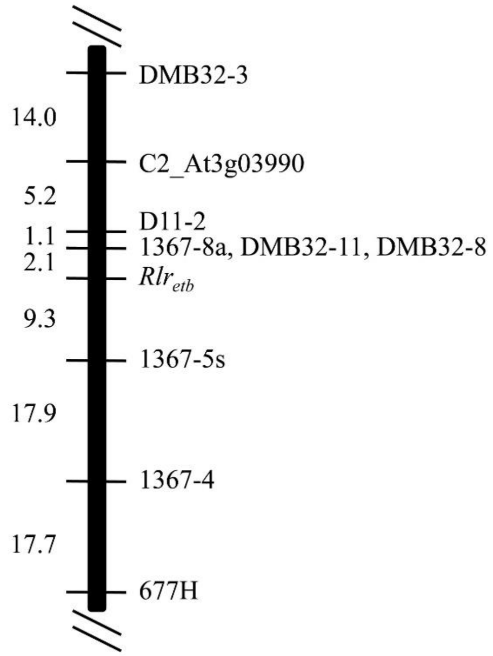

Figure 1.1 Linkage map derived from two BC_4 populations depicting the region surrounding Rlr_{etb}, the locus for potato leafroll virus resistance, on the long arm of chromosome 4 from Kuhl et al. 2016.

One potential problem with molecular markers is that they can be expensive and more labor intensive than other selection options. However, advancing technologies such as single nucleotide polymorphisms (SNPs) chips is significantly decreasing the cost per molecular marker (Brown and Caligari 2008).

Potato landrace line *S. tuberosum ssp. andigena* has been used to breed for resistance, specifically resistance to potato leafroll virus (PLRV) (Kasai et at. 2000). Recently a resistance gene analog (RGA) derived sequence characterized amplified region (SCAR) marker was successfully developed based on sequence homology with disease resistance genes of an amplified fragment length polymorphism (AFLP) molecular marker tightly linked to the Rl_{adg} gene of *S. tuberosum ssp. andigena* (Mihovilovich et al. 2014). This new marker was designated as “RGASC850” (RGA- derived SCAR) based on the size of the amplified fragment. This SCAR proved to be highly proficient in identifying Rl_{adg} based resistance while at the same time failing to amplify PLRV resistance from sources other than *S. tuberosum ssp. andigena.* This makes it useful in selecting cultivars with complimentary sources of resistance to PLRV. In addition, a cleaved amplified polymorphic sequence (CAPS) marker based on "RGASC850" was developed capable of distinguishing genotypes carrying Rl_{adg}. This CAPS marker could be useful in screening breeding populations from wide crosses and confirming the presence of the Rl_{adg} gene (Mihovilovich et al. 2014).

Modern linkage mapping has its history in the genetic segregation studies of Gregor Mendel. The genetic makeup of potato, autotetraploid, has caused some delay in linkage mapping efforts. However, a variety of other tools are available for genetic mapping which include some of the fore mentioned techniques. Marker assisted selection utilizing restriction fragment length polymorphisms (RFLP's), amplified fragment length polymorphisms (AFLP's) from PCR and short sequence repeats (SSR) all aid in developing ultra-high density (UHD) linkage maps. The first potato map was created by using an interspecific cross involving a diploid potato line and RFLP markers previously mapped in tomato (Bernatzky and Tanksley 1986; Bonierbale et al 1988). The successful use of tomato RFLP probes in potato mapping suggested a high level of synteny among the tomato and potato genomes.

The first intraspecific linkage potato map was developed using RFLP markers in a mapping population derived from a cross between two diploid *S. tuberosum* lines (Gebhardt et al. 1989). This first map contained 141 RFLP markers which were assigned to 12 linkage groups for a total of 690 centimorgans (cM). More tomato-potato derived RFLP markers were added to the linkage map by Gebhardt et al. (1989) which extended the total length to 1034 cM with 304 mapped loci. Tanksley et al. (1992) further enriched the potato genetic map with RFLP, isozyme and CAPS markers thus generating a map on which a marker could be found, on average, every 0.7 cM distance. Jacobs et al. (1995) added another 92 molecular markers to the potato linkage map. These markers were developed from a potato leaf cDNA library near flanking sites for T-DNA or the Ac transposable element. The same population was then used to map 264 AFLPs (van Eck et al. 1995). This was the first use of AFLP markers in potato. The AFLP map was integrated with the RFLP map of Jacobs et al. (1995). In 1998 Milbourne et al. (1998) identified 55 additional markers utilizing SSRs. Seven years later Feingold et al. (2005) reported development of SSR markers from a collection of more than 150,000 publicly available potato express sequence tag (EST) sequences. A total of 57 SSR markers were mapped in two diploid *S. tuberosum* mapping populations (Feingold et al. 2005). Linkage mapping efforts resulted in an ultra-high density UHD map in 2006 with a total of 10,365 markers (van Os et al. 2006). The mapping population was from diploid *S. tuberosum* lines. A bin system was utilized to develop this map. Each bin was described as a collection of markers separated by a single recombination event from an adjacent bin. Such a high density of markers meant that an average distance between markers was smaller than the average size of the potato artificial bacterial chromosome (BAC) library. This could facilitate chromosomal landing for cloning genes of interest. Additionally, the UHD map was integrated with the BAC-based potato physical map. This resource was used to facilitate in the whole genome sequencing of potato (van Os et al. 2006) and in July 2011 an international team of scientists from 14 countries published the full potato genome sequence in the journal Nature (PGSC 2012).

DArT technology has also become a useful and cost effective way to explore genomes. A DArT array consists of a microarray slide spotted with DNA fragments from a group of related species or a group of genotypes from within a species. The DNA fragments are a representation of an entire genome of each member of the group obtained by restriction digests and cloning. For linkage mapping, genomic representations from genotypes of a mapping population are hybridized to the DArT array. Maker segregation data are deduced from the presence or absence of hybridization at each microarray spot. Ongoing efforts between Dr. James Bradeen (University of Minnesota, USA) and Dr. Domenico Carputo (University of Naples, Italy) laboratories have published DArT-based linkage maps for disease resistant wild potato *S. bulbocastanum* (Iorizzo et al. 2014).

Economic Impact

Potato (*Solanum tuberosum ssp. tuberosum*) is one of the main staple food crops worldwide, ranked as number four behind only rice, wheat, and corn (Karasev and Gray 2013). World potato production exceeds that of many cereals such as barley, sorghum, millets, rye and oats. Despite Idaho’s reputation as “The Potato State”, the United States of

America falls fifth in potato production world-wide preceded by China, India, Russia and Ukraine (FAOSTAT data 2015). Idaho provides nearly one third of the U.S. potato crop and is the single largest potato producing state in the U.S. In 2000, 415,000 acres of potatoes were planted in Idaho which accounted for nearly 34 percent of the nation's fall harvest acreage (Stark and Love 2003). The Idaho potato industry provides about $2.7 billion to Idaho's economy and provides more than 30,000 jobs (Idaho Potato Commission 2015). The world dedicated nearly 460 million acres in 2010 for potato cultivation. The average world farm yield for potato was 8.7 tons per acre, in 2010. Potato farms in the United States were the most productive in 2000, with a production quantity average of 23.3 million tons per farm. (FAOSTAT data 2015).

The impact of potato on the world's economy has reached out to the poor and hungry in some of the worlds most impoverished areas. The potato contributes in at least two ways to developing countries. One way is food for sustenance. In some countries, like Rwanda, the potato is staple and grown to feed the poor while reducing hunger and improving nutritional status. The second way potatoes are assisting the poor is to provide employment. Potato is a high value crop in places like Cameroon, where the impoverished can find new employment and earn wages thus improving their quality of life (Thiele et al. 2010).

Wild Potato Species

Wild *Solanum* species in section *Petota* includes cultivated and wild species that have contributed to potato breeding efforts. These wild *Solanum* species have a large area of distribution and can be found growing in many of the southwestern states in the U.S. (Nebraska, Colorado, Utah, Arizona, New Mexico and Texas) (Hawkes 1990). Nearly every state in Mexico as well as other countries just south of Mexico such as Guatemala, Honduras, Costa Rica and Panama contain wild species of potato (Hawkes 1990). In South America, wild potato species are found in every country with the exception of the Guianas (Hijmans and Spooner 2001). Along with a wide geographical distribution, wild potato species also share a wide variety of resistances to common pathogens. It is not unusual to find resistance to fungal, bacterial and virus diseases as well as nematode pathogens in wild *Solanum* species (Gebhardt and Valkonen 2001). These characteristics make wild potato species highly valuable to breeders and economically valuable. Potatoes are an ancient food and have been domesticated for thousands of years (Morales Garzon 2007). Most evidence of this comes from ceramics made from coastal peoples of South America. Clothing and other forms of artwork show domestication of potatoes however, to find plant evidence one needs to look in rubbish piles and in graves (Hawkes 1990).

The center of origin for potato domestication may well have been in the Andes of southern Peru and northern Bolivia, where likely wild prototypes still exist. Archeological remains of potatoes and an unrelated tuber crop, *Ulluco*, have been radiocarbon-dated to 7000 years before present (Hawkes, 1990). The word potato comes from a blending of two terms for the vegetable. The first word “patata” originates from the Spanish vocabulary while the other word “batata” is Haitian and ultimately refers to a “sweet potato” which was much more desirable in the 1560’s. Because the sweet potato was more popular, the common potato, *Solanum tuberosum*, was referred to as the “bastard potato”. This is not the only unique name for this valuable vegetable. In France they call the potato “pomme de terre” or “earth apple”. In Sweden it’s called jordpäron, literally "earth-pear" (Online Etymology Dictionary, 2001-2015). Domesticated potatoes have at least one major trait that differs from its wild relatives. Shorter stolons and corresponding increase in tuber size. Wild potato species produce small tubers on long stolons that can be as long as a meter in length. This is an adaptive feature that allows for the production of asexual propagules over large areas. Domesticated potatoes have short stolons and larger tubers for high marketable yield (Spooner et al. 2014).

Taxonomy of the common potato follows thusly, Domain: Eukarya, Kingdom: Plantae, Phylum: Anthrophyta, Class: Magnoliopsida, Order: Solanales, Family: Solanaceae, Genus: *Solanum*, Species: *Solanum tuberosum* (Bradley 2009). Members of the family Solanaceae, nightshade family, produce glycoalkaloids, which are toxic and can cause DNA damage when consumed (Korpan et al. 2004). Glycoalkaloids are found in both leaves, tubers and fruit where they convey a bitter taste (Camire et al. 2009). Potatoes from wild *Solanum* species contain varying levels of glycoalkaloids (Friedman 2006). However, the cultivated potato contains low glycoalkaloid levels, typically only solanine and chaconine, suggesting these bitter compounds were selected against during domestication (Johns and Alonso 1990). The genus Solanum consists of approximately 1500 species. It contains more species than any other genus in the Solanaceae family and it's one of the larges among the angiosperms (D'Arcy 1991). Solanum section Petota, which includes potato and its wild relatives, contains about 200 wild species distributed from the southwestern United States, to central Argentina and adjacent Chile (Spooner et al. 2004).

While the introgression of a few specific genes from wild species has had a significant impact on cultivar development, only a handful of species have been used extensively. These include *S. acuale*, *S. chacoence*, *S. demissum*, *S. spegazzinii*, *S. stoloniferum* and *S vernei*, mainly as sources of major genes for resistance to late blight, viruses and potato cyst nematodes (Bradshaw et al. 2006).

Somatic Fusion

Somatic fusion, also called "protoplast fusion", is a genetic modification by which cells from two distinct species of plants are fused together to form a new hybrid cell with nuclear DNA of both. Somatic fusion is required to produce a hybrid that exhibits the characteristics of two sexually incompatible plants. In other words, to combine genomes of incompatible genotypes (Novy and Helgeson 1994a).

Somatic fusion generally occurs in 4 steps: First, removal of cell wall of one of each cell using cellulose enzyme to produce a somatic cell called a protoplast. Second, protoplasts are then fused together using electric shock (electrofusion) or chemical treatment to join the cells and fuse the nuclei. The resulting nucleus is called a heterokaryon. Third, the somatic hybrid cell then has its cell wall induced using hormones. Forth and lastly, the cells are then grown into callus which are then further grown into plantlets and finally grown into a full plant known as a somatic hybrid (Novy and Helgeson 1994a). Protoplast fusion is not a new technology, originally described by Kuster in 1909 (Pelletier 1993), later on animal and cell biologist began to use cell fusion to study developmental and differentiation problems in the

1960s (Barski et al. 1960; Ephrussi and Weiss 1965). Not until the early 1970s did plant cell biologists begin taking cell fusion seriously and start using protoplasts to produce new hybrid plants (Kao et al. 1974; Power et al. 1970). In the early days numerous optimistic ideas were proposed where hybrids of a root crop (carrots or turnips) would be fused to top-vegetable crop (cabbage or cucumber). To date, none of these ideas has been successful. This leads us to the fact that in some cases it is impossible for two nuclei to exist in the same cytoplasmic environment. Often there is selective elimination of some chromosomes and in extreme cases there is complete elimination of one nucleus. If this occurs there is still one cell where the two cytoplasms are fused. This fusion product is then known as a cytoplasmic hybrid or a cybrid. For extrachromosomal inheritance factors this has significant implications (Dodds 1985). Using electricity to fuse isolated protoplasts, sometimes known as the Zimmerman Method, allows the possibility of fusing two individually isolated protoplasts. Using chemical methods involves a large number of protoplasts and results in random fusion and mixture of possible products. It is common for similar protoplasts to fuse and this results in a number of aggregates ranging from two to eight cells forming a polynucleate fusion product. Ideally the desired product is a 1:1 fusion. Sorting the fusion products out can be done visually.

Dr. Richard Novy and colleagues used protoplast fusion to create the unique family of *Solanum*-like plants between a hybrid diploid line and *S. etuberosum* (Novy and Helgeson 1994a). A pedigree showing the protoplast fusion event and successive crosses is shown in Figure 1.2. Progeny from these crosses continue to be evaluated and included in hybridizations to this day.

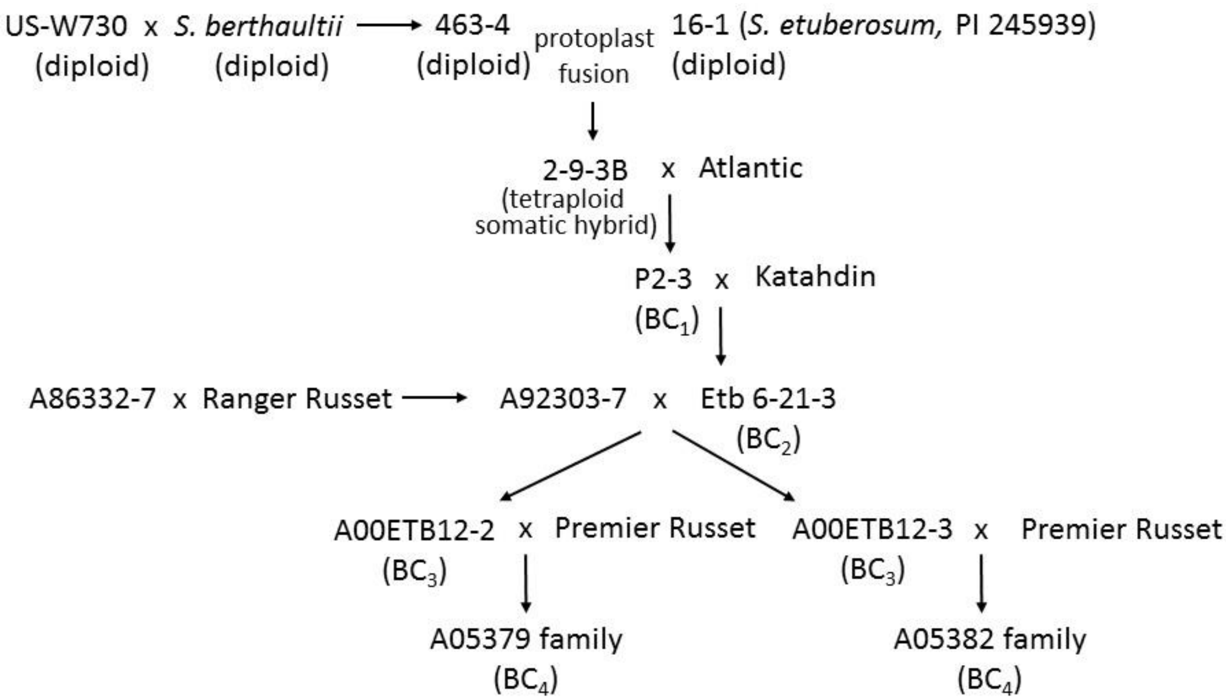

Figure 1.2 BC_4 pedigree derived from Kuhl et al. 2016. BC_4 families as adopted from the original *S. etuberosum* genotype. Diploid individuals, 2N=24, are labeled, 2-9-3B is tetraploid, 2n=48, and all other individuals are tetraploid.

Plant Viruses

Plant viruses are not the only source of disease in potato crops but can cause as much damage to crop yield and quality as any pathogen known today (Oerke 2006). Plant viruses are extremely small and cannot be seen with the naked eye or even the most powerful light microscope. An electron microscope is needed to visualize these “infectious molecules” as they are sometimes termed. A virus is a set of one or more nucleic acid template molecules, either RNA or DNA, normally encapsulated in a protective coat or coats of protein or lipoprotein that is able to self-organize within a suitable host cell (Hull 2009). Viruses can usually be horizontally transmitted between hosts. The number of plant viruses known today is far too exhaustive to cover in this literature review. However, there are 92 genera of plant viruses recognized of which 10 are “unassigned” to a specific family (King et al. 2012). There are 21 families that contain plant virus genera (some also include animal infecting genera) and 3 orders that contain plant virus genera, Mononegavirales, Picornavirales and Tymovirales (King et al. 2012).

There are several methods a virus can spread and infect a host. Potato viruses can spread through fungi infection (Potato Mop Top), mechanically (PVX), grafting of infected plants to healthy plants (nearly all viruses), insect vectors and nematodes. Several plant viruses (PVY, PVA and PLRV) are transmitted through insect vectors. Aphids are a common insect vector. For example, the green peach aphid (see section on Green Peach Aphid) is a vector for turnip mosaic virus (TuMV)(Casteel et al. 2014), Potato virus Y (Ren et al. 2015) and Cucumber Mosaic virus (CMV)(Krenz et al. 2015). Infection of a host plant typically falls into one of four types of transmission: stylet borne or non-persistent, semi-persistent, persistent or circulative and finally circulative propagative. There is no latent period between time of acquisition and potential of transmitting the virus for non-persistent transmission and virions are able to be transmitted mechanically whereas only a few persistent viruses can be transmitted in such a manner (Ng and Falk 2006). Semi-persistent (foregut) and non-persistent manners of transmission are very similar except for the fact that retention times and acquisition times are longer for the semi-persistent viruses. Persistent transmission can be further broken down into two subcategories; circulative (no virus replication) or circulative propagative (virus replication). In circulative transmission, viruses move from the foregut further to the mid- and hindgut, from where they are transported to the hemolymph and further to the salivary gland, where they are released into the plant tissue during feeding. Circulative propagative transmission is very similar in its route through the aphid with one exception, the virus multiplies in the aphid. Figure 1.3 shows an example of persistent circulative transmission, as is the case for PLRV.

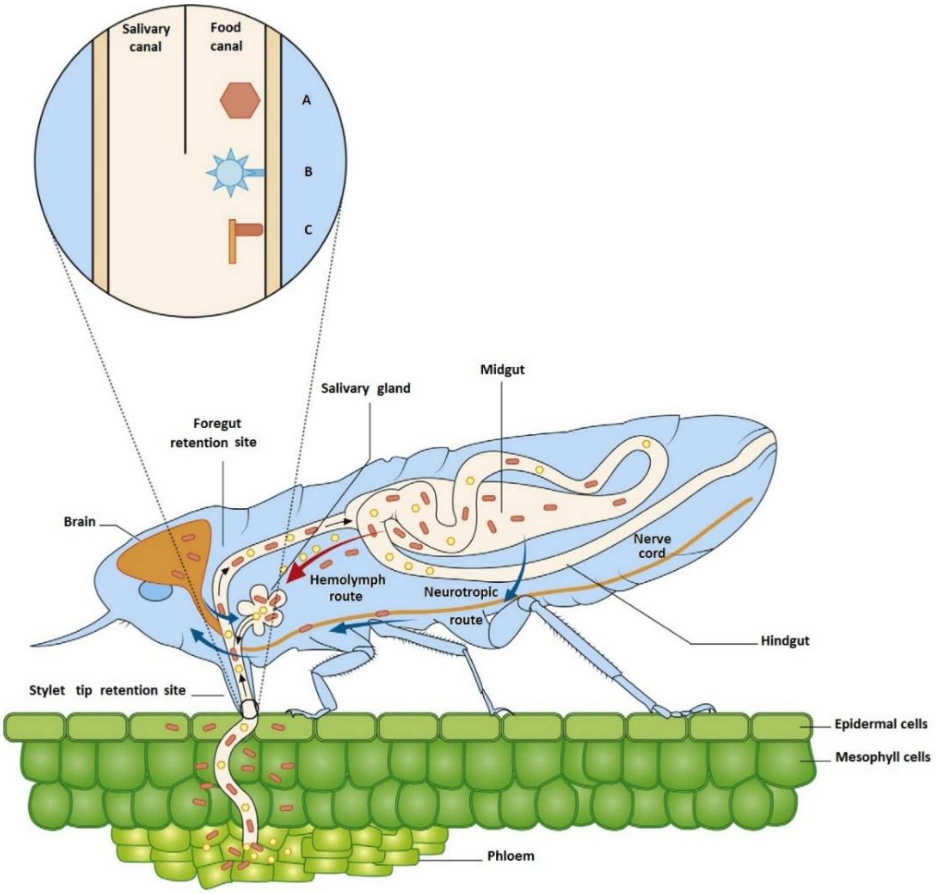

Figure 1.3 Viruses localize to different sites in the plant-feeding insect vector depending on their modes of transmission. Non-circulative viruses bind to the insect stylet (see inset) or foregut. Non-propagative circulative (yellow circles) viruses are generally phloem limited and move through the insect body via the midgut or hindgut. Circulative viruses enter the hemolymph and then enter the salivary glands. By contrast, circulative propagative viruses (red ovals) tend to enter the insect through the midgut and replicate in insect tissues. Some propagative viruses are phloem limited while others are widely distributed in plant tissues. The salivary glands are the final destination for circulative transmission, and viruses reach the salivary glands via the hemolymph or other routes such as the nervous tissue (neurotropic route) or through connective tissues. Inset: Magnification of an insect stylet showing the proposed site of virion attachment at the tip of the stylet in the common duct region. Letters represent the different methods for virion binding and retention in the stylet: *capsid strategy*, direct binding of coat protein to the stylet (A), *helper component strategies* for caulimoviruses, two virus proteins serve as a ‘bridge’ between the virion and the stylet (B) and *potyviruses*, one virus protein (HC-Pro) binds to the aphid stylet and to the virus (C). Derived from Whitfield et al. 2015.

Potato Leafroll Virus

Potato leafroll virus (PLRV) belongs to the genus Polerovirus of the family Luteoviridae. It is phloem limited and contains a positive sense strand RNA. PLRV is persistently transmitted by aphids in a circulative manner meaning it travels from the gut of the aphid to the haemolymph back to the salivary glands for transmission (Rouze-Jouan et al 2001). PLRV was first described by Quanjer et al. (1916). The genomes of the Luteoviridae family of viruses are linear and are roughly 5,700 nucleotides. Potato leafroll virus replicates within the cytoplasm of infected plant cells (Khan and Dijkstra 2006). The virion particle is non-enveloped while the nucleocapsid of PLRV is isometric 24nm in diameter (Loebenstein et al. 2001). Plants that are grown from PLRV infected seed do not fully develop and virtually no usable tubers are produced. These plants exhibit yellow rolled-up leaves that have a leathery texture. Plants infected later in the season can develop net necrosis tuber symptoms. The most distinguished sign of net necrosis is the discoloration of the vascular tissue (Hooker 1981). These infected vascular bundles are brown to black and can extend throughout the tuber. Potatoes showing signs of net necrosis are typically firm, similar to leafroll infected tubers, with a slightly blue coloration at the stem end (Schultz and Folsom 1921). A tuber showing net necrosis can be seen in Figure 1.4.

Figure 1.4 An example of net necrosis from Manzer et al. 1982. This is a Green Mountain cultivar showing significant signs of net necrosis in the phloem tissue of a potato leafroll virus infected tuber.

Infected seed is a primary source of PLRV in potato crops. Early season management can significantly impact subsequent crop growth. Purchase of certified seed is the first step in ensuring excellent vigor, yield potential and PLRV free crops. Natural host range for PLRV is mainly restricted to Solanaceae. Geographical distribution likely occurs worldwide in potato growing areas, especially in climate regions that favor high vector populations and in agro-systems where use of virus-tested “seed” potatoes is not common.

The PLRV genome consists of a single stranded, linear sense messenger RNA molecule, which is covalently linked to a small protein (VPg or viral genome linked protein) of 32 amino acids at its N-terminus (Rowhani and Smith 1979). The RNA does not contain a poly-A sequence at its 3’ terminus. The genomic sequence of PLRV consists of 8 known open reading frames (ORFs) (Kawchuck et al. 1990; Mayo and Ziegler-Graff 1996; Ashoub et al. 1998). The six major ORFs are separated into two gene clusters – ORFs 0, 1 and 2, and ORFs 3, 4 and 5. ORF 0 encodes a factor involved in symptom development. ORF 1 and 2, with motifs characteristic of helicases (ORF 1) and polymerases (ORF 2), form part of the viral replicase. The other ORFs are located in the 3’ half of the genome. ORF 3 encodes the capsid protein. Initiation of an internally located AUG codon within the coat protein gene (CP gene), but in a different reading frame, codes for the movement protein (ORF 4). Suppression of the CP amber stop codon results in formation of an ORF 3/ORF 5 read-through protein, which is supposedly involved in aphid transmission (Ashoub et al. 1998).

ORF 0, ORF 1 and ORF 2 are translated from genomic RNA or “gRNA” as seen in Figure 1.5. In addition, three subgenomic RNAs have been observed – sgRNA 1 (~2.3kb) (Smith and Harris 1990), sgRNA 2 (~0.8 kb) (Ashoub et al. 1998) and sgRNA 3 of unknown length (Hwang et al. 2012). sgRNA 1 serves as mRNA for ORF 3, ORF 3/5 and ORF 4. sgRNA 2 may code for two viral proteins of 17 kDa (ORF 6) and 14 kDa (ORF 7), respectively. The viral genome linked protein (VPg), is thought to act as a transcription enhancer sequence has been mapped to position 400-431 or ORF 1, downstream of the putative protease domain and in front of the RNA-dependent RNA polymerase (Carrington and Freed 1990; van der Wilk et al. 1997). ORF0 codes for a protein used in leafroll symptom development (Ashoub et al. 1998) and quite possibly codes for the VA protein which is indispensable for virus accumulation (Khan and Dijkstra 2006). ORF1 and ORF2, expressed by a -1 frame shift (Khan and Dijkstra 2006), encode helicase and polymerase (Ashoub et al. 1998; Khan and Dijkstra 2006). The capsid protein is from ORF3 but a different reading frame allows for a movement protein to be expressed from ORF4 and for on ORF3/5 read through factor that possibly codes for an aphid transmission factor (Ashoub et al. 1998; Khan and Dijkstra 2006). ORF2 also contains an RNA-dependent RNA polymerase (RdRp) motif. A full-scale representation of the PLRV genome is shown in Figure 1.5.

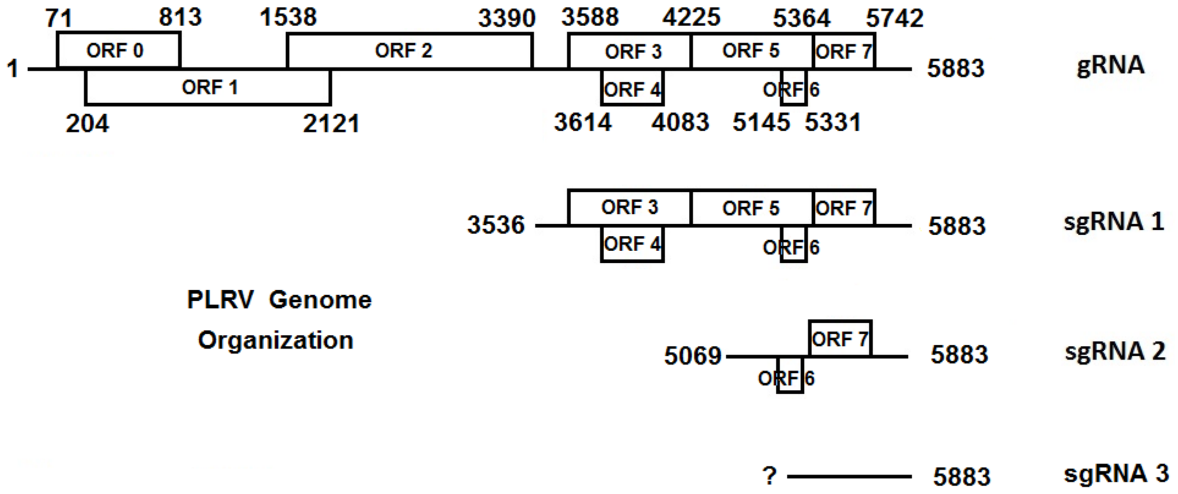

Figure 1.5 Illustration showing the genomic organization of PLRV. ORF0 = silencing suppressor, ORF1 = polyprotein precursor/protease, ORF1/ORF2 = viral RNA dependent RNA polymerase, Rap1 = replication-associated protein1; ORF3 = capsid protein, ORF4 = movement protein, ORF3/ORF5 = read through transmission protein, ORF6 = unknown function, ORF7 = PLRV genomic RNA binding protein and Rap 1 = replication-associated protein. Nucleotide positions for each ORF are shown. Solid lines represent the gRNA, sgRNA1, sgRNA2 and sgRNA3 of PLRV (Ashoub et al. 1998; Hwang et al. 2012; Kawchuck et al. 1990; Mayo and Ziegler-Graff 1996; Smith and Harris 1990).

PLRV can be detected in potato leaves by serology, using commercial ELISA kits. However, the concentration of PLRV varies and in plants grown at temperatures of 30°C or in older plants, ELISA may not always detect infection. Various methods based on PCR or nucleic acid probes have been developed and evaluated. Lotos et al. (2014) created a two-step RT-PCR assay capable of detecting the majority of known poleroviruses including PLRV. Their target for this RT-PCR is the RdRp coding region. They chose this site since it differs significantly from that of other members in the family Luteoviridae and its sequence can be more informative than other regions in the viral genome.

PLRV can be eliminated by keeping tubers for 25 days at 37.5C in a humid atmosphere (Kassanis 1950; Lizarraga et al. 1991). However, heat treatment causes tubers to deteriorate and therefore is not used for commercial stocks but is mainly employed to obtain virus-free plants of small specialty potato lines which can then be propagated. Tissue culture, with or without, thermotherapy, is the most common practice to retrieve virus-free potatoes in general and PLRV-free plants in particular (Lizarraga et al. 1991). It should, however, be emphasized that following virus elimination reliable testing for viruses is needed, preferably over two growing periods and evaluation of trueness-to-type of the cured lines are essential (Loebenstein et al. 2001).

Green Peach Aphid

The green peach aphid, *Myzus persicae,* is an efficient vector for PLRV transmission (Ragsdale et al. 2001). It is found throughout the world, including all areas of North America, where it is viewed as a pest principally due to its ability to transmit plant viruses (Tingey and Andaloro 1982). Development can be rapid, often 10 to 12 days for a complete generation, and with over 20 annual generations reported in mild climates (Capinera 2001). Where suitable host plants cannot persist, the aphid overwinters in the egg stage on *Prunus spp* (Tingey and Andaloro 1982). In the spring, soon after the plant breaks dormancy and begins to grow, the eggs hatch and the nymphs feed on flowers, young foliage, and stems. After several generations, winged dispersants from overwintering *Prunus spp*. deposit nymphs on summer hosts. In cold climates, adults return to *Prunus spp*. in the autumn, where mating occurs, and eggs are deposited. All generations except the autumn generation culminating in egg production are parthenogenetic (non-sexual) (Capinera 2001). Unlike the majority of insects, they can reproduce clonally and give birth to live young, and an aphid’s embryonic development begins before its mother’s birth (Goggin 2007). Green peach aphids feed on numerous plants including many common crop species such as artichoke, bean, carrot, cantaloupe, eggplant, potato, tomato and watermelon (Capinera 2001). A variety of natural enemies can provide some relief. Flower flies (Diptera*: Syrphidae*), lacewings (Neuroptera: mainly *Chrysopidae*), parasitic wasps (Hymenoptera: *Braconidae*), and entomopathogenic fungi (mainly *Entomophthorales*) are just a handful of the insects that feed on green peach aphid, however, lady beetles (Coleoptera: *Coccinellidae*) tend to provide the best control (Capinera 2001). Other means of control are making sure you use certified tuber seeds when growing potatoes. A regular application of insecticides can also reduce aphid infestation. Neonicotinoids have staved off aphid transmission of PLRV more recently but they have raised some controversy in that they are being blamed for the decrease in honey bee populations around the globe (Doublet et al. 2015). This is more commonly known as colony collapse disorder or CCD (van Engelsdorp et al. 2008).

Plant Defense

Plant disease resistance and susceptibility are governed by the combined genotypes of host and pathogen and depend on a complex exchange of signals and responses occurring under given environmental conditions. A key difference between resistant and susceptible plants is the timely recognition of the invading pathogen and the rapid and effective activation of host defense mechanisms (Yang et al. 1997). The activation of defense responses in plants is initiated by host recognition of pathogen-encoded molecules called elicitors (Nurnberger and Brunner 2002). The interaction of pathogen elicitors with host receptors (some of which may be encoded by R genes) likely activates a signal transduction cascade that may involve protein phosphorylation, ion fluxes, reactive oxygen species (ROS) and other signaling events (Sarwat et al. 2016). Subsequent transcriptional and/or post translational activation of transcription factors eventually lead to the induction of plant defense genes. Protein kinases and phosphatases play a pivotal role in the signal transduction processes leading to cell growth, differentiation, and responses to environmental stimuli (Jia et al. 1997). Mounting evidence indicates that phosphorylation and dephosphorylation are also essential to early as well as later events along the signaling pathways leading to plant defense responses (Yang et al. 1997). In addition to protein phosphorylation, early signaling events in plant defense responses may involve ion channels, ROS, GRP-binding proteins, phospholipases and/or other signaling components such as nucleotide sequences (W boxes and G boxes). Following the early signaling events activated by pathogen attack, elicitor signals are often amplified through the generation of secondary signal molecules such as salicylic acid, ethylene, and jasmonates. Mutational analysis has been a powerful tool for identifying the components of various signaling pathways in organisms as diverse as yeast, *Caenorhabditis elegans* and *Drosophila melanogaster*. Among plants, *Arabidopsis thaliana* serves as an excellent model organism to identify mutants with altered defense mechanisms.

When a plant is infected by a pathogen, the plant must recognize the pathogen and then initiate a defense response to limit the potential damage or spread that can be caused by the pathogen. Host recognition of the invading pathogen at the whole organism level is often determined by the so called "gene-for-gene" interaction between a dominant avirulence (Avr) gene of the pathogen and a corresponding dominant resistance gene or "R gene" in the host (Flor 1971). Although Pto from tomato is an exception (Dixon et al. 1996), most cloned R genes that confer gene-for-gene specificities contain leucine-rich-repeats (LRRs). Other common motifs include serine/threonine kinase domains, nucleotide binding sites, leucine zippers and Toll/interleuin-1 receptor-like domains. Furthermore, plant R genes are flanked frequently by multiple homologous paralogs (Lawrence et al. 1995). Therefore, the LRR-containing R genes may undergo active intragenic and intergenic recombination that contributes significantly to the evolution of new specificities. Interestingly, repetitive sequences are also found in some of the Avr genes from plant pathogens (Yang Y et al. 1997). Therefore, genomic recombination among homologous sequences appears to play an important role during the reciprocal evolution of gene-for-gene interactions.

Plant defense isn't just a battle between host plant and bacteria or fungi. There has been an animal-plant warfare that traces back to the eminent role of medicinal plants in the millennia-old history of humankind (Woll et al. 2013). Plants have reacted to herbivory by developing hard shells and thorns causing animals to develop stronger dermis, denser fur and stronger dentition. Plants also produce so called “chemical protection” by making alkaloids, terpenes, phenolics, glucosinolates and cyanogenic glycosides (Woll et al. 2013). Animals counteract by generating special enzymes, e.g. cytochrome 450 monooxigenases (CYP450) that metabolize xenobiotic phytochemicals (Woll et al. 2013). The next step in evolutionary competition between plants and animals, plant produced non-toxic pro-drugs, which become toxic only after ingestion and acted upon my enzymes such as CYP450. From here animals have taken a number of different paths to circumvent the toxic chemicals exuded by plants. Some have adapted their diets and consume only enough of a specific plant to avoid side effects of these chemicals while others have taken advantage of mutations allowing them to consume more of a given plant (e.g. possums and Eucalyptus plants containing terpenes) that would typically be poisonous to other animals (Woll et al. 2013).

In 2006 a “zig-zag” model was proposed by Jones and Dangl that encompassed the two branches of the plant immune system. The first branch recognizes conserved molecules shared among many classes of microbes (microbe associate or pathogen associated molecular patterns) and is called pattern triggered immunity (PTI). The second branch recognizes and responds to virulence factors called effectors which attempt to suppress PTI. This second branch is termed effector triggered immunity (ETI). This is an interesting theory and has captivated both researchers and students alike. However, in 2014 Pritchard and Birch (2014) noted the significance of this theory but point out several lacking features. Notably the molecular scope of the zig-zag model fails to mention anything about necrotrophic organisms or provide a viral example. There’s an absence of environment and how it could affect the model. There’s a strongly implied order of events in the zig-zag model. It seems apparent that not all plant cells would be going through the same steps in the model at the same time. Not only does it suggest all steps occur at the same time but it neglects to mention whether the steps occur in one cell or all cells involved in an infection event. Last but not least, the zig-zag model is entirely qualitative. Nowhere in the model does it present units of measure or values of any kind.

Plant Propagation

Solanum species related to cultivated potato are often propagated using *in vitro* techniques to maintain individual genotypes and disease-free plantlets. Plant propagation is the multiplication of plants by both sexual and asexual means. Propagation of plants have been around for thousands of years. Agriculture started some 10,000 years ago when mankind first started to plant and grow plants for nutritional needs (Hawkes 1990). Some technical considerations need to be taken into account when one considers the topic of plant propagation. First, a knowledge of mechanical, environmental and chemical manipulations, which require a certain amount of skill and expertise to be acquired. Second, successful propagation necessitates knowledge of the plant growth, development and morphology. Some of this knowledge can be gained through working directly with the plants but much of it is acquired through formal courses such as genetics, chemistry, botany and plant physiology. The ability to master these techniques will allow the grower to better cope with unexpected circumstances and know how to address unexpected outcomes, e.g. deviation from expected form (Hartmann et al. 1990). Third and lastly, the grower needs to have a thorough knowledge of the kinds of plants they work with and the various methods by which these plants can be propagated. To a large extent, the method utilized is directly linked to the plant and the situation under which it's being propagated. Plant propagation has advanced quite a bit since its beginning. Selective breeding, budding and grafting were among the first methods of plant propagation and they continue today (Hartmann et al. 1990). This has allowed people to manipulate crops to a condition much different than the wild species from which the crop originates. Such examples are tobacco, barley and maize. In more recent times biotechnology has allowed the development of aseptic micropropagation and *in vitro* tissue culture techniques.

References

Ashoub A, Rohde W and Prüfer D (1998) In Planta transcription of a second subgenomic RNA increases the complexity of the subgroup 2 luteovirus genome. Nucleic Acid Research 26: 420-426

Barski G (1960) Production of cells of a "hybrid" nature in cultivars in vitro of 2 cellular strains in combination. CR Hebd Seances Acad Sci Comptes rendus hebdomadaires des séances de l'Académie des sciences251: 1825-1827

Boglioli E, Richard M (2015) Rewriting The Book Of Life: A New Era in Precision Gene Editing. The Boston Consulting Group

Bradley A (2009) Potato (Solanum tuberosum). http://bioweb.uwlax.edu/bio203/s2009/bradley_adam/Classification.htm. Accessed 15 January 2016

Bradshaw JE, Bryan GJ and Ramsay G (2006) Genetic resources (including wild and cultivated Solanum species) and progress in their utilization in potato breeding. Potato Research 49: 49–65

Brown J and Caligari P (2008) An Introduction to Plant Breeding. Blackwell, Oxford

Camire ME, Kubow S and Donnelly DJ (2009) Potatoes and human health. Critical Reviews in Food Science and Nutrition 49: 823–840

Capinera J (2001) Handbook of Vegetable Pests. pp. 307-312

Carrington J and Freed DD (1990) Cap-Independent Enhancement of Translation by a Plant Potyvirus 5' Nontranslated Region. Journal of Virology 64: 1590-1597

Casteel CL, Yang C, Nanduri AC, De Jong HN, Whitham SA and Jander G (2014) The Nia-Pro protein of Turnip mosaic virus improves growth and reproduction of the aphid vector, Myzus persicae (green peach aphid). The Plant Journal 77: 653-663

Collard BCY, Jahufer MZZ, Brouwer JB and Pang ECK (2005) An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. Euphytca 142: 169-196

Daboussi F, Leduc S, Marechal A, Dubois G, Guyot V, Perez-Michaut C, Amato A, Falciatore A, Juilleratt A, Beurdeley M, Voytas DF, Cavarec L and Duchateau P (2014) Genome engineering empowers the diatom Phaeodactylum tricornutum for biotechnology. Nature Communications 5: article 3831

D'Arcy WG (1991) The Solanaceae since 1976, with a review of its biogeography. In: Hawkes JG Lester RN, Nee M and Estrada N ed(s). Solanaceae III. Taxonomy chemistry evolution. Royal Botanical Garden: Kew & Linnean Society: London. pp. 75-137. 114 Plant geography Biogeography, Solanaceae

Dixon MS, Jones DA, Keddie JS, Thomas CM, Harrison K and Jones JDG (1996) The tomato Cf-2 disease resistance locus comprises two functional genes encoding leucine-rich repeat proteins. Cell 84: 451-459

Dodds JH (1985) Plant genetic engineering. Cambridge University Press, New York

Doublet V, Labarussias M, de Miranda JR, Moritz RFA and Paxton RJ (2015) Bees under stress: sublethal doses of neonicotinoid pesticide and pathogens interact to elevate honey bee mortality across the life cycle. Environmental Microbiology 17: 969-983

Ephrussi B and Weiss MC (1965) Interspecific Hybridization of Somatic Cells. Proceedings of the National Academy of Sciences of the United States of America 53: 1040-1042

FAOSTAT (2015) Food and Agriculture Organization of the United Nations Statistics Division. http://faostat3.fao.org/download/Q/QC/E. Accessed 23 July 2015

Feingold S, Lloyd J, Norero N, Bonierbale M and Lorenzen J (2005) Mapping and characterization of new EST-derived microsatellites for potato (Solanum tuberosum L.). Theoretical and Applied Genetics 111: 456-466

Flor H (1971) Current status of gene-for-gene concept. Annual Review Phytopathology 9: 275-296

Friedman M (2006) Potato glycoalkaloids and metabolites: Roles in the plant and in the diet. Journal of Agricultural and Food Chemistry 54: 8655–8681

Gebhardt C, Ritter E and Debener T, Schachtschabel U, Walkemeier B, Uhrig H and Salamini F (1989) RFLP analysis and linkage mapping in Solanum tuberosum. Theoretical and Applied Genetics 78: 65-75

Gebhardt C, Valkonen JPT (2001) Organization of Genes Controlling Disease Resistance in the Potato Genome. Annual Review Phytopathology 39: 79-102

Goggin FL (2007) Plant–aphid interactions: molecular and ecological perspectives. Current Opinion in Plant Biology 10: 399–408

Hartmann HT, Kester DE and Davies FT Jr (1990) Plant Propagation, Principals and Practices. Prentice Hall, Englewood Cliffs, New Jersey

Haun W, Coffman A, Clasen BM, Demorest ZL, Lowry A, Ray E, Retterath A, Stoddard T, Juillerat A, Cedrone F, Mathis L, Voytas DF and Zhang F (2014) Improved soybean oil quality by targeted mutagenesis of the fatty acid desaturase 2 gene family. Plant Biotechnology Journal 12: 934-940

Hawkes JG (1990) The Potato. Evolution, Biodiversity & Genetic Resources. Smithsonian Institution Press, Washington DC

Hijmans RT, Spooner DM (2001) Geographic Distribution of Wild Potato Species. American Journal of Botany 88: 2101-2112

Hooker WJ (1981) Compendium of Potato Diseases pp 68-70

Hull (2009) Comparative Plant Virology 2nd Edition Elsevier Academic Press, London, England

Idaho Potato Commission (2015) Potato Harvest News Letter. https://idahopotato.com /uploads/ media/14-0423PotatoHarvest-History-HI.pdf. Accessed 2 September 2015

Iorizzo M, Liangliang G, Harpartap M, Traini A, Chiusano ML, Kilian A, Aversano R, Carputo D and Bradeen JM (2014) A DArT marker-based linkage map for wild potato *Solanum bulbocastanum* facilitates structural comparisons between *Solanum* A and B genomes. BMC Genetics 15: 123

Jacobs JME, Van Eck JH, Arens P, Verkerk-Bakker B, te Lintel Hekkert B, Bastiaanssen HJM, El-Kharbotly A, Pereira A, Jacobsen E and Stiekama JW (1995) A genetic map of potato: construction and applications. Theoretical and Applied Genetics 91: 289-300

Jia YL, YT Loh, JM Zhou and GB Martin (1997) Alleles of Pto and Fen occur in bacterial speck-susceptible and fenithion- insensitive tomato cultivars and encode active protein kinases. Plant Cell 9: 61-73

Johns T and JG Alonso (1990) Glycoalkaloid change during the domestication of the potato, Solanum Section Petota. Euphytica 50: 203–210

Jones JDG and Dangl JL (2006) The plant immune system. Nature 444: 323-329

Kao KN, Constabel F, Michayluk MR and Gamborg OL (1974) Plant Protoplast Fusion and Growth of Intergeneric Hybrid Cells. Planta 120: 215-227

Karasev AV and Gray SM (2013) Continuous and Emerging Challenges of Potato virus Y in Potato. Annual Review of Phytopathology 51: 571-586

Kassanis B (1950) Heat Inactivation of Leaf-Roll Virus in Potato Tubers. Annals of Applied Biology 37: 339-341

Kawchuck LM, Martin RR and McPherson (1990) Resistance in Transgenic Potato Expressing the Potato Leafroll Virus Coat Protein Gene. Molecular Plant-Microbe Interactions 3: 301-307

Khan JA and Dijkstra J (2006) Handbook of Plant Virology. The Haworth Press, Inc., 10 Alice Street, Binghamton, NY 113904-1580

King AMQ, Adams MJ, Lefkowitz EJ (2012) Virus Taxonomy Classification and Nomenclature of Viruses, Elsevier Academic Press

Korpan YI, Nazarenko EA, Skryshevskaya IV, Martelet C, Jaffrezic-Renault N and El'skaya AV (2004) Potato glycoalkaloids: true safety or false sense of security? Trends in Biotechnology 22: 147–151

Krenz B, Bronikowski A, Lu X, Ziebell H, Thompson JR and Perry KL (2015) Journal of General Virology 96: 2904-2912

Kuhl JC, Novy RG, Whitworth JL, Dibble MS, Schneider S and Hall D (2016) Development of Molecular Markers Closely Linked to the Potato Leafroll Virus Resistance Gene, *Rlr_{etb}*, for use in Marker-Assisted Selection. American Journal of Potato Research 93: 203-212

Lawrence GJ, Finnegan EJ, Ayliffe MA and Ellis JG (1995) The L6 gene for flax rust resistance is related to the Arabidopsis bacterial resistance gene RPS2 and the tobacco viral resistance gene. N. Plant Cell 7: 1195-1206

Ledford H (2015) CRISPR, The Disruptor. Nature 522: 20-24

Lizarraga R, Panta A, Jayasinghe U and Dodds J (1991) Cultivo de tejidos para la eliminacion de patogenos. CIP Research Guide 3, International Potato Center, Lima, Peru

Loebenstein G, Berber PH, Brunt AA and Lawson RH (Eds.) (2001) Virus and Virus-like Diseases of Potatoes and Production of Seed-Potatoes. Kluwer Academic Publishers. 101 Philip Drive, Norwell, MA 02064

Lotos L, Efthimiou K, Maliogka V and Katis N (2014) Generic detection of poleroviruses using RT-PCR assay targeting the RdRp coding sequence. Journal of Virological Methods 198: 1-11

Manzer FE, Merriam DC, Storch RH and Simpson GW (1982) Effect of Time of Inoculation with Potato Leafroll Virus Development of Net Necrosis and Stem-End Browning in Potato Tubers. American Potato Journal 59: 337-349

Mayo MA and Ziegler-Gaff V (1996) Molecular Biology of Luteoviruses. In: Maramorosch K, Murphy FA and Shatkin AJ (ed) Advances in Virus Research, Vol 46. San Diego, California p 413–463

Mihovilovich E, Aponte M, Lindqvist-Kreuze H and Bonierbale M (2014) An RGA-Derived SCAR Marker Linked to PLRV Resistance from Solanum tuberosum ssp. andigena. Plant Molecular Biology Reporter 32: 117-128

Milbourne D, Meyer RC, Collins AJ, Ramsay LD, Gebhardt C and Waugh R (1998) Isolation, characterization and mapping of simple sequence repeat loci in potato. Molecular and General Genetics 259: 233-245

Morales Garzón FJ (2007) Sociedades precolombinas asociadas a la domesticación y cultivo de la papa (Solanum tuberosum) en Sudamérica. Revista Latinoamericana de la Papa 14: 1–9

Ng JCK and Falk BW (2006) Virus-Vector Interactions Mediating Nonpersistent and Semipersistent Transmission of Plant Viruses. Annual Review of Phytopathology 44: 183-212

Novy RG and Helgeson JP (1994a) Somatic hybrids between *Solanum etuberosum* and diploid, tuber bearing solanum clones. Theoretical and Applied Genes 89: 775-782

Nurnberger T and Brunner F (2002) Innate immunity in plants and animals: emerging parallels between the recognition of general elicitors and pathogen-associated molecular patterns. Current Opinion in Plant Biology 5: 318-324

Oerke EC (2006) Crop losses to pathogens. Journal of Agricultural Science 144: 31-4

Online Etymology Dictionary (2001-2015) http://www.etymonline.com/index.php?allowed_in_frame=0&search=potato&searchmode=none. Accessed 15 September 2015

Pelletier G (1993) Plant Breeding: principals and prospects. In: Heyward MD, Bosemark NO, Romagosa I and Cerezo M (ed) Somatic Fusion, Chapman and Hall, London, p 93-106

Perez EE, Wang J, Miller JC, Jouvenot Y, Kim KA, Liu O, Wang N, Lee G, Bartsevich VV, Lee YL, Guschin DY, Rupniewski I, Waite AJ, Carpenito C, Carroll RG, Orange JS, Urnov FD, Rebar EJ, Ando D, Gregory PD, Riley JL, Holmes MC, June CH (2008) Establishment of HIV-1 resistance in CD4+ T cells by genome editing using zinc-finger nucleases. Nature Biotechnology 26: 808–816

Power JB, Cummins SE and Cocking EC (1970) Fusion of Isolated Plant Protoplasts. Nature 225: 1016-1018

Pritchard L and Birch PRJ (2014) The zigzag model of plant-microbe interactions: is it time to move on? Molecular Plant Pathology 15: 865-870

Quanjer HM, Van Der Lek HAA and Botjes JO (1916) On the Nature, Mode of Dissemination and Control of Phloem-Necrosis (Leaf Roll) and Related Diseases. Third Contribution to a Monograph of the Potato Diseases of the Netherlands

Ragsdale DW, Radcliffe EB and DiFonzo CD (2001) Epidemiology and Field Control of PVY and PLRV. Virus and Virus-like Diseases of Potatoes and Production of Seed Potatoes. Springer Netherlands

Ren G, Wang XF, Chen D, Wang XW, Fan XJ and Liu XD (2015) Potato virus Y-infected tobacco affects the growth, reproduction, and feeding behavior of a vector aphid, *Myzus persicae* (Hemiptera: Aphididae). Applied Entomology and Zoology 50: 239-243

Rowhani A and Stace-Smith R (1979) Purification and Characterization of Potato Leafroll Virus. Virology 98: 45-54

Rouze-Jouan J, Terradot L, Pasquer F, Tanguy S and Ducray-Bourdin DG (2001) The passage of Potato leafroll virus through Myzus persicae gut membrane regulates transmission efficiency. Journal of General Virology 82: 17-23

Sarwat M, Ahmad A, Abdin MZ and Ibrahim MM (2016) Stress Signaling in Plants: Genomics and Proteomics Perspective Volume 2, Springer

Schouten HJ, Krens FA and Jacobsen E (2006) Do cisgenic plants warrant less stringent oversight? Nature Biotechnology 24: 753

Schultz ES and Folsom D (1921) Leafroll, Net-Necrosis, and Spindling-Sprout of the Irish Potato. Journal of Agricultural Research 21: 47-99

Shalem O, Sanjana NE, Hartenian E, Shi X, Scott DA, Mikkelsen TS, Heckl D, Ebert BL, Root DE, Doench JG and Zhang F. (2014) Genome-scale CRISPR-Cas9 knockout screening in human cells. Science 343: 84-87

Smith OP and Harris KF (1990) Potato leafroll virus 3’ genome organization: sequence of the coat protein gene and identification of a viral subgenomic RNA. Phytopathology 80: 609-614

Spooner DM, Ven Den Berg RG, Rodriques A, Baberg J and Jijmans R (2004) Systematic Botany Monographs: Wild Potatoes (Solanum Section Petota; Solanaceae) of North & Central America. Amer Society of Plant Taxonomists

Spooner DM, Ghislain M, Simon R, Jansky SH and Gavrilenko T (2014) Systematics, Diversity, Genetics, and Evolution of Wild and Cultivated Potatoes. The Botanical Review 80: 283-383

Stark SC and Love SL (2003) Potato Production Systems. University of Idaho Agricultural Communications, Moscow, Idaho

Tanksley SD, Ganal MW, Prince JP, deVicente MC, Bonierbale MW, Broun P, Fulton TM, Giovannoni JJ, Grandillo S, Martin GB, Messeguer R, Miller JC, Miller L, Paterson AH, Pineda O, Roder MS, Wing RA, Wu W and Young ND (1992) High Density Molecular Linkage Maps of the Tomato and Potato Genomes. Genetics Society of America 132: 1141-1160

Thiele G, Theisen K, Bonierbale M and Walker T. (2010) Targeting the Poor and Hungry with Potato Science. Potato Journal 37: 75-86

van der Wilk F, Dullemans AM and van der Heuvel JFJM (1997) The Genome-Linked Protein of Potato Leafroll Virus Is Located Downstream of the Putative Domain of the ORF1 Product. Virology 234: 300-303

van Eck HJ, van der Voort JR, Draaistra J, Van Zandvoort P, van Enckevort E, Segers B, Peleman J, Jacobsen E, Helder J and Bakker J (1995) The inheritance and chromosomal localization of AFLP markers in a non-inbred potato offspring. Molecular Breeding 1: 397-410

van Engelsdorp D, Hayes J Jr, Underwood RM, Pettis J (2008) A Survey of Honey Bee Colony Losses in the United States Fall 2007 to Spring 2008. Plos ONE 3: 12

van Os H, Andrzejewski S, Bakker E, Barrena I, Bryann GJ, Bernard C, Ghareeb B, Isidore E, de Jong W, van Koert P, Lefebvre V, Milbourne D, Ritter E, van der Voort JNAMR, Rousselle-Bourgeois F, van Vliet J, Waugh R, Visser RGF, Bakker J and van Eck HJ (2006) Construction of a 10,000-Marker Ultradense Genetic Recombination Map of Potato: Providing a Framework for Accelerated Gene Isolation and a Genomewide Physical Map. Genetics Society of America 173: 1075-1087

Whitfield AE, Falk BW and Rotenberg D (2015) Insect vector-mediated transmission of plant viruses. Virology 479-480: 278–289

Woll S, Kim SH, Greten HJ and Efferth T (2013) Animal plant warfare and secondary metabolite evolution. Natural Products and Bioprospecting 3: 1–7

Yang Y, Shah J and Klessig DF (1997) Signal perception and transduction in plant defense responses, a review, Genes & Development 11: 1621-1639

CHAPTER 2

CREATION OF A TRANSCRIPTOME OF *S. ETUBEROSUM* WITH SEQUENCING OF A SEGREGATING POTATO POPULATION TO EVALUATE DIFFERENTIALL GENE EXPRESSION ASSOCIATED WITH POTATO LEAFROLL VIRUS RESISTANCE

Abstract

Wild species of cultivated potato (*Solanum tuberosum sp*.) are a rich source of disease resistance for the modern day breeder. A unique BC_4 population of cultivated potato was developed that exhibits resistance to potato leafroll virus (PLRV) derived from *S. etuberosum*. The PLRV resistance gene, Rlr_{etb}, has been mapped to potato chromosome 4. Pools of RNA were extracted from PLRV resistant and susceptible plants and short-read Illumina sequencing was used to compare transcript levels from each pool. Transcript differences between the two pools were identified and differences are discussed and possible candidates for Rlr_{etb} described.

Introduction

Potato Leafroll Virus (PLRV) belongs to the genus Polerovirus and family Luteoviridae. It is phloem limited and contains a positive sense strand RNA. PLRV is persistently transmitted by aphids in a circulative manner and can be detected in potato leaves by serology using commercial ELISA kits. Without crop protection almost 75% of attainable potato production would be lost to PLRV (Oerke et al. 2006). Potato leafroll virus is widely distributed and has been documented in crops from northern Africa to Europe as well as in the Americas.

Insects and pathogens often evolve to overcome resistance control measures. Because of this, breeding for resistance is still a primary objective of plant breeding. Wild *Solanum* species in section *Petota* includes cultivated and wild species that have contributed to potato breeding efforts. Wild potato species related to domesticated potato harbor resistance genes to fungal, bacterial, viral diseases as well as nematode pathogens (Novy et al. 2007; Spooner et al. 2014). These characteristics make wild potato species highly valuable to breeders and economically valuable to the industry.

Creating new cultivars with disease resistance has been a main focus for potato breeders for centuries. Wild species harbor many unique genes for disease resistance and other desirable traits (e.g. cold tolerance from *S. etuberosum*), and therefore the ability to cross wild species with potato cultivars is becoming an increasingly desirable tool for breeders. Unfortunately, there are genetic barriers to crossing certain wild species and domesticated potato cultivars (Austin et al 1988; Novy and Helgeson 1994a). Somatic fusion offers one means to overcome the genetic dilemma. Somatic fusion, also called "protoplast fusion", is a genetic modification by which cells from two distinct species of plants are fused together to form a new hybrid plant with nuclear DNA of both. Bridge species provide another means of overcoming such genetic barriers (Hermsen and Taylor 1979). However, somatic hybridization allows direct hybridization to *S. tuberosum* while bridge species requires close monitoring at each hybridization to ensure the desired trait is not lost before final crossing to *S. tuberosum*.

Novy and Helgeson (1994a) successfully accomplished somatic fusion of plants using an electrofusion technique with *Solanum etuberosum* and diploid hybrid potato line, 463-4, a hybrid between US-W730 and *Solanum berthaultii*. Confirmation of parental genomes in progeny plants was conducted with RFLP analysis. Since the absence of an RFLP marker could simply mean a deletion of a segment of chromosome there needed to be another way of identifying all parental genomes in the progeny. Dong et al (2001) employed genome in situ hybridization (GISH) as well as RFLP analysis to differentiate between genomes of different species. These experiments eventually led to the creation of the BC_4 family A05379 which exhibits beneficial characteristics such as disease resistance to PLRV (Kuhl et al. 2016).

The original somatic hybridization between diploid 463-4 with *S. etuberosum* conferred resistance to PLRV among other beneficial qualities (resistance to PVY, PVX, and green peach aphid) (Novy and Helgeson 1994b). During the subsequent backcrosses with common potato cultivars (performed to increase tuber size, quality and yield) PVY resistance was lost while PLRV resistance was retained (Novy et al. 2007; Kuhl et al. 2016). The resistance to PLRV from *S. tuberosum* was initially localized to tomato linkage group 4 of tomato with this major gene for resistance subsequently designated as *Rlr$_{etb}$* (Gillen and Novy 2007; Kelley et al. 2009). Additional mapping analysis further localized *Rlr$_{etb}$* and identified three molecular markers, DMB32-11, 1367-8a and DMB32-8 that were linked within 2.1cM of the gene (Kuhl et al. 2016).

Pacific Biosciences and Illumina RNA experiments were used to study PLRV resistance derived from *S. etuberosum*. RNA from selfed progeny of *S. etuberosum* was extracted and analyzed using Pacific Biosciences sequencing. Field evaluations for response to PLRV in BC$_4$ derived from *S. etuberosum* allowed the identification of nine clones that were immune, and nine that were susceptible to PLRV (Kuhl et al. 2016). Clone pools were bulked and Illumina sequenced. We report the expression of transcripts that might be associated with PLRV resistance from *S. etuberosum* associated with gene *Rlr$_{etb}$***.**

Materials and Methods

Plant Material

Nine immune and nine susceptible A05379 plants were identified based on 2 years of field innoculations (Table 1, Kuhl et al. 2016). Description of the field screening is documented in Novy et al. 2007 and Corsini et al. 1994. In brief, after field inoculation, ten tubers were harvested from each rep and progeny plants were grown out in the greenhouse. Tuber-progeny plants were assayed for PLRV infection using DAS-ELISA using PLRV antiserum was obtained from BioReba Ag (Reinach, Switzerland).

Immune or highly resistant lines shown in Table 2.1 were identified as lines which never produced progeny tubers which tested positive for PLRV after inoculation of plants in the field over a two year period. Susceptible lines shown in Table 2.1 had 90-100% PLRV infected progeny tubers in 2008 and above 70% infection in 2009. Molecular marker DMB32-11, 2.1 cM from *Rlr$_{etb}$*, was used to check for linkage to *Rlr$_{etb}$*. DMB32-11 was present in eight immune individuals, absent in immune line A05379-112, and absent in all susceptible progeny. Of interest might be the fact that immune plant A05379-112 did not have molecular marker 32-11 but was not infected with PLRV. This means there was likely a cross-over event between *Rlr*$_{etb}$ and 32-11 in this plant. Even though it didn't posess molecular marker 32-11 it was not infected with PLRV and was thus numbered among the immune plants. The eight clones used in this study were received as tubers and established in tissue culture from green sprouts. All plants were tested for viruses at the time they were placed in tissue culture. A low percentage of plantlets tested positive and were cleaned up using chemical and heat treatments. Tissue for RNA extraction was collected from growth chamber plants after transfer to soil from tissue culture.

Although the *S. etuberosum* genotype, 16-1, used by Novy and Helgeson (1994a) has been lost, selfed true potato seed of that clone is still available. Seeds were surfaced sterilized, germinated on artificial media and plantlets were maintained in tissue culture. Five 16-1 self seedlings (7, 11, 12, 19 and 27) were transferred to soil from tissue culture and tissue collected for RNA extraction. S. etuberosum is unique among diploid potato species in that it is self-fertile and has a high level of homozygosity. The bulking of selfed seedlings of 16-1 was felt to effectively reconstitute the homozygous genome of 16-1, with this approach previously demonstrated to be effective genomic reconstitution by Kelley et al. (2009). RNA was submitted for Iso-Seq sequencing on a Pacific Biosciences instrument at the National Center for Genome Resources.

BC$_4$ immune and susceptible RNA extractions were conducted by pooling tissue from 3 plants (Table 2.2), pools were identified as BC$_4$I and BC$_4$S, respectively. Equal amounts (100 mg) of leaf tissue from 3 individual immune plants were pooled for one extraction. This was done 3 times for a total of 9 immune plants with three independent pooled RNA samples. Similar pooling was done for the susceptible. BC$_4$I and BC$_4$S RNA samples were submitted for library preparation and Illumina sequencing at the National Center for Genome Resources.

Table 2.1 Immune and susceptible A05739 genotypes identified based on 2 years field inoculations. Each rep represents 10 progeny tubers grown out in the greenhouse and tested with ELISA for PLRV. Data courtesy of Dr. Richard Novy and Dr. Jonathan Whitworth.

		2008				2009			
	PLRV	% PLRV detection in tuber progeny				% PLRV detection in tuber progeny			
Clone	Response	Rep 1	Rep 2	Rep 3	Mean	Rep 1	Rep 2	Rep 3	Mean
A05379-16	Immune	0	0	0	0	0	0	0	0
A05379-34	Immune	0	0	0	0	0	0	0	0
A05379-61	Immune	0	0	0	0	0	0	0	0
A05379-63	Immune	0	0	0	0	0	0	0	0
A05379-90	Immune	0	0	0	0	0	0	0	0
A05379-100	Immune	0	0	0	0	0	0	0	0
A05379-112	Immune	0	0	0	0	0	0	0	0
A05379-214	Immune	0	0	0	0	0	0	0	0
A05379-219	Immune	0	0	0	0	0	0	0	0
A05379-24	Susceptible	100	100	100	100	100	70	67	79
A05379-38	Susceptible	100	100	100	100	80	70	90	80
A05379-55	Susceptible	100	100	100	100	90	100	40	77
A05379-94	Susceptible	100	100	100	100	70	50	100	73
A05379-111	Susceptible	100	100	90	97	80	70	100	83
A05379-116	Susceptible	.	100	90	95	50	100	70	73
A05379-210	Susceptible	100	100	100	100	100	86	100	95
A05379-215	Susceptible	100	100	100	100	70	100	90	87
A05379-216	Susceptible	100	100	100	100	80	100	70	83

Table 2.2 Quantification and quality data derived from a NanoDrop 2000c spectrophotometer and TapeStation 2200 for RNA extracted, purified and sent to the National Center for Genomic Research (NCGR) for sequencing.

Code	Tube Name	Plants[a] in each tube	Volume	Concentration NanoDrop 2000c	260/280 NanoDrop	260/230 NanoDrop	Concentration TapeStation 2200	RNA Integrity Number equivalent (RIN[e])
Setb[b]	16-1	7,11,12,19,27	95uL	291 ng/µl	2.01	2.43	386 ng/µl	9.1
BC_4I	Immune	16,34,61	95uL	115 ng/µl	2.05	0.92	197 ng/µl	8.8
BC_4I[c]	Immune	63,90,100	95uL	288 ng/µl	2.10	2.07	364 ng/µl	9.3
BC_4I[d]	Immune	112,214,219	95uL	207 ng/µl	2.02	2.31	196 ng/µl	9.5
BC_4S	Susceptible	24,38,55	95uL	161 ng/µl	2.03	1.95	177 ng/µl	9.5
BC_4S	Susceptible	94,111,116	95uL	469 ng/µl	2.20	2.33	453 ng/µl	9.2
BC_4S	Susceptible	210,215,216	95uL	409 ng/µl	2.10	2.23	365 ng/µl	9.1

[a] "Plants" refers to the individual plant number from each phenotype group of family A05379. For example, Plant #63 is and individual plant in the immune phenotype group (A05379-63) that was pooled with plant #90 and plant #100 (Table 2.1). Each of these plants makes up the immune pool BC_4I and was diluted 1:2 to report the above data seen in the 4th row from the top of the table. All other plants follow the same scheme.

[b] This set of data is from a diluted sample. It was diluted 1:1 in Millipore purified H_20.

[c] This set of data is from a diluted sample. It was diluted 1:2 in Millipore purified H_20.

[d] This set of data is from a diluted sample. It was diluted 1:1 in Millipore purified H_20.

Protocol for Extracting RNA from Plant Tissue

Freshly harvested tissue (~100mg of apical meristem) was placed in a chilled coffee grinder chamber (Hamilton Beach Custom Grind™ Deluxe) with dry ice and ground to a fine powder. Ground sample was transferred to a 50mL polypropylene. For every 100mg of plant tissue 1.5mL of RNAzol® RT (Molecular Research Center Inc.) was added. Plant tissue was allowed to thaw in the RNAzol RT. Once thawed the solution was transferred to 15mL polypropylene tube. CTAB buffer stock (1% CTAB buffer stock was prepared containing 1M NaCl 0.05M Tris, pH 8.0, 0.01 M ethylenediaminetetraacetic acid (EDTA) and 2% Polyvinylpyrrolidone-40.5%. β-mercaptoethanol was added to the CTAB stock prior to use.) was added at about 40-50% of thawed solution and hand shaken for 15 seconds and then incubated at room temperature for 15 minutes. Samples were then centrifuge at 12,000 rcf for 15 minutes. Supernatant was pipetted to new 15mL tube being careful not to disturb the interphase. Equal volumes of Chloroform/Isoamyl (24:1) were added and incubated at room temperature for 5 minutes. While incubating, samples were shaken by hand repeatedly in order to gain a complete homogenate mixture and then centrifuged at 7500 rcf for 5 minutes. Supernatant was pipetted into a new 15mL polypropylene tube avoiding interphase. Forty percent of the volume was determined and that amount of 75% ethanol was added to the solution. Solution was then shake by hand and then incubated for 10 minutes at room temperature, with 2mL of solution added to a 2mL tube, while the remaining volume retained in a 15mL tube. The 2mL tubes were then centrifuged at 12,000 g for 8 minutes, with the supernatant then discarded. This was then repeated until all the solution from the 15mL tube had also been centrifuged and there was still a small but obvious white pellet in the bottom of the 2mL tubes. Any remaining supernatant was removed before washing the pellet twice with 500uL of 75% ethanol, with each washing involving spinning of the 2mL tubes for 1.5 minutes at 12,000g, with subsequent discard of supernatant. Pellet was spun in a mini-centrifuge to remove any residual ethanol left from the washes, and then allowed to dry on ice for 1 minute; filtered nuclease-free water (Thermo Scientific, Waltham, MA) was then added. The amount of water added depended on the size of the pellet; typically starting with 100uL and pipetting very gently until RNA became slightly gelatinous. Additional water was then added until the pellet was completed dissolved.

RNA concentration was measured on a NanoDrop 2000c (Thermo Scientific, Waltham, MA). If readings above 600ng/ul were observed, then the sample was diluted 1:10 in filtered nuclease-free water and measured again. Quality measurements were determined on a TapeStation 2200 (Agilent Technologies, Santa Clara, CA). Five ul of sample buffer was added to PCR tubes in addition to 1 uL of RNA. PCR tubes were then vortexed for 1 minute and briefly spin in a tabletop centrifuge, and then incubated for 3 minutes at 72°C and then in ice water for 2 minutes. A quick centrifugation was again conducted and product then placed in the TapeStation for quality measurement. Manufacturer directions were followed.

Agilent High Sensitivity RNA Assay

RNA samples were then assayed in the Agilent TapeStation 2200 as per protocols using High Sensitivity RNA tapes (Agilent Technologies, Santa Clera, CA).

National Center for Genome Resources (NCGR) – sequencing and analysis

RNA from 16-1 selfed seedlings was evaluated according to NCGR quality standards and converted to cDNA using CloneTech SMARTer PCR cDNA Synthesis (Takara Bio USA, Mountain View, CA). Multiple cDNA conversions were conducted, one each for small and medium size fragment selection and two-three for 3+kb larger size bins. Size selection from small (1-2kb), medium (2-3kb) and large (3+kb) bins was conducted using BluePippin (Sage Science, Beverly, MA). Medium and large bins required two selections each. Eight Pacific Biosciences single molecular, real-time (SMRT) cells were used for sequencing, two cells on 1-2kb, two cells on 2-3kb, and four cells on 3+kb. Isoform sequencing (Iso-Seq) application generates full-length cDNA sequences from the 5’ end of transcripts to the poly-A tail.

Sequence analysis was determined using the transcript landscape for *S. etuberosum* using PacBio’s IsoSeq analysis. Consensus sequences for each insert were generated in cases where the polymerase was able to pass over the insert multiple times. Reads identified as containing both the 5’ and 3’ primers as well as the polyA tail were labeled as full-length. All full-length reads were clustered to group suspected isoforms together, and these isoforms were processed with quiver polishing to create a higher accuracy consensus through alignments. A matrix file for peptide prediction using tomato, *Solanum lycopersicum*, was used as the reference. Annotation was provided using Pfam, Superfam and Tigrfam databases.

RNA from the nine immune genotypes and nine susceptible genotypes were pooled together into BC_4I and BC_4S pools for Illumina library prep. Library preps were run on one lane of Illumina HiSeq 2000. Illumina read counts were mapped to the *S. etuberosum* transcriptome generated from PacBio IsoSeq analysis. A Venn diagram was used to identify unique gene sets in immune and susceptible BC_4 pools. Functional annotation was determined using *S. lycopersicum* as the model organism.

Results

Quantification and quality assessment of RNA for next generation sequencing.

RNA was extracted in sets of pooled-tissue as indicated in Table 2.2, where RNA from 16-1 was extracted in a single set of five plants, while BC_4I and BC_4S samples were extracted in three sets of three plants each (Table 2.2). Initial quantification and quality evaluation of these samples was conducted on a NanoDrop 2000C spectrophotometer and shown in Table 2.2. Spectrophotometer 260/280 ratio for pure RNA is expected to be 2.0. Additional quality assessment was conducted using a TapeStation 2200 shown in Figures 2.1, 2.2, and 2.3. All samples meet this expectation except the first BCI extraction, 2.10, and the second and third BC_4S extractions, 2.20 and 2.10, respectively. Although these samples had 260/280 higher than expected the resulting RIN^e scores were still very good, above 9.0. Spectrophotometer 260/230 ratio for pure nucleic acid is expected 2.0-2.2. Three samples were outside this range including *S.etuberosum* 16-1 and the second BC_4S extractions both higher than 2.2, 2.43 and 2.33, respectively. The first BC_4I extraction had a 260/230 ratio of 0.92, much lower than expected. Interestingly the first BC_4I extraction also had the lowest RIN^e score of 8.8, the only RNA sample with a RIN^e below 9.0. Overall RIN^e values suggest extremely high quality RNA. RINe score takes into account the ratio of 28S and 18S peaks as well as any small molecular weight RNA fragments suggesting RNA degradation (Figures 2.1, 2.2, and 2.3). Interestingly, RIN scores generated by NCGR prior to library preparation match RIN^e scores reported here for four out of the seven samples. The remaining three samples were within 0.1 or 0.2. RNA concentrations were higher on the TapeStation 2200 compared to the spectrophotometer for four out of seven samples. The third BC_4I and second BC_4S extractions were approximately the same for RNA concentration between the TapeStation 2200 and the spectrophotometer, while the third BC_4S extraction was ~11% lower on the TapeStation 2200.

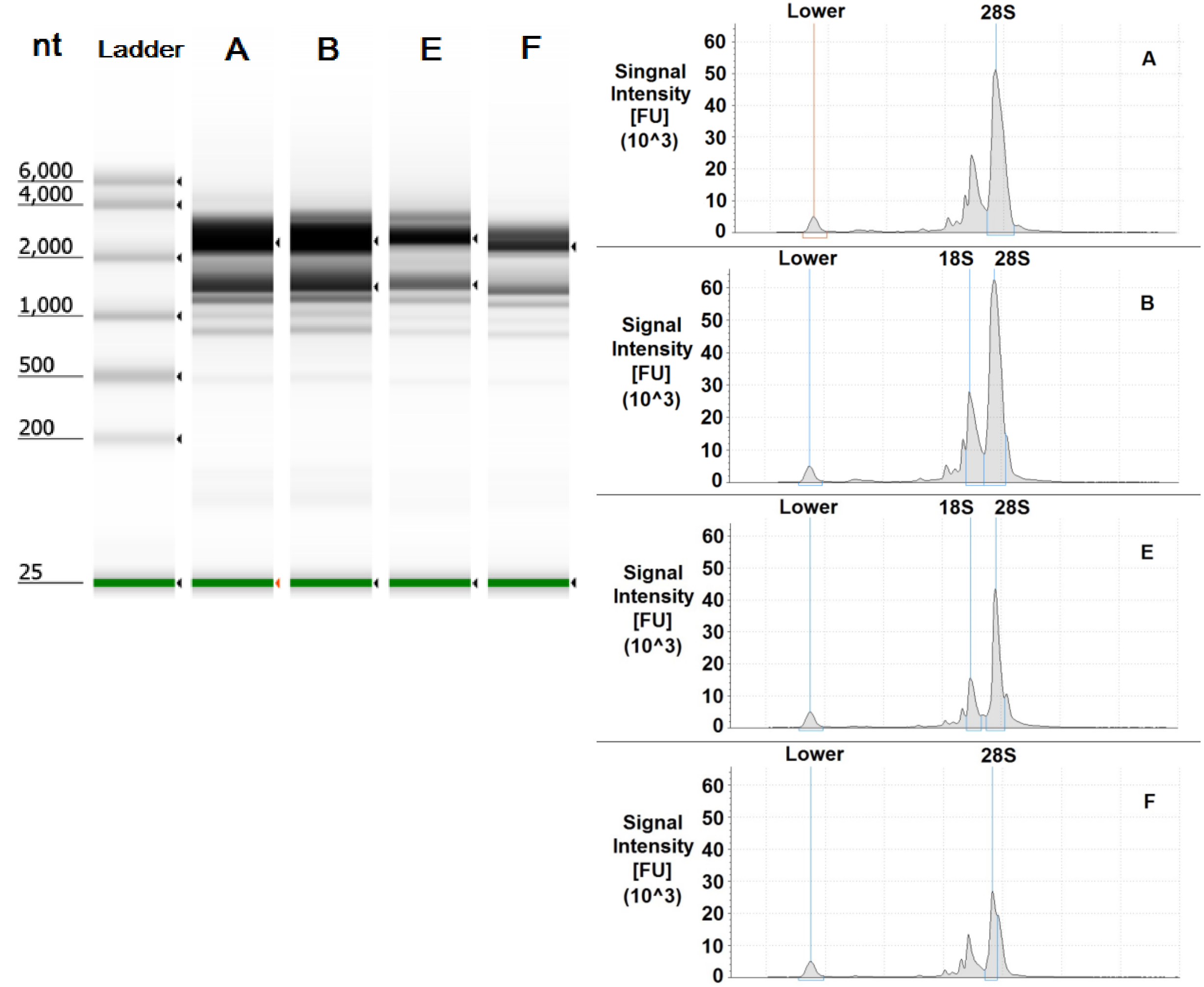

Figure 2.1 TapeStation 2200 gel image and electropherograms for *S. etuberosum*, 16-1, samples. Electropherograms are presented in the right column while the gel image is shown in the left column. Each electropherogram is labeled with an individual letter corresponding to a lane visible in the gel image. Peak intensity in each electropherogram is represented in fluorescent units (FU) to the 10^3 magnitude. “Lower” indicates a control peak provided with the TapeStation reagents and should be visible in all TapeStation 2200 electropherogram images. Number of nucleotides are shown in the far-left lane in the gel image with a description of “nt”. Each band in the gel ladder corresponds with a number of nucleotides seen in the nt lane. Sample loaded in lane A represents extracted RNA samples from five pooled 16-1 *Solanum etuberosum* plants used for Pac Bio sequencing (see table 2.2 first row). Electropherogram B (see also lane B on gel image) is a duplicate of electropherogram A and contains the same five pooled 16-1 RNA samples. Electropherogram E is a 1:1 (5µl Millipore purified H_20 + 5µl Sample) dilution of electropherogram B. Electropherogram F is a 1:1 (5µl Millipore purified H_20 + 5µl Sample) dilution of electropherogram A.

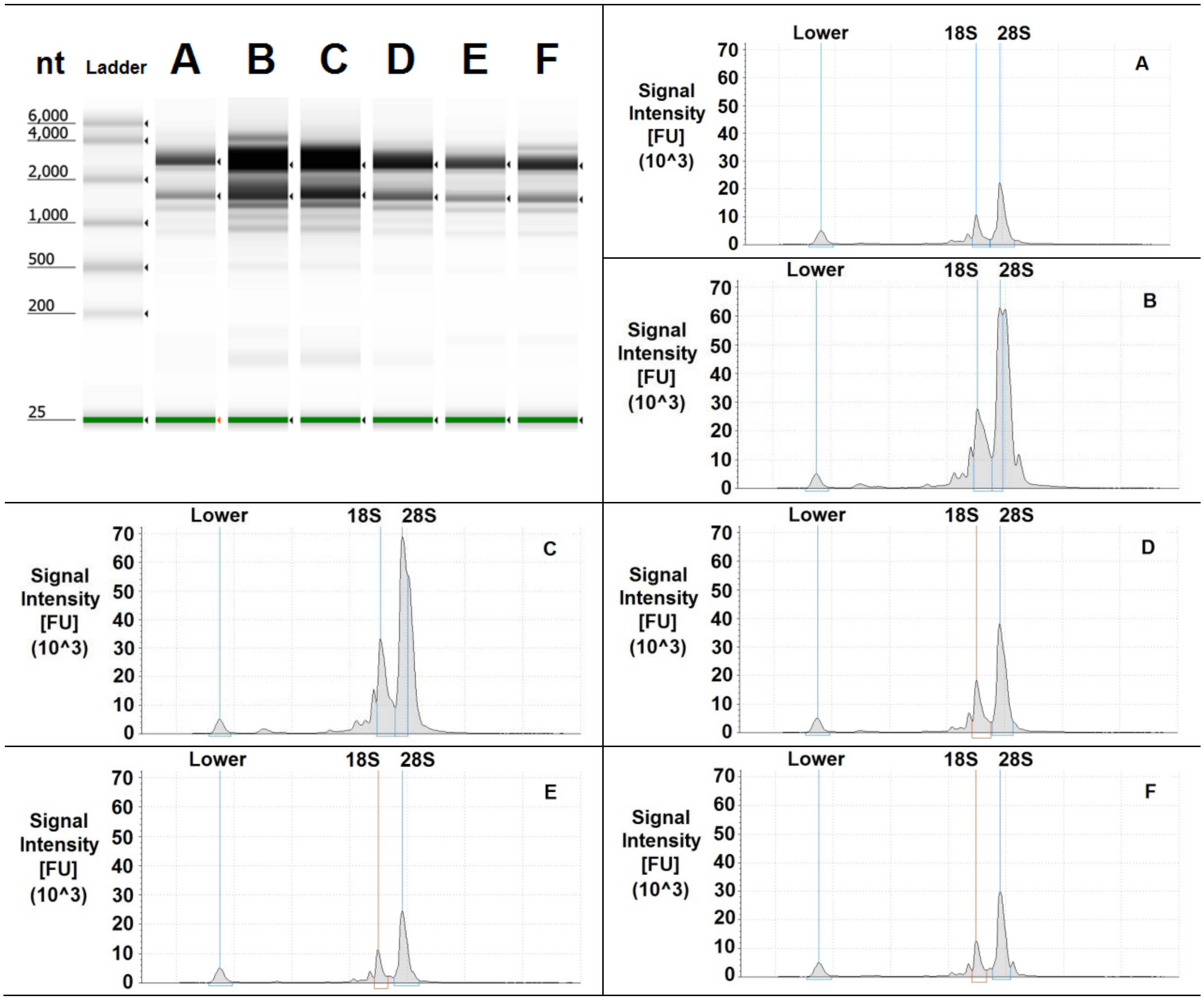

Figure 2.2 TapeStation 2200 gel image and electropherograms for immune (BC$_4$I) samples. Each electropherogram is labeled with an individual letter (A-F) corresponding to a lane visible in the gel image (top left). Peak intensity in each electropherogram is represented in fluorescent units (FU) to the 10^3 magnitude. “Lower” indicates a control peak provided with the TapeStation reagents and should be visible in all TapeStation 2200 electropherogram images. Number of nucleotides are shown in the far-left lane in the gel image with a description of “nt”. Each band in the gel ladder correlates with a number of nucleotides seen in the nt lane. Electropherogram A represents extracted RNA from three separate immune plants, each individually numbered 16, 34 and 61 then pooled to make one sample (see Table 2.2 row 2). Electropherogram B represents extracted RNA from a different set of immune plants. Each plant individually numbered 63, 90 and 100 respectively (see Table 2.2 row 3). Electropherogram C represents yet another set of three immune plants numbered 112, 214 and 219 respectively (see Table 2.2 row 4). Samples producing electropherogram F are a 1:1 dilution (5µl Millipore purified H$_2$0 + 5µl Sample) of the samples seen in electropherogram B. Samples producing electropherogram E are a 1:1 dilution (5µl Millipore purified H$_2$0 + 5µl Sample) of the samples seen in electropherogram A. Samples producing electropherogram D are a 1:1 dilution (5µl Millipore purified H$_2$0 + 5µl Sample) of the samples seen in electropherogram C.

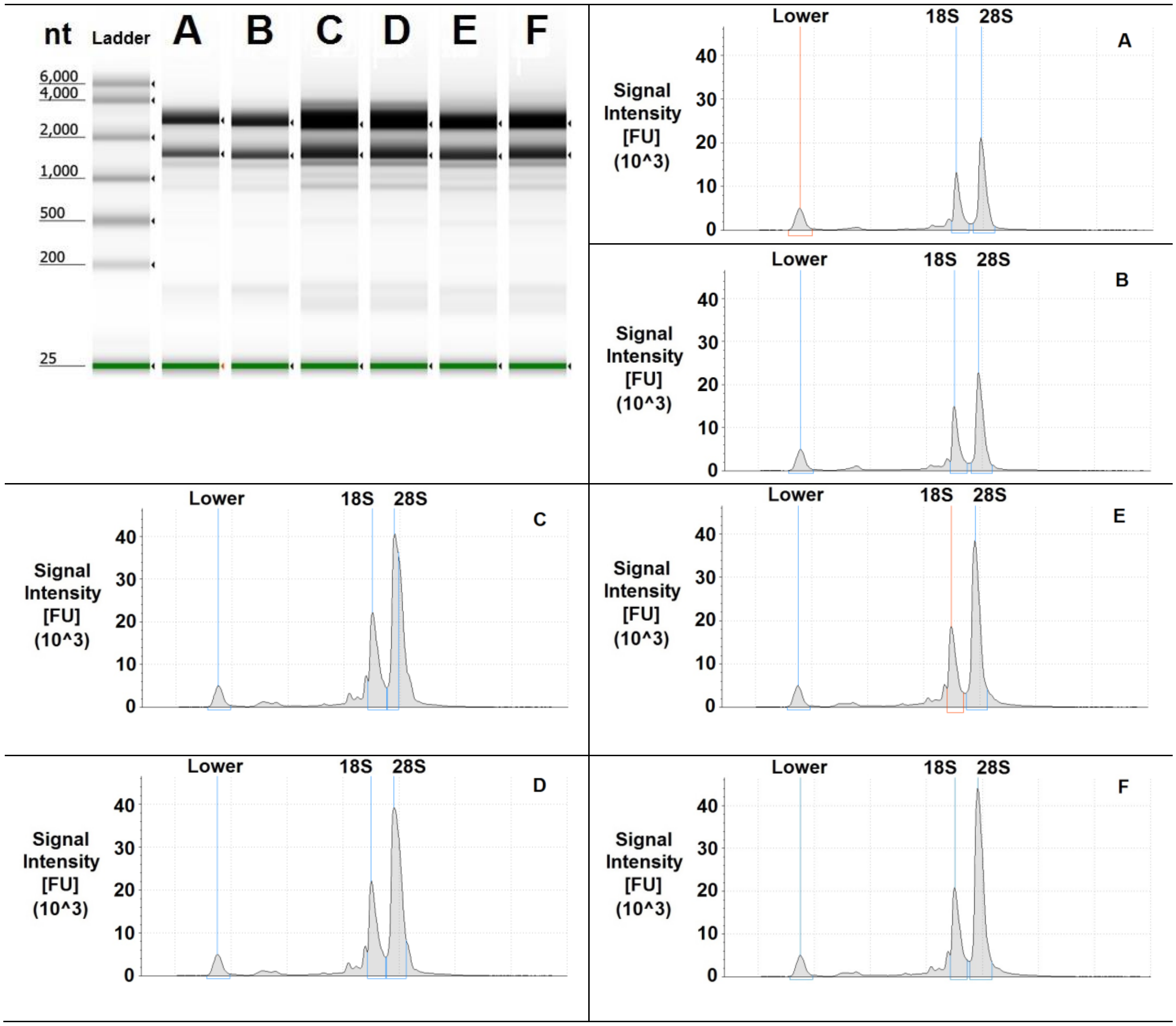

Figure 2.3 TapeStation 2200 gel image and electropherograms for susceptible (BC_4S) samples. Each electropherogram is labeled with an individual letter corresponding to a lane visible in the gel image. Peak intensity in each electropherogram is represented in fluorescent units (FU) to the 10^3 magnitude. “Lower” indicates a control peak provided with the TapeStation reagents and should be visible in all TapeStation 2200 electropherogram images. Number of nucleotides are shown in the far-left lane in the gel image with a description of “nt”. Each band in the gel ladder corresponds with a number of nucleotides seen in the nt lane. Electropherogram A represents extracted RNA from three separate susceptible plants, each individually numbered 24, 38 and 55 then pooled to make one sample (see Table 2.2 row 5). Electropherogram B represents extracted RNA from a different set of susceptible plants. Each plant individually numbered 94, 111 and 116 respectively (see Table 2.2 row 6). Electropherogram C represents yet another set of three susceptible plants numbered 210, 215 and 216 respectively (see Table 2.2 row 7). Electropherogram A is run in duplicate and this data is shown in electropherogram B. Electropherogram C is run in duplicate and this data is shown in electropherogram D. Electropherogram E is run in duplicate and this data is shown in electropherogram F.

Pacific Biosciences IsoSeq and Illumina dataset

The National Center for Genome Resources conducted Pacific Biosciences IsoSeq analysis on *S. etuberosum* 16-1 pooled sample of five self-pollinated plants. Sequence results are shown in Table 2.3. A total of 35,942 contigs were identified with a total length of 64,897,966 bp, representing putative gene transcripts from leaf tissue at the time of extraction. The mean contig length was 1,806 with a maximum contig of 7,196. Average GC content was 41.01%. Peptide prediction using ESTScan with a *S. lycopersicum* dataset identified 35,633 peptides. Protein models were identified using three database, PFAM, TIGRFAM, and SUPERFAM, identifying 33,625, 18,490, and 31,013 proteins, respectively. Alignment of *S. etuberosum* transcripts with UNIREF 100 database using BLASTN identified 35,552 protein encoding regions. Illumina sequencing generated 64,180,732 and 73,074,458 reads corresponding to BC_4I and BC_4S RNA pools, respectively. BC_4I and BC_4S reads were mapped to *S. etuberosum* transcripts and unique genes (not present in the other dataset) were identified in BC_4I and BC_4S, with 385 and 381 transcripts, respectively. Results of these transcripts aligned with UNIREF 100 are shown in Appendix A and B. All transcripts from both BC_4I and BC_4S are represented.

Table 2.3 *Solanum etuberosum* 16-1 selfed progeny RNA analyzed with Pacific Biosciences IsoSeq as reported by the National Center for Genome Resources.

Sequence Character	Sequence Character Quantification
Contigs	35,942
Maximum contig	7,196 bp
Mean contig	1,806 bp
Contig N50	1,888 bp
Contig N90	1,148 bp
Total contig length	64,897,966 bp
Assembly GC[a]	41.41%

[a] Percent Guanine/Cytosine in all contigs

Discussion

Solanum etuberosum RNA was extracted from five plants in a single extraction. Even though the original 16-1 somatic fusion plant has been lost, selfed seed (courtesy of Dr. Richard Novy) had been generated. Since *S. etuberosum* does not tuberize, and reproduces primarily through self pollination, the original 16-1 is expected to have been homozygous at most genetic loci therefore, a pool of five plants from self-pollination is expected to recover the majority alleles in the original 16-1 plant. Such an approach was demonstrated to tbe valid by Kelley at al. (2009) using CAPs markers, where no differences were observed in marker representation between 16-1 remnant DNA and pooled DNA of its selfed plants; albeit the number of selfed plants of 16-1 that were pooled was much higher at 65 plants relative to the five used in this study. Transcripts generated from Pacific Biosciences Iso-Seq should capture many of the expressed genes in the original 16-1 plant.

The 35,942 transcripts identified in this study is very close to the total number of protein-coding regions, 39,031, identified by the Potato Genome Sequencing Consortium (2011). The number of contigs shown here is most likely is an over estimate of the total number of genes expresses in leaf tissue at the time of extraction. The number of transcripts might be reduced by reducing highly similar sequences using software such as CD-HIT. There were also a large number of “uncharacterized” proteins (~1023) which provides little or no information regarding function. By removing these uncharacterized proteins the total number of transcripts will decrease. In addition to the uncharacterized proteins there are approximately 167 “predicted” proteins that also provides little information as to their functionality but does offer the organism from which close homologs were identified.

Illumina sequencing of PLRV immune plants and PLRV susceptible plants identified 381 and 385 unique *S. etuberosum* transcripts, respectively. The close similarity of these two numbers might be expected since any selection pressure for or against *S. etuberosum* DNA fragments in the A05379 BC family would have been uniformly distributed between PLRV resistance or susceptibility progeny, except for *S. etuberosum* genes linked to Rlr_{etb}. Therefore, *S. etuberosum* transcripts would be expected to be equally distributed between

PLRV immune and susceptible progeny. It is curious that over 380 transcripts were found to be unique to each nine plant pool, however as noted above, some of these transcripts could be reduced by removing highly similar sequences and uninformative transcript descriptions.

Only immune related RNA transcripts were investigated in this study. Further investigation of the susceptible transcripts might elucidate other informative transcripts. There could be additional resistance genes to other pathogens. For example, polyneuridine-aldehyde esterase was found among the susceptible transcripts. This enzyme is a part of the pathway of indole alkaloid biosynthesis. The indole alkaloids that result from this metabolic pathway are used by many plant species as a defense against herbivores and parasites (Pasquali et al 1992). Many of these transcripts could simply belong to general plant functions. Ubiquitin-conjugating protein and sometimes called the ubiquitin-carrier enzymes, perform the second step in the ubiquitination reaction that targets a protein for degradation via the proteasome (Nandi et al. 2006). Light harvesting chlorophyll a/b-binding protein also found among susceptible transcripts (LHCII), represents a system for balancing the excitation energy between the two photosystems (Mayfield and Taylor 1984). There are two photosystems in the photosynthesis pathway critical to the conversion of light energy into chemical energy that can later be released to fuel the organism's activities.

Inoculating the plants with PLRV or other pathogens before extracting nucleic acids could possibly show differences in gene expression more closely related to infection. Goriach et al (1996) showed the onset of resistance and the induction of resistance genes by inoculating wheat plants with powdery mildew. This was also accomplished in potatoes with the fungus *Botritys cinerea* (Berrocal-Lobo et al. 2002). Snakin-2 (StSN2) gene is developmentally expressed in tubers but not in roots, or stolons, and is locally up-regulated by wounding. Expression of this gene is up-regulated after infection of potato tubers with fungus *Botritys cinerea*.

The fourth backcross after the original somatic fusion might be expected to contain ~3.125% *S. etuberosum* DNA assuming unbiased inheritance of *S. etuberosum* chromosomes segments. Assuming the same number of protein encoding genes as the potato genome, 39,031, this works out to be ~1,219 coding regions. A surprisingly high number of transcripts are unique to immune and susceptible pools considering each pool is composed of nine plants and with the inherent genetic homozygosity of self compatible *S. etuberosum*. A venn diagram representing these common genes in addition to the unique coding regions to immune and susceptible is shown in figure 2.4.

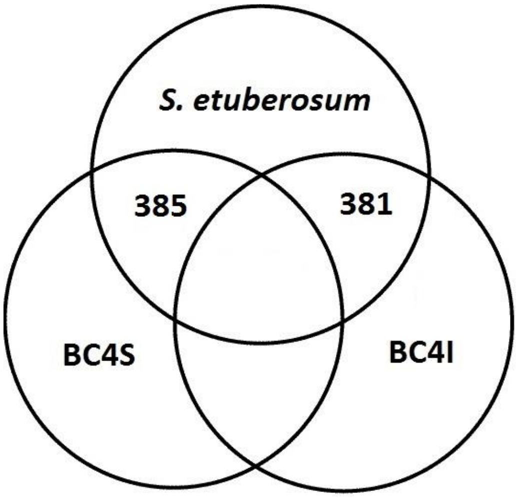

Figure 2.4 Venn diagram illustrating 381 unique transcripts to immune pool, 385 unique transcripts to susceptible pool.

Potato leafroll virus is a potentially devastating disease in *Solanum tuberosum*. Crop losses range in severity but pest control through the use of systemic insecticides has allowed potato growers to effectively manage the aphid vector of PLRV, and therefore the virus. However, PLRV will find a way to overcome these control measures and new methods of virus control will be needed. With the use of resistance genes from a wild species we have been able to obtain plants with phenotypes showing resistance to PLRV. Being able to acquire these plants and obtain putative R gene sequences is a positive gain.

A number of candidate genes were identified that should provide useful for research further down the road. Approximately 50 kinases were discovered in the UNIREF 100 database unique to BC_4 immune sequences. These show a wide variety of potential disease resistance genes (see appendix A). After further investigation of these kinase genes, MAP kinase c26812/f3p1/2052, and leucine-rich repeat receptor-like protein kinase c97673/f6p14/3359, were found to be potential candidate genes, and are discussed here. MAP kinase or mitogen activated protein kinases have been shown to be involved in signaling pathways activated by abiotic stresses including salt, touch and wounding (Sinha et al. 2011). Furthermore, MAP kinases have been shown to be involved in innate immunity due to pathogen detection (Rasmussen et al. 2012). Leucine-rich repeat receptor kinases (LRR-RKs) manage a wide variety of cellular processes. Among which are cellular division, cell proliferation, hormone perception and plant defense (Torii 2004). Albert et al (2015) were able to demonstrate LRR-RKs providing enhanced defense towards bacterial and fungal pathogens. Necrosis and ethylene-inducing peptide 1-like proteins (NLPs) are unique elicitors. These proteins are produced by multiple prokaryotic (bacterial) and eukaryotic (fungal, oomycete) plant pathogens. A leucine-rich repeat receptor protein (LRR-RP) RLP23 binds *in vivo* to a conserved 20-amino-acid fragment found in most NLPs (nlp20), thereby mediating immune activation in *Arabidopsis thaliana*. Stable, ectopic expression of RLP23 in potato (*Solanum tuberosum*) confers nlp20 pattern recognition and enhanced immunity to destructive oomycete and fungal plant pathogens, such as *Phytophthora infestans* and *Sclerotinia sclerotiorum* (Albert et al. 2015).

Further studies (gene association) need to be conducted in order to confirm the validity of these gene candidates. One possibility is to use a series of bacterial artificial chromosomes (BACs) containing genomic DNA inserts from *S. etuberosum* 16-1 selfed seedlings created by Dr. Joseph Kuhl. An alignment software program from DNAStar called Lasergene, or similar software, might be used to create a continuous segment of DNA that could possibly contain Rlr_{etb}. Using this we could locate new molecular markers which could lead us to new BACs or we could move on to exploring new BC_4s. The availability of a BAC library opens avenues for the further development of the linkage map shown in figure 1.1 and positional gene cloning. Using gene knockouts could also be used to determine a number of characteristics not investigated in this study. What is the actual factor necessary for PRLV to infect cells? By knocking out genes in the immune or susceptible plants we might elucidate the factor or factors necessary for PLRV to infect cells. Lee et al. (2002) noted 17-kDa protein (P17) is necessary for movement of PLRV within the plant once infection has already occurred. But what is necessary for the potato leafroll virus to infect cells in the first place? Does it have to do with the infection of the main vector green peach aphid? We do know the mechanisms of movement through the aphid vector and that it requires approximately 6 hours from initial uptake from an infected leaf into the aphid and back to the stylet for infection of additional plants (Kotzampigikis et al. 2010). But we still don't know the exact method used by the virus to enter cells. Perhaps this could be discovered through knockout plants. Knockout plants have been used previously to elucidate methods of resistance (Zhang et al. 2003; Piquerez et al. 2014; van der Hoorna and Kamounb 2008). There's also an "N" gene found in tobacco that confers N-mediated resistance response to tobacco mosaic virus in tomato (Whitham et al. 1996). This demonstrates the utility of using isolated resistance genes to protect crop plants from diseases. This is perhaps a possibility in *S. tuberosum* especially considering the tomato and potato are members of the same family, Solanaceae.

References

Albert I, Böhm H, Albert M, Feiler CE, Imkampe J, Niklas Wallmeroth N, Brancato C, Raaymakers TM, Oome S, Zhang H, Krol E, Grefen C, Gust AA, Chai J, Hedrich R, Van den Ackerveken G and Thorsten Nürnberger T (2015) An RLP23–SOBIR1–BAK1 complex mediates NLP-triggered immunity. Nature Plants 1: Article 15140

Austin S, Lojkowska E, Ehlenfeldt MK, Kelman A, Helgeson JP (1988) Fertile Intraspacific Somatic Hybrids of Solanum: A Novel Source of Resistance to Erwinia Soft Rot. Phytopathology 78: 1216-1220

Berrocal-Lobo M, Segura A, Moreno M, Lopez G, Garcia-Olmedo F and Molina A (2002) Snakin-2, an Antimicrobial Peptide from Potato Whose Gene Is Locally Induced by Wounding and Responds to Pathogen Infection. Plant Physiology 128: 951-961

Corsini DL, JJ Pavek, MW Martin, and CR Brown (1994) Potato germplasm with combined resistance to leafroll virus and viruses X and Y. American Potato Journal 71:377-359

Dong F, McGrath JM, Helgeson JP and Jiang J (2001) The genetic identity of alien chromosomes in potato breeding lines revealed by sequential GISH and FISH analyses using chromosome-specific cytogenetic DNA markers Genome 44: 729-734

Goriach J, Volrath S, Knauf-Beiter G, Hengy G, Beckhove U, Kogel KH, Oostendorp M, Staub T, Ward E, Kessmann H and Ryals J (1996) Benzothiadiazole, A Novel Class of Inducers of Systemic Acquired Resistance, Activates Gene Expression and Disease Resistance in Wheat. The Plant Cell 8: 629-643

Hermsen JGTH and Taylor LM (1979) Successful hybridization of non-tuberous Solanum etuberosumLind. and tuberbearing S. pinnatisectumDun. Euphytica 28: 1-7

Kasai K, Morikawa Y, Sorri VA, Valkonen JPT, Gebhardt C and Watanabe KN (2000) Development of SCAR markers to the PVY resistance gene Ryadg based on a common feature of plant disease resistance genes. Genome 43: 1-8

Kelley KB, Whitworth JL and Novy RG (2009) Mapping of the potato leafroll virus resistance gene, *Rlr*$_{etb}$, from *Solanum etuberosum* identifies interchromosomal translocations among its E-genome chromosomes 4 and 9 relative to the A-genome of *Solanum* L. sect. *Petota*. Molecular Breeding 23: 489-500

Kotzampigikis A, Hristova D and Tasheva-Terzieva E (2010) Virus-vector relationship between potato leafroll virus plrv and myzus persicae sulzer. Bulgarian Journal of Agricultural Science 16: 412-421

Kuhl JC, Novy RG, Whitworth JL, Dibble MS, Schneider S and Hall D (2016) Development of Molecular Markers Closely Linked to the Potato Leafroll Virus Resistance Gene, *Rlr*$_{etb}$, for use in Marker-Assisted Selection. American Journal of Potato Research 93: 203-212

Lee L, Palukaitis P and Gray S. (2002) Host-Dependent Requirement for the Potato leafroll virus 17-kDa Protein in Virus Movement. Molecular Plant-Microbe Ineractions 15 : 1086–1094

Mayfield SP and Taylor WC (1984) Carotenoid-deficient maize seedlings fail to accumulate light-harvesting chlorophyll a/b binding protein (LHCP) mRNA. European Journal of Biochemistry 144: 79- 84

Nandi D, Tahiliani P, Kumar A and Chandu D (2006) The ubiquitin-proteasome system. Journal of biosciences. 31: 137–55.

Novy RG and Helgeson JP (1994a) Somatic hybrids between *Solanum etuberosum* and diploid, tuber bearing solanum clones. Theoretical and Applied Genes 89: 775-782

Novy RG and Helgeson JP (1994b) resistance to potato virus Y in somatic hybrids between *Solanum etuberosum* and *S. tuberosum* x *S. berthaultii* hybrid. Theoretical and Applied Genes 89: 783-786

Novy RG, Gillen AM, and Whitworth JL (2007) Characterization of the expression and inheritance of potato leafroll virus (PLRV) and potato virus Y (PVY) resistance in three generations of germplasm derived from *Solanum etuberosum*. Theoretical and Applied Genetics 114: 1161-1172

Oerke EC (2006) Crop losses to pathogens. Journal of Agricultural Science 144: 31-4

Pasquali G, Goddijn OJM, de Waal A, Verpoorte R, Schilperoort RA, Hoge JHC and Memelink J (1992) Plant Molecular Biology 18: 1121-1131

Piquerez SJM, Harvey SE, Beynon JL and Ntoukakis V (2014) Improving crop disease resistance : lessons from research on Arabidopsis and tomato. www.frontiersin.org December 2014, Volume 5, Article 671

Potato Genome Sequencing Consortium (2011) Genome sequence and analysis of the tuber crop potato. Nature 475: 189-197

Rasmussen MW, Roux M, Petersen M and Mundy J (2012) MAP kinase cascades in Arabidopsis innate immunity. Frontiers in Plant Science volume 3 July 2012

Sinha AK, Jaggi M, Raghuram B and Tuteja N (2011) Mitogen-activated protein kinase signaling in plants under abiotic stress. Plant Signaling & Behavior 6: 196-203

Torii (2004) Leucine-Rich Repeat Receptor Kinases in Plants: Structure, Function, and Signal Transduction Pathways. International Review of Cytology 234: 1-46

van der Hoorna RAL and Kamounb S (2008) From Guard to Decoy: A New Model for Perception of Plant Pathogen Effectors. The Plant Cell 20: 2009–2017

Whitham S, McCormick S and Baker B (1996) The N gene of tobacco confers resistance to tobacco mosaic virus in transgenic tomato. Plant Biology 93: 8776-8781

Zhang Y, Tessaro MJ, Lassner M and Lia X (2003) Knockout Analysis of Arabidopsis Transcription Factors TGA2, TGA5, and TGA6 Reveals Their Redundant and Essential Roles in Systemic Acquired Resistance. Plant Cell 15: 2647-2653

Appendix A *Solanum etuberosum* genes expressed in the BC$_4$I pool but absent from the BC$_4$S pool as detected by Illumina sequencing, mapped to the *S. etuberosum* 16-1 reference database, and aligned to the UNIREF100 dataset.

c1816/f18p6/1124	proteasome subunit alpha type n 1 tax solanum lycopersicum score=511.53 evalue=2.40e-179;
c1816/f18p6/1124	proteasome subunit alpha type n 1 tax nicotiana benthamiana score=492.27 evalue=3.94e-172;
c1816/f18p6/1124	proteasome subunit alpha type n 2 tax populus trichocarpa score=460.30 evalue=1.93e-159;
c1816/f18p6/1124	proteasome subunit alpha type n 1 tax ricinus communis score=456.83 evalue=4.59e-158;
c1816/f18p6/1124	proteasome subunit alpha type n 1 tax vitis vinifera score=454.14 evalue=6.11e-157;
c2076/f3p3/1163	uncharacterized protein n 1 tax solanum lycopersicum score=672.16 evalue=0.00e+00;
c2076/f3p3/1163	ftsh-like protein n 1 tax solanum lycopersicum score=668.31 evalue=0.00e+00;
c2076/f3p3/1163	atp-dependent zinc metalloprotease ftsh chloroplastic n 1 tax nicotiana tabacum score=659.45 evalue=0.00e+00;
c2076/f3p3/1163	uncharacterized protein n 1 tax glycine max score=658.29 evalue=0.00e+00;
c2076/f3p3/1163	uncharacterized protein n 1 tax glycine max score=657.52 evalue=0.00e+00;
c2170/f5p28/1097	chlorophyll a-b binding protein 6a chloroplastic n 1 tax solanum lycopersicum score=462.23 evalue=8.83e-161;
c2170/f5p28/1097	uncharacterized protein n 1 tax solanum lycopersicum score=443.74 evalue=1.65e-153;
c2170/f5p28/1097	photosystem i light-harvesting chlorophyll a/b-binding protein n 1 tax nicotiana tabacum score=413.31 evalue=1.23e-141;
c2170/f5p28/1097	uncharacterized protein n 2 tax lotus japonicus score=402.52 evalue=2.32e-137;
c2170/f5p28/1097	uncharacterized protein n 1 tax glycine max score=400.98 evalue=1.12e-136;
c2384/f9p8/949	atp synthase subunit delta' mitochondrial n 1 tax ipomoea batatas score=372.09 evalue=5.97e-127;
c2384/f9p8/949	uncharacterized protein n 1 tax solanum lycopersicum score=358.22 evalue=1.92e-121;
c2384/f9p8/949	putative invasin/intimin protein (fragment) n 4 tax escherichia coli score=374.40 evalue=1.60e-117;
c2384/f9p8/949	atp synthase delta subunit 2 n 1 tax gossypium hirsutum score=319.70 evalue=2.38e-106;
c2384/f9p8/949	uncharacterized protein n 1 tax lotus japonicus score=318.55 evalue=6.59e-106;
c2811/f4p4/1161	uncharacterized protein n 2 tax magnoliophyta score=580.48 evalue=0.00e+00;
c2811/f4p4/1161	kda outer mitochondrial membrane protein porin-like protein n 1 tax solanum tuberosum score=556.98 evalue=0.00e+00;
c2811/f4p4/1161	voltage-dependent anion channel n 1 tax nicotiana tabacum score=513.84 evalue=2.04e-180;
c2811/f4p4/1161	mitochondrial outer membrane protein porin of 34 kda n 1 tax solanum tuberosum score=497.28 evalue=7.01e-174;
c2811/f4p4/1161	uncharacterized protein n 1 tax solanum lycopersicum score=496.89 evalue=1.16e-173;
c2998/f5p1/1377	d-type cyclin family 3 subgroup 3 n 1 tax solanum tuberosum score=593.96 evalue=0.00e+00;
c2998/f5p1/1377	cycd3 3 protein n 1 tax solanum lycopersicum score=580.10 evalue=0.00e+00;
c2998/f5p1/1377	uncharacterized protein n 1 tax solanum lycopersicum score=385.57 evalue=4.07e-128;

c2998/f5p1/1377	cyclin d3a (fragment) n 1 tax antirrhinum majus score=337.81 evalue=3.84e-109;
c2998/f5p1/1377	d3-type cyclin n 1 tax malus x domestica score=328.56 evalue=3.57e-105;
c3437/f1p1/1513	uncharacterized protein n 1 tax solanum lycopersicum score=617.46 evalue=0.00e+00;
c3437/f1p1/1513	uncharacterized protein n 1 tax vitis vinifera score=515.00 evalue=0.00e+00;
c3437/f1p1/1513	uncharacterized protein n 1 tax vitis vinifera score=175.25 evalue=0.00e+00;
c3437/f1p1/1513	peptidase s41 family protein n 1 tax arabidopsis thaliana score=474.94 evalue=1.17e-174;
c3437/f1p1/1513	peptidase s41 family protein n 1 tax arabidopsis thaliana score=166.78 evalue=1.17e-174;
c3655/f1p1/928	predicted protein n 2 tax populus trichocarpa score=202.99 evalue=1.27e-64;
c3655/f1p1/928	predicted protein n 2 tax populus trichocarpa score=70.86 evalue=1.27e-64;
c3655/f1p1/928	uncharacterized protein n 1 tax picea sitchensis score=199.52 evalue=3.66e-64;
c3655/f1p1/928	uncharacterized protein n 1 tax picea sitchensis score=72.79 evalue=3.66e-64;
c3655/f1p1/928	uncharacterized protein n 1 tax vitis vinifera score=199.13 evalue=6.02e-64;
c4052/f2p21/1422	proline-rich protein n 1 tax solanum tuberosum score=282.34 evalue=1.25e-85;
c4052/f2p21/1422	proline-rich protein n 1 tax nicotiana glauca score=222.25 evalue=2.46e-65;
c4052/f2p21/1422	uncharacterized protein n 1 tax solanum lycopersicum score=203.76 evalue=8.41e-59;
c4052/f2p21/1422	predicted protein (fragment) n 1 tax populus trichocarpa score=199.13 evalue=1.40e-56;
c4052/f2p21/1422	predicted protein (fragment) n 1 tax populus trichocarpa score=196.44 evalue=2.45e-55;
c4197/f1p5/1409	uncharacterized protein n 1 tax solanum lycopersicum score=806.59 evalue=0.00e+00;
c4197/f1p5/1409	atp-citrate synthase n 1 tax medicago truncatula score=758.06 evalue=0.00e+00;
c4197/f1p5/1409	atp-citrate synthase putative n 1 tax ricinus communis score=756.90 evalue=0.00e+00;
c4197/f1p5/1409	uncharacterized protein n 1 tax medicago truncatula score=754.98 evalue=0.00e+00;
c4197/f1p5/1409	uncharacterized protein n 1 tax vitis vinifera score=754.98 evalue=0.00e+00;
c5012/f1p0/1425	udp-sulfoquinovose synthase n 2 tax solanum lycopersicum score=880.94 evalue=0.00e+00;
c5012/f1p0/1425	predicted protein n 1 tax populus trichocarpa score=729.17 evalue=0.00e+00;
c5012/f1p0/1425	uncharacterized protein n 3 tax magnoliophyta score=729.17 evalue=0.00e+00;
c5012/f1p0/1425	uncharacterized protein n 1 tax glycine max score=722.62 evalue=0.00e+00;
c5012/f1p0/1425	uncharacterized protein n 1 tax glycine max score=719.92 evalue=0.00e+00;
c5403/f2p6/1455	uncharacterized protein n 1 tax solanum lycopersicum score=499.59 evalue=1.98e-172;
c5403/f2p6/1455	tuber-specific and sucrose-responsive element binding factor (fragment) n 1 tax solanum tuberosum score=472.24 evalue=5.44e-162;
c5403/f2p6/1455	myb-like protein n 1 tax nicotiana tabacum score=447.97 evalue=3.72e-152;
c5403/f2p6/1455	uncharacterized protein n 1 tax vitis vinifera score=338.96 evalue=8.91e-110;

c5403/f2p6/1455	uncharacterized protein n 1 tax vitis vinifera score=331.64 evalue=7.08e-107;
c5895/f4p2/1192	uncharacterized protein n 1 tax solanum lycopersicum score=419.08 evalue=3.99e-143;
c5895/f4p2/1192	uncharacterized protein n 1 tax solanum lycopersicum score=334.72 evalue=5.81e-110;
c5895/f4p2/1192	kda seed maturation protein n 1 tax elaeis guineensis score=330.10 evalue=2.24e-108;
c5895/f4p2/1192	uncharacterized protein n 1 tax vitis vinifera score=329.72 evalue=3.65e-108;
c5895/f4p2/1192	uncharacterized protein n 1 tax medicago truncatula score=328.18 evalue=1.85e-107;
c6089/f1p13/1385	uncharacterized protein n 1 tax solanum lycopersicum score=674.86 evalue=0.00e+00;
c6089/f1p13/1385	protein n 1 tax jatropha curcas score=585.49 evalue=0.00e+00;
c6089/f1p13/1385	auxin-induced protein 5ng4 putative n 1 tax ricinus communis score=583.95 evalue=0.00e+00;
c6089/f1p13/1385	uncharacterized protein n 1 tax vitis vinifera score=582.02 evalue=0.00e+00;
c6089/f1p13/1385	mtn21-like protein n 1 tax populus trichocarpa score=573.55 evalue=0.00e+00;
c6152/f7p3/1524	acyltransferase-like n 1 tax solanum melongena score=837.02 evalue=0.00e+00;
c6152/f7p3/1524	uncharacterized protein n 1 tax solanum lycopersicum score=828.93 evalue=0.00e+00;
c6152/f7p3/1524	protein n 1 tax nicotiana tabacum score=801.20 evalue=0.00e+00;
c6152/f7p3/1524	3'-n-debenzoyl-2'-deoxytaxol n-benzoyltransferase putative n 1 tax ricinus communis score=579.33 evalue=0.00e+00;
c6152/f7p3/1524	protein n 1 tax populus trichocarpa score=577.40 evalue=0.00e+00;
c6269/f2p4/979	allene oxide cyclase n 2 tax solanum score=380.56 evalue=2.49e-129;
c6269/f2p4/979	allene oxide cyclase n 1 tax nicotiana tabacum score=368.24 evalue=1.59e-124;
c6269/f2p4/979	allene oxide cyclase n 1 tax hyoscyamus niger score=363.23 evalue=1.85e-122;
c6269/f2p4/979	allene oxide cyclase n 2 tax solanum lycopersicum score=359.38 evalue=4.18e-121;
c6269/f2p4/979	b2zfd7 aoc n 2 tax solanaceae b2zfd7_pethy score=354.37 evalue=4.65e-119;
c6500/f1p5/1040	b2-type cyclin dependent kinase n 1 tax solanum lycopersicum score=559.30 evalue=0.00e+00;
c6500/f1p5/1040	cdk putative n 1 tax ricinus communis score=503.44 evalue=2.66e-176;
c6500/f1p5/1040	uncharacterized protein n 1 tax lotus japonicus score=500.75 evalue=2.41e-175;
c6500/f1p5/1040	cyclin-dependent kinase n 1 tax camellia sinensisi score=497.28 evalue=5.81e-174;
c6500/f1p5/1040	cyclin-dependent kinase b n 1 tax populus tomentosa score=496.12 evalue=1.22e-173;
c6938/f2p6/1322	sgt1 n 2 tax solanum tuberosum score=681.40 evalue=0.00e+00;
c6938/f2p6/1322	uncharacterized protein n 1 tax solanum lycopersicum score=676.01 evalue=0.00e+00;
c6938/f2p6/1322	sgt1 n 1 tax nicotiana benthamiana score=641.34 evalue=0.00e+00;
c6938/f2p6/1322	sgt1 n 1 tax nicotiana attenuata score=640.57 evalue=0.00e+00;
c6938/f2p6/1322	sgt1 n 2 tax nicotiana benthamiana score=634.79 evalue=0.00e+00;

c7083/f7p2/1279	uncharacterized protein n 2 tax solanum lycopersicum score=679.09 evalue=0.00e+00;
c7083/f7p2/1279	geranylgeranyl pyrophosphate synthase 3 n 1 tax solanum pennellii score=677.94 evalue=0.00e+00;
c7083/f7p2/1279	chloroplast geranylgeranyl diphosphate synthase 3 n 1 tax nicotiana tabacum score=603.21 evalue=0.00e+00;
c7083/f7p2/1279	geranyl diphosphate synthase large subunit n 1 tax antirrhinum majus score=519.24 evalue=2.61e-180;
c7083/f7p2/1279	geranylgeranyl diphosphate synthase n 1 tax ipomoea batatas score=516.92 evalue=1.38e-179;
c7237/f1p5/1235	uncharacterized protein n 1 tax solanum lycopersicum score=372.47 evalue=1.55e-125;
c7237/f1p5/1235	rac-like gtpase 1 n 1 tax nicotiana tabacum score=368.62 evalue=4.01e-124;
c7237/f1p5/1235	rac/rop-like small gtpase n 1 tax scoparia dulcis score=366.70 evalue=2.31e-123;
c7237/f1p5/1235	ntgp2 n 1 tax nicotiana tabacum score=365.93 evalue=4.89e-123;
c7237/f1p5/1235	gtp-binding rop/rac gtpase n 1 tax petunia integrifolia subsp. inflata score=365.54 evalue=6.85e-123;
c7305/f1p1/1522	uncharacterized protein n 1 tax solanum lycopersicum score=803.51 evalue=0.00e+00;
c7305/f1p1/1522	predicted protein n 1 tax populus trichocarpa b9iel3_poptr score=746.12 evalue=0.00e+00;
c7305/f1p1/1522	mannose-1-phosphate guanyltransferase putative n 1 tax ricinus communis b9r8y9_ricco score=745.35 evalue=0.00e+00;
c7305/f1p1/1522	putative uncharacterized protein n 1 tax vitis vinifera d7shy4_vitvi score=730.71 evalue=0.00e+00;
c7305/f1p1/1522	putative gdp-mannose pyrophosphorylase n 2 tax linum usitatissimum q1hga9_linus score=721.08 evalue=0.00e+00;
c7465/f1p10/1226	uncharacterized protein n 1 tax solanum lycopersicum k4b075_sollc score=631.33 evalue=0.00e+00;
c7465/f1p10/1226	putative uncharacterized protein n 1 tax vitis vinifera e0cux2_vitvi score=565.07 evalue=0.00e+00;
c7465/f1p10/1226	prolyl-trna synthetase putative n 1 tax ricinus communis b9riu3_ricco score=556.98 evalue=0.00e+00;
c7465/f1p10/1226	predicted protein (fragment) n 1 tax populus trichocarpa b9mwz9_poptr score=551.59 evalue=0.00e+00;
c7465/f1p10/1226	uncharacterized protein n 1 tax glycine max i1l332_soybn score=552.36 evalue=0.00e+00;
c7665/f1p0/1466	uncharacterized protein n 1 tax solanum lycopersicum k4d9m0_sollc score=739.57 evalue=0.00e+00;
c7665/f1p0/1466	putative uncharacterized protein n 1 tax vitis vinifera f6gv27_vitvi score=622.08 evalue=0.00e+00;
c7665/f1p0/1466	inner membrane protein n 1 tax populus trichocarpa b9gjq3_poptr score=608.22 evalue=0.00e+00;
c7665/f1p0/1466	uncharacterized protein n 1 tax glycine max i1lk36_soybn score=588.19 evalue=0.00e+00;
c7665/f1p0/1466	inner membrane protein ppf-1 chloroplast putative n 1 tax ricinus communis b9sze3_ricco score=583.18 evalue=0.00e+00;
c8270/f8p11/1031	uncharacterized protein n 1 tax solanum lycopersicum k4db71_sollc score=493.43 evalue=2.39e-173;
c8270/f8p11/1031	uncharacterized protein n 1 tax solanum lycopersicum k4ch72_sollc score=484.57 evalue=7.12e-170;
c8270/f8p11/1031	ribosomal protein l8 n 1 tax solanum lycopersicum k4cxi9_sollc score=482.64 evalue=4.36e-169;
c8270/f8p11/1031	ribosomal protein l2-like n 1 tax solanum tuberosum q2xtd6_soltu score=482.64 evalue=4.52e-169;
c8270/f8p11/1031	ribosomal protein l8 n 1 tax solanum lycopersicum rl8_sollc score=482.26 evalue=6.68e-169;
c8408/f4p1/1329	uncharacterized protein n 1 tax solanum lycopersicum k4b1c4_sollc score=711.84 evalue=0.00e+00;

c8408/f4p1/1329	putative uncharacterized protein n 1 tax vitis vinifera f6i4v4_vitvi score=543.50 evalue=0.00e+00;
c8408/f4p1/1329	zinc finger protein putative n 1 tax ricinus communis b9rfn2_ricco score=536.95 evalue=0.00e+00;
c8408/f4p1/1329	gdsl esterase/lipase n 1 tax medicago truncatula g7kwh3_medtr score=507.68 evalue=9.17e-176;
c8408/f4p1/1329	predicted protein n 1 tax populus trichocarpa b9n445_poptr score=503.44 evalue=1.71e-174;
c8440/f1p5/1025	uncharacterized protein n 1 tax solanum lycopersicum k4dh64_sollc score=513.84 evalue=5.23e-178;
c8440/f1p5/1025	cysteine protease n 1 tax solanum lycopersicum q18lc4_sollc score=513.84 evalue=5.96e-178;
c8440/f1p5/1025	vascular processing enzyme-3 n 1 tax capsicum annuum b2czk0_capan score=489.19 evalue=2.77e-168;
c8440/f1p5/1025	vacuolar processing enzyme-3 n 1 tax nicotiana tabacum q852t0_tobac score=481.49 evalue=2.44e-165;
c8440/f1p5/1025	vacuolar processing enzyme-1b n 1 tax nicotiana tabacum q852t2_tobac score=441.43 evalue=2.18e-149;
c8491/f1p0/746	uncharacterized protein n 1 tax solanum lycopersicum k4c219_sollc score=380.18 evalue=2.48e-131;
c8491/f1p0/746	putative uncharacterized protein n 1 tax vitis vinifera f6h713_vitvi score=319.32 evalue=2.35e-107;
c8491/f1p0/746	prefoldin subunit putative n 1 tax ricinus communis b9rzt0_ricco score=312.00 evalue=1.44e-104;
c8491/f1p0/746	prefoldin subunit 3 n 1 tax zea mays b6tke7_maize score=309.30 evalue=2.28e-103;
c8491/f1p0/746	probable prefoldin subunit 3 n 2 tax arabidopsis thaliana pfd3_arath score=308.14 evalue=7.36e-103;
c8711/f7p6/1549	uncharacterized protein n 1 tax solanum lycopersicum k4cbv8_sollc score=678.32 evalue=0.00e+00;
c8711/f7p6/1549	uncharacterized protein n 1 tax solanum lycopersicum k4cbv7_sollc score=638.26 evalue=0.00e+00;
c8711/f7p6/1549	spermidine hydroxycinnamoyl transferase n 1 tax nicotiana attenuata g9htf5_nicat score=380.18 evalue=2.02e-123;
c8711/f7p6/1549	uncharacterized protein n 1 tax solanum lycopersicum k4dhf0_sollc score=353.21 evalue=4.64e-113;
c8711/f7p6/1549	putative spermidine hydroxycinnamoyl transferase n 1 tax nicotiana attenuata g9htf6_nicat score=352.83 evalue=7.68e-113;
c8882/f1p4/912	chlorophyll a-b binding protein 3c chloroplastic n 1 tax solanum lycopersicum cb2g_sollc score=483.80 evalue=4.99e-170;
c8882/f1p4/912	chlorophyll a-b binding protein 40 chloroplastic n 1 tax nicotiana tabacum cb24_tobac score=481.87 evalue=2.43e-169;
c8882/f1p4/912	light harvesting chlorophyll a/b-binding protein n 1 tax nicotiana sylvestris o64447_nicsy score=481.87 evalue=2.68e-169;
c8882/f1p4/912	uncharacterized protein n 1 tax solanum lycopersicum k4be01_sollc score=481.49 evalue=3.31e-169;
c8882/f1p4/912	light harvesting chlorophyll a/b-binding protein n 1 tax nicotiana sylvestris o64446_nicsy score=481.49 evalue=3.57e-169;
c9556/f2p1/1383	uncharacterized protein n 1 tax solanum lycopersicum k4b344_sollc score=694.89 evalue=0.00e+00;
c9556/f2p1/1383	sucrose non-fermenting 1-related protein kinase 2 family member n 1 tax solanum tuberosum j9un52_soltu score=693.73 evalue=0.00e+00;
c9556/f2p1/1383	serine/threonine-protein kinase sapk10 putative n 1 tax ricinus communis b9s768_ricco score=652.51 evalue=0.00e+00;
c9556/f2p1/1383	uncharacterized protein n 1 tax glycine max i1nd33_soybn score=647.12 evalue=0.00e+00;
c9556/f2p1/1383	predicted protein n 1 tax populus trichocarpa b9n4u7_poptr score=645.20 evalue=0.00e+00;
c9562/f1p2/1424	uncharacterized protein n 2 tax solanum lycopersicum k4d3y9_sollc score=799.27 evalue=0.00e+00;
c9562/f1p2/1424	enolase n 1 tax solanum lycopersicum eno_sollc score=778.47 evalue=0.00e+00;

c9562/f1p2/1424	enolase n 1 tax nicotiana tabacum c5j0g6_tobac score=772.70 evalue=0.00e+00;
c9562/f1p2/1424	acetyltransferase family protein n 1 tax shigella flexneri 2850-71 i6bgq2_shifl score=781.17 evalue=0.00e+00;
c9562/f1p2/1424	los2 n 2 tax capsella bursa-pastoris q6q4z3_capbu score=744.19 evalue=0.00e+00;
c9645/f1p0/1417	uncharacterized protein n 1 tax solanum lycopersicum k4bld5_sollc score=581.25 evalue=0.00e+00;
c9645/f1p0/1417	putative uncharacterized protein n 1 tax vitis vinifera d7sid0_vitvi score=416.77 evalue=3.84e-140;
c9645/f1p0/1417	uncharacterized protein n 1 tax glycine max i1kcs1_soybn score=407.91 evalue=8.40e-137;
c9645/f1p0/1417	uncharacterized protein n 1 tax glycine max k7kvy0_soybn score=407.53 evalue=1.29e-136;
c9645/f1p0/1417	putative uncharacterized protein n 1 tax glycine max c6tk19_soybn score=402.90 evalue=9.04e-135;
c11756/f5p1/991	uncharacterized protein n 3 tax solanum k4bv76_sollc score=384.80 evalue=7.50e-132;
c11756/f5p1/991	ubiquitin-conjugating enzyme n 1 tax capsicum annuum q06ac9_capan score=374.01 evalue=1.26e-127;
c11756/f5p1/991	putative uncharacterized protein n 2 tax vitis vinifera f6hqj9_vitvi score=358.99 evalue=2.69e-121;
c11756/f5p1/991	uncharacterized protein n 1 tax solanum lycopersicum k4dgx4_sollc score=357.84 evalue=2.75e-121;
c11756/f5p1/991	ubiquitin-conjugating enzyme m putative n 1 tax ricinus communis b9sgh9_ricco score=357.07 evalue=5.18e-121;
c11907/f2p0/1177	uncharacterized protein n 1 tax solanum lycopersicum k4d7y7_sollc score=411.76 evalue=1.98e-140;
c11907/f2p0/1177	predicted protein (fragment) n 1 tax populus trichocarpa b9gmw6_poptr score=295.43 evalue=3.91e-95;
c11907/f2p0/1177	putative uncharacterized protein n 1 tax vitis vinifera f6hj85_vitvi score=288.89 evalue=3.45e-92;
c11907/f2p0/1177	putative uncharacterized protein n 1 tax ricinus communis b9rg32_ricco score=285.42 evalue=8.62e-91;
c11907/f2p0/1177	f27f5.5 n 2 tax arabidopsis thaliana q9mal1_arath score=278.49 evalue=7.06e-88;
c13733/f1p1/1390	uncharacterized protein n 1 tax solanum lycopersicum k4cul8_sollc score=717.23 evalue=0.00e+00;
c13733/f1p1/1390	putative uncharacterized protein n 1 tax vitis vinifera f6gxm3_vitvi score=515.00 evalue=9.34e-178;
c13733/f1p1/1390	magnesium transporter n 1 tax populus trichocarpa b9hke1_poptr score=502.29 evalue=7.85e-173;
c13733/f1p1/1390	rna splicing protein mrs2 mitochondrial putative n 1 tax ricinus communis b9s4t3_ricco score=498.82 evalue=1.78e-171;
c13733/f1p1/1390	uncharacterized protein n 1 tax glycine max i1nia1_soybn score=498.82 evalue=2.62e-171;
c14350/f1p4/1099	fructose-bisphosphate aldolase n 1 tax solanum tuberosum q38hv4_soltu score=590.11 evalue=0.00e+00;
c14350/f1p4/1099	fructose-bisphosphate aldolase n 1 tax solanum lycopersicum k4d3e4_sollc score=590.11 evalue=0.00e+00;
c14350/f1p4/1099	fructose-bisphosphate aldolase n 1 tax solanum tuberosum q308a5_soltu score=589.34 evalue=0.00e+00;
c14350/f1p4/1099	fructose-bisphosphate aldolase n 1 tax solanum lycopersicum k4cqv5_sollc score=559.30 evalue=0.00e+00;
c14350/f1p4/1099	fructose-bisphosphate aldolase n 1 tax solanum tuberosum q2pyx3_soltu score=557.75 evalue=0.00e+00;
c14515/f2p1/1461	uncharacterized protein n 1 tax solanum lycopersicum k4c8k0_sollc score=513.46 evalue=2.48e-177;
c14515/f2p1/1461	putative uncharacterized protein n 1 tax solanum lycopersicum q0kih9_sollc score=453.37 evalue=1.63e-154;
c14515/f2p1/1461	uncharacterized protein n 1 tax solanum lycopersicum k4bkm2_sollc score=327.79 evalue=7.67e-105;

c14515/f2p1/1461	putative uncharacterized protein n 1 tax vitis vinifera f6gsx8_vitvi score=224.94 evalue=3.17e-65;
c14515/f2p1/1461	putative anti-virus transcriptional factor n 1 tax vitis pseudoreticulata b6va58_9rosi score=223.02 evalue=1.82e-64;
c14664/f3p3/1599	uncharacterized protein n 1 tax solanum lycopersicum k4cet1_sollc score=373.24 evalue=6.63e-122;
c14664/f3p3/1599	g-strand specific single-stranded telomere-binding protein 2 n 1 tax nicotiana tabacum e2f3s9_tobac score=346.28 evalue=1.57e-111;
c14664/f3p3/1599	g-strand specific single-stranded telomere-binding protein 3 n 1 tax nicotiana tabacum e2f3t0_tobac score=331.26 evalue=1.19e-105;
c14664/f3p3/1599	g-strand specific single-stranded telomere-binding protein 1 n 1 tax nicotiana tabacum e2f3s8_tobac score=322.01 evalue=4.48e-102;
c14664/f3p3/1599	uncharacterized protein n 1 tax glycine max i1lxp8_soybn score=281.57 evalue=2.27e-86;
c14757/f1p4/1411	uncharacterized protein n 1 tax solanum lycopersicum q40131_sollc score=484.18 evalue=8.22e-173;
c14757/f1p4/1411	uncharacterized protein n 1 tax solanum lycopersicum q40131_sollc score=151.37 evalue=8.22e-173;
c14757/f1p4/1411	2-oxoglutarate-dependent dioxygenase n 1 tax solanum chacoense q9zsh4_solch score=462.61 evalue=1.39e-169;
c14757/f1p4/1411	2-oxoglutarate-dependent dioxygenase n 1 tax solanum chacoense q9zsh4_solch score=162.16 evalue=1.39e-169;
c14757/f1p4/1411	dioxygenase n 1 tax solanum melongena q43640_solme score=417.93 evalue=8.07e-156;
c14798/f1p1/1487	uncharacterized protein n 1 tax solanum lycopersicum k4cw92_sollc score=748.43 evalue=0.00e+00;
c14798/f1p1/1487	putative uncharacterized protein n 1 tax vitis vinifera d7szn5_vitvi score=650.59 evalue=0.00e+00;
c14798/f1p1/1487	predicted protein n 1 tax populus trichocarpa b9hku6_poptr score=639.03 evalue=0.00e+00;
c14798/f1p1/1487	predicted protein n 1 tax populus trichocarpa b9hst8_poptr score=626.71 evalue=0.00e+00;
c14798/f1p1/1487	pre-mrna-splicing factor putative n 1 tax ricinus communis b9squ0_ricco score=626.32 evalue=0.00e+00;
c15321/f1p1/1057	uncharacterized protein n 1 tax solanum lycopersicum k4bvu1_sollc score=522.32 evalue=2.67e-180;
c15321/f1p1/1057	ps60 protein n 1 tax nicotiana tabacum q40473_tobac score=486.49 evalue=3.66e-166;
c15321/f1p1/1057	pectinesterase (fragment) n 1 tax solanum lycopersicum o04870_sollc score=481.49 evalue=1.05e-164;
c15321/f1p1/1057	multicopper oxidase n 1 tax cucumis melo subsp. melo e5gcd6_cucme score=422.55 evalue=3.24e-141;
c15321/f1p1/1057	multicopper oxidase putative n 1 tax ricinus communis b9r8i7_ricco score=420.24 evalue=2.93e-140;
c15570/f1p0/1562	uncharacterized protein n 1 tax solanum lycopersicum k4b202_sollc score=375.94 evalue=3.73e-165;
c15570/f1p0/1562	uncharacterized protein n 1 tax solanum lycopersicum k4b202_sollc score=234.19 evalue=3.73e-165;
c15570/f1p0/1562	putative uncharacterized protein n 1 tax vitis vinifera f6h966_vitvi score=326.25 evalue=1.14e-132;
c15570/f1p0/1562	putative uncharacterized protein n 1 tax vitis vinifera f6h966_vitvi score=176.02 evalue=1.14e-132;
c15570/f1p0/1562	uncharacterized protein n 1 tax glycine max i1kuk8_soybn score=323.17 evalue=9.66e-129;
c15929/f2p1/1358	uncharacterized protein n 1 tax solanum lycopersicum k4ca21_sollc score=441.43 evalue=4.17e-151;
c15929/f2p1/1358	uncharacterized protein n 1 tax solanum lycopersicum k4c367_sollc score=240.35 evalue=3.92e-73;
c15929/f2p1/1358	predicted protein n 1 tax populus trichocarpa a9paj2_poptr score=185.65 evalue=1.13e-52;
c15929/f2p1/1358	putative uncharacterized protein n 2 tax populus trichocarpa a9pe12_poptr score=184.50 evalue=2.64e-52;

c15929/f2p1/1358	protein binding protein putative n 1 tax ricinus communis b9s385_ricco score=171.40 evalue=4.50e-47;
c16552/f2p9/1377	uncharacterized protein n 1 tax solanum lycopersicum k4bhr9_sollc score=650.20 evalue=0.00e+00;
c16552/f2p9/1377	uncharacterized protein n 3 tax solanum k4d4e6_sollc score=648.66 evalue=0.00e+00;
c16552/f2p9/1377	uncharacterized protein n 3 tax fabaceae i1jy56_soybn score=648.28 evalue=0.00e+00;
c16552/f2p9/1377	actin n 13 tax core eudicotyledons b8y645_helan score=647.89 evalue=0.00e+00;
c16552/f2p9/1377	actin n 1 tax stevia rebaudiana q8h6a3_stere score=647.89 evalue=0.00e+00;
c16928/f1p5/1154	uncharacterized protein n 2 tax solanum k4b413_sollc score=528.09 evalue=0.00e+00;
c16928/f1p5/1154	ascorbate peroxidase n 1 tax capsicum frutescens j9z324_capfr score=526.94 evalue=0.00e+00;
c16928/f1p5/1154	ascorbate peroxidase n 1 tax capsicum annuum q8w4v7_capan score=523.86 evalue=0.00e+00;
c16928/f1p5/1154	cytosolic ascorbate peroxidase isoform 4 n 1 tax solanum lycopersicum q09y77_sollc score=519.62 evalue=0.00e+00;
c16928/f1p5/1154	papx (fragment) n 1 tax solanum nigrum c5j0h7_solni score=467.62 evalue=1.99e-162;
c17087/f1p4/883	uncharacterized protein n 1 tax solanum lycopersicum k4bi65_sollc score=451.06 evalue=6.67e-158;
c17087/f1p4/883	chloroplast thylakoid lumenal 17.4 kda protein n 1 tax solanum tuberosum k7vkb9_soltu score=435.65 evalue=6.34e-152;
c17087/f1p4/883	thylakoid lumenal 17.4 kda protein chloroplast putative n 1 tax ricinus communis b9sjt2_ricco score=347.82 evalue=3.04e-117;
c17087/f1p4/883	putative uncharacterized protein n 1 tax vitis vinifera e0cv77_vitvi score=346.28 evalue=1.17e-116;
c17087/f1p4/883	predicted protein n 1 tax populus trichocarpa b9i1y5_poptr score=338.58 evalue=2.13e-113;
c18537/f3p3/1283	uncharacterized protein n 1 tax solanum lycopersicum k4c874_sollc score=661.76 evalue=0.00e+00;
c18537/f3p3/1283	learca1 protein n 1 tax solanum lycopersicum q9sxr9_sollc score=660.60 evalue=0.00e+00;
c18537/f3p3/1283	uncharacterized protein n 1 tax solanum lycopersicum k4bm53_sollc score=632.48 evalue=0.00e+00;
c18537/f3p3/1283	uncharacterized protein n 1 tax solanum lycopersicum k4deu5_sollc score=632.10 evalue=0.00e+00;
c18537/f3p3/1283	learca2 protein n 1 tax solanum lycopersicum q9sxs0_sollc score=630.17 evalue=0.00e+00;
c18638/f2p4/1035	cysteine synthase n 1 tax solanum tuberosum q9fs26_soltu score=496.51 evalue=1.80e-172;
c18638/f2p4/1035	cysteine synthase n 1 tax solanum lycopersicum k4cj67_sollc score=494.20 evalue=1.34e-171;
c18638/f2p4/1035	cysteine synthase chloroplastic/chromoplastic n 1 tax solanum tuberosum cyskp_soltu score=493.43 evalue=2.58e-171;
c18638/f2p4/1035	alpha-glucosidase n 1 tax sphingobium indicum b90a i5bf64_9sphn score=495.74 evalue=5.36e-170;
c18638/f2p4/1035	cysteine synthase (fragment) n 1 tax nicotiana tabacum q3lag6_tobac score=481.87 evalue=4.51e-167;
c18674/f5p1/2162	uncharacterized protein n 1 tax solanum lycopersicum k4bmy1_sollc score=932.94 evalue=0.00e+00;
c18674/f5p1/2162	uncharacterized protein n 1 tax solanum lycopersicum k4c710_sollc score=813.91 evalue=0.00e+00;
c18674/f5p1/2162	putative uncharacterized protein n 1 tax vitis vinifera d7tzw6_vitvi score=772.70 evalue=0.00e+00;
c18674/f5p1/2162	casein kinase putative n 1 tax ricinus communis b9s5v9_ricco score=762.68 evalue=0.00e+00;
c18674/f5p1/2162	caesin kinase i isoform delta like protein n 1 tax cucumis sativus k8dvf4_cucsa score=741.88 evalue=0.00e+00;

c18742/f2p7/798	uncharacterized protein n 1 tax solanum lycopersicum k4bby2_sollc score=166.39 evalue=1.82e-45;
c18742/f2p7/798	putative uncharacterized protein n 1 tax vitis vinifera f6h5v8_vitvi score=88.20 evalue=2.81e-17;
c18742/f2p7/798	putative uncharacterized protein n 1 tax vitis vinifera f6h5v8_vitvi score=78.95 evalue=5.81e-14;
c18742/f2p7/798	putative uncharacterized protein n 1 tax vitis vinifera f6h5v8_vitvi score=74.33 evalue=2.10e-12;
c18742/f2p7/798	uncharacterized protein n 1 tax solanum lycopersicum k4b747_sollc score=67.01 evalue=6.66e-10;
c18839/f77p15/1844	glucose-1-phosphate adenylyltransferase small subunit chloroplastic/amyloplastic n 1 tax solanum tuberosum glgs_soltu score=1051.20 evalue=0.00e+00;
c18839/f77p15/1844	glucose-1-phosphate adenylyltransferase n 1 tax solanum lycopersicum k4cge7_sollc score=1046.19 evalue=0.00e+00;
c18839/f77p15/1844	glucose-1-phosphate adenylyltransferase n 1 tax solanum lycopersicum var. cerasiforme d5l5q9_sollc score=1046.19 evalue=0.00e+00;
c18839/f77p15/1844	glucose-1-phosphate adenylyltransferase n 1 tax solanum tuberosum q38m81_soltu score=1043.49 evalue=0.00e+00;
c18839/f77p15/1844	glucose-1-phosphate adenylyltransferase n 1 tax solanum tuberosum q2pxi9_soltu score=1042.34 evalue=0.00e+00;
c19201/f3p0/1658	uncharacterized protein n 1 tax solanum lycopersicum k4bva7_sollc score=89.74 evalue=2.64e-18;
c19860/f1p3/1216	uncharacterized protein n 1 tax solanum lycopersicum k4cla0_sollc score=591.65 evalue=0.00e+00;
c19860/f1p3/1216	zinc transporter 4 chloroplastic n 1 tax arabidopsis thaliana zip4_arath score=378.25 evalue=2.40e-125;
c19860/f1p3/1216	zip family metal transporter n 1 tax thlaspi japonicum q5ccl8_thlja score=377.48 evalue=6.82e-125;
c19860/f1p3/1216	zip-like zinc transporter n 2 tax noccaea caerulescens q93xe8_nocca score=374.40 evalue=2.81e-123;
c19860/f1p3/1216	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata d7kll3_arall score=373.24 evalue=9.02e-123;
c19923/f1p0/899	uncharacterized protein n 1 tax solanum lycopersicum k4c948_sollc score=172.94 evalue=2.95e-84;
c19923/f1p0/899	uncharacterized protein n 1 tax solanum lycopersicum k4c948_sollc score=157.53 evalue=2.95e-84;
c19923/f1p0/899	uncharacterized protein n 1 tax solanum lycopersicum k4c948_sollc score=30.42 evalue=2.95e-84;
c19923/f1p0/899	predicted protein n 1 tax populus trichocarpa b9my30_poptr score=130.95 evalue=2.18e-57;
c19923/f1p0/899	predicted protein n 1 tax populus trichocarpa b9my30_poptr score=118.63 evalue=2.18e-57;
c20264/f2p2/1131	14-3-3 protein n 1 tax nicotiana tabacum q948k3_tobac score=512.69 evalue=2.58e-180;
c20264/f2p2/1131	14-3-3 protein 9 n 1 tax solanum lycopersicum 14339_sollc score=512.30 evalue=3.04e-180;
c20264/f2p2/1131	14-3-3 protein n 1 tax solanum berthaultii a3few3_9soln score=464.54 evalue=2.69e-161;
c20264/f2p2/1131	14-3-3 protein 8 n 1 tax solanum lycopersicum 14338_sollc score=462.61 evalue=1.59e-160;
c20264/f2p2/1131	14-3-3 protein putative n 1 tax ricinus communis b9sbk7_ricco score=459.91 evalue=1.66e-159;
c20559/f4p0/2294	uncharacterized protein n 1 tax solanum lycopersicum k4b7e2_sollc score=864.37 evalue=0.00e+00;
c20559/f4p0/2294	putative uncharacterized protein n 1 tax vitis vinifera f6h3y6_vitvi score=716.46 evalue=0.00e+00;
c20559/f4p0/2294	putative uncharacterized protein n 1 tax vitis vinifera a5az58_vitvi score=714.15 evalue=0.00e+00;
c20559/f4p0/2294	uncharacterized protein n 1 tax glycine max k7kp05_soybn score=714.15 evalue=0.00e+00;
c20559/f4p0/2294	uncharacterized protein n 1 tax glycine max i1n798_soybn score=709.52 evalue=0.00e+00;

c20722/f1p3/1413	uncharacterized protein n 1 tax solanum lycopersicum k4d5c2_sollc score=636.72 evalue=0.00e+00;
c20722/f1p3/1413	uncharacterized protein n 1 tax glycine max i1l677_soybn score=548.89 evalue=0.00e+00;
c20722/f1p3/1413	uncharacterized protein n 1 tax glycine max k7muh9_soybn score=545.81 evalue=0.00e+00;
c20722/f1p3/1413	4-nitrophenylphosphatase putative n 1 tax ricinus communis b9rm24_ricco score=545.43 evalue=0.00e+00;
c20722/f1p3/1413	putative uncharacterized protein n 1 tax medicago truncatula b7fj10_medtr score=543.12 evalue=0.00e+00;
c20917/f2p2/2071	putative uncharacterized protein n 1 tax vitis vinifera e0cqh3_vitvi score=521.16 evalue=2.51e-177;
c20917/f2p2/2071	nicotiana tabacum wound inducive mrna complete cds n 1 tax nicotiana tabacum q9lw93_tobac score=501.13 evalue=4.63e-170;
c20917/f2p2/2071	predicted protein n 1 tax populus trichocarpa b9grk6_poptr score=497.28 evalue=2.05e-168;
c20917/f2p2/2071	putative uncharacterized protein n 1 tax ricinus communis b9r7y6_ricco score=482.64 evalue=9.71e-163;
c20917/f2p2/2071	predicted protein n 1 tax populus trichocarpa b9h4e6_poptr score=473.01 evalue=4.78e-159;
c21188/f1p0/1316	putative uncharacterized protein n 1 tax vitis vinifera e0cqh3_vitvi score=517.69 evalue=7.08e-180;
c21188/f1p0/1316	nicotiana tabacum wound inducive mrna complete cds n 1 tax nicotiana tabacum q9lw93_tobac score=498.43 evalue=9.03e-173;
c21188/f1p0/1316	predicted protein n 1 tax populus trichocarpa b9grk6_poptr score=494.20 evalue=5.07e-171;
c21188/f1p0/1316	putative uncharacterized protein n 1 tax ricinus communis b9r7y6_ricco score=479.94 evalue=2.23e-165;
c21188/f1p0/1316	predicted protein n 1 tax populus trichocarpa b9h4e6_poptr score=470.70 evalue=1.11e-161;
c21202/f3p1/1819	uncharacterized protein n 1 tax solanum lycopersicum k4dam3_sollc score=391.73 evalue=1.50e-125;
c21202/f3p1/1819	putative uncharacterized protein n 1 tax vitis vinifera d7tdy1_vitvi score=286.19 evalue=8.58e-86;
c21202/f3p1/1819	predicted protein n 1 tax populus trichocarpa b9gsm4_poptr score=284.65 evalue=1.05e-84;
c21202/f3p1/1819	atp binding protein putative n 1 tax ricinus communis b9ruc4_ricco score=282.34 evalue=1.07e-83;
c21202/f3p1/1819	uncharacterized protein n 1 tax glycine max i1jf97_soybn score=280.03 evalue=3.60e-83;
c21226/f2p0/1095	uncharacterized protein n 1 tax lotus japonicus i3str8_lotja score=127.10 evalue=4.02e-32;
c21226/f2p0/1095	putative uncharacterized protein n 1 tax glycine max c6t2w3_soybn score=126.33 evalue=8.21e-32;
c21226/f2p0/1095	uncharacterized protein n 1 tax glycine max i1jnz8_soybn score=125.18 evalue=1.41e-31;
c21226/f2p0/1095	uncharacterized protein n 1 tax glycine max c6syi0_soybn score=122.86 evalue=1.68e-30;
c21226/f2p0/1095	putative uncharacterized protein n 1 tax medicago truncatula b7fhc2_medtr score=122.09 evalue=2.95e-30;
c21832/f5p6/2066	cyclin a1 n 1 tax solanum lycopersicum q9xgi5_sollc score=837.41 evalue=0.00e+00;
c21832/f5p6/2066	cyclin a-like protein n 1 tax nicotiana tabacum q40490_tobac score=776.93 evalue=0.00e+00;
c21832/f5p6/2066	a-type cyclin n 1 tax nicotiana tabacum q40514_tobac score=775.39 evalue=0.00e+00;
c21832/f5p6/2066	cyclin a-like protein n 1 tax nicotiana tabacum q40491_tobac score=759.99 evalue=0.00e+00;
c21832/f5p6/2066	cyclin a n 1 tax scutellaria baicalensis q4jf77_scuba score=609.76 evalue=0.00e+00;
c22142/f13p14/1898	protoporphyrinogen oxidase n 1 tax solanum tuberosum o64384_soltu score=1021.54 evalue=0.00e+00;

c22142/f13p14/1898	uncharacterized protein n 1 tax solanum lycopersicum k4axf5_sollc score=1013.83 evalue=0.00e+00;
c22142/f13p14/1898	protoporphyrinogen oxidase px-1 n 1 tax nicotiana tabacum q9sbi4_tobac score=942.95 evalue=0.00e+00;
c22142/f13p14/1898	phosphoenolpyruvate synthase n 10 tax helicobacter pylori i9ruz7_helpx score=941.80 evalue=0.00e+00;
c22142/f13p14/1898	plastidal protoporphyrinogen oxidase n 1 tax nicotiana tabacum q9sax9_tobac score=940.26 evalue=0.00e+00;
c22400/f1p1/886	oxygen-evolving enhancer protein 2 chloroplastic n 1 tax solanum tuberosum psbp_soltu score=339.73 evalue=1.17e-113;
c22400/f1p1/886	oxygen-evolving enhancer protein 2 chloroplastic n 1 tax solanum lycopersicum k4cep4_sollc score=325.87 evalue=4.02e-108;
c22400/f1p1/886	oxygen-evolving enhancer protein 2 chloroplastic n 1 tax solanum lycopersicum psbp_sollc score=325.48 evalue=4.29e-108;
c22400/f1p1/886	transcription-repair coupling factor n 1 tax helicobacter pylori hp h-41 i9svn3_helpx score=338.58 evalue=6.22e-105;
c22400/f1p1/886	transcription-repair coupling factor n 1 tax helicobacter pylori hp h-41 i9svn3_helpx score=323.94 evalue=2.31e-99;
c22570/f2p2/1316	uncharacterized protein n 1 tax solanum lycopersicum k4bkc0_sollc score=629.02 evalue=0.00e+00;
c22570/f2p2/1316	putative uncharacterized protein n 1 tax vitis vinifera f6gsl6_vitvi score=387.11 evalue=1.36e-128;
c22570/f2p2/1316	putative uncharacterized protein n 1 tax ricinus communis b9raz2_ricco score=367.08 evalue=7.57e-121;
c22570/f2p2/1316	predicted protein n 1 tax populus trichocarpa b9ieu7_poptr score=356.68 evalue=7.05e-117;
c22570/f2p2/1316	putative uncharacterized protein n 1 tax vitis vinifera a5c6w9_vitvi score=344.74 evalue=9.41e-113;
c22598/f1p0/872	udp-glc-4-epimerase n 1 tax solanum tuberosum q6xp48_soltu score=508.83 evalue=7.98e-179;
c22598/f1p0/872	uncharacterized protein n 1 tax solanum lycopersicum k4cp57_sollc score=503.83 evalue=8.29e-177;
c22598/f1p0/872	predicted protein n 1 tax populus trichocarpa b9gwf3_poptr score=449.13 evalue=2.41e-155;
c22598/f1p0/872	putative uncharacterized protein n 1 tax vitis vinifera d7tw56_vitvi score=444.12 evalue=2.13e-153;
c22598/f1p0/872	udp-glucose 4-epimerase 1 n 2 tax arabidopsis thaliana gale1_arath score=441.04 evalue=3.27e-152;
c23083/f1p2/726	uncharacterized protein n 1 tax solanum lycopersicum k4b429_sollc score=182.96 evalue=1.06e-54;
c23083/f1p2/726	expressed protein putative n 1 tax ricinus communis b9s5k9_ricco score=125.18 evalue=1.19e-36;
c23083/f1p2/726	expressed protein putative n 1 tax ricinus communis b9s5k9_ricco score=54.68 evalue=1.19e-36;
c23083/f1p2/726	uncharacterized protein n 1 tax solanum lycopersicum k4bg78_sollc score=112.85 evalue=1.56e-32;
c23083/f1p2/726	uncharacterized protein n 1 tax solanum lycopersicum k4bg78_sollc score=53.14 evalue=1.56e-32;
c23459/f6p6/2077	uncharacterized protein n 1 tax solanum lycopersicum k4bv39_sollc score=684.10 evalue=0.00e+00;
c23459/f6p6/2077	putative uncharacterized protein n 2 tax vitis vinifera a5at48_vitvi score=442.58 evalue=2.13e-146;
c23459/f6p6/2077	predicted protein n 1 tax populus trichocarpa b9mvj2_poptr score=418.70 evalue=3.00e-137;
c23459/f6p6/2077	thylakoidal processing peptidase n 2 tax medicago truncatula g7j5q2_medtr score=394.43 evalue=1.17e-127;
c23459/f6p6/2077	uncharacterized protein n 2 tax glycine max i1jtg1_soybn score=387.88 evalue=2.79e-125;
c23473/f2p3/1346	uncharacterized protein n 1 tax solanum lycopersicum k4aye6_sollc score=677.94 evalue=0.00e+00;
c23473/f2p3/1346	s-adenosyl-methionine-sterol-c-methyltransferase n 1 tax nicotiana tabacum o82720_tobac score=653.28 evalue=0.00e+00;

c23473/f2p3/1346	s-adenosyl-methionine cycloartenol-c24-methyltransferase n 1 tax nicotiana tabacum o82434_tobac score=599.36 evalue=0.00e+00;
c23473/f2p3/1346	putative uncharacterized protein n 1 tax vitis vinifera f6hbc7_vitvi score=571.24 evalue=0.00e+00;
c23473/f2p3/1346	uncharacterized protein n 1 tax oryza brachyantha j3kug9_orybr score=568.15 evalue=0.00e+00;
c23772/f2p3/1662	xylulose kinase putative n 1 tax ricinus communis b9rhb4_ricco score=310.07 evalue=7.81e-180;
c23772/f2p3/1662	xylulose kinase putative n 1 tax ricinus communis b9rhb4_ricco score=295.82 evalue=7.81e-180;
c23772/f2p3/1662	xylulose kinase putative n 1 tax ricinus communis b9rhb4_ricco score=75.87 evalue=7.81e-180;
c23772/f2p3/1662	putative uncharacterized protein n 1 tax vitis vinifera f6i198_vitvi score=315.46 evalue=3.71e-165;
c23772/f2p3/1662	putative uncharacterized protein n 1 tax vitis vinifera f6i198_vitvi score=295.05 evalue=3.71e-165;
c23787/f1p0/1387	uncharacterized protein n 1 tax solanum lycopersicum k4b6a3_sollc score=644.81 evalue=0.00e+00;
c23787/f1p0/1387	uncharacterized protein n 1 tax glycine max i1jcg8_soybn score=607.06 evalue=0.00e+00;
c23787/f1p0/1387	putative uncharacterized protein n 1 tax vitis vinifera e0cq75_vitvi score=596.66 evalue=0.00e+00;
c23787/f1p0/1387	chloroplast ferredoxin-nadp+ oxidoreductase n 1 tax capsicum annuum q9m4d2_capan score=594.73 evalue=0.00e+00;
c23787/f1p0/1387	ferredoxin--nadp reductase leaf-type isozyme chloroplastic n 1 tax nicotiana tabacum fenr1_tobac score=592.42 evalue=0.00e+00;
c23986/f1p0/2277	uncharacterized protein n 1 tax solanum lycopersicum k4cg51_sollc score=534.26 evalue=0.00e+00;
c23986/f1p0/2277	uncharacterized protein n 1 tax solanum lycopersicum k4cg51_sollc score=358.22 evalue=0.00e+00;
c23986/f1p0/2277	uncharacterized protein n 1 tax solanum lycopersicum k4cg51_sollc score=154.45 evalue=0.00e+00;
c23986/f1p0/2277	max2a n 1 tax petunia x hybrida i1ssi5_pethy score=483.03 evalue=0.00e+00;
c23986/f1p0/2277	max2a n 1 tax petunia x hybrida i1ssi5_pethy score=386.34 evalue=0.00e+00;
c25762/f22p5/827	ribosomal protein l15 n 1 tax solanum lycopersicum k4c793_sollc score=360.15 evalue=7.95e-123;
c25762/f22p5/827	ribosomal protein l15 n 1 tax solanum lycopersicum k4bp02_sollc score=358.61 evalue=3.62e-122;
c25762/f22p5/827	ribosomal protein l15 n 1 tax solanum lycopersicum k4c6m0_sollc score=357.07 evalue=1.51e-121;
c25762/f22p5/827	60s ribosomal protein l15 n 1 tax petunia x hybrida rl15_pethy score=348.59 evalue=3.38e-118;
c25762/f22p5/827	ribosomal protein l15 n 1 tax populus trichocarpa b9gpa1_poptr score=345.89 evalue=3.09e-117;
c26530/f13p5/1747	uncharacterized protein n 1 tax solanum lycopersicum k4cwq9_sollc score=865.14 evalue=0.00e+00;
c26530/f13p5/1747	putative uncharacterized protein n 1 tax vitis vinifera f6gwe5_vitvi score=755.75 evalue=0.00e+00;
c26530/f13p5/1747	putative uncharacterized protein n 1 tax vitis vinifera a5bn70_vitvi score=747.27 evalue=0.00e+00;
c26530/f13p5/1747	predicted protein n 1 tax populus trichocarpa a9p9k8_poptr score=729.55 evalue=0.00e+00;
c26530/f13p5/1747	udp-d-glucuronic acid 4-epimerase n 1 tax medicago truncatula g7ja85_medtr score=727.24 evalue=0.00e+00;
c26618/f5p13/2013	uncharacterized protein n 1 tax solanum lycopersicum k4at31_sollc score=1080.47 evalue=0.00e+00;
c26618/f5p13/2013	putative acetyl co-enzyme a carboxylase biotin carboxylase subunit n 1 tax capsicum annuum b5las7_capan score=1044.65 evalue=0.00e+00;
c26618/f5p13/2013	acetyl-coa carboxylase n 1 tax nicotiana tabacum h9cch6_tobac score=1027.31 evalue=0.00e+00;

c26618/f5p13/2013	biotin carboxylase subunit n 1 tax nicotiana tabacum q40475_tobac score=1006.51 evalue=0.00e+00;
c26618/f5p13/2013	biotin carboxylase 1 chloroplastic n 1 tax populus trichocarpa accc1_poptr score=958.75 evalue=0.00e+00;
c26744/f6p5/1608	uncharacterized protein n 1 tax solanum lycopersicum k4b8t5_sollc score=735.33 evalue=0.00e+00;
c26744/f6p5/1608	uncharacterized protein n 1 tax solanum lycopersicum k4be45_sollc score=599.74 evalue=0.00e+00;
c26744/f6p5/1608	uncharacterized protein n 1 tax glycine max i1mer4_soybn score=520.00 evalue=6.48e-179;
c26744/f6p5/1608	putative uncharacterized protein n 1 tax medicago truncatula g7ikb9_medtr score=518.46 evalue=1.43e-178;
c26744/f6p5/1608	predicted protein n 1 tax populus trichocarpa b9i1n2_poptr score=516.92 evalue=7.06e-178;
c26784/f3p1/1928	uncharacterized protein n 1 tax solanum lycopersicum k4ceh3_sollc score=1167.91 evalue=0.00e+00;
c26784/f3p1/1928	putative uncharacterized protein n 1 tax vitis vinifera f6gu74_vitvi score=943.73 evalue=0.00e+00;
c26784/f3p1/1928	bzip domain class transcription factor n 1 tax malus x domestica d9ziq5_maldo score=904.05 evalue=0.00e+00;
c26784/f3p1/1928	bzip domain class transcription factor n 1 tax malus x domestica d9ziq0_maldo score=902.51 evalue=0.00e+00;
c26784/f3p1/1928	predicted protein n 1 tax populus trichocarpa b9i769_poptr score=900.58 evalue=0.00e+00;
c26812/f3p1/2052	uncharacterized protein n 1 tax solanum lycopersicum k4dew2_sollc score=1040.80 evalue=0.00e+00;
c26812/f3p1/2052	mitogen-activated protein kinase 16 n 1 tax solanum lycopersicum f8ufc5_sollc score=1037.71 evalue=0.00e+00;
c26812/f3p1/2052	map kinase n 1 tax nicotiana tabacum i7ee96_tobac score=975.31 evalue=0.00e+00;
c26812/f3p1/2052	map kinase n 1 tax nicotiana tabacum i7fjj2_tobac score=874.77 evalue=0.00e+00;
c26812/f3p1/2052	uncharacterized protein n 1 tax solanum lycopersicum k4c872_sollc score=851.66 evalue=0.00e+00;
c27381/f4p3/2177	uncharacterized protein n 1 tax solanum lycopersicum k4b985_sollc score=977.24 evalue=0.00e+00;
c27381/f4p3/2177	uncharacterized protein n 1 tax solanum lycopersicum k4be75_sollc score=857.05 evalue=0.00e+00;
c27381/f4p3/2177	uncharacterized protein n 1 tax glycine max i1m0d7_soybn score=828.16 evalue=0.00e+00;
c27381/f4p3/2177	uncharacterized protein n 1 tax glycine max i1m281_soybn score=823.16 evalue=0.00e+00;
c27381/f4p3/2177	uncharacterized protein n 1 tax glycine max i1mef2_soybn score=814.30 evalue=0.00e+00;
c27407/f3p3/2022	uncharacterized protein n 1 tax solanum lycopersicum k4c7d1_sollc score=950.66 evalue=0.00e+00;
c27407/f3p3/2022	putative uncharacterized protein n 1 tax vitis vinifera f6i3z1_vitvi score=814.68 evalue=0.00e+00;
c27407/f3p3/2022	putative uncharacterized protein n 1 tax vitis vinifera f6i400_vitvi score=784.25 evalue=0.00e+00;
c27407/f3p3/2022	putative uncharacterized protein n 1 tax vitis vinifera a5c8t7_vitvi score=781.17 evalue=0.00e+00;
c27407/f3p3/2022	putative uncharacterized protein n 1 tax vitis vinifera d7u9b0_vitvi score=776.93 evalue=0.00e+00;
c27908/f1p1/1640	uncharacterized protein n 1 tax solanum lycopersicum k4bi08_sollc score=791.96 evalue=0.00e+00;
c27908/f1p1/1640	uncharacterized protein n 1 tax solanum lycopersicum k4cpx7_sollc score=501.13 evalue=9.63e-171;
c27908/f1p1/1640	putative uncharacterized protein n 1 tax vitis vinifera f6hu88_vitvi score=497.66 evalue=5.10e-169;
c27908/f1p1/1640	predicted protein n 1 tax populus trichocarpa b9i215_poptr score=490.73 evalue=5.27e-167;

c27908/f1p1/1640	phosphatidylcholine transfer protein putative n 1 tax ricinus communis b9ryw5_ricco score=488.03 evalue=2.24e-165;
c27998/f3p1/1219	c-4 methyl sterol oxidase n 1 tax solanum lycopersicum f6m7c4_sollc score=555.83 evalue=0.00e+00;
c27998/f3p1/1219	c-4 methyl sterol oxidase putative n 1 tax ricinus communis b9s3d6_ricco score=499.59 evalue=1.55e-174;
c27998/f3p1/1219	sterol 4-alpha-methyl-oxidase 2 n 1 tax arabidopsis lyrata subsp. lyrata d7kh21_arall score=489.57 evalue=1.30e-170;
c27998/f3p1/1219	putative sterol 4-alpha-methyl-oxidase n 1 tax gossypium arboreum q8gta1_gosar score=489.57 evalue=1.36e-170;
c27998/f3p1/1219	predicted protein n 1 tax populus trichocarpa b9gj78_poptr score=489.19 evalue=2.13e-170;
c28086/f1p1/1740	uncharacterized protein n 1 tax solanum lycopersicum k4bnb2_sollc score=614.76 evalue=0.00e+00;
c28086/f1p1/1740	uncharacterized protein n 1 tax solanum lycopersicum k4bwh5_sollc score=322.40 evalue=2.65e-98;
c28086/f1p1/1740	putative uncharacterized protein n 1 tax vitis vinifera d7tnk1_vitvi score=228.79 evalue=5.73e-64;
c28086/f1p1/1740	uncharacterized protein n 2 tax glycine max k7l9m7_soybn score=190.66 evalue=2.45e-50;
c28086/f1p1/1740	putative uncharacterized protein n 1 tax ricinus communis b9s2i4_ricco score=191.04 evalue=5.37e-50;
c28368/f1p1/1669	predicted protein n 1 tax populus trichocarpa b9i6v5_poptr score=619.39 evalue=0.00e+00;
c28368/f1p1/1669	putative uncharacterized protein n 1 tax vitis vinifera d7sjj6_vitvi score=620.16 evalue=0.00e+00;
c28368/f1p1/1669	putative uncharacterized protein n 1 tax ricinus communis b9rx17_ricco score=589.34 evalue=0.00e+00;
c28368/f1p1/1669	uncharacterized protein n 1 tax glycine max i1mzr2_soybn score=590.11 evalue=0.00e+00;
c28368/f1p1/1669	metalloendopeptidase n 1 tax arabidopsis lyrata subsp. lyrata d7kg76_arall score=567.77 evalue=0.00e+00;
c28900/f4p2/2106	uncharacterized protein n 1 tax solanum lycopersicum k4az60_sollc score=825.08 evalue=0.00e+00;
c28900/f4p2/2106	uncharacterized protein n 1 tax solanum lycopersicum k4c1d1_sollc score=753.82 evalue=0.00e+00;
c28900/f4p2/2106	uncharacterized protein n 1 tax solanum lycopersicum k4cyv0_sollc score=736.87 evalue=0.00e+00;
c28900/f4p2/2106	putative uncharacterized protein n 2 tax vitis vinifera f6i3a1_vitvi score=724.16 evalue=0.00e+00;
c28900/f4p2/2106	uncharacterized protein n 1 tax glycine max i1j7u8_soybn score=720.31 evalue=0.00e+00;
c29076/f1p4/1579	uncharacterized protein n 1 tax solanum lycopersicum k4b438_sollc score=799.27 evalue=0.00e+00;
c29076/f1p4/1579	v-type atp synthase beta chain n 1 tax medicago truncatula g7ksi7_medtr score=790.03 evalue=0.00e+00;
c29076/f1p4/1579	predicted protein n 1 tax populus trichocarpa a9pck1_poptr score=786.95 evalue=0.00e+00;
c29076/f1p4/1579	uncharacterized protein n 1 tax solanum lycopersicum k4d1f7_sollc score=785.79 evalue=0.00e+00;
c29076/f1p4/1579	vacuolar atpase subunit b n 1 tax mesembryanthemum crystallinum q8gub5_mescr score=785.02 evalue=0.00e+00;
c29231/f1p4/1740	uncharacterized protein n 1 tax solanum lycopersicum k4dht7_sollc score=896.73 evalue=0.00e+00;
c29231/f1p4/1740	predicted protein n 1 tax populus trichocarpa b9hx57_poptr score=677.55 evalue=0.00e+00;
c29231/f1p4/1740	uncharacterized protein n 1 tax glycine max i1mru5_soybn score=655.98 evalue=0.00e+00;
c29231/f1p4/1740	putative uncharacterized protein n 1 tax vitis vinifera f6h704_vitvi score=649.43 evalue=0.00e+00;
c29231/f1p4/1740	uncharacterized protein n 1 tax glycine max i1kmn0_soybn score=644.81 evalue=0.00e+00;

c29806/f2p1/1703	uncharacterized protein n 1 tax solanum lycopersicum k4def3_sollc score=457.22 evalue=0.00e+00;
c29806/f2p1/1703	uncharacterized protein n 1 tax solanum lycopersicum k4def3_sollc score=412.92 evalue=0.00e+00;
c29806/f2p1/1703	uncharacterized protein n 1 tax glycine max i1jmm6_soybn score=426.79 evalue=0.00e+00;
c29806/f2p1/1703	uncharacterized protein n 1 tax glycine max i1jmm6_soybn score=353.21 evalue=0.00e+00;
c29806/f2p1/1703	actin-related protein n 1 tax medicago truncatula g7kbn0_medtr score=422.94 evalue=0.00e+00;
c29987/f2p6/1642	uncharacterized protein n 1 tax solanum lycopersicum k4b113_sollc score=715.69 evalue=0.00e+00;
c29987/f2p6/1642	putative uncharacterized protein n 1 tax vitis vinifera f6i4m0_vitvi score=539.65 evalue=0.00e+00;
c29987/f2p6/1642	putative uncharacterized protein n 1 tax vitis vinifera a5b3s4_vitvi score=515.77 evalue=4.05e-176;
c29987/f2p6/1642	uncharacterized protein n 1 tax glycine max i1lba0_soybn score=511.92 evalue=1.18e-174;
c29987/f2p6/1642	uncharacterized protein n 1 tax glycine max i1nj17_soybn score=508.83 evalue=2.69e-173;
c30007/f1p0/1025	uncharacterized protein n 1 tax solanum lycopersicum k4azk4_sollc score=130.18 evalue=9.20e-34;
c30007/f1p0/1025	putative uncharacterized protein n 1 tax vitis vinifera d7sj36_vitvi score=96.29 evalue=4.70e-21;
c30007/f1p0/1025	putative uncharacterized protein n 1 tax medicago truncatula q2htj3_medtr score=92.43 evalue=2.47e-19;
c30007/f1p0/1025	putative uncharacterized protein n 2 tax glycine max c6t0g9_soybn score=90.51 evalue=4.49e-19;
c30007/f1p0/1025	uncharacterized protein n 1 tax medicago truncatula i3sfh2_medtr score=89.74 evalue=9.05e-19;
c30437/f3p2/2103	uncharacterized protein n 1 tax solanum lycopersicum k4chh4_sollc score=951.43 evalue=0.00e+00;
c30437/f3p2/2103	putative uncharacterized protein n 1 tax vitis vinifera d7t838_vitvi score=715.30 evalue=0.00e+00;
c30437/f3p2/2103	trigger factor putative n 1 tax ricinus communis b9syy0_ricco score=708.75 evalue=0.00e+00;
c30437/f3p2/2103	predicted protein n 1 tax populus trichocarpa b9ieg6_poptr score=690.65 evalue=0.00e+00;
c30437/f3p2/2103	uncharacterized protein n 1 tax glycine max i1jje0_soybn score=688.34 evalue=0.00e+00;
c30590/f1p5/1503	monodehydroascorbate reductase n 1 tax solanum lycopersicum k4cqw8_sollc score=870.15 evalue=0.00e+00;
c30590/f1p5/1503	monodehydroascorbate reductase n 1 tax solanum lycopersicum mdar_sollc score=869.38 evalue=0.00e+00;
c30590/f1p5/1503	monodehydroascorbate reductase n 1 tax ipomoea batatas d2cgm8_ipoba score=782.33 evalue=0.00e+00;
c30590/f1p5/1503	monodehydroascorbate reductase n 1 tax acanthus ebracteatus a0mq80_acaeb score=764.61 evalue=0.00e+00;
c30590/f1p5/1503	predicted protein n 1 tax populus trichocarpa a9p7v5_poptr score=756.90 evalue=0.00e+00;
c30656/f2p2/1494	uncharacterized protein n 1 tax solanum lycopersicum k4crc9_sollc score=786.56 evalue=0.00e+00;
c30656/f2p2/1494	predicted protein (fragment) n 1 tax populus trichocarpa b9hbt8_poptr score=609.37 evalue=0.00e+00;
c30656/f2p2/1494	predicted protein n 1 tax populus trichocarpa b9ifw6_poptr score=608.60 evalue=0.00e+00;
c30656/f2p2/1494	uncharacterized protein n 1 tax glycine max i1j702_soybn score=600.13 evalue=0.00e+00;
c30656/f2p2/1494	uncharacterized protein n 1 tax glycine max i1jm15_soybn score=590.50 evalue=0.00e+00;
c30899/f1p3/1537	uncharacterized protein n 1 tax solanum lycopersicum k4cl10_sollc score=620.16 evalue=0.00e+00;

c30899/f1p3/1537	ya2 n 1 tax antirrhinum majus a5pgu1_antma score=249.98 evalue=5.09e-75;
c30899/f1p3/1537	ya2 (fragment) n 1 tax petunia x hybrida a5pgv0_pethy score=223.79 evalue=2.71e-67;
c30899/f1p3/1537	predicted protein n 1 tax populus trichocarpa b9hdv6_poptr score=192.20 evalue=1.03e-52;
c30899/f1p3/1537	nuclear transcription factor y subunit a-3 putative n 1 tax ricinus communis b9s5t3_ricco score=177.56 evalue=1.92e-47;
c31375/f4p7/1481	mitochondrial protein putative n 1 tax medicago truncatula g7i9t8_medtr score=168.70 evalue=2.05e-72;
c31375/f4p7/1481	mitochondrial protein putative n 1 tax medicago truncatula g7i9t8_medtr score=132.11 evalue=2.05e-72;
c31375/f4p7/1481	uncharacterized protein n 1 tax solanum lycopersicum k4d065_sollc score=221.86 evalue=1.31e-66;
c31375/f4p7/1481	uncharacterized protein n 1 tax nicotiana tabacum q5m9r1_tobac score=189.50 evalue=2.19e-54;
c31375/f4p7/1481	mitochondrial protein putative n 1 tax medicago truncatula g7i9t8_medtr score=176.79 evalue=2.33e-54;
c31623/f1p2/1272	putative uncharacterized protein n 1 tax vitis vinifera e0cqh3_vitvi score=482.64 evalue=2.57e-166;
c31623/f1p2/1272	nicotiana tabacum wound inducive mrna complete cds n 1 tax nicotiana tabacum q9lw93_tobac score=458.37 evalue=3.09e-157;
c31623/f1p2/1272	predicted protein n 1 tax populus trichocarpa b9grk6_poptr score=457.99 evalue=4.68e-157;
c31623/f1p2/1272	predicted protein n 1 tax populus trichocarpa b9h4e6_poptr score=444.12 evalue=1.69e-151;
c31623/f1p2/1272	putative uncharacterized protein n 1 tax ricinus communis b9r7y6_ricco score=442.19 evalue=7.67e-151;
c31943/f1p0/2124	uncharacterized protein n 1 tax solanum lycopersicum k4d2f4_sollc score=1053.89 evalue=0.00e+00;
c31943/f1p0/2124	calcium-dependent protein kinase 4 n 1 tax capsicum annuum q5edd1_capan score=1045.03 evalue=0.00e+00;
c31943/f1p0/2124	calcium-dependent protein kinase 8 n 1 tax nicotiana tabacum e3vjp8_tobac score=1017.68 evalue=0.00e+00;
c31943/f1p0/2124	calcium-dependent protein kinase n 1 tax hevea brasiliensis f8v179_hevbr score=904.05 evalue=0.00e+00;
c31943/f1p0/2124	calcium-dependent protein kinase putative n 1 tax ricinus communis b9suf1_ricco score=895.58 evalue=0.00e+00;
c32136/f1p3/1717	udp-glucose 6-dehydrogenase n 1 tax solanum lycopersicum k4bl40_sollc score=967.99 evalue=0.00e+00;
c32136/f1p3/1717	udp-glucose 6-dehydrogenase n 1 tax vitis vinifera f6hf82_vitvi score=919.84 evalue=0.00e+00;
c32136/f1p3/1717	udp-glucose 6-dehydrogenase n 2 tax vitis vinifera a5avx9_vitvi score=912.52 evalue=0.00e+00;
c32136/f1p3/1717	udp-glucose 6-dehydrogenase n 1 tax gossypium hirsutum d2wk27_goshi score=911.37 evalue=0.00e+00;
c32136/f1p3/1717	udp-glucose 6-dehydrogenase n 1 tax gossypium hirsutum d2wk26_goshi score=911.37 evalue=0.00e+00;
c32643/f1p2/1671	uncharacterized protein n 1 tax solanum lycopersicum k4cf40_sollc score=917.15 evalue=0.00e+00;
c32643/f1p2/1671	predicted protein n 1 tax populus trichocarpa a9p7u9_poptr score=738.03 evalue=0.00e+00;
c32643/f1p2/1671	predicted protein n 1 tax populus trichocarpa b9gtt7_poptr score=726.47 evalue=0.00e+00;
c32643/f1p2/1671	putative uncharacterized protein n 1 tax vitis vinifera f6hie6_vitvi score=725.70 evalue=0.00e+00;
c32643/f1p2/1671	uncharacterized protein n 1 tax glycine max i1jij8_soybn score=711.84 evalue=0.00e+00;
c32692/f1p1/1900	uncharacterized protein n 1 tax solanum lycopersicum k4bwc5_sollc score=1107.82 evalue=0.00e+00;
c32692/f1p1/1900	uncharacterized protein n 1 tax solanum lycopersicum k4bwb8_sollc score=967.99 evalue=0.00e+00;

c32692/f1p1/1900	uncharacterized protein n 1 tax solanum lycopersicum k4bwc1_sollc score=921.00 evalue=0.00e+00;
c32692/f1p1/1900	uncharacterized protein n 1 tax solanum lycopersicum k4bwb9_sollc score=919.46 evalue=0.00e+00;
c32692/f1p1/1900	uncharacterized protein n 1 tax solanum lycopersicum k4bwc4_sollc score=915.99 evalue=0.00e+00;
c32815/f2p5/1868	uncharacterized protein n 1 tax solanum lycopersicum k4chv7_sollc score=805.82 evalue=0.00e+00;
c32815/f2p5/1868	putative uncharacterized protein n 1 tax vitis vinifera d7sx10_vitvi score=625.16 evalue=0.00e+00;
c32815/f2p5/1868	at1g79050 protein n 1 tax arabidopsis thaliana c0z2k2_arath score=620.16 evalue=0.00e+00;
c32815/f2p5/1868	dna repair protein reca homolog 1 chloroplastic n 1 tax arabidopsis thaliana recac_arath score=619.77 evalue=0.00e+00;
c32815/f2p5/1868	predicted protein (fragment) n 1 tax populus trichocarpa b9nab1_poptr score=611.68 evalue=0.00e+00;
c33033/f7p3/1491	uncharacterized protein n 1 tax solanum lycopersicum k4bsn9_sollc score=325.48 evalue=8.34e-105;
c33033/f7p3/1491	transcription factor dreb2a n 1 tax nicotiana benthamiana e6z277_nicbe score=270.01 evalue=1.54e-82;
c33033/f7p3/1491	ap2/erf domain-containing transcription factor n 2 tax populus trichocarpa b9h544_poptr score=255.76 evalue=1.54e-76;
c33033/f7p3/1491	dehydrate responsive element-binding protein n 1 tax populus euphratica d2ckb5_popeu score=255.37 evalue=2.12e-76;
c33033/f7p3/1491	putative uncharacterized protein n 1 tax vitis vinifera f6h885_vitvi score=246.90 evalue=3.11e-73;
c33123/f1p5/1655	uncharacterized protein n 1 tax solanum lycopersicum k4cb31_sollc score=845.88 evalue=0.00e+00;
c33123/f1p5/1655	endosomal p24a protein putative n 1 tax ricinus communis b9str3_ricco score=790.03 evalue=0.00e+00;
c33123/f1p5/1655	predicted protein n 1 tax populus trichocarpa b9hb25_poptr score=783.48 evalue=0.00e+00;
c33123/f1p5/1655	putative uncharacterized protein n 1 tax vitis vinifera d7sv44_vitvi score=776.55 evalue=0.00e+00;
c33123/f1p5/1655	putative uncharacterized protein n 1 tax vitis vinifera f6hyj2_vitvi score=775.39 evalue=0.00e+00;
c33158/f1p1/1691	uncharacterized protein n 1 tax solanum lycopersicum k4bw90_sollc score=656.37 evalue=0.00e+00;
c33158/f1p1/1691	putative uncharacterized protein n 1 tax ricinus communis b9sh84_ricco score=295.05 evalue=2.23e-85;
c33158/f1p1/1691	predicted protein n 1 tax populus trichocarpa b9hvb3_poptr score=291.20 evalue=2.75e-84;
c33158/f1p1/1691	putative uncharacterized protein n 1 tax vitis vinifera f6hpn7_vitvi score=288.89 evalue=4.83e-83;
c33158/f1p1/1691	uncharacterized protein n 2 tax glycine max i1j5a4_soybn score=248.05 evalue=1.35e-68;
c34902/f2p12/1044	uncharacterized protein n 1 tax solanum lycopersicum k4cbv6_sollc score=488.42 evalue=1.46e-171;
c34902/f2p12/1044	thaliana 60s ribosomal protein l7 (at2g44120) n 1 tax solanum tuberosum q38hu4_soltu score=486.49 evalue=8.84e-171;
c34902/f2p12/1044	uncharacterized protein n 1 tax solanum lycopersicum k4cmm7_sollc score=464.54 evalue=1.76e-157;
c34902/f2p12/1044	uncharacterized protein n 1 tax solanum lycopersicum k4dh95_sollc score=455.29 evalue=1.50e-151;
c34902/f2p12/1044	uncharacterized protein n 1 tax glycine max k7mbv6_soybn score=437.57 evalue=5.94e-151;
c34939/f3p2/1559	uncharacterized protein n 1 tax solanum lycopersicum k4bka5_sollc score=530.79 evalue=0.00e+00;
c34939/f3p2/1559	putative uncharacterized protein n 1 tax vitis vinifera d7shm0_vitvi score=402.13 evalue=2.25e-133;
c34939/f3p2/1559	fkbp12-interacting protein of 37 kda putative n 1 tax ricinus communis b9rax6_ricco score=386.73 evalue=1.54e-127;

c34939/f3p2/1559	uncharacterized protein n 1 tax glycine max i1mte4_soybn score=372.47 evalue=5.98e-122;
c34939/f3p2/1559	uncharacterized protein n 1 tax glycine max i1k033_soybn score=367.85 evalue=4.22e-120;
c35475/f52p33/1607	uncharacterized protein n 1 tax solanum lycopersicum k4c9c7_sollc score=831.63 evalue=0.00e+00;
c35475/f52p33/1607	uncharacterized protein n 1 tax solanum lycopersicum k4atc7_sollc score=739.18 evalue=0.00e+00;
c35475/f52p33/1607	putative uncharacterized protein n 1 tax vitis vinifera f6gyl5_vitvi score=712.61 evalue=0.00e+00;
c35475/f52p33/1607	predicted protein n 2 tax populus trichocarpa b9hv17_poptr score=704.90 evalue=0.00e+00;
c35475/f52p33/1607	sterol delta-7 reductase dwf5 n 1 tax gossypium hirsutum q2qcx7_goshi score=699.12 evalue=0.00e+00;
c36126/f3p1/1164	uncharacterized protein n 1 tax solanum lycopersicum k4c289_sollc score=533.49 evalue=0.00e+00;
c36126/f3p1/1164	putative uncharacterized protein n 1 tax vitis vinifera a5bzu9_vitvi score=471.08 evalue=6.26e-164;
c36126/f3p1/1164	predicted protein n 1 tax populus trichocarpa b9ih79_poptr score=461.45 evalue=3.08e-160;
c36126/f3p1/1164	predicted protein n 1 tax populus trichocarpa b9hcs0_poptr score=459.91 evalue=1.57e-159;
c36126/f3p1/1164	protein pob putative n 1 tax ricinus communis b9s3i8_ricco score=459.53 evalue=2.11e-159;
c36668/f4p2/1828	thioredoxin reductase n 1 tax solanum lycopersicum k4d2p9_sollc score=986.10 evalue=0.00e+00;
c36668/f4p2/1828	thioredoxin reductase n 1 tax populus trichocarpa b9h9s9_poptr score=812.76 evalue=0.00e+00;
c36668/f4p2/1828	thioredoxin reductase n 1 tax glycine max i1l9y6_soybn score=814.68 evalue=0.00e+00;
c36668/f4p2/1828	thioredoxin reductase n 1 tax glycine max i1jga5_soybn score=811.22 evalue=0.00e+00;
c36668/f4p2/1828	thioredoxin reductase n 1 tax vitis vinifera f6hkv5_vitvi score=810.83 evalue=0.00e+00;
c36672/f2p0/1471	uncharacterized protein n 1 tax solanum lycopersicum k4bpq5_sollc score=557.75 evalue=0.00e+00;
c36672/f2p0/1471	zinc finger protein putative n 1 tax ricinus communis b9se95_ricco score=472.63 evalue=2.28e-160;
c36672/f2p0/1471	predicted protein n 1 tax populus trichocarpa b9h7v0_poptr score=469.93 evalue=2.78e-159;
c36672/f2p0/1471	predicted protein n 1 tax populus trichocarpa b9gt84_poptr score=449.51 evalue=3.06e-151;
c36672/f2p0/1471	palmitoyltransferase swf1 n 1 tax medicago truncatula g7ibw6_medtr score=446.82 evalue=3.95e-150;
c36693/f14p3/1563	uncharacterized protein n 1 tax solanum lycopersicum k4ash7_sollc score=662.91 evalue=0.00e+00;
c36693/f14p3/1563	tap46 n 1 tax nicotiana benthamiana d2k8n5_nicbe score=613.61 evalue=0.00e+00;
c36693/f14p3/1563	putative uncharacterized protein n 1 tax vitis vinifera e0cv55_vitvi score=531.18 evalue=0.00e+00;
c36693/f14p3/1563	uncharacterized protein n 1 tax glycine max i1jyq8_soybn score=513.84 evalue=2.71e-176;
c36693/f14p3/1563	predicted protein n 1 tax populus trichocarpa b9i1x0_poptr score=503.44 evalue=4.37e-172;
c36810/f5p7/1818	sucrose transport protein n 1 tax solanum tuberosum q43653_soltu score=879.01 evalue=0.00e+00;
c36810/f5p7/1818	uncharacterized protein n 2 tax solanum lycopersicum k4d6k5_sollc score=868.23 evalue=0.00e+00;
c36810/f5p7/1818	sucrose transporter n 1 tax nicotiana tabacum a8e0n3_tobac score=817.38 evalue=0.00e+00;
c36810/f5p7/1818	sucrose transporter n 1 tax nicotiana tabacum b5m9j3_tobac score=810.83 evalue=0.00e+00;

c36810/f5p7/1818	sucrose transporter n 1 tax nicotiana tabacum b5m9j4_tobac score=809.29 evalue=0.00e+00;
c37265/f3p2/1614	uncharacterized protein n 1 tax solanum lycopersicum k4btv1_sollc score=800.04 evalue=0.00e+00;
c37265/f3p2/1614	putative uncharacterized protein n 1 tax vitis vinifera f6h0q0_vitvi score=529.63 evalue=0.00e+00;
c37265/f3p2/1614	protein brittle-1 chloroplast putative n 2 tax ricinus communis b9rjj9_ricco score=517.69 evalue=6.83e-177;
c37265/f3p2/1614	uncharacterized protein n 1 tax glycine max i1jve6_soybn score=506.14 evalue=8.12e-173;
c37265/f3p2/1614	uncharacterized protein n 1 tax glycine max i1k9z1_soybn score=499.98 evalue=2.34e-170;
c37673/f3p2/1961	uncharacterized protein n 1 tax solanum lycopersicum k4d5d1_sollc score=891.72 evalue=0.00e+00;
c37673/f3p2/1961	putative uncharacterized protein n 1 tax vitis vinifera f6h502_vitvi score=645.97 evalue=0.00e+00;
c37673/f3p2/1961	30s ribosomal protein s5 putative n 1 tax ricinus communis b9sdg2_ricco score=643.65 evalue=0.00e+00;
c37673/f3p2/1961	30s ribosomal protein s5 n 1 tax medicago truncatula g7le23_medtr score=571.24 evalue=0.00e+00;
c37673/f3p2/1961	predicted protein n 1 tax populus trichocarpa b9i6u1_poptr score=567.38 evalue=0.00e+00;
c38218/f1p3/2229	putative uncharacterized protein n 1 tax vitis vinifera d7tyt5_vitvi score=592.42 evalue=0.00e+00;
c38218/f1p3/2229	predicted protein n 1 tax populus trichocarpa b9gz36_poptr score=578.17 evalue=0.00e+00;
c38218/f1p3/2229	uncharacterized protein n 1 tax solanum lycopersicum k4bzl6_sollc score=545.43 evalue=0.00e+00;
c38218/f1p3/2229	uncharacterized protein n 1 tax glycine max k7n5k3_soybn score=546.58 evalue=0.00e+00;
c38218/f1p3/2229	uncharacterized protein n 2 tax glycine max i1kby5_soybn score=546.97 evalue=0.00e+00;
c38448/f1p0/1546	uncharacterized protein n 1 tax solanum lycopersicum k4ay41_sollc score=757.29 evalue=0.00e+00;
c38448/f1p0/1546	rna polymerase sigma factor rpod1 putative n 1 tax ricinus communis b9sda3_ricco score=528.48 evalue=1.12e-179;
c38448/f1p0/1546	putative uncharacterized protein n 1 tax vitis vinifera d7ub90_vitvi score=515.77 evalue=1.49e-174;
c38448/f1p0/1546	uncharacterized protein n 1 tax glycine max k7khd7_soybn score=500.75 evalue=7.26e-169;
c38448/f1p0/1546	sigma factor n 1 tax spinacia oleracea q710c3_spiol score=499.20 evalue=4.53e-168;
c38550/f1p5/1210	glutamate-1-semialdehyde 2 1-aminomutase chloroplastic n 1 tax solanum lycopersicum gsa_sollc score=725.32 evalue=0.00e+00;
c38550/f1p5/1210	uncharacterized protein n 1 tax solanum lycopersicum k4bp76_sollc score=724.55 evalue=0.00e+00;
c38550/f1p5/1210	urea amidolyase n 2 tax amycolatopsis mediterranei i7dxe1_amymd score=724.93 evalue=0.00e+00;
c38550/f1p5/1210	glutamate-1-semialdehyde 2 1-aminomutase chloroplastic n 1 tax nicotiana tabacum gsa_tobac score=691.42 evalue=0.00e+00;
c38550/f1p5/1210	predicted protein n 1 tax populus trichocarpa b9ifg3_poptr score=657.14 evalue=0.00e+00;
c38804/f4p0/2016	external rotenone-insensitive nadph dehydrogenase n 1 tax solanum tuberosum q9st62_soltu score=907.13 evalue=0.00e+00;
c38804/f4p0/2016	uncharacterized protein n 1 tax solanum lycopersicum k4cy40_sollc score=895.96 evalue=0.00e+00;
c38804/f4p0/2016	uncharacterized protein n 1 tax solanum lycopersicum k4cg06_sollc score=725.70 evalue=0.00e+00;
c38804/f4p0/2016	uncharacterized protein n 1 tax solanum lycopersicum k4cg06_sollc score=235.73 evalue=0.00e+00;
c38804/f4p0/2016	putative uncharacterized protein n 1 tax vitis vinifera d7td11_vitvi score=684.87 evalue=0.00e+00;

c38886/f1p1/1635	uncharacterized protein n 1 tax solanum lycopersicum k4b0r3_sollc score=194.51 evalue=2.14e-52;
c38886/f1p1/1635	uncharacterized protein n 1 tax solanum lycopersicum k4b0r3_sollc score=171.78 evalue=3.41e-44;
c38886/f1p1/1635	putative uncharacterized protein n 1 tax vitis vinifera a5c7l7_vitvi score=115.93 evalue=2.99e-25;
c38886/f1p1/1635	putative uncharacterized protein n 1 tax vitis vinifera f6hyy0_vitvi score=115.93 evalue=9.70e-25;
c38886/f1p1/1635	chloroplast-targeted copper chaperone putative n 1 tax ricinus communis b9rtt9_ricco score=113.62 evalue=6.89e-24;
c39082/f2p3/1662	adenylyl-sulfate reductase n 1 tax solanum lycopersicum q672q8_sollc score=898.27 evalue=0.00e+00;
c39082/f2p3/1662	paps-reductase-like protein n 1 tax catharanthus roseus q39619_catro score=785.02 evalue=0.00e+00;
c39082/f2p3/1662	uncharacterized protein n 1 tax solanum lycopersicum k4b5n0_sollc score=781.56 evalue=0.00e+00;
c39082/f2p3/1662	putative uncharacterized protein n 1 tax vitis vinifera f6h7k9_vitvi score=765.38 evalue=0.00e+00;
c39082/f2p3/1662	uncharacterized protein n 1 tax solanum lycopersicum k4bfd4_sollc score=755.36 evalue=0.00e+00;
c39117/f1p4/1978	uncharacterized protein n 1 tax solanum lycopersicum k4aw47_sollc score=1001.12 evalue=0.00e+00;
c39117/f1p4/1978	galactokinase putative n 1 tax ricinus communis b9rzt4_ricco score=865.53 evalue=0.00e+00;
c39117/f1p4/1978	uncharacterized protein n 2 tax glycine max i1kmp3_soybn score=861.68 evalue=0.00e+00;
c39117/f1p4/1978	uncharacterized protein n 2 tax glycine max i1mrt3_soybn score=860.52 evalue=0.00e+00;
c39117/f1p4/1978	putative uncharacterized protein n 1 tax vitis vinifera f6h710_vitvi score=859.75 evalue=0.00e+00;
c39268/f1p4/1982	uncharacterized protein n 1 tax solanum lycopersicum k4csn1_sollc score=870.15 evalue=0.00e+00;
c39268/f1p4/1982	putative uncharacterized protein n 1 tax vitis vinifera d7sk13_vitvi score=783.87 evalue=0.00e+00;
c39268/f1p4/1982	predicted protein n 1 tax populus trichocarpa b9hp62_poptr score=781.94 evalue=0.00e+00;
c39268/f1p4/1982	sodium-dependent phosphate transport protein putative n 1 tax ricinus communis b9shz0_ricco score=780.01 evalue=0.00e+00;
c39268/f1p4/1982	predicted protein (fragment) n 1 tax populus trichocarpa b9git9_poptr score=770.00 evalue=0.00e+00;
c39714/f1p4/1679	uncharacterized protein n 1 tax solanum lycopersicum k4c9g9_sollc score=1007.67 evalue=0.00e+00;
c39714/f1p4/1679	2-carboxy-d-arabinitol 1-phosphate (ca1p) phosphatase n 1 tax nicotiana tabacum h2a0j7_tobac score=922.15 evalue=0.00e+00;
c39714/f1p4/1679	putative uncharacterized protein n 1 tax vitis vinifera f6gw48_vitvi score=703.36 evalue=0.00e+00;
c39714/f1p4/1679	phosphoglycerate mutase putative (fragment) n 1 tax ricinus communis b9t5t3_ricco score=694.89 evalue=0.00e+00;
c39714/f1p4/1679	2-carboxy-d-arabinitol 1-phosphate (ca1p) phosphatase n 1 tax phaseolus vulgaris g4vuy8_phavu score=685.26 evalue=0.00e+00;
c40094/f1p4/1523	uncharacterized protein n 1 tax solanum lycopersicum k4cc33_sollc score=759.99 evalue=0.00e+00;
c40094/f1p4/1523	26s proteasome subunit rpn7 n 1 tax capsicum annuum a0mkc7_capan score=717.23 evalue=0.00e+00;
c40094/f1p4/1523	26s proteasome non-atpase regulatory subunit putative n 1 tax ricinus communis b9ram4_ricco score=672.54 evalue=0.00e+00;
c40094/f1p4/1523	predicted protein n 1 tax populus trichocarpa b9if58_poptr score=669.08 evalue=0.00e+00;
c40094/f1p4/1523	26s proteasome non-atpase regulatory subunit n 1 tax cucumis melo subsp. melo e5gbw6_cucme score=666.38 evalue=0.00e+00;
c40322/f1p1/596	uncharacterized protein n 1 tax solanum lycopersicum k4c950_sollc score=287.73 evalue=1.06e-95;

c40322/f1p1/596	putative uncharacterized protein n 1 tax solanum tuberosum q307x4_soltu score=286.57 evalue=3.03e-95;
c40322/f1p1/596	uncharacterized protein n 1 tax solanum lycopersicum k4cj85_sollc score=276.56 evalue=2.77e-91;
c40322/f1p1/596	uncharacterized protein n 2 tax solanum k4dhe3_sollc score=275.79 evalue=5.21e-91;
c40322/f1p1/596	60s ribosomal protein l9 n 1 tax cucumis melo subsp. melo e5gbd5_cucme score=268.08 evalue=5.08e-88;
c40335/f2p0/1537	uncharacterized protein n 1 tax solanum lycopersicum k4bee6_sollc score=598.59 evalue=0.00e+00;
c40335/f2p0/1537	uncharacterized protein n 1 tax solanum lycopersicum k4c5y0_sollc score=345.89 evalue=3.04e-110;
c40335/f2p0/1537	protein phosphatase 2c putative n 1 tax ricinus communis b9rik1_ricco score=295.82 evalue=3.97e-92;
c40335/f2p0/1537	putative uncharacterized protein n 1 tax vitis vinifera d7tvf2_vitvi score=291.58 evalue=7.75e-90;
c40335/f2p0/1537	probable protein phosphatase 2c 51 n 3 tax oryza sativa p2c51_orysj score=277.33 evalue=1.63e-84;
c40380/f2p2/1546	uncharacterized protein n 1 tax solanum lycopersicum k4ckd3_sollc score=895.19 evalue=0.00e+00;
c40380/f2p2/1546	putative uncharacterized protein n 1 tax vitis vinifera f6hbc9_vitvi score=669.08 evalue=0.00e+00;
c40380/f2p2/1546	predicted protein n 1 tax populus trichocarpa b9hns1_poptr score=641.34 evalue=0.00e+00;
c40380/f2p2/1546	uncharacterized protein n 1 tax glycine max k7m485_soybn score=628.25 evalue=0.00e+00;
c40380/f2p2/1546	pentatricopeptide repeat-containing protein putative n 1 tax ricinus communis b9rvl0_ricco score=628.25 evalue=0.00e+00;
c40735/f1p4/1864	uncharacterized protein n 1 tax solanum lycopersicum k4ayj9_sollc score=1001.89 evalue=0.00e+00;
c40735/f1p4/1864	putative esterase n 1 tax nicotiana tabacum a7wpl1_tobac score=874.00 evalue=0.00e+00;
c40735/f1p4/1864	putative uncharacterized protein n 1 tax vitis vinifera f6hhx5_vitvi score=651.74 evalue=0.00e+00;
c40735/f1p4/1864	putative uncharacterized protein n 1 tax vitis vinifera a5ag79_vitvi score=646.74 evalue=0.00e+00;
c40735/f1p4/1864	predicted protein n 1 tax populus trichocarpa b9hnv3_poptr score=623.62 evalue=0.00e+00;
c40896/f5p7/2072	glutamyl-trna reductase (fragment) n 1 tax nicotiana tabacum a6q0f0_tobac score=919.46 evalue=0.00e+00;
c40896/f5p7/2072	glutamyl-trna reductase n 1 tax vitis vinifera a5bzy3_vitvi score=842.80 evalue=0.00e+00;
c40896/f5p7/2072	glutamyl-trna reductase 1 chloroplastic n 2 tax cucumis sativus hem11_cucsa score=831.63 evalue=0.00e+00;
c40896/f5p7/2072	glutamyl-trna reductase 1 chloroplast putative n 1 tax ricinus communis b9r6q2_ricco score=807.75 evalue=0.00e+00;
c40896/f5p7/2072	glutamyl-trna reductase n 1 tax glycine max i1jv15_soybn score=796.58 evalue=0.00e+00;
c40970/f3p2/2270	uncharacterized protein n 1 tax solanum lycopersicum k4cp55_sollc score=1041.57 evalue=0.00e+00;
c40970/f3p2/2270	increased size exclusion limit 1a n 1 tax nicotiana benthamiana d5kxm9_nicbe score=965.68 evalue=0.00e+00;
c40970/f3p2/2270	increased size exclusion limit 1b n 1 tax nicotiana benthamiana d5kxn0_nicbe score=939.10 evalue=0.00e+00;
c40970/f3p2/2270	predicted protein n 1 tax populus trichocarpa b9gwf2_poptr score=731.48 evalue=0.00e+00;
c40970/f3p2/2270	putative uncharacterized protein n 1 tax vitis vinifera a5ak59_vitvi score=729.17 evalue=0.00e+00;
c41333/f2p2/1462	uncharacterized protein n 1 tax solanum lycopersicum k4blb3_sollc score=693.73 evalue=0.00e+00;
c41333/f2p2/1462	putative uncharacterized protein n 1 tax vitis vinifera f6gt81_vitvi score=545.43 evalue=0.00e+00;

c41333/f2p2/1462	putative uncharacterized protein n 1 tax medicago truncatula g7jr01_medtr score=533.10 evalue=0.00e+00;
c41333/f2p2/1462	uncharacterized protein n 1 tax medicago truncatula i3sck7_medtr score=531.56 evalue=0.00e+00;
c41333/f2p2/1462	uncharacterized protein n 1 tax glycine max i1mtt3_soybn score=526.17 evalue=0.00e+00;
c41406/f1p1/1699	chloroplast protease n 2 tax magnoliophyta o99018_capan score=908.67 evalue=0.00e+00;
c41406/f1p1/1699	ftsh-like protein pftf n 1 tax nicotiana tabacum q9zp50_tobac score=904.05 evalue=0.00e+00;
c41406/f1p1/1699	cell division protein ftsh putative n 1 tax ricinus communis b9s304_ricco score=895.19 evalue=0.00e+00;
c41406/f1p1/1699	predicted protein (fragment) n 1 tax populus trichocarpa b9ia25_poptr score=885.56 evalue=0.00e+00;
c41406/f1p1/1699	putative uncharacterized protein n 1 tax vitis vinifera f6h539_vitvi score=885.17 evalue=0.00e+00;
c41762/f1p1/1754	uncharacterized protein n 1 tax solanum lycopersicum k4brx8_sollc score=593.96 evalue=0.00e+00;
c41762/f1p1/1754	putative uncharacterized protein n 1 tax vitis vinifera f6hni8_vitvi score=414.07 evalue=3.45e-135;
c41762/f1p1/1754	putative uncharacterized protein n 1 tax vitis vinifera a5aes9_vitvi score=410.99 evalue=4.88e-134;
c41762/f1p1/1754	predicted protein (fragment) n 1 tax populus trichocarpa b9hu29_poptr score=342.81 evalue=4.52e-108;
c41762/f1p1/1754	putative uncharacterized protein n 1 tax vitis vinifera f6hqz6_vitvi score=340.89 evalue=7.08e-107;
c44251/f2p5/1481	uncharacterized protein n 1 tax solanum lycopersicum k4dbr8_sollc score=687.57 evalue=0.00e+00;
c44251/f2p5/1481	putative uncharacterized protein n 1 tax vitis vinifera d7tbj2_vitvi score=602.44 evalue=0.00e+00;
c44251/f2p5/1481	uncharacterized protein n 1 tax glycine max i1kpy5_soybn score=585.87 evalue=0.00e+00;
c44251/f2p5/1481	lactoylglutathione lyase n 1 tax medicago truncatula g7l865_medtr score=585.49 evalue=0.00e+00;
c44251/f2p5/1481	uncharacterized protein n 2 tax medicago truncatula b7fjh9_medtr score=583.95 evalue=0.00e+00;
c45101/f127p23/910	chlorophyll a-b binding protein cp24 10b chloroplastic n 1 tax solanum lycopersicum cb4b_sollc score=497.28 evalue=1.63e-175;
c45101/f127p23/910	chloroplast pigment-binding protein cp24 n 1 tax nicotiana tabacum q0pws6_tobac score=466.08 evalue=3.23e-163;
c45101/f127p23/910	poly (3-hydroxybutyrate) depolymerase n 1 tax rhodanobacter sp. 116-2 i4wva4_9gamm score=459.14 evalue=3.01e-159;
c45101/f127p23/910	chlorophyll a-b binding protein cp24 10a chloroplastic n 1 tax solanum lycopersicum cb4a_sollc score=450.28 evalue=5.42e-157;
c45101/f127p23/910	chloroplast chlorophyll a/b-binding protein cp24 n 1 tax medicago truncatula g7int9_medtr score=438.73 evalue=2.17e-152;
c45334/f54p28/3163	uncharacterized protein n 1 tax solanum lycopersicum k4c785_sollc score=1802.72 evalue=0.00e+00;
c45334/f54p28/3163	uncharacterized protein n 1 tax glycine max i1ks56_soybn score=1422.91 evalue=0.00e+00;
c45334/f54p28/3163	uncharacterized protein n 1 tax glycine max i1k3r3_soybn score=1420.99 evalue=0.00e+00;
c45334/f54p28/3163	aspartokinase-homoserine dehydrogenase n 1 tax glycine max o63067_soybn score=1419.83 evalue=0.00e+00;
c45334/f54p28/3163	predicted protein (fragment) n 1 tax populus trichocarpa b9mwj3_poptr score=1419.06 evalue=0.00e+00;
c45394/f47p41/2808	mitochondrial protein putative n 1 tax medicago truncatula g7i9t8_medtr score=453.37 evalue=0.00e+00;
c45394/f47p41/2808	mitochondrial protein putative n 1 tax medicago truncatula g7i9t8_medtr score=171.01 evalue=0.00e+00;
c45394/f47p41/2808	mitochondrial protein putative n 1 tax medicago truncatula g7i9t8_medtr score=168.70 evalue=0.00e+00;

c45394/f47p41/2808	mitochondrial protein putative n 1 tax medicago truncatula g7i9t8_medtr score=132.11 evalue=0.00e+00;
c45394/f47p41/2808	mitochondrial protein putative n 1 tax medicago truncatula g7i9t8_medtr score=106.69 evalue=0.00e+00;
c45538/f27p9/2653	uncharacterized protein n 1 tax solanum lycopersicum k4bva7_sollc score=89.74 evalue=6.30e-18;
c45637/f10p8/3288	atp-dependent clp protease atp-binding subunit clpa homolog cd4a chloroplastic n 1 tax solanum lycopersicum k4bly5_sollc score=1618.21 evalue=0.00e+00;
c45637/f10p8/3288	atp-dependent clp protease atp-binding subunit clpa homolog cd4a chloroplastic n 1 tax solanum lycopersicum clpaa_sollc score=1615.51 evalue=0.00e+00;
c45637/f10p8/3288	atp-dependent clp protease atp-binding subunit clpa homolog cd4b chloroplastic n 1 tax solanum lycopersicum k4df00_sollc score=1529.23 evalue=0.00e+00;
c45637/f10p8/3288	atp-dependent clp protease atp-binding subunit clpa homolog cd4b chloroplastic n 1 tax solanum lycopersicum clpab_sollc score=1527.69 evalue=0.00e+00;
c45637/f10p8/3288	putative uncharacterized protein n 1 tax vitis vinifera f6gt40_vitvi score=1491.09 evalue=0.00e+00;
c45933/f12p36/3311	atp-dependent clp protease atp-binding subunit clpa homolog cd4b chloroplastic n 1 tax solanum lycopersicum k4df00_sollc score=1672.52 evalue=0.00e+00;
c45933/f12p36/3311	atp-dependent clp protease atp-binding subunit clpa homolog cd4b chloroplastic n 1 tax solanum lycopersicum clpab_sollc score=1667.90 evalue=0.00e+00;
c45933/f12p36/3311	atp-dependent clp protease atp-binding subunit clpa homolog cd4a chloroplastic n 1 tax solanum lycopersicum k4bly5_sollc score=1570.06 evalue=0.00e+00;
c45933/f12p36/3311	atp-dependent clp protease atp-binding subunit clpa homolog cd4a chloroplastic n 1 tax solanum lycopersicum clpaa_sollc score=1568.13 evalue=0.00e+00;
c45933/f12p36/3311	uncharacterized protein n 1 tax vitis vinifera f6gt40_vitvi score=1528.07 evalue=0.00e+00;
c46003/f2p2/2838	uncharacterized protein n 1 tax solanum lycopersicum k4bne9_sollc score=1164.06 evalue=0.00e+00;
c46003/f2p2/2838	uncharacterized protein n 1 tax solanum lycopersicum k4bxw8_sollc score=989.95 evalue=0.00e+00;
c46003/f2p2/2838	uncharacterized protein n 1 tax solanum lycopersicum k4atn2_sollc score=964.53 evalue=0.00e+00;
c46003/f2p2/2838	atp binding protein putative n 1 tax ricinus communis b9ref5_ricco score=889.41 evalue=0.00e+00;
c46003/f2p2/2838	putative uncharacterized protein n 2 tax vitis vinifera f6hf73_vitvi score=877.86 evalue=0.00e+00;
c46152/f5p6/3523	uncharacterized protein n 1 tax solanum lycopersicum k4cbj2_sollc score=1914.04 evalue=0.00e+00;
c46152/f5p6/3523	putative uncharacterized protein n 1 tax vitis vinifera a5brs2_vitvi score=1858.19 evalue=0.00e+00;
c46152/f5p6/3523	116 kd u5 small nuclear ribonucleoprotein component putative n 1 tax ricinus communis b9t2n2_ricco score=1785.39 evalue=0.00e+00;
c46152/f5p6/3523	uncharacterized protein n 1 tax glycine max i1lzw4_soybn score=1782.69 evalue=0.00e+00;
c46152/f5p6/3523	uncharacterized protein n 1 tax glycine max i1mtz8_soybn score=1781.92 evalue=0.00e+00;
c46241/f3p4/2722	methionine synthase n 1 tax solanum tuberosum q9lm03_soltu score=862.06 evalue=0.00e+00;
c46241/f3p4/2722	methionine synthase n 1 tax solanum tuberosum q9lm03_soltu score=649.82 evalue=0.00e+00;
c46241/f3p4/2722	uncharacterized protein n 1 tax solanum lycopersicum k4d338_sollc score=855.51 evalue=0.00e+00;
c46241/f3p4/2722	uncharacterized protein n 1 tax solanum lycopersicum k4d338_sollc score=650.97 evalue=0.00e+00;
c46241/f3p4/2722	methionine synthase n 1 tax nicotiana suaveolens q069k2_9sola score=812.37 evalue=0.00e+00;
c46418/f5p5/3435	uncharacterized protein n 1 tax solanum lycopersicum k4d7u2_sollc score=1596.64 evalue=0.00e+00;
c46418/f5p5/3435	putative uncharacterized protein n 1 tax vitis vinifera d7tgm4_vitvi score=1318.91 evalue=0.00e+00;
c46418/f5p5/3435	putative uncharacterized protein n 1 tax vitis vinifera d7sn01_vitvi score=1311.98 evalue=0.00e+00;

c46418/f5p5/3435	drp n 1 tax cucumis melo q5dmx3_cucme score=1301.58 evalue=0.00e+00;
c46418/f5p5/3435	uncharacterized protein n 1 tax glycine max i1mqt0_soybn score=1300.42 evalue=0.00e+00;
c46615/f5p4/2656	uncharacterized protein n 1 tax solanum lycopersicum k4cpj0_sollc score=1157.90 evalue=0.00e+00;
c46615/f5p4/2656	predicted protein n 1 tax populus trichocarpa b9gx60_poptr score=832.40 evalue=0.00e+00;
c46615/f5p4/2656	predicted protein n 1 tax populus trichocarpa b9gl93_poptr score=824.70 evalue=0.00e+00;
c46615/f5p4/2656	putative uncharacterized protein n 1 tax vitis vinifera f6hur5_vitvi score=804.28 evalue=0.00e+00;
c46615/f5p4/2656	uncharacterized protein n 1 tax glycine max i1kph8_soybn score=794.27 evalue=0.00e+00;
c46676/f5p2/2985	uncharacterized protein n 1 tax solanum lycopersicum k4aw53_sollc score=1093.95 evalue=0.00e+00;
c46676/f5p2/2985	putative uncharacterized protein n 1 tax vitis vinifera f6h711_vitvi score=594.73 evalue=0.00e+00;
c46676/f5p2/2985	flowering time control protein fca putative n 1 tax ricinus communis b9rzt3_ricco score=499.59 evalue=9.25e-159;
c46676/f5p2/2985	rna binding / abscisic acid binding protein n 1 tax arabidopsis thaliana f4jlr7_arath score=422.17 evalue=5.52e-131;
c46676/f5p2/2985	flowering time control protein fca n 3 tax arabidopsis thaliana fca_arath score=424.09 evalue=1.01e-130;
c47159/f1p14/3596	uncharacterized protein n 1 tax solanum lycopersicum k4bq77_sollc score=2268.43 evalue=0.00e+00;
c47159/f1p14/3596	mg protoporphyrin ix chelatase n 1 tax nicotiana tabacum o22435_tobac score=2191.77 evalue=0.00e+00;
c47159/f1p14/3596	protoporphyrin ix:mg chelatase n 1 tax antirrhinum majus q07893_antma score=2105.49 evalue=0.00e+00;
c47159/f1p14/3596	magnesium chelatase h subunit n 1 tax camellia sinensis f8spg3_camsi score=2093.93 evalue=0.00e+00;
c47159/f1p14/3596	uncharacterized protein n 1 tax glycine max i1laa1_soybn score=2083.53 evalue=0.00e+00;
c47490/f4p10/3020	uncharacterized protein n 1 tax solanum lycopersicum k4bvk0_sollc score=1600.10 evalue=0.00e+00;
c47490/f4p10/3020	predicted protein n 1 tax populus trichocarpa b9gqy2_poptr score=571.24 evalue=0.00e+00;
c47490/f4p10/3020	putative uncharacterized protein n 1 tax vitis vinifera f6h068_vitvi score=544.27 evalue=6.98e-176;
c47490/f4p10/3020	putative uncharacterized protein n 1 tax ricinus communis b9r858_ricco score=533.87 evalue=3.45e-171;
c47490/f4p10/3020	predicted protein n 1 tax populus trichocarpa b9h4k1_poptr score=519.24 evalue=5.61e-166;
c48143/f1p2/1453	uncharacterized protein n 1 tax solanum lycopersicum k4b1f9_sollc score=433.72 evalue=8.25e-141;
c48310/f1p2/1910	uncharacterized protein n 1 tax solanum lycopersicum k4dap1_sollc score=612.45 evalue=0.00e+00;
c48310/f1p2/1910	putative uncharacterized protein n 1 tax vitis vinifera f6haf1_vitvi score=363.61 evalue=2.19e-115;
c48310/f1p2/1910	predicted protein n 1 tax populus trichocarpa b9hq80_poptr score=324.71 evalue=1.17e-100;
c48310/f1p2/1910	predicted protein n 1 tax populus trichocarpa b9ghl2_poptr score=314.31 evalue=3.53e-97;
c48310/f1p2/1910	calmodulin binding protein putative n 1 tax ricinus communis b9rj06_ricco score=305.06 evalue=3.99e-93;
c48392/f3p5/3449	uncharacterized protein n 1 tax solanum lycopersicum k4bnn5_sollc score=1381.70 evalue=0.00e+00;
c48392/f3p5/3449	putative uncharacterized protein n 1 tax vitis vinifera f6hua4_vitvi score=986.48 evalue=0.00e+00;
c48392/f3p5/3449	nucleoporin 98 n 1 tax daucus carota a9zp15_dauca score=907.13 evalue=0.00e+00;

c48392/f3p5/3449	predicted protein n 1 tax populus trichocarpa b9i0p2_poptr score=793.50 evalue=0.00e+00;
c48392/f3p5/3449	uncharacterized protein n 1 tax glycine max i1lvb2_soybn score=770.00 evalue=0.00e+00;
c48767/f2p3/3047	dna repair and recombination protein rad54b putative n 1 tax ricinus communis b9ryj2_ricco score=1293.10 evalue=0.00e+00;
c48767/f2p3/3047	putative uncharacterized protein n 1 tax vitis vinifera f6hqc0_vitvi score=1236.09 evalue=0.00e+00;
c48767/f2p3/3047	rad54-like protein n 1 tax arabidopsis thaliana q0pcs3_arath score=1235.71 evalue=0.00e+00;
c48767/f2p3/3047	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata d7l9w7_arall score=1232.24 evalue=0.00e+00;
c48767/f2p3/3047	putative uncharacterized protein n 1 tax vitis vinifera a5bi61_vitvi score=1230.31 evalue=0.00e+00;
c48783/f1p6/1528	uncharacterized protein n 1 tax solanum lycopersicum k4bak9_sollc score=761.91 evalue=0.00e+00;
c48783/f1p6/1528	amine oxidase putative n 1 tax ricinus communis b9rnm3_ricco score=529.25 evalue=0.00e+00;
c48783/f1p6/1528	putative uncharacterized protein n 1 tax vitis vinifera d7st93_vitvi score=513.84 evalue=1.76e-175;
c48783/f1p6/1528	amine oxidase family protein n 1 tax arabidopsis lyrata subsp. lyrata d7l8a1_arall score=497.28 evalue=7.99e-169;
c48783/f1p6/1528	fad/nad(p)-binding oxidoreductase domain-containing protein n 1 tax arabidopsis thaliana q9sf45_arath score=494.20 evalue=1.25e-167;
c48834/f1p5/3545	uncharacterized protein n 1 tax solanum lycopersicum k4cvw5_sollc score=1791.93 evalue=0.00e+00;
c48834/f1p5/3545	putative uncharacterized protein n 1 tax vitis vinifera f6hdz1_vitvi score=493.81 evalue=9.40e-152;
c48834/f1p5/3545	putative uncharacterized protein n 1 tax ricinus communis b9rte3_ricco score=474.94 evalue=1.54e-144;
c48834/f1p5/3545	uncharacterized protein n 1 tax glycine max k7lme3_soybn score=407.53 evalue=1.08e-120;
c48834/f1p5/3545	uncharacterized protein n 1 tax glycine max k7k5h3_soybn score=404.06 evalue=8.06e-119;
c48940/f1p1/2265	uncharacterized protein n 1 tax solanum lycopersicum k4bd04_sollc score=869.38 evalue=0.00e+00;
c48940/f1p1/2265	putative uncharacterized protein n 1 tax vitis vinifera f6hri9_vitvi score=523.86 evalue=6.10e-174;
c48940/f1p1/2265	putative uncharacterized protein n 1 tax vitis vinifera a5cay7_vitvi score=512.69 evalue=4.27e-171;
c48940/f1p1/2265	predicted protein n 1 tax populus trichocarpa b9ibm4_poptr score=457.60 evalue=3.88e-148;
c48940/f1p1/2265	putative uncharacterized protein n 1 tax vitis vinifera f6h175_vitvi score=450.67 evalue=2.05e-145;
c49116/f1p3/3017	serine/threonine-protein kinase n 1 tax solanum lycopersicum k4b9i0_sollc score=1623.99 evalue=0.00e+00;
c49116/f1p3/3017	serine/threonine-protein kinase n 1 tax solanum lycopersicum k4bea0_sollc score=1244.57 evalue=0.00e+00;
c49116/f1p3/3017	serine/threonine-protein kinase n 1 tax ipomoea trifida q40096_ipotf score=1157.90 evalue=0.00e+00;
c49116/f1p3/3017	serine/threonine-protein kinase n 3 tax vitis vinifera f6hct4_vitvi score=1073.92 evalue=0.00e+00;
c49116/f1p3/3017	serine/threonine-protein kinase n 1 tax populus trichocarpa b9h1v2_poptr score=1041.18 evalue=0.00e+00;
c49357/f1p2/2552	uncharacterized protein n 1 tax solanum lycopersicum k4ax76_sollc score=1316.21 evalue=0.00e+00;
c49357/f1p2/2552	trna uridine 5-carboxymethylaminomethyl modification enzyme mnmg n 1 tax medicago truncatula g7le56_medtr score=1115.14 evalue=0.00e+00;
c49357/f1p2/2552	ncharacterized protein n 1 tax glycine max i1k513_soybn score=1113.60 evalue=0.00e+00;
c49357/f1p2/2552	putative uncharacterized protein n 1 tax vitis vinifera f6i0c6_vitvi score=1113.21 evalue=0.00e+00;

c49357/f1p2/2552	uncharacterized protein n 1 tax glycine max i1knw3_soybn score=1100.50 evalue=0.00e+00;
c49538/f1p1/2280	uncharacterized protein n 2 tax solanum lycopersicum k4ay44_sollc score=1216.45 evalue=0.00e+00;
c49538/f1p1/2280	utp-glucose-1-phosphate uridylyltransferase putative n 1 tax ricinus communis b9sd97_ricco score=622.85 evalue=0.00e+00;
c49538/f1p1/2280	putative udp-glucose pyrophosphorylase n 1 tax trifolium pratense q2pev2_tripr score=578.17 evalue=0.00e+00;
c49538/f1p1/2280	utp-glucose-1-phosphate uridylyltransferase n 1 tax medicago truncatula g7j8l5_medtr score=533.10 evalue=5.82e-177;
c49538/f1p1/2280	uncharacterized protein n 1 tax glycine max k7ks97_soybn score=462.61 evalue=2.22e-152;
c49644/f1p0/2988	uncharacterized protein n 1 tax solanum lycopersicum k4b2f3_sollc score=1337.01 evalue=0.00e+00;
c49644/f1p0/2988	sentrin/sumo-specific protease putative n 1 tax ricinus communis b9s9i8_ricco score=476.48 evalue=6.30e-149;
c49644/f1p0/2988	uncharacterized protein n 1 tax glycine max k7m1w1_soybn score=444.51 evalue=1.44e-136;
c49644/f1p0/2988	predicted protein n 1 tax populus trichocarpa b9heb6_poptr score=410.22 evalue=4.14e-124;
c49644/f1p0/2988	sentrin-specific protease n 1 tax medicago truncatula g7is57_medtr score=409.45 evalue=1.15e-122;
c49699/f1p3/744	uncharacterized protein n 1 tax solanum lycopersicum k4bxd1_sollc score=239.19 evalue=3.03e-76;
c49699/f1p3/744	plastid-specific 30s ribosomal protein 3 chloroplast putative n 1 tax ricinus communis b9st11_ricco score=176.02 evalue=2.07e-51;
c49699/f1p3/744	predicted protein n 1 tax populus trichocarpa b9hwj9_poptr score=173.33 evalue=3.20e-50;
c49699/f1p3/744	predicted protein n 1 tax populus trichocarpa b9hj10_poptr score=172.94 evalue=4.81e-50;
c49699/f1p3/744	putative uncharacterized protein n 1 tax vitis vinifera f6hse3_vitvi score=164.85 evalue=3.22e-47;
c49749/f1p7/1856	uncharacterized protein n 2 tax solanum lycopersicum k4bsm2_sollc score=987.64 evalue=0.00e+00;
c49749/f1p7/1856	inositol-3-phosphate synthase n 1 tax nicotiana tabacum ino1_tobac score=979.55 evalue=0.00e+00;
c49749/f1p7/1856	inositol-3-phosphate synthase n 1 tax nicotiana paniculata ino1_nicpa score=977.24 evalue=0.00e+00;
c49749/f1p7/1856	uncharacterized protein n 1 tax solanum lycopersicum k4c1l6_sollc score=950.66 evalue=0.00e+00;
c49749/f1p7/1856	myo-inositol 1-phosphate synthase n 1 tax passiflora edulis f. flavicarpa q1hg62_pased score=946.81 evalue=0.00e+00;
c49806/f2p3/3212	uncharacterized protein n 1 tax solanum lycopersicum k4bxg7_sollc score=1581.62 evalue=0.00e+00;
c49806/f2p3/3212	uncharacterized protein n 1 tax glycine max i1j6r6_soybn score=1117.06 evalue=0.00e+00;
c49806/f2p3/3212	protein chup1 n 1 tax medicago truncatula g7jx26_medtr score=1075.85 evalue=0.00e+00;
c49806/f2p3/3212	uncharacterized protein n 1 tax brachypodium distachyon i1hg51_bradi score=778.86 evalue=0.00e+00;
c49806/f2p3/3212	putative uncharacterized protein n 1 tax vitis vinifera f6hf24_vitvi score=692.96 evalue=0.00e+00;
c49921/f1p3/3295	uncharacterized protein n 1 tax solanum lycopersicum k4bc59_sollc score=934.10 evalue=0.00e+00;
c49921/f1p3/3295	putative uncharacterized protein n 1 tax vitis vinifera f6h494_vitvi score=256.53 evalue=1.82e-123;
c49921/f1p3/3295	putative uncharacterized protein n 1 tax vitis vinifera f6h494_vitvi score=216.08 evalue=1.82e-123;
c49921/f1p3/3295	uncharacterized protein n 1 tax solanum lycopersicum k4bc59_sollc score=397.51 evalue=6.42e-120;
c49921/f1p3/3295	putative uncharacterized protein n 1 tax vitis vinifera a5c8l9_vitvi score=229.18 evalue=6.13e-82;

c50287/f2p15/1638	uncharacterized protein n 1 tax solanum lycopersicum k4bs97_sollc score=845.88 evalue=0.00e+00;
c50287/f2p15/1638	uncharacterized protein n 1 tax solanum lycopersicum k4bpq6_sollc score=777.32 evalue=0.00e+00;
c50287/f2p15/1638	uncharacterized protein n 1 tax glycine max i1k4u3_soybn score=753.44 evalue=0.00e+00;
c50287/f2p15/1638	predicted protein n 1 tax populus trichocarpa b9hg65_poptr score=753.05 evalue=0.00e+00;
c50287/f2p15/1638	putative uncharacterized protein n 1 tax populus trichocarpa a9ph46_poptr score=752.67 evalue=0.00e+00;
c50351/f1p2/3040	uncharacterized protein n 1 tax solanum lycopersicum k4df01_sollc score=1584.70 evalue=0.00e+00;
c50351/f1p2/3040	auxin response factor 2 n 1 tax solanum lycopersicum q2laj3_sollc score=1261.90 evalue=0.00e+00;
c50351/f1p2/3040	putative uncharacterized protein n 1 tax vitis vinifera d7sh69_vitvi score=1128.62 evalue=0.00e+00;
c50351/f1p2/3040	putative uncharacterized protein n 1 tax vitis vinifera a5bg94_vitvi score=1105.12 evalue=0.00e+00;
c50351/f1p2/3040	auxin-response factor n 1 tax citrus sinensis g9i820_citsi score=1070.46 evalue=0.00e+00;
c50567/f2p1/1423	uncharacterized protein n 1 tax solanum lycopersicum k4b9z1_sollc score=508.06 evalue=6.01e-177;
c50567/f2p1/1423	expansin n 1 tax solanum lycopersicum q9zp33_sollc score=441.04 evalue=1.91e-150;
c50567/f2p1/1423	expansin (fragment) n 1 tax solanum tuberosum d3ye74_soltu score=430.25 evalue=4.25e-147;
c50567/f2p1/1423	putative uncharacterized protein n 1 tax vitis vinifera f6hfw4_vitvi score=412.15 evalue=4.59e-139;
c50567/f2p1/1423	uncharacterized protein n 1 tax glycine max i1mbr5_soybn score=410.99 evalue=9.81e-139;
c51141/f1p3/1516	uncharacterized protein n 1 tax solanum lycopersicum k4ci87_sollc score=409.45 evalue=5.89e-136;
c51141/f1p3/1516	chloroplast zebra-necrosis protein n 1 tax nicotiana benthamiana b1a8t8_nicbe score=399.82 evalue=3.90e-132;
c51141/f1p3/1516	uncharacterized protein n 1 tax solanum lycopersicum k4b424_sollc score=399.05 evalue=5.33e-132;
c51141/f1p3/1516	putative uncharacterized protein n 1 tax vitis vinifera a5bbj4_vitvi score=359.76 evalue=5.53e-118;
c51141/f1p3/1516	putative uncharacterized protein n 1 tax vitis vinifera f6i101_vitvi score=358.61 evalue=4.99e-116;
c51229/f2p2/3967	uncharacterized protein n 1 tax solanum lycopersicum k4bdj4_sollc score=1913.27 evalue=0.00e+00;
c51229/f2p2/3967	uncharacterized protein n 1 tax solanum lycopersicum k4bdt0_sollc score=748.81 evalue=0.00e+00;
c51229/f2p2/3967	putative uncharacterized protein n 1 tax vitis vinifera f6i5k3_vitvi score=657.52 evalue=0.00e+00;
c51229/f2p2/3967	putative uncharacterized protein n 1 tax ricinus communis b9rbl2_ricco score=615.15 evalue=0.00e+00;
c51229/f2p2/3967	uncharacterized protein n 1 tax glycine max k7mfe9_soybn score=599.36 evalue=0.00e+00;
c51732/f1p4/2941	granule-bound starch synthase 2 chloroplastic/amyloplastic n 1 tax solanum tuberosum ssy2_soltu score=1474.53 evalue=0.00e+00;
c51732/f1p4/2941	uncharacterized protein n 2 tax solanum k4bbv6_sollc score=1472.60 evalue=0.00e+00;
c51732/f1p4/2941	putative uncharacterized protein n 1 tax vitis vinifera f6h5u3_vitvi score=1028.85 evalue=0.00e+00;
c51732/f1p4/2941	starch synthase putative n 1 tax ricinus communis b9t0t7_ricco score=1008.44 evalue=0.00e+00;
c51732/f1p4/2941	starch synthase isoform ii n 1 tax manihot esculenta b3srp3_manes score=1002.66 evalue=0.00e+00;
c52239/f1p4/2908	uncharacterized protein n 2 tax glycine max i1l2g5_soybn score=638.65 evalue=0.00e+00;

c52239/f1p4/2908	uncharacterized protein n 2 tax glycine max i1l2g5_soybn score=138.66 evalue=0.00e+00;
c52239/f1p4/2908	uncharacterized protein n 2 tax glycine max i1l2g5_soybn score=132.88 evalue=0.00e+00;
c52239/f1p4/2908	uncharacterized protein n 1 tax glycine max i1mjp7_soybn score=635.95 evalue=0.00e+00;
c52239/f1p4/2908	uncharacterized protein n 1 tax glycine max i1mjp7_soybn score=132.88 evalue=0.00e+00;
c52321/f1p0/2762	uncharacterized protein n 1 tax solanum lycopersicum k4bvz7_sollc score=1397.88 evalue=0.00e+00;
c52321/f1p0/2762	sugar transporter putative n 1 tax ricinus communis b9r8s3_ricco score=1148.27 evalue=0.00e+00;
c52321/f1p0/2762	putative hexose transporter n 1 tax vitis vinifera q4u339_vitvi score=1119.38 evalue=0.00e+00;
c52321/f1p0/2762	putative uncharacterized protein n 1 tax vitis vinifera a5bh92_vitvi score=1117.45 evalue=0.00e+00;
c52321/f1p0/2762	predicted protein n 1 tax populus trichocarpa b9h5v3_poptr score=1114.37 evalue=0.00e+00;
c52435/f2p0/3276	uncharacterized protein n 1 tax solanum lycopersicum k4cvt7_sollc score=1482.23 evalue=0.00e+00;
c52435/f2p0/3276	putative uncharacterized protein n 1 tax vitis vinifera f6hdw9_vitvi score=1077.77 evalue=0.00e+00;
c52435/f2p0/3276	pentatricopeptide repeat-containing protein putative n 1 tax ricinus communis b9rtg3_ricco score=1041.95 evalue=0.00e+00;
c52435/f2p0/3276	pentatricopeptide repeat-containing protein at3g23020 n 1 tax arabidopsis thaliana pp250_arath score=939.87 evalue=0.00e+00;
c52435/f2p0/3276	pentatricopeptide repeat-containing protein n 1 tax arabidopsis lyrata subsp. lyrata d7l2i5_arall score=938.33 evalue=0.00e+00;
c52828/f1p5/3355	uncharacterized protein n 1 tax solanum lycopersicum k4c689_sollc score=1764.20 evalue=0.00e+00;
c52828/f1p5/3355	uncharacterized protein n 1 tax solanum lycopersicum k4c692_sollc score=1472.60 evalue=0.00e+00;
c52828/f1p5/3355	putative uncharacterized protein n 1 tax vitis vinifera d7t712_vitvi score=1105.89 evalue=0.00e+00;
c52828/f1p5/3355	putative uncharacterized protein n 1 tax vitis vinifera a5bbr8_vitvi score=1098.19 evalue=0.00e+00;
c52828/f1p5/3355	putative uncharacterized protein rhel901 n 1 tax populus trichocarpa b9nbn6_poptr score=1056.20 evalue=0.00e+00;
c53114/f2p3/3330	uncharacterized protein n 1 tax solanum lycopersicum k4c1t0_sollc score=1323.53 evalue=0.00e+00;
c53114/f2p3/3330	putative uncharacterized protein n 1 tax vitis vinifera a5aeg1_vitvi score=866.68 evalue=0.00e+00;
c53114/f2p3/3330	putative uncharacterized protein n 1 tax vitis vinifera d7t4j9_vitvi score=866.30 evalue=0.00e+00;
c53114/f2p3/3330	adenosine diphosphatase putative n 1 tax ricinus communis b9t6c6_ricco score=835.48 evalue=0.00e+00;
c53114/f2p3/3330	mtn21-like protein n 1 tax populus trichocarpa b9n0r4_poptr score=808.13 evalue=0.00e+00;
c53164/f4p1/2663	uncharacterized protein n 1 tax solanum lycopersicum k4cvm7_sollc score=1450.26 evalue=0.00e+00;
c53164/f4p1/2663	putative uncharacterized protein n 1 tax vitis vinifera f6hds9_vitvi score=721.08 evalue=0.00e+00;
c53164/f4p1/2663	predicted protein n 1 tax populus trichocarpa b9hk03_poptr score=645.58 evalue=0.00e+00;
c53164/f4p1/2663	tso1 putative n 1 tax ricinus communis b9rtm0_ricco score=625.55 evalue=0.00e+00;
c53164/f4p1/2663	uncharacterized protein n 1 tax glycine max i1jar5_soybn score=611.68 evalue=0.00e+00;
c53351/f2p4/1695	uncharacterized protein n 1 tax solanum lycopersicum k4c3e5_sollc score=979.93 evalue=0.00e+00;
c53351/f2p4/1695	putative uncharacterized protein n 1 tax solanum tuberosum q2v9c4_soltu score=953.74 evalue=0.00e+00;

c53351/f2p4/1695	putative uncharacterized protein n 1 tax solanum tuberosum q2vci1_soltu score=911.75 evalue=0.00e+00;
c53351/f2p4/1695	putative uncharacterized protein (fragment) n 1 tax capsicum annuum a0mlw5_capan score=768.07 evalue=0.00e+00;
c53351/f2p4/1695	uncharacterized protein n 1 tax solanum lycopersicum k4cae8_sollc score=755.75 evalue=0.00e+00;
c53493/f1p0/2108	uncharacterized protein n 1 tax solanum lycopersicum k4ce62_sollc score=1256.51 evalue=0.00e+00;
c53493/f1p0/2108	putative uncharacterized protein n 1 tax vitis vinifera f6hgs6_vitvi score=989.95 evalue=0.00e+00;
c53493/f1p0/2108	predicted protein n 2 tax populus b9msz9_poptr score=969.15 evalue=0.00e+00;
c53493/f1p0/2108	xylem serine proteinase 1 putative n 1 tax ricinus communis b9rr97_ricco score=966.84 evalue=0.00e+00;
c53493/f1p0/2108	predicted protein n 1 tax arabidopsis lyrata subsp. lyrata d7l9b5_arall score=945.65 evalue=0.00e+00;
c53506/f1p7/3416	uncharacterized protein n 1 tax solanum lycopersicum k4bmh6_sollc score=1828.53 evalue=0.00e+00;
c53506/f1p7/3416	uncharacterized protein n 1 tax solanum lycopersicum k4c7u7_sollc score=1703.72 evalue=0.00e+00;
c53506/f1p7/3416	uncharacterized protein n 1 tax solanum lycopersicum k4df88_sollc score=1670.21 evalue=0.00e+00;
c53506/f1p7/3416	coatomer beta subunit putative n 1 tax ricinus communis b9sqc0_ricco score=1628.22 evalue=0.00e+00;
c53506/f1p7/3416	uncharacterized protein n 1 tax glycine max k7m8y1_soybn score=1627.45 evalue=0.00e+00;
c53759/f2p5/5028	uncharacterized protein n 1 tax solanum lycopersicum k4cg46_sollc score=1575.07 evalue=0.00e+00;
c53759/f2p5/5028	uncharacterized protein n 1 tax solanum lycopersicum k4cg46_sollc score=999.96 evalue=0.00e+00;
c53759/f2p5/5028	uncharacterized protein n 1 tax solanum lycopersicum k4cg46_sollc score=638.65 evalue=0.00e+00;
c53759/f2p5/5028	phosphoenolpyruvate carboxylase putative n 1 tax ricinus communis b9rwb8_ricco score=1479.54 evalue=0.00e+00;
c53759/f2p5/5028	phosphoenolpyruvate carboxylase putative n 1 tax ricinus communis b9rwb8_ricco score=959.13 evalue=0.00e+00;
c53953/f1p1/1856	uncharacterized protein n 1 tax solanum lycopersicum k4bxv2_sollc score=421.39 evalue=0.00e+00;
c53953/f1p1/1856	uncharacterized protein n 1 tax solanum lycopersicum k4bxv2_sollc score=365.93 evalue=0.00e+00;
c53953/f1p1/1856	putative uncharacterized protein n 1 tax vitis vinifera d7t9w6_vitvi score=310.84 evalue=7.27e-162;
c53953/f1p1/1856	putative uncharacterized protein n 1 tax vitis vinifera d7t9w6_vitvi score=288.89 evalue=7.27e-162;
c53953/f1p1/1856	putative uncharacterized protein n 1 tax medicago truncatula g7jy02_medtr score=303.91 evalue=1.45e-146;
c54308/f1p8/2447	uncharacterized protein n 1 tax solanum lycopersicum k4bmv8_sollc score=1286.17 evalue=0.00e+00;
c54308/f1p8/2447	uncharacterized protein n 1 tax solanum lycopersicum k4dfh4_sollc score=1046.19 evalue=0.00e+00;
c54308/f1p8/2447	protein sey1 putative n 1 tax ricinus communis b9sn36_ricco score=1020.76 evalue=0.00e+00;
c54308/f1p8/2447	putative uncharacterized protein n 1 tax vitis vinifera f6hy18_vitvi score=1000.35 evalue=0.00e+00;
c54308/f1p8/2447	predicted protein n 1 tax populus trichocarpa b9mws5_poptr score=993.42 evalue=0.00e+00;
c54601/f2p1/3156	uncharacterized protein n 1 tax solanum lycopersicum k4b0j6_sollc score=1426.77 evalue=0.00e+00;
c54601/f2p1/3156	putative uncharacterized protein n 1 tax vitis vinifera f6htw0_vitvi score=1311.59 evalue=0.00e+00;
c54601/f2p1/3156	nucleotide binding protein putative n 1 tax ricinus communis b9rev1_ricco score=1306.58 evalue=0.00e+00;

c54601/f2p1/3156	predicted protein n 1 tax populus trichocarpa b9mzj8_poptr score=1303.89 evalue=0.00e+00;
c54601/f2p1/3156	predicted protein n 1 tax populus trichocarpa b9i893_poptr score=1248.80 evalue=0.00e+00;
c54631/f1p0/1917	glucose-6-phosphate isomerase n 1 tax solanum tuberosum q68hc9_soltu score=1121.30 evalue=0.00e+00;
c54631/f1p0/1917	glucose-6-phosphate isomerase n 1 tax solanum lycopersicum q1pcd2_sollc score=1106.28 evalue=0.00e+00;
c54631/f1p0/1917	glucose-6-phosphate isomerase cytosolic n 4 tax oenothera g6pi_oenme score=997.65 evalue=0.00e+00;
c54631/f1p0/1917	glucose-6-phosphate isomerase cytosolic 1 n 1 tax clarkia mildrediae g6pi1_clami score=994.96 evalue=0.00e+00;
c54631/f1p0/1917	glucose-6-phosphate isomerase n 1 tax clarkia gracilis q9smj2_9myrt score=994.57 evalue=0.00e+00;
c54644/f1p18/5400	uncharacterized protein n 1 tax solanum lycopersicum k4bje6_sollc score=1432.93 evalue=0.00e+00;
c54644/f1p18/5400	uncharacterized protein n 1 tax solanum lycopersicum k4bje6_sollc score=825.47 evalue=0.00e+00;
c54644/f1p18/5400	uncharacterized protein n 1 tax solanum lycopersicum k4bje6_sollc score=446.05 evalue=0.00e+00;
c54644/f1p18/5400	uncharacterized protein n 1 tax solanum lycopersicum k4bje6_sollc score=187.58 evalue=0.00e+00;
c54644/f1p18/5400	putative uncharacterized protein n 1 tax vitis vinifera f6hf38_vitvi score=1196.42 evalue=0.00e+00;
c54645/f1p1/1474	uncharacterized protein n 1 tax solanum lycopersicum k4bx18_sollc score=238.81 evalue=1.02e-70;
c54645/f1p1/1474	putative uncharacterized protein n 1 tax solanum tuberosum q38m44_soltu score=186.81 evalue=8.92e-52;
c54645/f1p1/1474	putative uncharacterized protein n 1 tax solanum tuberosum q38m63_soltu score=106.30 evalue=2.59e-23;
c54645/f1p1/1474	predicted protein n 1 tax populus trichocarpa b9hj82_poptr score=56.61 evalue=6.38e-06;
c54729/f2p5/1458	uncharacterized protein n 1 tax solanum lycopersicum k4cnr6_sollc score=440.65 evalue=0.00e+00;
c54729/f2p5/1458	uncharacterized protein n 1 tax solanum lycopersicum k4cnr6_sollc score=310.07 evalue=0.00e+00;
c54729/f2p5/1458	transaldolase total2 n 1 tax solanum lycopersicum q941r1_sollc score=428.33 evalue=0.00e+00;
c54729/f2p5/1458	transaldolase total2 n 1 tax solanum lycopersicum q941r1_sollc score=308.14 evalue=0.00e+00;
c54729/f2p5/1458	putative uncharacterized protein n 1 tax vitis vinifera d7t5j5_vitvi score=374.01 evalue=5.23e-161;
c54878/f1p4/2939	uncharacterized protein n 1 tax solanum lycopersicum k4dgq0_sollc score=1490.32 evalue=0.00e+00;
c54878/f1p4/2939	uncharacterized protein n 1 tax solanum lycopersicum k4buk5_sollc score=1143.26 evalue=0.00e+00;
c54878/f1p4/2939	predicted protein n 1 tax populus trichocarpa b9gnn7_poptr score=1068.14 evalue=0.00e+00;
c54878/f1p4/2939	putative uncharacterized protein n 1 tax vitis vinifera f6h187_vitvi score=1056.59 evalue=0.00e+00;
c54878/f1p4/2939	predicted protein n 2 tax populus trichocarpa b9ibq2_poptr score=1055.43 evalue=0.00e+00;
c54926/f1p2/3081	uncharacterized protein n 1 tax solanum lycopersicum k4cv75_sollc score=1415.59 evalue=0.00e+00;
c54926/f1p2/3081	dna mismatch repair protein pms2 putative n 1 tax ricinus communis b9san7_ricco score=1025.00 evalue=0.00e+00;
c54926/f1p2/3081	predicted protein n 2 tax populus trichocarpa b9i9s8_poptr score=961.44 evalue=0.00e+00;
c54926/f1p2/3081	dna mismatch repair protein n 1 tax medicago truncatula g7if83_medtr score=931.78 evalue=0.00e+00;
c54926/f1p2/3081	uncharacterized protein n 2 tax glycine max k7lgx1_soybn score=931.40 evalue=0.00e+00;

c55139/f2p4/2804	uncharacterized protein n 1 tax solanum lycopersicum k4bva7_sollc score=89.74 evalue=6.95e-18;
c55233/f3p1/1659	uncharacterized protein n 1 tax solanum lycopersicum k4bm95_sollc score=330.10 evalue=1.06e-105;
c55233/f3p1/1659	predicted protein n 1 tax populus trichocarpa b9i2l7_poptr score=258.45 evalue=1.09e-76;
c55233/f3p1/1659	uncharacterized protein n 3 tax glycine max i1k5r4_soybn score=222.25 evalue=2.91e-63;
c55233/f3p1/1659	proline-rich protein putative n 1 tax ricinus communis b9t1n4_ricco score=214.54 evalue=8.41e-61;
c55233/f3p1/1659	uncharacterized protein n 1 tax glycine max c6t790_soybn score=210.31 evalue=1.05e-58;
c55239/f2p0/1519	uncharacterized protein n 1 tax solanum lycopersicum k4cqz8_sollc score=633.64 evalue=0.00e+00;
c55239/f2p0/1519	putative uncharacterized protein n 1 tax vitis vinifera d7tj39_vitvi score=563.53 evalue=0.00e+00;
c55239/f2p0/1519	inosine-uridine preferring ribonucleoside hydrolase n 1 tax medicago truncatula g7l609_medtr score=546.58 evalue=0.00e+00;
c55239/f2p0/1519	inosine-uridine preferring nucleoside hydrolase putative n 1 tax ricinus communis b9sru5_ricco score=543.12 evalue=0.00e+00;
c55239/f2p0/1519	predicted protein n 1 tax populus trichocarpa b9hbj9_poptr score=543.89 evalue=0.00e+00;
c56954/f3p1/1944	pyruvate kinase n 1 tax solanum lycopersicum k4bp30_sollc score=1035.02 evalue=0.00e+00;
c56954/f3p1/1944	pyruvate kinase cytosolic isozyme n 1 tax solanum tuberosum kpyc_soltu score=1028.47 evalue=0.00e+00;
c56954/f3p1/1944	pyruvate kinase n 1 tax solanum tuberosum q3s1n4_soltu score=1028.08 evalue=0.00e+00;
c56954/f3p1/1944	pyruvate kinase n 1 tax capsicum annuum q1i0x5_capan score=975.70 evalue=0.00e+00;
c56954/f3p1/1944	pyruvate kinase n 1 tax vitis vinifera f6hvy1_vitvi score=967.99 evalue=0.00e+00;
c57141/f2p1/1838	uncharacterized protein n 1 tax solanum lycopersicum k4dbg9_sollc score=687.18 evalue=0.00e+00;
c57141/f2p1/1838	uncharacterized protein n 1 tax solanum lycopersicum k4cen4_sollc score=593.96 evalue=0.00e+00;
c57141/f2p1/1838	putative uncharacterized protein n 1 tax vitis vinifera a5ah66_vitvi score=525.01 evalue=1.73e-175;
c57141/f2p1/1838	putative uncharacterized protein n 1 tax vitis vinifera f6hp06_vitvi score=524.24 evalue=3.65e-175;
c57141/f2p1/1838	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata d7l1n4_arall score=503.44 evalue=1.04e-167;
c57506/f2p11/3090	uncharacterized protein n 1 tax solanum lycopersicum k4cpc9_sollc score=1681.77 evalue=0.00e+00;
c57506/f2p11/3090	predicted protein n 2 tax populus trichocarpa b9gwt9_poptr score=1530.77 evalue=0.00e+00;
c57506/f2p11/3090	predicted protein n 1 tax populus trichocarpa b9gkf2_poptr score=1521.52 evalue=0.00e+00;
c57506/f2p11/3090	ap-2 complex subunit beta-1 putative n 1 tax ricinus communis b9sb76_ricco score=1509.58 evalue=0.00e+00;
c57506/f2p11/3090	uncharacterized protein n 1 tax glycine max i1lpd3_soybn score=1506.89 evalue=0.00e+00;
c57907/f48p56/2753	uncharacterized protein n 2 tax lycopersicon k4cbn0_sollc score=1425.99 evalue=0.00e+00;
c57907/f48p56/2753	vacuolar h+-pyrophosphatase n 1 tax solanum lycopersicum k4q1y8_sollc score=1424.45 evalue=0.00e+00;
c57907/f48p56/2753	inorganic pyrophosphatase n 1 tax nicotiana tabacum q43797_tobac score=1379.00 evalue=0.00e+00;
c57907/f48p56/2753	uncharacterized protein n 1 tax solanum lycopersicum k4dc72_sollc score=1352.42 evalue=0.00e+00;
c57907/f48p56/2753	vacuolar proton-pumping ppase n 1 tax chenopodium rubrum q8l5b2_cheru score=1336.63 evalue=0.00e+00;

c58389/f2p4/3534	uncharacterized protein n 1 tax solanum lycopersicum k4cqu3_sollc score=1811.58 evalue=0.00e+00;
c58389/f2p4/3534	putative uncharacterized protein n 1 tax vitis vinifera f6hlh4_vitvi score=1247.65 evalue=0.00e+00;
c58389/f2p4/3534	gamma-tubulin complex component putative n 1 tax ricinus communis b9t277_ricco score=1238.79 evalue=0.00e+00;
c58389/f2p4/3534	tubulin gamma complex-associated protein n 1 tax populus trichocarpa b9ha09_poptr score=1213.36 evalue=0.00e+00;
c58389/f2p4/3534	tubulin gamma complex-associated protein n 1 tax populus trichocarpa b9iib0_poptr score=1202.19 evalue=0.00e+00;
c58552/f2p0/3298	uncharacterized protein n 1 tax solanum lycopersicum k4cgz5_sollc score=1128.62 evalue=0.00e+00;
c58552/f2p0/3298	putative uncharacterized protein n 1 tax vitis vinifera f6h242_vitvi score=719.15 evalue=0.00e+00;
c58552/f2p0/3298	putative uncharacterized protein n 1 tax vitis vinifera f6h242_vitvi score=332.41 evalue=0.00e+00;
c58552/f2p0/3298	predicted protein (fragment) n 1 tax populus trichocarpa b9hzu8_poptr score=687.95 evalue=0.00e+00;
c58552/f2p0/3298	predicted protein (fragment) n 1 tax populus trichocarpa b9hzu8_poptr score=338.58 evalue=0.00e+00;
c58569/f2p7/3120	uncharacterized protein n 1 tax solanum lycopersicum k4bnl3_sollc score=1331.62 evalue=0.00e+00;
c58569/f2p7/3120	uncharacterized protein n 1 tax solanum lycopersicum k4bnl4_sollc score=1224.15 evalue=0.00e+00;
c58569/f2p7/3120	uncharacterized protein n 1 tax solanum lycopersicum k4bnl0_sollc score=1085.86 evalue=0.00e+00;
c58569/f2p7/3120	uncharacterized protein n 1 tax solanum lycopersicum k4czz5_sollc score=783.87 evalue=0.00e+00;
c58569/f2p7/3120	uncharacterized protein n 1 tax solanum lycopersicum k4bq24_sollc score=776.93 evalue=0.00e+00;
c58644/f3p3/3399	uncharacterized protein n 1 tax solanum lycopersicum k4bjf4_sollc score=1839.31 evalue=0.00e+00;
c58644/f3p3/3399	putative uncharacterized protein n 1 tax vitis vinifera f6he84_vitvi score=1406.73 evalue=0.00e+00;
c58644/f3p3/3399	dna-binding protein smubp-2 putative n 1 tax ricinus communis b9sde3_ricco score=1396.72 evalue=0.00e+00;
c58644/f3p3/3399	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata d7mhy2_arall score=1333.93 evalue=0.00e+00;
c58644/f3p3/3399	uncharacterized protein n 1 tax glycine max i1l7b1_soybn score=1322.38 evalue=0.00e+00;
c58925/f2p1/2553	putative uncharacterized protein n 1 tax vitis vinifera f6hvg4_vitvi score=450.28 evalue=7.91e-143;
c58925/f2p1/2553	putative uncharacterized protein n 1 tax ricinus communis b9rgc7_ricco score=440.27 evalue=1.22e-138;
c58925/f2p1/2553	uncharacterized protein n 1 tax glycine max k7lqm1_soybn score=417.54 evalue=8.70e-131;
c58925/f2p1/2553	uncharacterized protein n 1 tax glycine max k7lql9_soybn score=412.54 evalue=5.80e-129;
c58925/f2p1/2553	predicted protein n 1 tax populus trichocarpa b9gm26_poptr score=391.35 evalue=1.04e-120;
c59521/f1p4/2907	uncharacterized protein n 1 tax solanum lycopersicum k4b9z0_sollc score=1353.96 evalue=0.00e+00;
c59521/f1p4/2907	hop-interacting protein thi142 n 1 tax solanum lycopersicum g8z293_sollc score=1092.80 evalue=0.00e+00;
c59521/f1p4/2907	uncharacterized protein n 1 tax solanum lycopersicum k4b5s9_sollc score=1090.49 evalue=0.00e+00;
c59521/f1p4/2907	predicted protein n 1 tax populus trichocarpa b9n8h2_poptr score=1011.13 evalue=0.00e+00;
c59521/f1p4/2907	predicted protein n 1 tax populus trichocarpa b9hzh5_poptr score=1004.97 evalue=0.00e+00;
c59743/f1p253/1442	putative uncharacterized protein n 1 tax medicago truncatula g7k0e3_medtr score=154.45 evalue=2.01e-81;

c59743/f1p253/1442	putative uncharacterized protein n 1 tax medicago truncatula g7k0e3_medtr score=88.97 evalue=2.01e-81;
c59743/f1p253/1442	putative uncharacterized protein n 1 tax medicago truncatula g7k0e3_medtr score=79.72 evalue=2.01e-81;
c59743/f1p253/1442	putative uncharacterized protein n 1 tax medicago truncatula g7k0e3_medtr score=49.68 evalue=2.01e-81;
c59743/f1p253/1442	uncharacterized protein n 1 tax oxytricha trifallax j9i0r4_9spit score=231.88 evalue=1.51e-69;
c59750/f1p2/1189	uncharacterized protein n 1 tax solanum lycopersicum k4bq58_sollc score=689.11 evalue=0.00e+00;
c59750/f1p2/1189	b-1 4-glucanase n 1 tax gossypium gossypioides i1t8b8_gosgo score=547.35 evalue=0.00e+00;
c59750/f1p2/1189	predicted protein n 1 tax populus trichocarpa b9i5v9_poptr score=545.81 evalue=0.00e+00;
c59750/f1p2/1189	b-1 4-glucanase n 4 tax gossypium i1t8a1_gostu score=546.58 evalue=0.00e+00;
c59750/f1p2/1189	b-1 4-glucanase n 1 tax gossypium aridum i1t8b7_gosai score=546.20 evalue=0.00e+00;
c59827/f1p8/3128	uncharacterized protein n 1 tax solanum lycopersicum k4bnl3_sollc score=1331.62 evalue=0.00e+00;
c59827/f1p8/3128	uncharacterized protein n 1 tax solanum lycopersicum k4bnl4_sollc score=1224.15 evalue=0.00e+00;
c59827/f1p8/3128	uncharacterized protein n 1 tax solanum lycopersicum k4bnl0_sollc score=1085.09 evalue=0.00e+00;
c59827/f1p8/3128	uncharacterized protein n 1 tax solanum lycopersicum k4czz5_sollc score=783.87 evalue=0.00e+00;
c59827/f1p8/3128	uncharacterized protein n 1 tax solanum lycopersicum k4bq24_sollc score=776.93 evalue=0.00e+00;
c60008/f1p3/2716	uncharacterized protein n 1 tax solanum lycopersicum k4cwx5_sollc score=1487.24 evalue=0.00e+00;
c60008/f1p3/2716	glucan/water dikinase n 1 tax solanum tuberosum d2jrz6_soltu score=1472.60 evalue=0.00e+00;
c60008/f1p3/2716	putative uncharacterized protein n 1 tax vitis vinifera f6i490_vitvi score=1156.74 evalue=0.00e+00;
c60008/f1p3/2716	chloroplast alpha-glucan water dikinase putative n 1 tax ricinus communis b9rxz3_ricco score=1143.64 evalue=0.00e+00;
c60008/f1p3/2716	uncharacterized protein n 1 tax glycine max i1lfl5_soybn score=1035.40 evalue=0.00e+00;
c60079/f1p3/3762	uncharacterized protein n 1 tax solanum lycopersicum k4biv0_sollc score=1166.76 evalue=0.00e+00;
c60079/f1p3/3762	uncharacterized protein n 1 tax solanum lycopersicum k4biv0_sollc score=760.75 evalue=0.00e+00;
c60079/f1p3/3762	uncharacterized protein n 1 tax solanum lycopersicum k4c594_sollc score=816.61 evalue=0.00e+00;
c60079/f1p3/3762	uncharacterized protein n 1 tax solanum lycopersicum k4c594_sollc score=442.19 evalue=0.00e+00;
c60079/f1p3/3762	putative uncharacterized protein n 1 tax vitis vinifera f6hce8_vitvi score=457.99 evalue=0.00e+00;
c60336/f1p5/2945	uncharacterized protein n 1 tax solanum lycopersicum k4chv6_sollc score=1311.98 evalue=0.00e+00;
c60336/f1p5/2945	putative uncharacterized protein n 1 tax ricinus communis b9t478_ricco score=305.45 evalue=5.64e-88;
c60336/f1p5/2945	uncharacterized protein n 1 tax glycine max k7m997_soybn score=295.82 evalue=4.50e-83;
c60336/f1p5/2945	uncharacterized protein n 1 tax glycine max k7m996_soybn score=295.43 evalue=5.70e-83;
c60336/f1p5/2945	uncharacterized protein n 1 tax glycine max k7lpg9_soybn score=288.89 evalue=2.00e-81;
c60725/f1p4/2571	uncharacterized protein n 1 tax solanum lycopersicum k4bjs3_sollc score=1376.69 evalue=0.00e+00;
c60725/f1p4/2571	putative uncharacterized protein n 2 tax vitis vinifera f6hvr5_vitvi score=1308.12 evalue=0.00e+00;

c60725/f1p4/2571	predicted protein n 1 tax populus trichocarpa b9i4z5_poptr score=1283.86 evalue=0.00e+00;
c60725/f1p4/2571	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata d7kje9_arall score=1266.14 evalue=0.00e+00;
c60725/f1p4/2571	predicted protein n 1 tax populus trichocarpa b9n358_poptr score=1251.50 evalue=0.00e+00;
c60827/f1p2/2980	uncharacterized protein n 1 tax solanum lycopersicum k4brx7_sollc score=938.33 evalue=0.00e+00;
c60827/f1p2/2980	mitochondrial carrier protein putative n 1 tax ricinus communis b9sun5_ricco score=561.61 evalue=0.00e+00;
c60827/f1p2/2980	mitochondrial carrier protein putative n 1 tax ricinus communis b9sun5_ricco score=429.48 evalue=0.00e+00;
c60827/f1p2/2980	mitochondrial carrier protein putative n 1 tax ricinus communis b9sun5_ricco score=75.48 evalue=0.00e+00;
c60827/f1p2/2980	putative uncharacterized protein n 1 tax vitis vinifera d7tmd3_vitvi score=560.07 evalue=0.00e+00;
c60936/f1p3/3212	uncharacterized protein n 1 tax solanum lycopersicum k4dhl1_sollc score=1257.66 evalue=0.00e+00;
c60936/f1p3/3212	putative uncharacterized protein n 1 tax vitis vinifera d7snt6_vitvi score=425.25 evalue=6.22e-130;
c60936/f1p3/3212	putative uncharacterized protein n 1 tax vitis vinifera a5c2x9_vitvi score=387.50 evalue=2.08e-115;
c60936/f1p3/3212	putative uncharacterized protein n 1 tax ricinus communis b9rwi0_ricco score=220.32 evalue=3.28e-58;
c60936/f1p3/3212	predicted protein n 1 tax populus trichocarpa b9ijh5_poptr score=211.46 evalue=5.25e-55;
c61081/f1p6/2951	uncharacterized protein n 1 tax solanum lycopersicum k4bq77_sollc score=1936.00 evalue=0.00e+00;
c61081/f1p6/2951	mg protoporphyrin ix chelatase n 1 tax nicotiana tabacum o22435_tobac score=1866.66 evalue=0.00e+00;
c61081/f1p6/2951	uncharacterized protein n 1 tax glycine max i1laa1_soybn score=1825.83 evalue=0.00e+00;
c61081/f1p6/2951	protoporphyrin ix:mg chelatase n 1 tax antirrhinum majus q07893_antma score=1813.12 evalue=0.00e+00;
c61081/f1p6/2951	magnesium chelatase h subunit n 1 tax camellia sinensis f8spg3_camsi score=1811.19 evalue=0.00e+00;
c61400/f1p3/3089	uncharacterized protein n 1 tax solanum lycopersicum k4dfm1_sollc score=1837.39 evalue=0.00e+00;
c61400/f1p3/3089	predicted protein n 1 tax populus trichocarpa b9n7f7_poptr score=1390.17 evalue=0.00e+00;
c61400/f1p3/3089	putative uncharacterized protein n 1 tax ricinus communis b9st78_ricco score=1370.53 evalue=0.00e+00;
c61400/f1p3/3089	uncharacterized protein n 1 tax arabidopsis thaliana f4jfr5_arath score=1358.20 evalue=0.00e+00;
c61400/f1p3/3089	at3g14120/mag2_7 n 1 tax arabidopsis thaliana q84me0_arath score=1356.27 evalue=0.00e+00;
c61764/f1p7/2166	beta-galactosidase n 1 tax solanum lycopersicum k4bew1_sollc score=1289.25 evalue=0.00e+00;
c61764/f1p7/2166	beta-galactosidase n 1 tax solanum lycopersicum a2jgx1_sollc score=1288.09 evalue=0.00e+00;
c61764/f1p7/2166	beta-galactosidase n 1 tax solanum lycopersicum e3uvw9_sollc score=1287.32 evalue=0.00e+00;
c61764/f1p7/2166	beta-galactosidase n 1 tax vitis vinifera d7swf1_vitvi score=962.21 evalue=0.00e+00;
c61764/f1p7/2166	beta-galactosidase n 1 tax pyrus pyrifolia q5ccq0_pyrpy score=904.82 evalue=0.00e+00;
c61767/f1p2/3290	uncharacterized protein n 1 tax solanum lycopersicum k4d1n9_sollc score=1033.09 evalue=0.00e+00;
c61767/f1p2/3290	uncharacterized protein n 1 tax solanum lycopersicum k4b466_sollc score=795.81 evalue=0.00e+00;
c61767/f1p2/3290	putative uncharacterized protein n 1 tax vitis vinifera f6i0v6_vitvi score=630.17 evalue=0.00e+00;

c61767/f1p2/3290	predicted protein n 1 tax populus trichocarpa b9hqy0_poptr score=607.45 evalue=0.00e+00;
c61767/f1p2/3290	putative uncharacterized protein n 1 tax ricinus communis b9sid1_ricco score=600.90 evalue=0.00e+00;
c62003/f1p2/3383	uncharacterized protein n 1 tax solanum lycopersicum k4ddz1_sollc score=1534.62 evalue=0.00e+00;
c62003/f1p2/3383	uncharacterized protein n 1 tax solanum lycopersicum k4bbf9_sollc score=956.05 evalue=0.00e+00;
c62003/f1p2/3383	putative uncharacterized protein n 1 tax vitis vinifera f6hux2_vitvi score=799.27 evalue=0.00e+00;
c62003/f1p2/3383	rrm/rnp domain putative n 1 tax ricinus communis b9sf86_ricco score=762.68 evalue=0.00e+00;
c62003/f1p2/3383	predicted protein n 1 tax populus trichocarpa b9ijm5_poptr score=731.48 evalue=0.00e+00;
c62216/f1p6/2966	uncharacterized protein n 1 tax solanum lycopersicum k4cg46_sollc score=1277.69 evalue=0.00e+00;
c62216/f1p6/2966	uncharacterized protein n 1 tax solanum lycopersicum k4cg46_sollc score=638.26 evalue=0.00e+00;
c62216/f1p6/2966	phosphoenolpyruvate carboxylase 1 n 1 tax gossypium hirsutum o23946_goshi score=1202.58 evalue=0.00e+00;
c62216/f1p6/2966	phosphoenolpyruvate carboxylase 1 n 1 tax gossypium hirsutum o23946_goshi score=577.78 evalue=0.00e+00;
c62216/f1p6/2966	phosphoenolpyruvate carboxylase putative n 1 tax ricinus communis b9rwb8_ricco score=1198.34 evalue=0.00e+00;
c62300/f1p3/2374	uncharacterized protein n 1 tax solanum lycopersicum k4cgp6_sollc score=1261.90 evalue=0.00e+00;
c62300/f1p3/2374	putative uncharacterized protein n 2 tax vitis vinifera f6h2k4_vitvi score=1246.49 evalue=0.00e+00;
c62300/f1p3/2374	uncharacterized protein n 1 tax glycine max i1ktg8_soybn score=1233.01 evalue=0.00e+00;
c62300/f1p3/2374	uncharacterized protein n 1 tax glycine max i1mi49_soybn score=1231.47 evalue=0.00e+00;
c62300/f1p3/2374	uncharacterized protein n 1 tax glycine max i1m2v7_soybn score=1228.00 evalue=0.00e+00;
c62646/f1p9/2676	uncharacterized protein n 2 tax solanum lycopersicum k4c390_sollc score=1352.42 evalue=0.00e+00;
c62646/f1p9/2676	thiamine biosynthesis protein thic variant l1 n 1 tax solanum lycopersicum b9tu32_sollc score=1344.72 evalue=0.00e+00;
c62646/f1p9/2676	uncharacterized protein n 1 tax glycine max i1n019_soybn score=1162.13 evalue=0.00e+00;
c62646/f1p9/2676	putative uncharacterized protein n 1 tax vitis vinifera f6guu1_vitvi score=1160.98 evalue=0.00e+00;
c62646/f1p9/2676	mrna clone: rtfl01-17-g05 n 1 tax eutrema halophilum e4mx93_theha score=1157.90 evalue=0.00e+00;
c62763/f1p3/3427	uncharacterized protein n 1 tax solanum lycopersicum k4bnk4_sollc score=2060.42 evalue=0.00e+00;
c62763/f1p3/3427	phosphoenolpyruvate carboxylase n 1 tax ricinus communis a6ym33_ricco score=1721.83 evalue=0.00e+00;
c62763/f1p3/3427	putative uncharacterized protein n 1 tax vitis vinifera f6hfq3_vitvi score=1703.72 evalue=0.00e+00;
c62763/f1p3/3427	putative uncharacterized protein n 1 tax vitis vinifera a5aev0_vitvi score=1696.40 evalue=0.00e+00;
c62763/f1p3/3427	atppc4 n 1 tax arabidopsis lyrata subsp. lyrata d7kqt7_arall score=1662.51 evalue=0.00e+00;
c62888/f1p1/3250	uncharacterized protein n 1 tax solanum lycopersicum k4dhv3_sollc score=1608.19 evalue=0.00e+00;
c62888/f1p1/3250	putative uncharacterized protein n 1 tax vitis vinifera f6h736_vitvi score=1195.65 evalue=0.00e+00;
c62888/f1p1/3250	putative uncharacterized protein n 1 tax ricinus communis b9rzn3_ricco score=1166.76 evalue=0.00e+00;
c62888/f1p1/3250	predicted protein n 1 tax populus trichocarpa b9hwx8_poptr score=1155.20 evalue=0.00e+00;

c62888/f1p1/3250	predicted protein n 2 tax populus trichocarpa b9hiq7_poptr score=1145.95 evalue=0.00e+00;
c63338/f1p7/1002	cellulose synthase (fragment) n 1 tax solanum tuberosum q6xp44_soltu score=499.98 evalue=9.33e-169;
c63338/f1p7/1002	uncharacterized protein n 1 tax solanum lycopersicum k4ckq2_sollc score=508.06 evalue=3.34e-168;
c63338/f1p7/1002	cellulose synthase catalytic subunit (fragment) n 1 tax gossypium hirsutum c6kf43_goshi score=473.01 evalue=1.20e-159;
c63338/f1p7/1002	cellulose synthase cesa1 (fragment) n 1 tax boehmeria nivea q4pkb6_boeni score=473.78 evalue=1.76e-156;
c63338/f1p7/1002	cellulose synthase n 1 tax populus tremuloides q6ybv2_poptm score=476.86 evalue=3.92e-156;
c63582/f1p0/3374	uncharacterized protein n 1 tax solanum lycopersicum k4bjk2_sollc score=1649.41 evalue=0.00e+00;
c63582/f1p0/3374	putative uncharacterized protein n 1 tax vitis vinifera f6i606_vitvi score=1137.48 evalue=0.00e+00;
c63582/f1p0/3374	putative uncharacterized protein n 1 tax vitis vinifera a5c8u0_vitvi score=1134.01 evalue=0.00e+00;
c63582/f1p0/3374	uncharacterized protein n 1 tax glycine max k7m8g3_soybn score=1072.77 evalue=0.00e+00;
c63582/f1p0/3374	pentatricopeptide repeat-containing protein n 1 tax arabidopsis lyrata subsp. lyrata d7m889_arall score=1011.52 evalue=0.00e+00;
c63621/f1p2/3219	uncharacterized protein n 1 tax solanum lycopersicum k4bab6_sollc score=1860.50 evalue=0.00e+00;
c63621/f1p2/3219	putative uncharacterized protein n 1 tax vitis vinifera d7swc0_vitvi score=1578.92 evalue=0.00e+00;
c63621/f1p2/3219	mitotic control protein dis3 putative n 1 tax ricinus communis b9s6w9_ricco score=1545.02 evalue=0.00e+00;
c63621/f1p2/3219	uncharacterized protein n 1 tax glycine max i1kb85_soybn score=1536.16 evalue=0.00e+00;
c63621/f1p2/3219	predicted protein n 1 tax populus trichocarpa b9gz79_poptr score=1532.31 evalue=0.00e+00;
c63870/f1p0/3203	uncharacterized protein n 1 tax solanum lycopersicum k4bhx8_sollc score=954.12 evalue=0.00e+00;
c63870/f1p0/3203	putative uncharacterized protein n 1 tax vitis vinifera f6h7a2_vitvi score=608.22 evalue=0.00e+00;
c63870/f1p0/3203	putative uncharacterized protein n 1 tax vitis vinifera f6h7a2_vitvi score=325.48 evalue=0.00e+00;
c63870/f1p0/3203	uncharacterized protein n 1 tax glycine max i1jh75_soybn score=537.72 evalue=0.00e+00;
c63870/f1p0/3203	uncharacterized protein n 1 tax glycine max i1jh75_soybn score=326.63 evalue=0.00e+00;
c64530/f1p3/4014	uncharacterized protein n 1 tax solanum lycopersicum k4d9x7_sollc score=1595.48 evalue=0.00e+00;
c64530/f1p3/4014	putative uncharacterized protein n 1 tax vitis vinifera d7tcx9_vitvi score=1072.77 evalue=0.00e+00;
c64530/f1p3/4014	uncharacterized protein n 1 tax glycine max k7lvp9_soybn score=1041.18 evalue=0.00e+00;
c64530/f1p3/4014	uncharacterized protein n 1 tax glycine max i1ltu3_soybn score=1039.25 evalue=0.00e+00;
c64530/f1p3/4014	uncharacterized protein n 1 tax glycine max k7m317_soybn score=1022.31 evalue=0.00e+00;
c64961/f1p2/2838	uncharacterized protein n 1 tax solanum lycopersicum k4d486_sollc score=1538.09 evalue=0.00e+00;
c64961/f1p2/2838	uncharacterized protein n 1 tax solanum lycopersicum k4crc1_sollc score=1313.52 evalue=0.00e+00;
c64961/f1p2/2838	putative uncharacterized protein n 1 tax vitis vinifera d7skc8_vitvi score=1193.33 evalue=0.00e+00;
c64961/f1p2/2838	predicted protein n 1 tax populus trichocarpa b9ifv8_poptr score=1168.30 evalue=0.00e+00;
c64961/f1p2/2838	mitochondrial respiratory chain complexes assembly protein afg3 putative n 1 tax ricinus communis b9syc0_ricco score=1152.50 evalue=0.00e+00;

c65489/f1p0/2645	putative reca protein n 1 tax solanum lycopersicum b1n670_sollc score=666.77 evalue=0.00e+00;
c65489/f1p0/2645	putative uncharacterized protein n 1 tax vitis vinifera d7tsa5_vitvi score=432.95 evalue=5.10e-140;
c65489/f1p0/2645	dna repair protein reca homolog 2 mitochondrial n 1 tax arabidopsis thaliana recam_arath score=390.96 evalue=5.50e-124;
c65489/f1p0/2645	uncharacterized protein n 1 tax glycine max i1n8w7_soybn score=382.49 evalue=9.73e-121;
c65489/f1p0/2645	uncharacterized protein n 1 tax glycine max k7my79_soybn score=382.10 evalue=1.16e-120;
c65568/f1p0/1546	uncharacterized protein n 3 tax solanum k4d4e6_sollc score=784.64 evalue=0.00e+00;
c65568/f1p0/1546	uncharacterized protein n 1 tax solanum lycopersicum k4bhr9_sollc score=781.94 evalue=0.00e+00;
c65568/f1p0/1546	actin n 13 tax core eudicotyledons g7jax4_medtr score=778.47 evalue=0.00e+00;
c65568/f1p0/1546	uncharacterized protein n 3 tax fabaceae i1jy56_soybn score=777.32 evalue=0.00e+00;
c65568/f1p0/1546	actin1 n 1 tax morella rubra f8wth6_9rosi score=777.32 evalue=0.00e+00;
c65578/f1p42/3640	uncharacterized protein n 1 tax solanum lycopersicum k4ckq2_sollc score=2016.89 evalue=0.00e+00;
c65578/f1p42/3640	putative uncharacterized protein n 1 tax vitis vinifera f6h311_vitvi score=1879.76 evalue=0.00e+00;
c65578/f1p42/3640	cellulose synthase a catalytic subunit 6 [udp-forming] putative n 1 tax ricinus communis b9rp67_ricco score=1845.48 evalue=0.00e+00;
c65578/f1p42/3640	cellulose synthase n 1 tax populus trichocarpa b9ikv7_poptr score=1836.23 evalue=0.00e+00;
c65578/f1p42/3640	cellulose synthase a n 1 tax eucalyptus camaldulensis g0z2c3_eucca score=1835.85 evalue=0.00e+00;
c66155/f1p2/3596	uncharacterized protein n 1 tax solanum lycopersicum k4bdb2_sollc score=1876.29 evalue=0.00e+00;
c66155/f1p2/3596	putative uncharacterized protein n 1 tax vitis vinifera f6h4h9_vitvi score=834.71 evalue=0.00e+00;
c66155/f1p2/3596	putative uncharacterized protein n 1 tax vitis vinifera a5bfy8_vitvi score=827.01 evalue=0.00e+00;
c66155/f1p2/3596	myosin-9 putative n 1 tax ricinus communis b9scb4_ricco score=759.21 evalue=0.00e+00;
c66155/f1p2/3596	uncharacterized protein n 1 tax glycine max k7ln67_soybn score=691.03 evalue=0.00e+00;
c66285/f1p1/2867	uncharacterized protein n 1 tax solanum lycopersicum k4cbr2_sollc score=1606.65 evalue=0.00e+00;
c66285/f1p1/2867	hydrolase hydrolyzing o-glycosyl compounds putative n 1 tax ricinus communis b9t139_ricco score=1260.36 evalue=0.00e+00;
c66285/f1p1/2867	alkaline alpha galactosidase 3 n 1 tax cucumis sativus h6wx41_cucsa score=1240.33 evalue=0.00e+00;
c66285/f1p1/2867	putative uncharacterized protein n 1 tax vitis vinifera f6hhb0_vitvi score=1239.94 evalue=0.00e+00;
c66285/f1p1/2867	predicted protein n 1 tax populus trichocarpa b9ha87_poptr score=1219.53 evalue=0.00e+00;
c66298/f1p1/2815	phenylalanine ammonia-lyase n 1 tax solanum lycopersicum k4cqi0_sollc score=1415.21 evalue=0.00e+00;
c66298/f1p1/2815	phenylalanine ammonia-lyase n 1 tax solanum lycopersicum pal5_sollc score=1407.89 evalue=0.00e+00;
c66298/f1p1/2815	apolipoprotein a1/a4/e domain-containing protein n 1 tax rhizobium leguminosarum bv. viciae usda 2370 i9mth1_rhilv score=1405.19 evalue=0.00e+00;
c66298/f1p1/2815	apolipoprotein a1/a4/e domain-containing protein n 1 tax rhizobium leguminosarum bv. viciae usda 2370 i9mth1_rhilv score=1172.15 evalue=0.00e+00;
c66298/f1p1/2815	apolipoprotein a1/a4/e domain-containing protein n 1 tax rhizobium leguminosarum bv. viciae usda 2370 i9mth1_rhilv score=1008.44 evalue=0.00e+00;
c66334/f1p2/2755	uncharacterized protein n 1 tax solanum lycopersicum k4bp58_sollc score=1207.59 evalue=0.00e+00;

c66334/f1p2/2755	putative uncharacterized protein n 1 tax vitis vinifera d7syl4_vitvi score=851.66 evalue=0.00e+00;
c66334/f1p2/2755	putative uncharacterized protein n 1 tax vitis vinifera a5bbk3_vitvi score=836.25 evalue=0.00e+00;
c66334/f1p2/2755	pre-mrna splicing factor putative n 1 tax ricinus communis b9rzq3_ricco score=830.48 evalue=0.00e+00;
c66334/f1p2/2755	predicted protein (fragment) n 1 tax populus trichocarpa b9hx17_poptr score=811.99 evalue=0.00e+00;
c66493/f1p4/3109	uncharacterized protein n 1 tax solanum lycopersicum k4bwn3_sollc score=1694.86 evalue=0.00e+00;
c66493/f1p4/3109	plastid alpha-amylase n 1 tax actinidia chinensis q5bly1_actch score=1253.04 evalue=0.00e+00;
c66493/f1p4/3109	plastid alpha-amylase n 1 tax malus x domestica q5bly3_maldo score=1244.18 evalue=0.00e+00;
c66493/f1p4/3109	putative uncharacterized protein n 1 tax vitis vinifera f6hpf1_vitvi score=1236.48 evalue=0.00e+00;
c66493/f1p4/3109	alpha-amylase putative n 1 tax ricinus communis b9s2b5_ricco score=1211.82 evalue=0.00e+00;
c66901/f3p5/3411	uncharacterized protein n 1 tax solanum lycopersicum k4bq85_sollc score=1714.89 evalue=0.00e+00;
c66901/f3p5/3411	uncharacterized protein n 1 tax solanum lycopersicum k4d2q1_sollc score=1435.62 evalue=0.00e+00;
c66901/f3p5/3411	predicted protein n 2 tax populus trichocarpa b9ii82_poptr score=1305.43 evalue=0.00e+00;
c66901/f3p5/3411	putative uncharacterized protein n 1 tax vitis vinifera d7thv1_vitvi score=1271.53 evalue=0.00e+00;
c66901/f3p5/3411	actin bundling protein abp135 n 1 tax lilium longiflorum q9sqh4_lillo score=1235.32 evalue=0.00e+00;
c67185/f1p1/2471	uncharacterized protein n 1 tax solanum lycopersicum k4cxs6_sollc score=1393.64 evalue=0.00e+00;
c67185/f1p1/2471	putative uncharacterized protein n 1 tax vitis vinifera e0cs09_vitvi score=969.15 evalue=0.00e+00;
c67185/f1p1/2471	putative uncharacterized protein n 1 tax vitis vinifera a5agq6_vitvi score=955.28 evalue=0.00e+00;
c67185/f1p1/2471	predicted protein n 1 tax populus trichocarpa b9n7r8_poptr score=934.10 evalue=0.00e+00;
c67185/f1p1/2471	uncharacterized protein n 1 tax glycine max k7mcq2_soybn score=918.30 evalue=0.00e+00;
c67191/f17p41/3624	putative rna-dependent rna-polymerase n 1 tax solanum tuberosum a4uv17_soltu score=1798.87 evalue=0.00e+00;
c67191/f17p41/3624	rna dependent rna polymerase family protein n 1 tax solanum demissum q6l3v2_solde score=1795.02 evalue=0.00e+00;
c67191/f17p41/3624	rna-directed rna polymerase putative n 1 tax solanum demissum q6l3w8_solde score=1777.30 evalue=0.00e+00;
c67191/f17p41/3624	rna-directed rna polymerase n 1 tax solanum lycopersicum q9zr58_sollc score=1774.60 evalue=0.00e+00;
c67191/f17p41/3624	rna dependent rna polymerase family protein n 1 tax solanum demissum q0kir2_solde score=1774.60 evalue=0.00e+00;
c67402/f8p2/1172	uncharacterized protein n 1 tax solanum lycopersicum k4b978_sollc score=440.27 evalue=1.33e-150;
c67402/f8p2/1172	uncharacterized protein n 1 tax solanum lycopersicum k4be74_sollc score=285.03 evalue=4.54e-90;
c67402/f8p2/1172	putative uncharacterized protein n 1 tax vitis vinifera a5bxh1_vitvi score=250.75 evalue=1.22e-76;
c67402/f8p2/1172	putative uncharacterized protein n 1 tax vitis vinifera f6hws4_vitvi score=251.91 evalue=2.60e-76;
c67402/f8p2/1172	uncharacterized protein n 1 tax medicago truncatula i3s047_medtr score=215.31 evalue=5.15e-63;
c68147/f47p7/1227	arca2 protein-like n 1 tax solanum tuberosum q2v991_soltu score=651.36 evalue=0.00e+00;
c68147/f47p7/1227	uncharacterized protein n 1 tax solanum lycopersicum k4bm53_sollc score=650.20 evalue=0.00e+00;

c68147/f47p7/1227	learca2 protein n 1 tax solanum lycopersicum q9sxs0_sollc score=647.51 evalue=0.00e+00;
c68147/f47p7/1227	g protein beta-subunit-like protein n 1 tax nicotiana plumbaginifolia q40403_nicpl score=630.17 evalue=0.00e+00;
c68147/f47p7/1227	uncharacterized protein n 1 tax solanum lycopersicum k4c874_sollc score=625.93 evalue=0.00e+00;
c69039/f34p10/2779	uncharacterized protein n 1 tax solanum lycopersicum k4bvn6_sollc score=1374.76 evalue=0.00e+00;
c69039/f34p10/2779	heat shock protein 90 n 1 tax nicotiana tabacum g9md86_tobac score=1264.21 evalue=0.00e+00;
c69039/f34p10/2779	heat shock protein 90 n 1 tax nicotiana tabacum g9md87_tobac score=1258.82 evalue=0.00e+00;
c69039/f34p10/2779	putative uncharacterized protein n 1 tax vitis vinifera e0cq80_vitvi score=1219.14 evalue=0.00e+00;
c69039/f34p10/2779	endoplasmin putative n 1 tax ricinus communis b9r8a7_ricco score=1207.20 evalue=0.00e+00;
c69219/f83p26/1680	gamma aminobutyrate transaminase 2 n 1 tax solanum lycopersicum k4dbi4_sollc score=918.30 evalue=0.00e+00;
c69219/f83p26/1680	viroid rna-binding protein (fragment) n 1 tax solanum lycopersicum q8rvv4_sollc score=910.60 evalue=0.00e+00;
c69219/f83p26/1680	gamma aminobutyrate transaminase 2 n 1 tax solanum lycopersicum gatp2_sollc score=909.83 evalue=0.00e+00;
c69219/f83p26/1680	uncharacterized protein n 1 tax solanum lycopersicum k4cj91_sollc score=835.48 evalue=0.00e+00;
c69219/f83p26/1680	putative aminotransferase n 1 tax capsicum annuum e1aqy3_capan score=820.46 evalue=0.00e+00;
c69890/f48p18/3035	uncharacterized protein n 1 tax solanum lycopersicum k4b894_sollc score=1425.99 evalue=0.00e+00;
c69890/f48p18/3035	uncharacterized protein n 1 tax solanum lycopersicum k4bdz9_sollc score=975.70 evalue=0.00e+00;
c69890/f48p18/3035	putative uncharacterized protein n 1 tax vitis vinifera f6hmg9_vitvi score=788.10 evalue=0.00e+00;
c69890/f48p18/3035	pputative uncharacterized protein n 1 tax ricinus communis b9s173_ricco score=762.68 evalue=0.00e+00;
c69890/f48p18/3035	ppredicted protein n 1 tax populus trichocarpa b9i113_poptr score=749.20 evalue=0.00e+00;
c70141/f4p9/2726	puncharacterized protein n 1 tax solanum lycopersicum k4bvn6_sollc score=1374.76 evalue=0.00e+00;
c70141/f4p9/2726	pheat shock protein 90 n 1 tax nicotiana tabacum g9md86_tobac score=1264.21 evalue=0.00e+00;
c70141/f4p9/2726	pheat shock protein 90 n 1 tax nicotiana tabacum g9md87_tobac score=1258.82 evalue=0.00e+00;
c70141/f4p9/2726	pputative uncharacterized protein n 1 tax vitis vinifera e0cq80_vitvi score=1219.14 evalue=0.00e+00;
c70141/f4p9/2726	pendoplasmin putative n 1 tax ricinus communis b9r8a7_ricco score=1207.20 evalue=0.00e+00;
c70441/f3p0/1411	puncharacterized protein n 1 tax solanum lycopersicum k4cvz5_sollc score=709.91 evalue=0.00e+00;
c70441/f3p0/1411	uncharacterized protein n 1 tax solanum lycopersicum k4cw02_sollc score=543.89 evalue=0.00e+00;
c70441/f3p0/1411	uncharacterized protein n 1 tax solanum lycopersicum k4cvz9_sollc score=537.34 evalue=0.00e+00;
c70441/f3p0/1411	uncharacterized protein n 1 tax solanum lycopersicum k4cvz4_sollc score=474.17 evalue=4.79e-162;
c70441/f3p0/1411	desacetoxyvindoline 4-hydroxylase putative n 1 tax ricinus communis b9sti5_ricco score=459.91 evalue=1.57e-156;
c70623/f1p0/1275	uncharacterized protein n 1 tax solanum lycopersicum k4atj2_sollc score=622.85 evalue=0.00e+00;
c70623/f1p0/1275	predicted protein n 1 tax populus trichocarpa a9pgt3_poptr score=436.42 evalue=6.28e-149;
c70623/f1p0/1275	putative uncharacterized protein n 1 tax vitis vinifera f6i1n0_vitvi score=434.49 evalue=1.40e-147;

c70623/f1p0/1275	at2g35450 n 1 tax arabidopsis lyrata subsp. lyrata d7lhw4_arall score=424.86 evalue=2.20e-144;
c70623/f1p0/1275	putative uncharacterized protein n 2 tax medicago truncatula g7kus9_medtr score=421.39 evalue=1.81e-142;
c70647/f2p0/1738	uncharacterized protein n 1 tax solanum lycopersicum k4dg29_sollc score=394.81 evalue=3.16e-130;
c70647/f2p0/1738	erf transcription factor 8 n 1 tax nicotiana tabacum k7xd40_tobac score=254.99 evalue=1.17e-76;
c70647/f2p0/1738	dehydration-responsive element binding protein 3 n 1 tax solanum lycopersicum q8gze8_sollc score=228.41 evalue=1.03e-66;
c70647/f2p0/1738	dehydration-responsive element-binding protein dreb4 n 1 tax solanum tuberosum g9izq6_soltu score=223.40 evalue=1.40e-63;
c70647/f2p0/1738	dehydration responsive element binding protein 3 n 1 tax solanum tuberosum i6m4h9_soltu score=212.23 evalue=1.12e-60;
c70690/f1p3/1983	uncharacterized protein n 1 tax solanum lycopersicum k4bjy9_sollc score=845.11 evalue=0.00e+00;
c70690/f1p3/1983	putative uncharacterized protein n 1 tax vitis vinifera f6gst5_vitvi score=626.71 evalue=0.00e+00;
c70690/f1p3/1983	putative uncharacterized protein n 1 tax ricinus communis b9rai2_ricco score=600.13 evalue=0.00e+00;
c70690/f1p3/1983	predicted protein n 1 tax populus trichocarpa b9i3p4_poptr score=597.04 evalue=0.00e+00;
c70690/f1p3/1983	uncharacterized protein n 1 tax glycine max i1jxi6_soybn score=569.31 evalue=0.00e+00;
c71060/f1p0/1002	uncharacterized protein n 1 tax solanum lycopersicum k4dcx5_sollc score=515.77 evalue=0.00e+00;
c71060/f1p0/1002	uncharacterized protein n 1 tax glycine max i1kyb0_soybn score=491.89 evalue=8.28e-172;
c71060/f1p0/1002	predicted protein n 1 tax populus trichocarpa b9gjh1_poptr score=491.50 evalue=9.39e-172;
c71060/f1p0/1002	predicted protein n 1 tax populus trichocarpa b9i150_poptr score=488.80 evalue=1.12e-170;
c71060/f1p0/1002	uncharacterized protein n 1 tax medicago truncatula i3suc7_medtr score=485.72 evalue=1.16e-169;
c71664/f2p2/1460	uncharacterized protein n 1 tax solanum lycopersicum k4az11_sollc score=793.88 evalue=0.00e+00;
c71664/f2p2/1460	putative uncharacterized protein n 1 tax vitis vinifera d7slu2_vitvi score=565.84 evalue=0.00e+00;
c71664/f2p2/1460	catalytic putative n 1 tax ricinus communis b9rd44_ricco score=562.38 evalue=0.00e+00;
c71664/f2p2/1460	3-hydroxyisobutyryl-coa hydrolase-like protein n 1 tax medicago truncatula g7lbk0_medtr score=558.52 evalue=0.00e+00;
c71664/f2p2/1460	uncharacterized protein n 1 tax glycine max i1jmv6_soybn score=558.52 evalue=0.00e+00;
c72849/f1p3/1967	sigma factor n 1 tax nicotiana tabacum q9slx3_tobac score=389.04 evalue=0.00e+00;
c72849/f1p3/1967	sigma factor n 1 tax nicotiana tabacum q9slx3_tobac score=234.19 evalue=0.00e+00;
c72849/f1p3/1967	sigma factor n 1 tax nicotiana tabacum q9slx3_tobac score=171.40 evalue=0.00e+00;
c72849/f1p3/1967	uncharacterized protein n 1 tax solanum lycopersicum k4c8z1_sollc score=506.91 evalue=0.00e+00;
c72849/f1p3/1967	uncharacterized protein n 1 tax solanum lycopersicum k4c8z1_sollc score=241.12 evalue=0.00e+00;
c73080/f1p2/1798	alpha-glucosidase n 1 tax solanum tuberosum q9lec9_soltu score=1009.21 evalue=0.00e+00;
c73080/f1p2/1798	uncharacterized protein n 1 tax solanum lycopersicum k4bxc1_sollc score=1005.36 evalue=0.00e+00;
c73080/f1p2/1798	putative uncharacterized protein n 1 tax vitis vinifera f6hex2_vitvi score=794.27 evalue=0.00e+00;
c73080/f1p2/1798	predicted protein n 1 tax populus trichocarpa b9hj23_poptr score=782.71 evalue=0.00e+00;

c73080/f1p2/1798	predicted protein n 1 tax populus trichocarpa b9hwi3_poptr score=778.86 evalue=0.00e+00;
c73387/f1p10/1950	uncharacterized protein n 1 tax solanum lycopersicum k4c9g9_sollc score=1007.28 evalue=0.00e+00;
c73387/f1p10/1950	2-carboxy-d-arabinitol 1-phosphate (ca1p) phosphatase n 1 tax nicotiana tabacum h2a0j7_tobac score=921.38 evalue=0.00e+00;
c73387/f1p10/1950	putative uncharacterized protein n 1 tax vitis vinifera f6gw48_vitvi score=701.82 evalue=0.00e+00;
c73387/f1p10/1950	phosphoglycerate mutase putative (fragment) n 1 tax ricinus communis b9t5t3_ricco score=693.73 evalue=0.00e+00;
c73387/f1p10/1950	2-carboxy-d-arabinitol 1-phosphate (ca1p) phosphatase n 1 tax phaseolus vulgaris g4vuy8_phavu score=684.49 evalue=0.00e+00;
c73636/f1p2/1369	uncharacterized protein n 1 tax solanum lycopersicum k4blh5_sollc score=677.17 evalue=0.00e+00;
c73636/f1p2/1369	delta-9 fatty acid desaturase n 1 tax vernicia fordii d3ylk2_verfo score=478.02 evalue=1.29e-164;
c73636/f1p2/1369	delta 9 desaturase putative n 1 tax ricinus communis b9rv72_ricco score=478.79 evalue=1.08e-163;
c73636/f1p2/1369	uncharacterized protein n 1 tax glycine max k7kzd0_soybn score=472.63 evalue=2.48e-161;
c73636/f1p2/1369	mrna clone: rtfl01-01-g02 n 1 tax eutrema halophilum e4mvq1_theha score=469.54 evalue=2.39e-160;
c73767/f1p6/1583	uncharacterized protein n 1 tax solanum lycopersicum k4cx91_sollc score=276.17 evalue=1.68e-83;
c73767/f1p6/1583	putative arginine/serine-rich protein-like n 1 tax solanum tuberosum q2xtd4_soltu score=270.40 evalue=1.19e-81;
c73767/f1p6/1583	putative arginine/serine-rich protein n 1 tax solanum tuberosum q2xpw2_soltu score=270.01 evalue=1.75e-81;
c73767/f1p6/1583	putative uncharacterized protein n 1 tax vitis vinifera d7swx8_vitvi score=199.90 evalue=1.14e-54;
c73767/f1p6/1583	uncharacterized protein n 1 tax glycine max i1mj68_soybn score=182.96 evalue=1.83e-48;
c74050/f1p4/1735	uncharacterized protein n 1 tax solanum lycopersicum k4d276_sollc score=930.24 evalue=0.00e+00;
c74050/f1p4/1735	putative uncharacterized protein n 1 tax vitis vinifera d7tqt9_vitvi score=698.35 evalue=0.00e+00;
c74050/f1p4/1735	putative uncharacterized protein n 1 tax cucumis melo subsp. melo e5gbn1_cucme score=676.78 evalue=0.00e+00;
c74050/f1p4/1735	putative uncharacterized protein n 1 tax ricinus communis b9ru60_ricco score=667.15 evalue=0.00e+00;
c74050/f1p4/1735	uncharacterized protein n 1 tax glycine max k7my36_soybn score=656.75 evalue=0.00e+00;
c74299/f1p0/1245	uncharacterized protein n 1 tax solanum lycopersicum k4clg8_sollc score=468.77 evalue=4.53e-158;
c74299/f1p0/1245	uncharacterized protein n 1 tax solanum lycopersicum k4dag7_sollc score=271.94 evalue=9.56e-82;
c74299/f1p0/1245	putative uncharacterized protein n 1 tax vitis vinifera d7stk8_vitvi score=248.44 evalue=2.58e-72;
c74299/f1p0/1245	uncharacterized protein n 1 tax glycine max i1m8y5_soybn score=224.17 evalue=1.41e-63;
c74299/f1p0/1245	uncharacterized protein n 1 tax glycine max i1mxe8_soybn score=214.93 evalue=4.25e-60;
c74417/f2p4/1639	uncharacterized protein n 1 tax solanum lycopersicum k4cx59_sollc score=647.51 evalue=0.00e+00;
c74417/f2p4/1639	uncharacterized protein n 1 tax solanum lycopersicum k4b9r3_sollc score=565.84 evalue=0.00e+00;
c74417/f2p4/1639	uncharacterized protein n 1 tax solanum lycopersicum k4bfe4_sollc score=531.95 evalue=0.00e+00;
c74417/f2p4/1639	nuclear acid binding protein putative n 1 tax ricinus communis b9rxn0_ricco score=476.86 evalue=5.73e-161;
c74417/f2p4/1639	putative uncharacterized protein n 1 tax vitis vinifera f6hej3_vitvi score=471.86 evalue=1.61e-158;

c74505/f1p16/2812	arginine decarboxylase n 7 tax lycopersicon q5f307_sollc score=1300.03 evalue=0.00e+00;
c74505/f1p16/2812	arginine decarboxylase n 1 tax nicotiana tabacum q76bk9_tobac score=1205.66 evalue=0.00e+00;
c74505/f1p16/2812	arginine decarboxylase n 1 tax nicotiana tabacum q9ldm9_tobac score=1100.50 evalue=0.00e+00;
c74505/f1p16/2812	arginine decarboxylase n 1 tax datura stramonium q9scf0_datst score=1097.42 evalue=0.00e+00;
c74505/f1p16/2812	arginine decarboxylase n 1 tax nicotiana tabacum q71s28_tobac score=1090.87 evalue=0.00e+00;
c74699/f1p4/1635	uncharacterized protein n 1 tax solanum lycopersicum k4bvr9_sollc score=818.92 evalue=0.00e+00;
c74699/f1p4/1635	putative uncharacterized protein n 1 tax vitis vinifera f6h0e3_vitvi score=569.31 evalue=0.00e+00;
c74699/f1p4/1635	predicted protein n 1 tax populus trichocarpa b9h525_poptr score=555.44 evalue=0.00e+00;
c74699/f1p4/1635	nucleoredoxin putative n 1 tax ricinus communis b9r8f0_ricco score=521.55 evalue=4.00e-179;
c74699/f1p4/1635	uncharacterized protein n 1 tax glycine max i1jsz5_soybn score=503.83 evalue=9.77e-172;
c75157/f2p1/1962	uncharacterized protein n 1 tax solanum lycopersicum k4cu19_sollc score=755.75 evalue=0.00e+00;
c75157/f2p1/1962	putative uncharacterized protein n 1 tax vitis vinifera a5c4q9_vitvi score=669.46 evalue=0.00e+00;
c75157/f2p1/1962	putative uncharacterized protein n 1 tax vitis vinifera d7u3e6_vitvi score=669.08 evalue=0.00e+00;
c75157/f2p1/1962	putative uncharacterized protein n 2 tax vitis vinifera d7ts74_vitvi score=663.68 evalue=0.00e+00;
c75157/f2p1/1962	uncharacterized protein n 1 tax solanum lycopersicum k4cal3_sollc score=661.37 evalue=0.00e+00;
c75658/f2p5/2639	uncharacterized protein n 2 tax lycopersicon k4cbn0_sollc score=1423.68 evalue=0.00e+00;
c75658/f2p5/2639	vacuolar h+-pyrophosphatase n 1 tax solanum lycopersicum k4q1y8_sollc score=1420.60 evalue=0.00e+00;
c75658/f2p5/2639	inorganic pyrophosphatase n 1 tax nicotiana tabacum q43797_tobac score=1377.46 evalue=0.00e+00;
c75658/f2p5/2639	uncharacterized protein n 1 tax solanum lycopersicum k4dc72_sollc score=1347.03 evalue=0.00e+00;
c75658/f2p5/2639	vacuolar proton-pumping ppase n 1 tax chenopodium rubrum q8l5b2_cheru score=1332.39 evalue=0.00e+00;
c75939/f4p24/2780	arginine decarboxylase n 2 tax solanum lycopersicum g8z275_sollc score=1261.90 evalue=0.00e+00;
c75939/f4p24/2780	arginine decarboxylase n 1 tax datura stramonium q9scf0_datst score=1234.17 evalue=0.00e+00;
c75939/f4p24/2780	arginine decarboxylase n 1 tax nicotiana tabacum q9ldm9_tobac score=1147.50 evalue=0.00e+00;
c75939/f4p24/2780	arginine decarboxylase n 1 tax nicotiana tabacum q71s28_tobac score=1145.57 evalue=0.00e+00;
c75939/f4p24/2780	arginine decarboxylase n 1 tax nicotiana tabacum q9m7k9_tobac score=1140.95 evalue=0.00e+00;
c76607/f1p14/1000	uncharacterized protein n 1 tax solanum lycopersicum k4dfv3_sollc score=521.16 evalue=0.00e+00;
c76607/f1p14/1000	water channel protein n 1 tax nicotiana excelsior o09224_9sola score=517.69 evalue=0.00e+00;
c76607/f1p14/1000	major intrinsic protein n 1 tax solanum tuberosum a0fi89_soltu score=517.31 evalue=0.00e+00;
c76607/f1p14/1000	major intrinsic protein 1-like protein n 1 tax solanum tuberosum q38hu9_soltu score=516.15 evalue=0.00e+00;
c76607/f1p14/1000	water channel protein n 1 tax nicotiana tabacum q06bk4_tobac score=514.61 evalue=0.00e+00;
c77376/f1p7/1583	uncharacterized protein n 1 tax solanum lycopersicum k4bpd2_sollc score=701.05 evalue=0.00e+00;

c77376/f1p7/1583	dnaj-like protein n 1 tax solanum tuberosum q38ht9_soltu score=642.11 evalue=0.00e+00;
c77376/f1p7/1583	dnaj protein n 1 tax solanum tuberosum q43177_soltu score=635.57 evalue=0.00e+00;
c77376/f1p7/1583	uncharacterized protein n 1 tax solanum lycopersicum k4d4q9_sollc score=635.57 evalue=0.00e+00;
c77376/f1p7/1583	dnaj-like protein n 1 tax solanum tuberosum q38hu8_soltu score=635.18 evalue=0.00e+00;
c77631/f6p4/1973	uncharacterized protein n 1 tax solanum lycopersicum k4cpb9_sollc score=1098.96 evalue=0.00e+00;
c77631/f6p4/1973	cytochrome p450 fatty acid omega-hydroxylase n 1 tax petunia x hybrida b3rfj6_pethy score=1036.56 evalue=0.00e+00;
c77631/f6p4/1973	putative uncharacterized protein n 1 tax vitis vinifera a5ag84_vitvi score=879.78 evalue=0.00e+00;
c77631/f6p4/1973	putative uncharacterized protein n 1 tax vitis vinifera f6hub7_vitvi score=879.40 evalue=0.00e+00;
c77631/f6p4/1973	uncharacterized protein n 1 tax solanum lycopersicum k4azl5_sollc score=840.88 evalue=0.00e+00;
c77909/f10p8/1559	uncharacterized protein n 1 tax solanum lycopersicum k4d7r1_sollc score=803.90 evalue=0.00e+00;
c77909/f10p8/1559	eukaryotic initiation factor 4a-3 n 1 tax nicotiana plumbaginifolia if4a3_nicpl score=792.34 evalue=0.00e+00;
c77909/f10p8/1559	putative uncharacterized protein n 1 tax vitis vinifera f6hhf5_vitvi score=773.47 evalue=0.00e+00;
c77909/f10p8/1559	dh n 1 tax medicago sativa a8dx61_medsa score=759.21 evalue=0.00e+00;
c77909/f10p8/1559	uncharacterized protein n 1 tax glycine max i1l171_soybn score=756.90 evalue=0.00e+00;
c78258/f34p10/1613	acyl-[acyl-carrier-protein] desaturase n 1 tax solanum lycopersicum k4c635_sollc score=818.92 evalue=0.00e+00;
c78258/f34p10/1613	acyl-[acyl-carrier-protein] desaturase chloroplastic n 2 tax ricinus communis stad_ricco score=732.25 evalue=0.00e+00;
c78258/f34p10/1613	acyl-[acyl-carrier-protein] desaturase n 2 tax jatropha curcas q4jij4_9rosi score=729.55 evalue=0.00e+00;
c78258/f34p10/1613	acyl-[acyl-carrier-protein] desaturase n 1 tax manihot esculenta k0e5t2_manes score=725.70 evalue=0.00e+00;
c78258/f34p10/1613	acyl-[acyl-carrier-protein] desaturase n 1 tax sesamum indicum q43140_sesin score=724.93 evalue=0.00e+00;
c79784/f3p5/2212	uncharacterized protein n 5 tax magnoliophyta k4d9l5_sollc score=1216.83 evalue=0.00e+00;
c79784/f3p5/2212	heat shock protein 70-3 n 1 tax nicotiana tabacum q67bd0_tobac score=1204.12 evalue=0.00e+00;
c79784/f3p5/2212	heat shock protein 70 n 1 tax nicotiana tabacum q84qj3_tobac score=1195.26 evalue=0.00e+00;
c79784/f3p5/2212	heat shock cognate 70 kda protein 2 n 1 tax solanum lycopersicum k4d473_sollc score=1191.41 evalue=0.00e+00;
c79784/f3p5/2212	heat shock protein 70 n 1 tax cyclamen persicum a4zx75_9eric score=1191.41 evalue=0.00e+00;
c79860/f3p0/1739	uncharacterized protein n 1 tax solanum lycopersicum k4b2k0_sollc score=886.33 evalue=0.00e+00;
c79860/f3p0/1739	putative uncharacterized protein n 1 tax vitis vinifera f6hw60_vitvi score=386.73 evalue=7.95e-125;
c79860/f3p0/1739	atp binding protein putative n 1 tax ricinus communis b9rx51_ricco score=383.26 evalue=1.92e-123;
c79860/f3p0/1739	predicted protein n 1 tax populus trichocarpa b9gj10_poptr score=376.33 evalue=1.22e-120;
c79860/f3p0/1739	putative uncharacterized protein n 1 tax vitis vinifera f6gzk7_vitvi score=357.45 evalue=3.17e-113;
c79903/f3p16/1442	uncharacterized protein n 1 tax solanum lycopersicum k4cgi6_sollc score=716.07 evalue=0.00e+00;
c79903/f3p16/1442	glycolate oxidase n 1 tax nicotiana benthamiana e1axt8_nicbe score=697.20 evalue=0.00e+00;

c79903/f3p16/1442	glycolate oxidase n 1 tax mangifera indica f1cwa9_manin score=681.79 evalue=0.00e+00;
c79903/f3p16/1442	(s)-2-hydroxy-acid oxidase putative n 1 tax ricinus communis b9s0y9_ricco score=679.09 evalue=0.00e+00;
c79903/f3p16/1442	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata d7kva4_arall score=677.55 evalue=0.00e+00;
c80085/f2p1/2017	uncharacterized protein n 1 tax solanum lycopersicum k4cqr3_sollc score=746.50 evalue=0.00e+00;
c80085/f2p1/2017	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata d7lj57_arall score=555.44 evalue=0.00e+00;
c80085/f2p1/2017	predicted protein n 1 tax populus trichocarpa b9mtm3_poptr score=553.13 evalue=0.00e+00;
c80085/f2p1/2017	putative uncharacterized protein n 1 tax ricinus communis b9srl3_ricco score=547.74 evalue=0.00e+00;
c80085/f2p1/2017	at2g36630/f1o11.26 n 1 tax arabidopsis thaliana q8s9j0_arath score=546.97 evalue=0.00e+00;
c80371/f2p1/2120	uncharacterized protein n 1 tax solanum lycopersicum k4bbt2_sollc score=1000.35 evalue=0.00e+00;
c80371/f2p1/2120	putative uncharacterized protein n 1 tax vitis vinifera f6h5p3_vitvi score=457.22 evalue=5.96e-149;
c80371/f2p1/2120	putative uncharacterized protein n 1 tax vitis vinifera f6gt98_vitvi score=413.31 evalue=2.32e-131;
c80371/f2p1/2120	predicted protein n 1 tax populus trichocarpa b9n4b0_poptr score=369.01 evalue=7.41e-115;
c80371/f2p1/2120	putative uncharacterized protein n 1 tax vitis vinifera d7tnd0_vitvi score=367.08 evalue=3.28e-114;
c80685/f1p2/2133	uncharacterized protein n 1 tax solanum lycopersicum k4ca36_sollc score=1186.79 evalue=0.00e+00;
c80685/f1p2/2133	putative uncharacterized protein n 1 tax vitis vinifera f6guu3_vitvi score=890.95 evalue=0.00e+00;
c80685/f1p2/2133	hydrolase hydrolyzing o-glycosyl compounds putative n 1 tax ricinus communis b9shx7_ricco score=885.95 evalue=0.00e+00;
c80685/f1p2/2133	uncharacterized protein n 1 tax solanum lycopersicum k4c379_sollc score=882.86 evalue=0.00e+00;
c80685/f1p2/2133	putative uncharacterized protein n 1 tax vitis vinifera a5bkf4_vitvi score=874.77 evalue=0.00e+00;
c80893/f2p1/1889	uncharacterized protein n 1 tax solanum lycopersicum k4bu99_sollc score=904.05 evalue=0.00e+00;
c80893/f2p1/1889	putative uncharacterized protein n 1 tax vitis vinifera f6h149_vitvi score=373.24 evalue=1.71e-119;
c80893/f2p1/1889	putative uncharacterized protein n 1 tax ricinus communis b9smz5_ricco score=368.62 evalue=1.38e-117;
c80893/f2p1/1889	uncharacterized protein n 1 tax glycine max k7m7t9_soybn score=314.69 evalue=1.89e-96;
c80893/f2p1/1889	uncharacterized protein n 1 tax glycine max i1jh17_soybn score=310.46 evalue=7.90e-95;
c81023/f2p5/1590	uncharacterized protein n 1 tax solanum lycopersicum k4chp7_sollc score=801.59 evalue=0.00e+00;
c81023/f2p5/1590	putative uncharacterized protein n 1 tax vitis vinifera f6i570_vitvi score=533.87 evalue=0.00e+00;
c81023/f2p5/1590	putative uncharacterized protein n 1 tax vitis vinifera a5c0d9_vitvi score=512.69 evalue=8.62e-175;
c81023/f2p5/1590	putative uncharacterized protein n 1 tax ricinus communis b9s9w4_ricco score=496.89 evalue=7.61e-169;
c81023/f2p5/1590	predicted protein n 2 tax populus trichocarpa b9gfy7_poptr score=494.58 evalue=5.42e-168;
c81787/f1p2/1960	plasma membrane atpase 1 n 2 tax solanum lycopersicum pma1_sollc score=1043.11 evalue=0.00e+00;
c81787/f1p2/1960	plasma membrane atpase 3 n 1 tax nicotiana plumbaginifolia pma3_nicpl score=1022.31 evalue=0.00e+00;
c81787/f1p2/1960	n.plumbaginifolia h+-translocating atpase mrna n 2 tax nicotiana plumbaginifolia q42932_nicpl score=1013.06 evalue=0.00e+00;

c81787/f1p2/1960	plasma membrane atpase 2 n 1 tax solanum lycopersicum q9spd5_sollc score=1012.29 evalue=0.00e+00;
c81787/f1p2/1960	h(+)-transporting atpase n 1 tax solanum tuberosum q43182_soltu score=1012.29 evalue=0.00e+00;
c81930/f1p0/1531	proline-rich protein n 1 tax solanum tuberosum o82066_soltu score=282.34 evalue=3.38e-85;
c81930/f1p0/1531	proline-rich protein n 1 tax nicotiana glauca q9m6t7_nicgl score=222.25 evalue=6.00e-65;
c81930/f1p0/1531	uncharacterized protein n 1 tax solanum lycopersicum k4d183_sollc score=203.76 evalue=1.77e-58;
c81930/f1p0/1531	predicted protein (fragment) n 1 tax populus trichocarpa b9h154_poptr score=199.13 evalue=3.34e-56;
c81930/f1p0/1531	predicted protein (fragment) n 1 tax populus trichocarpa b9hra6_poptr score=196.44 evalue=5.77e-55;
c82918/f1p6/1909	serine hydroxymethyltransferase n 1 tax solanum lycopersicum k4clc9_sollc score=1075.46 evalue=0.00e+00;
c82918/f1p6/1909	serine hydroxymethyltransferase n 1 tax solanum lycopersicum k4dh66_sollc score=926.39 evalue=0.00e+00;
c82918/f1p6/1909	serine hydroxymethyltransferase putative n 1 tax ricinus communis b9s1d7_ricco score=902.12 evalue=0.00e+00;
c82918/f1p6/1909	serine hydroxymethyltransferase 8 n 1 tax populus trichocarpa b9hdq7_poptr score=901.74 evalue=0.00e+00;
c82918/f1p6/1909	putative uncharacterized protein n 1 tax vitis vinifera d7stm0_vitvi score=900.20 evalue=0.00e+00;
c82925/f1p0/1646	uncharacterized protein n 1 tax solanum lycopersicum k4d433_sollc score=771.15 evalue=0.00e+00;
c82925/f1p0/1646	uncharacterized protein n 1 tax solanum lycopersicum k4cqa7_sollc score=619.00 evalue=0.00e+00;
c82925/f1p0/1646	receptor serine-threonine protein kinase putative n 1 tax ricinus communis b9sgd4_ricco score=602.44 evalue=0.00e+00;
c82925/f1p0/1646	putative uncharacterized protein n 1 tax vitis vinifera d7tqb4_vitvi score=597.43 evalue=0.00e+00;
c82925/f1p0/1646	uncharacterized protein n 1 tax glycine max i1na42_soybn score=588.57 evalue=0.00e+00;
c83016/f1p2/2286	uncharacterized protein n 1 tax solanum lycopersicum k4be65_sollc score=1232.24 evalue=0.00e+00;
c83016/f1p2/2286	predicted protein n 1 tax populus trichocarpa b9hnv8_poptr score=1002.66 evalue=0.00e+00;
c83016/f1p2/2286	origin recognition complex subunit putative n 1 tax ricinus communis b9ric0_ricco score=1001.50 evalue=0.00e+00;
c83016/f1p2/2286	uncharacterized protein n 1 tax glycine max i1m507_soybn score=991.10 evalue=0.00e+00;
c83016/f1p2/2286	putative uncharacterized protein n 1 tax vitis vinifera f6gu49_vitvi score=983.40 evalue=0.00e+00;
c83075/f1p0/1348	uncharacterized protein n 1 tax solanum lycopersicum k4c9p9_sollc score=725.70 evalue=0.00e+00;
c83075/f1p0/1348	putative carbamoyl phosphate synthase large subunit n 1 tax nicotiana tabacum q8l6j9_tobac score=706.83 evalue=0.00e+00;
c83075/f1p0/1348	at1g29900 protein (fragment) n 1 tax arabidopsis thaliana b9di51_arath score=612.45 evalue=0.00e+00;
c83075/f1p0/1348	putative uncharacterized protein n 1 tax vitis vinifera f6gtx9_vitvi score=622.85 evalue=0.00e+00;
c83075/f1p0/1348	putative uncharacterized protein n 1 tax vitis vinifera a5b6e2_vitvi score=622.85 evalue=0.00e+00;
c83236/f1p0/1561	uncharacterized protein n 1 tax solanum lycopersicum k4cxa9_sollc score=874.00 evalue=0.00e+00;
c83236/f1p0/1561	uncharacterized protein n 1 tax solanum lycopersicum k4chp9_sollc score=816.61 evalue=0.00e+00;
c83236/f1p0/1561	uncharacterized protein n 1 tax solanum lycopersicum k4bq16_sollc score=766.15 evalue=0.00e+00;
c83236/f1p0/1561	predicted protein (fragment) n 1 tax populus trichocarpa b9ih04_poptr score=758.06 evalue=0.00e+00;

c83236/f1p0/1561	uncharacterized protein n 2 tax glycine max k7lb98_soybn score=761.14 evalue=0.00e+00;
c83276/f1p2/1621	uncharacterized protein n 1 tax solanum lycopersicum k4cl77_sollc score=474.55 evalue=4.92e-162;
c83276/f1p2/1621	putative uncharacterized protein n 1 tax vitis vinifera f6h3m5_vitvi score=444.12 evalue=6.23e-148;
c83276/f1p2/1621	putative uncharacterized protein n 1 tax vitis vinifera a5bxd3_vitvi score=442.19 evalue=1.19e-140;
c83276/f1p2/1621	calmodulin binding protein putative n 1 tax ricinus communis b9rqr6_ricco score=412.92 evalue=9.96e-136;
c83276/f1p2/1621	uncharacterized protein n 1 tax glycine max i1jtx8_soybn score=363.61 evalue=1.22e-116;
c83325/f1p1/1950	uncharacterized protein n 1 tax solanum lycopersicum k4clq3_sollc score=1028.47 evalue=0.00e+00;
c83325/f1p1/1950	putative uncharacterized protein n 1 tax vitis vinifera f6h3e4_vitvi score=669.46 evalue=0.00e+00;
c83325/f1p1/1950	ankyrin repeat-containing protein putative n 1 tax ricinus communis b9rs18_ricco score=664.07 evalue=0.00e+00;
c83325/f1p1/1950	putative uncharacterized protein n 1 tax vitis vinifera a5ank4_vitvi score=657.52 evalue=0.00e+00;
c83325/f1p1/1950	predicted protein n 1 tax populus trichocarpa b9ikj8_poptr score=645.20 evalue=0.00e+00;
c83570/f1p2/1618	uncharacterized protein n 1 tax solanum lycopersicum k4car9_sollc score=847.04 evalue=0.00e+00;
c83570/f1p2/1618	uncharacterized protein n 1 tax solanum lycopersicum k4cui2_sollc score=746.50 evalue=0.00e+00;
c83570/f1p2/1618	putative uncharacterized protein n 1 tax vitis vinifera d7te10_vitvi score=694.89 evalue=0.00e+00;
c83570/f1p2/1618	sulfate/bicarbonate/oxalate exchanger and transporter sat-1 n 1 tax populus trichocarpa b9h8c3_poptr score=686.41 evalue=0.00e+00;
c83570/f1p2/1618	sulfate transporter (fragment) n 1 tax populus tremula x populus alba a7ygi2_popcn score=682.17 evalue=0.00e+00;
c84231/f2p1/1593	uncharacterized protein n 1 tax solanum lycopersicum k4b406_sollc score=834.71 evalue=0.00e+00;
c84231/f2p1/1593	senescence-related protein n 1 tax camellia sinensis b5tv63_camsi score=576.63 evalue=0.00e+00;
c84231/f2p1/1593	putative uncharacterized protein n 1 tax vitis vinifera f6i108_vitvi score=562.38 evalue=0.00e+00;
c84231/f2p1/1593	predicted protein n 1 tax populus trichocarpa b9h186_poptr score=531.95 evalue=0.00e+00;
c84231/f2p1/1593	uncharacterized protein n 1 tax glycine max i1j8j9_soybn score=524.63 evalue=1.23e-179;
c84375/f1p3/1590	uncharacterized protein n 1 tax solanum lycopersicum k4bmz4_sollc score=825.47 evalue=0.00e+00;
c84375/f1p3/1590	uncharacterized protein n 1 tax solanum lycopersicum k4c718_sollc score=646.35 evalue=0.00e+00;
c84375/f1p3/1590	putative uncharacterized protein n 1 tax vitis vinifera a5bp62_vitvi score=640.96 evalue=0.00e+00;
c84375/f1p3/1590	phosphatidylcholine: diacylglycerol acyltransferase n 1 tax ricinus communis b9s5t1_ricco score=638.26 evalue=0.00e+00;
c84375/f1p3/1590	phospholipid:diacylglycerol acyl transferase n 1 tax ricinus communis f2vr35_ricco score=637.88 evalue=0.00e+00;
c84433/f1p3/2043	hop-interacting protein thi012 n 1 tax solanum lycopersicum g8z251_sollc score=910.98 evalue=0.00e+00;
c84433/f1p3/2043	uncharacterized protein n 1 tax solanum lycopersicum k4d9l1_sollc score=908.29 evalue=0.00e+00;
c84433/f1p3/2043	hop-interacting protein thi033 n 1 tax solanum lycopersicum g8z262_sollc score=779.63 evalue=0.00e+00;
c84433/f1p3/2043	predicted protein n 2 tax populus trichocarpa b9gjp4_poptr score=698.74 evalue=0.00e+00;
c84433/f1p3/2043	ring zinc finger protein n 1 tax artemisia desertorum q2te73_9astr score=684.87 evalue=0.00e+00;

c84579/f1p1/2255	transport inhibitor response 1 n 1 tax nicotiana tabacum c7e4r3_tobac score=944.88 evalue=0.00e+00;
c84579/f1p1/2255	tir1-like protein n 1 tax solanum lycopersicum c8c507_sollc score=926.78 evalue=0.00e+00;
c84579/f1p1/2255	uncharacterized protein n 1 tax glycine max i1jqg9_soybn score=906.36 evalue=0.00e+00;
c84579/f1p1/2255	f-box/leucine rich repeat protein n 1 tax phaseolus vulgaris e9nzt3_phavu score=904.05 evalue=0.00e+00;
c84579/f1p1/2255	uncharacterized protein n 1 tax glycine max i1nb13_soybn score=897.12 evalue=0.00e+00;
c85886/f1p2/1640	uncharacterized protein n 1 tax solanum lycopersicum k4bly8_sollc score=724.55 evalue=0.00e+00;
c85886/f1p2/1640	predicted protein n 1 tax populus trichocarpa b9i3y5_poptr score=674.47 evalue=0.00e+00;
c85886/f1p2/1640	putative uncharacterized protein n 1 tax vitis vinifera a5blt6_vitvi score=674.86 evalue=0.00e+00;
c85886/f1p2/1640	serine carboxypeptidase putative n 1 tax ricinus communis b9ra79_ricco score=672.54 evalue=0.00e+00;
c85886/f1p2/1640	serine carboxypeptidase putative n 1 tax ricinus communis b9rfy7_ricco score=670.23 evalue=0.00e+00;
c87094/f1p5/1595	phosphoglycerate kinase n 1 tax solanum tuberosum o81394_soltu score=909.06 evalue=0.00e+00;
c87094/f1p5/1595	phosphoglycerate kinase-like protein n 1 tax solanum tuberosum q2xpv6_soltu score=905.98 evalue=0.00e+00;
c87094/f1p5/1595	phosphoglycerate kinase-like n 1 tax solanum tuberosum q2v9b3_soltu score=905.98 evalue=0.00e+00;
c87094/f1p5/1595	phosphoglycerate kinase n 1 tax solanum lycopersicum k4chy4_sollc score=902.51 evalue=0.00e+00;
c87094/f1p5/1595	phosphoglycerate kinase chloroplastic n 1 tax nicotiana tabacum pgkh_tobac score=875.93 evalue=0.00e+00;
c87198/f7p1/2942	uncharacterized protein n 1 tax solanum lycopersicum k4bnl4_sollc score=871.69 evalue=0.00e+00;
c87198/f7p1/2942	uncharacterized protein n 1 tax solanum lycopersicum k4bnl4_sollc score=603.59 evalue=0.00e+00;
c87198/f7p1/2942	uncharacterized protein n 1 tax solanum lycopersicum k4bnl3_sollc score=706.06 evalue=0.00e+00;
c87198/f7p1/2942	uncharacterized protein n 1 tax solanum lycopersicum k4bnl3_sollc score=447.97 evalue=0.00e+00;
c87198/f7p1/2942	uncharacterized protein n 1 tax solanum lycopersicum k4bnl0_sollc score=689.49 evalue=0.00e+00;
c87339/f6p21/1030	uncharacterized protein n 1 tax solanum lycopersicum k4c8w9_sollc score=454.91 evalue=4.46e-158;
c87339/f6p21/1030	ribosomal protein s3a-like n 1 tax solanum tuberosum q2vch9_soltu score=454.91 evalue=4.51e-158;
c87339/f6p21/1030	uncharacterized protein n 1 tax solanum lycopersicum k4bjk7_sollc score=454.52 evalue=5.20e-158;
c87339/f6p21/1030	cyc07-like n 1 tax solanum tuberosum q2xpx9_soltu score=453.75 evalue=1.32e-157;
c87339/f6p21/1030	cyc07-like n 1 tax solanum tuberosum q2xpv8_soltu score=452.98 evalue=2.32e-157;
c89061/f2p1/1304	uncharacterized protein n 1 tax solanum lycopersicum k4bvx2_sollc score=506.14 evalue=2.69e-176;
c89061/f2p1/1304	putative uncharacterized protein n 1 tax vitis vinifera f6h085_vitvi score=182.96 evalue=1.60e-50;
c89061/f2p1/1304	putative uncharacterized protein n 1 tax vitis vinifera a5c7c8_vitvi score=185.27 evalue=2.29e-49;
c89061/f2p1/1304	uncharacterized protein n 1 tax glycine max i1jsa6_soybn score=115.55 evalue=4.78e-26;
c89061/f2p1/1304	uncharacterized protein n 1 tax glycine max i1k6v1_soybn score=115.16 evalue=6.93e-26;
c89188/f26p16/1649	isph protein n 1 tax solanum lycopersicum d0vny3_sollc score=926.39 evalue=0.00e+00;

c89188/f26p16/1649	lytb-like protein-like n 1 tax solanum tuberosum q2xtb5_soltu score=902.51 evalue=0.00e+00;
c89188/f26p16/1649	1-hydroxy-2-methyl-2-(e)-butenyl 4-diphosphate reductase n 1 tax nicotiana langsdorffii x nicotiana sanderae b3f8g9_nicls score=880.55 evalue=0.00e+00;
c89188/f26p16/1649	g0t511 1-hydroxy-2-methyl-butenyl 4-diphosphate reductase n 2 tax nicotiana benthamiana g0t511_nicbe score=879.40 evalue=0.00e+00;
c89188/f26p16/1649	chloroplast 1-hydroxy-2-methyl-butenyl 4-diphosphate reductase n 1 tax nicotiana tabacum q9spl9_tobac score=872.46 evalue=0.00e+00;
c89282/f3p5/1018	uncharacterized protein n 1 tax solanum lycopersicum k4c5k1_sollc score=256.53 evalue=6.70e-81;
c89282/f3p5/1018	pra1 family protein b1 n 1 tax medicago truncatula g7k792_medtr score=202.99 evalue=1.20e-59;
c89282/f3p5/1018	predicted protein n 1 tax populus trichocarpa b9hhw1_poptr score=198.75 evalue=1.11e-58;
c89282/f3p5/1018	putative uncharacterized protein n 1 tax vitis vinifera f6hca0_vitvi score=211.46 evalue=8.15e-58;
c89282/f3p5/1018	uncharacterized protein n 1 tax glycine max i1jic8_soybn score=190.66 evalue=2.21e-55;
c89890/f15p9/1905	sucrose transport protein n 1 tax solanum tuberosum q43653_soltu score=878.24 evalue=0.00e+00;
c89890/f15p9/1905	uncharacterized protein n 2 tax solanum lycopersicum k4d6k5_sollc score=867.84 evalue=0.00e+00;
c89890/f15p9/1905	sucrose transporter n 1 tax nicotiana tabacum a8e0n3_tobac score=816.61 evalue=0.00e+00;
c89890/f15p9/1905	sucrose transporter n 1 tax nicotiana tabacum b5m9j3_tobac score=810.83 evalue=0.00e+00;
c89890/f15p9/1905	sucrose transporter n 1 tax nicotiana tabacum b5m9j4_tobac score=809.29 evalue=0.00e+00;
c90028/f5p16/1316	uncharacterized protein n 1 tax solanum lycopersicum k4c945_sollc score=522.70 evalue=0.00e+00;
c90028/f5p16/1316	os12g0420200 protein n 1 tax oryza sativa japonica group q2qsr7_orysj score=393.27 evalue=5.50e-167;
c90028/f5p16/1316	os12g0420200 protein n 1 tax oryza sativa japonica group q2qsr7_orysj score=222.63 evalue=5.50e-167;
c90028/f5p16/1316	uncharacterized protein n 1 tax oryza glaberrima i1r5x3_orygl score=391.73 evalue=1.56e-166;
c90028/f5p16/1316	uncharacterized protein n 1 tax oryza glaberrima i1r5x3_orygl score=222.63 evalue=1.56e-166;
c90499/f1p1/1615	uncharacterized protein n 1 tax solanum lycopersicum k4d6f3_sollc score=831.25 evalue=0.00e+00;
c90499/f1p1/1615	avr9 elicitor response protein n 1 tax nicotiana tabacum q9zs49_tobac score=806.98 evalue=0.00e+00;
c90499/f1p1/1615	uncharacterized protein n 1 tax glycine max i1man3_soybn score=678.71 evalue=0.00e+00;
c90499/f1p1/1615	uncharacterized protein n 1 tax glycine max i1lw28_soybn score=677.17 evalue=0.00e+00;
c90499/f1p1/1615	beta-1 3-galactosyltransferase sqv-2 putative n 1 tax ricinus communis b9rjc3_ricco score=676.40 evalue=0.00e+00;
c90649/f1p2/1507	uncharacterized protein n 1 tax solanum lycopersicum k4bf28_sollc score=470.31 evalue=0.00e+00;
c90649/f1p2/1507	uncharacterized protein n 1 tax solanum lycopersicum k4bf28_sollc score=252.68 evalue=0.00e+00;
c90649/f1p2/1507	putative uncharacterized protein n 1 tax vitis vinifera a5bnp3_vitvi score=384.42 evalue=1.02e-158;
c90649/f1p2/1507	putative uncharacterized protein n 1 tax vitis vinifera a5bnp3_vitvi score=204.14 evalue=1.02e-158;
c90649/f1p2/1507	uncharacterized protein n 1 tax glycine max i1ngu8_soybn score=379.79 evalue=2.00e-156;
c91310/f1p11/1889	uncharacterized protein n 1 tax solanum lycopersicum k4dex3_sollc score=1007.28 evalue=0.00e+00;
c91310/f1p11/1889	phosphoethanolamine n-methyltransferase n 1 tax solanum lycopersicum q9axh3_sollc score=900.58 evalue=0.00e+00;

c91310/f1p11/1889	phosphoethanolamine n-methyltransferase putative n 1 tax ricinus communis b9t1h8_ricco score=866.68 evalue=0.00e+00;
c91310/f1p11/1889	putative uncharacterized protein n 1 tax vitis vinifera d7sja7_vitvi score=858.98 evalue=0.00e+00;
c91310/f1p11/1889	putative uncharacterized protein n 1 tax vitis vinifera a5anl8_vitvi score=855.90 evalue=0.00e+00;
c91443/f1p1/2073	uncharacterized protein n 1 tax solanum lycopersicum k4bbu6_sollc score=768.46 evalue=0.00e+00;
c91443/f1p1/2073	uncharacterized protein n 1 tax solanum lycopersicum k4bbu6_sollc score=393.27 evalue=0.00e+00;
c91443/f1p1/2073	uncharacterized protein n 1 tax solanum lycopersicum k4bbu6_sollc score=164.85 evalue=0.00e+00;
c91443/f1p1/2073	putative uncharacterized protein n 1 tax vitis vinifera a5c158_vitvi score=704.52 evalue=0.00e+00;
c91443/f1p1/2073	putative uncharacterized protein n 1 tax vitis vinifera a5c158_vitvi score=345.12 evalue=0.00e+00;
c91670/f1p5/1764	uncharacterized protein n 1 tax solanum lycopersicum k4bli3_sollc score=966.84 evalue=0.00e+00;
c91670/f1p5/1764	signal recognition particle 54 kda protein 1 n 1 tax solanum lycopersicum sr541_sollc score=950.66 evalue=0.00e+00;
c91670/f1p5/1764	signal recognition particle 54 kda protein 2 n 1 tax solanum lycopersicum sr542_sollc score=915.61 evalue=0.00e+00;
c91670/f1p5/1764	uncharacterized protein n 1 tax glycine max i1mce2_soybn score=895.19 evalue=0.00e+00;
c91670/f1p5/1764	uncharacterized protein n 1 tax glycine max i1kvg2_soybn score=894.80 evalue=0.00e+00;
c92075/f1p5/1946	phenylalanine ammonia-lyase n 1 tax solanum lycopersicum k4d451_sollc score=1178.70 evalue=0.00e+00;
c92075/f1p5/1946	phenylalanine ammonia-lyase n 1 tax nicotiana attenuata d2cfq1_nicat score=1165.21 evalue=0.00e+00;
c92075/f1p5/1946	phenylalanine ammonia-lyase n 1 tax nicotiana tabacum pal2_tobac score=1158.67 evalue=0.00e+00;
c92075/f1p5/1946	phenylalanine ammonia-lyase n 2 tax nicotiana tabacum pal3_tobac score=1152.12 evalue=0.00e+00;
c92075/f1p5/1946	phenylalanine ammonia-lyase n 1 tax nicotiana attenuata a5h1i7_nicat score=1134.78 evalue=0.00e+00;
c92090/f1p2/1875	uncharacterized protein n 1 tax solanum lycopersicum k4c828_sollc score=922.15 evalue=0.00e+00;
c92090/f1p2/1875	uncharacterized protein n 1 tax solanum lycopersicum k4blr9_sollc score=561.99 evalue=0.00e+00;
c92090/f1p2/1875	putative uncharacterized protein n 1 tax vitis vinifera f6hym2_vitvi score=446.43 evalue=3.56e-146;
c92090/f1p2/1875	predicted protein n 1 tax populus trichocarpa b9glp3_poptr score=438.73 evalue=7.37e-144;
c92090/f1p2/1875	putative uncharacterized protein n 1 tax ricinus communis b9rgp4_ricco score=434.88 evalue=3.30e-142;
c92287/f1p0/1990	hydrolase alpha/beta fold family protein n 1 tax solanum demissum q6l459_solde score=1011.52 evalue=0.00e+00;
c92287/f1p0/1990	uncharacterized protein n 1 tax solanum lycopersicum k4dav1_sollc score=1004.97 evalue=0.00e+00;
c92287/f1p0/1990	putative uncharacterized protein n 1 tax vitis vinifera f6gty2_vitvi score=599.36 evalue=0.00e+00;
c92287/f1p0/1990	putative uncharacterized protein n 1 tax vitis vinifera d7tqh3_vitvi score=588.96 evalue=0.00e+00;
c92287/f1p0/1990	uncharacterized protein n 1 tax glycine max i1lkc7_soybn score=582.02 evalue=0.00e+00;
c92474/f2p0/2331	gras6 n 1 tax solanum lycopersicum q00lp3_sollc score=856.28 evalue=0.00e+00;
c92474/f2p0/2331	uncharacterized protein n 1 tax solanum lycopersicum k4bt46_sollc score=850.89 evalue=0.00e+00;
c92474/f2p0/2331	gras family transcription factor n 1 tax populus trichocarpa b9h7m7_poptr score=498.82 evalue=0.00e+00;

c92474/f2p0/2331	gras family transcription factor n 1 tax populus trichocarpa b9h7m7_poptr score=197.21 evalue=0.00e+00;
c92474/f2p0/2331	putative uncharacterized protein n 2 tax vitis vinifera f6h091_vitvi score=492.27 evalue=0.00e+00;
c92908/f1p4/1562	uncharacterized protein n 1 tax solanum lycopersicum k4d272_sollc score=692.96 evalue=0.00e+00;
c92908/f1p4/1562	putative uncharacterized protein n 1 tax vitis vinifera a5amt9_vitvi score=430.64 evalue=2.51e-144;
c92908/f1p4/1562	predicted protein n 1 tax populus trichocarpa b9ihm5_poptr score=416.39 evalue=7.81e-139;
c92908/f1p4/1562	predicted protein n 1 tax populus trichocarpa b9h8r7_poptr score=410.22 evalue=2.21e-136;
c92908/f1p4/1562	uncharacterized protein n 2 tax glycine max i1jn16_soybn score=402.90 evalue=1.42e-133;
c93056/f1p2/1790	ribonucleoside-diphosphate reductase n 1 tax solanum lycopersicum k4bpq8_sollc score=1017.68 evalue=0.00e+00;
c93056/f1p2/1790	ribonucleoside-diphosphate reductase n 1 tax nicotiana tabacum q9zr56_tobac score=1000.35 evalue=0.00e+00;
c93056/f1p2/1790	ribonucleoside-diphosphate reductase n 1 tax solanum lycopersicum k4bs95_sollc score=969.15 evalue=0.00e+00;
c93056/f1p2/1790	ribonucleoside-diphosphate reductase n 1 tax nicotiana tabacum q9zr57_tobac score=966.07 evalue=0.00e+00;
c93056/f1p2/1790	ribonucleoside-diphosphate reductase n 1 tax glycine max q8gzu9_soybn score=941.03 evalue=0.00e+00;
c93102/f2p0/1721	uncharacterized protein n 1 tax solanum lycopersicum k4cui5_sollc score=682.56 evalue=0.00e+00;
c93102/f2p0/1721	putative uncharacterized protein n 1 tax vitis vinifera d7te14_vitvi score=417.16 evalue=1.43e-136;
c93102/f2p0/1721	putative uncharacterized protein n 1 tax vitis vinifera a5bj67_vitvi score=417.16 evalue=1.52e-136;
c93102/f2p0/1721	uncharacterized protein n 1 tax glycine max i1n9k2_soybn score=413.69 evalue=3.46e-135;
c93102/f2p0/1721	putative uncharacterized protein n 1 tax medicago truncatula g7idk3_medtr score=409.07 evalue=2.61e-133;
c93106/f2p7/1848	uncharacterized protein n 1 tax solanum lycopersicum k4cw78_sollc score=421.39 evalue=1.10e-137;
c93106/f2p7/1848	putative uncharacterized protein n 1 tax vitis vinifera a5bk88_vitvi score=350.13 evalue=3.03e-110;
c93106/f2p7/1848	putative uncharacterized protein n 1 tax vitis vinifera f6h8s2_vitvi score=350.13 evalue=3.49e-110;
c93106/f2p7/1848	uncharacterized protein n 1 tax solanum lycopersicum k4bdz2_sollc score=343.58 evalue=2.81e-108;
c93106/f2p7/1848	uncharacterized protein n 1 tax glycine max k7lka7_soybn score=340.12 evalue=2.53e-106;
c93134/f2p6/895	uncharacterized protein n 1 tax solanum lycopersicum k4bvl2_sollc score=355.52 evalue=1.69e-120;
c93134/f2p6/895	putative uncharacterized protein n 1 tax ricinus communis b9ses2_ricco score=271.17 evalue=2.20e-87;
c93134/f2p6/895	uncharacterized protein n 2 tax glycine max k7m082_soybn score=256.53 evalue=1.71e-81;
c93134/f2p6/895	uncharacterized protein n 1 tax oryza glaberrima i1pvg9_orygl score=252.29 evalue=3.32e-80;
c93134/f2p6/895	uncharacterized protein n 1 tax setaria italica k3yvf7_setit score=253.06 evalue=4.88e-80;
c93409/f1p4/2276	uncharacterized protein n 1 tax solanum lycopersicum k4bvv2_sollc score=1343.56 evalue=0.00e+00;
c93409/f1p4/2276	ftsh-like protein n 1 tax solanum lycopersicum a1kxm7_sollc score=1337.01 evalue=0.00e+00;
c93409/f1p4/2276	atp-dependent zinc metalloprotease ftsh chloroplastic n 1 tax nicotiana tabacum ftsh_tobac score=1261.51 evalue=0.00e+00;
c93409/f1p4/2276	atp-dependent zinc metalloprotease ftsh chloroplastic (fragment) n 1 tax capsicum annuum ftsh_capan score=1202.58 evalue=0.00e+00;

c93409/f1p4/2276	putative uncharacterized protein n 1 tax vitis vinifera f6h0b6_vitvi score=1174.46 evalue=0.00e+00;
c94042/f23p4/1949	uncharacterized protein n 1 tax solanum lycopersicum k4b8v5_sollc score=679.86 evalue=0.00e+00;
c94042/f23p4/1949	gtp-binding protein era putative n 1 tax ricinus communis b9s6c9_ricco score=537.72 evalue=0.00e+00;
c94042/f23p4/1949	putative uncharacterized protein n 1 tax vitis vinifera d7spa6_vitvi score=532.33 evalue=0.00e+00;
c94042/f23p4/1949	predicted protein n 1 tax populus trichocarpa b9hf36_poptr score=530.02 evalue=1.71e-180;
c94042/f23p4/1949	putative uncharacterized protein n 1 tax eutrema halophilum q0zr46_theha score=525.78 evalue=1.49e-178;
c94085/f9p35/1579	chloroplast sedoheptulose-1 7-bisphosphatase n 12 tax solanoideae c5iu71_sollc score=731.10 evalue=0.00e+00;
c94085/f9p35/1579	putative uncharacterized protein n 1 tax vitis vinifera d7tmh3_vitvi score=660.60 evalue=0.00e+00;
c94085/f9p35/1579	predicted protein n 1 tax populus trichocarpa a9pf94_poptr score=647.89 evalue=0.00e+00;
c94085/f9p35/1579	sedoheptulose-1 7-bisphosphatase chloroplast putative n 1 tax ricinus communis b9swp6_ricco score=642.50 evalue=0.00e+00;
c94085/f9p35/1579	predicted protein n 1 tax populus trichocarpa b9hhk5_poptr score=642.50 evalue=0.00e+00;
c94470/f2p6/1837	uncharacterized protein n 1 tax solanum lycopersicum k4cy98_sollc score=801.97 evalue=0.00e+00;
c94470/f2p6/1837	putative uncharacterized protein n 1 tax vitis vinifera d7u819_vitvi score=587.80 evalue=0.00e+00;
c94470/f2p6/1837	uncharacterized protein n 1 tax glycine max i1ncq2_soybn score=587.03 evalue=0.00e+00;
c94470/f2p6/1837	uncharacterized protein n 1 tax glycine max i1js33_soybn score=578.17 evalue=0.00e+00;
c94470/f2p6/1837	putative uncharacterized protein (fragment) n 1 tax glycine max c6tnj7_soybn score=567.00 evalue=0.00e+00;
c94919/f43p64/1834	catalase isozyme 1 n 2 tax solanum cata1_sollc score=1027.31 evalue=0.00e+00;
c94919/f43p64/1834	catalase n 1 tax solanum tuberosum q2pyw5_soltu score=1025.39 evalue=0.00e+00;
c94919/f43p64/1834	catalase isozyme 2 n 1 tax solanum tuberosum cata2_soltu score=1023.46 evalue=0.00e+00;
c94919/f43p64/1834	glutamate synthase subunit alpha n 1 tax rhodanobacter thiooxydans lcs2 i4wtb3_9gamm score=1022.69 evalue=0.00e+00;
c94919/f43p64/1834	glutamate synthase subunit alpha n 1 tax rhodanobacter thiooxydans lcs2 i4wtb3_9gamm score=775.78 evalue=0.00e+00;
c95119/f16p1/1931	uncharacterized protein n 1 tax solanum lycopersicum k4dbu6_sollc score=941.41 evalue=0.00e+00;
c95119/f16p1/1931	putative uncharacterized protein n 1 tax vitis vinifera d7tbe8_vitvi score=786.56 evalue=0.00e+00;
c95119/f16p1/1931	glucan endo-1 3-beta-glucosidase putative n 1 tax ricinus communis b9rkf7_ricco score=771.93 evalue=0.00e+00;
c95119/f16p1/1931	uncharacterized protein n 1 tax glycine max i1kpw0_soybn score=770.38 evalue=0.00e+00;
c95119/f16p1/1931	uncharacterized protein n 1 tax glycine max k7krr7_soybn score=764.99 evalue=0.00e+00;
c95806/f5p11/3292	uncharacterized protein n 1 tax solanum lycopersicum k4b991_sollc score=1465.29 evalue=0.00e+00;
c95806/f5p11/3292	putative uncharacterized protein n 1 tax vitis vinifera f6gzf1_vitvi score=630.94 evalue=0.00e+00;
c95806/f5p11/3292	putative uncharacterized protein n 1 tax ricinus communis b9rz42_ricco score=569.70 evalue=0.00e+00;
c95806/f5p11/3292	uncharacterized protein n 1 tax glycine max i1m287_soybn score=477.63 evalue=5.79e-148;
c95806/f5p11/3292	uncharacterized protein n 2 tax glycine max k7ma29_soybn score=466.85 evalue=1.20e-143;

c96041/f9p8/3094	uncharacterized protein n 1 tax solanum lycopersicum k4bm94_sollc score=1461.82 evalue=0.00e+00;
c96041/f9p8/3094	putative uncharacterized protein n 1 tax vitis vinifera d7siz8_vitvi score=909.44 evalue=0.00e+00;
c96041/f9p8/3094	putative uncharacterized protein n 1 tax vitis vinifera a5bq84_vitvi score=908.29 evalue=0.00e+00;
c96041/f9p8/3094	predicted protein n 1 tax populus trichocarpa b9i2l6_poptr score=865.53 evalue=0.00e+00;
c96041/f9p8/3094	crs1 / yhby (crm) domain-containing protein n 1 tax arabidopsis thaliana q9ls51_arath score=833.94 evalue=0.00e+00;
c96062/f3p7/2048	uncharacterized protein n 1 tax solanum lycopersicum k4byc0_sollc score=1091.64 evalue=0.00e+00;
c96062/f3p7/2048	uncharacterized protein n 1 tax glycine max i1lne6_soybn score=1047.34 evalue=0.00e+00;
c96062/f3p7/2048	uncharacterized protein n 1 tax glycine max i1myl7_soybn score=1045.42 evalue=0.00e+00;
c96062/f3p7/2048	chaperonin containing t-complex protein 1 epsilon subunit tcpe putative n 1 tax ricinus communis b9rmr9_ricco score=1045.42 evalue=0.00e+00;
c96062/f3p7/2048	uncharacterized protein n 1 tax setaria italica k3zs67_setit score=1036.17 evalue=0.00e+00;
c96153/f59p15/1668	uncharacterized protein n 1 tax solanum lycopersicum k4buy7_sollc score=794.27 evalue=0.00e+00;
c96153/f59p15/1668	uncharacterized protein n 1 tax solanum lycopersicum k4bpg6_sollc score=713.38 evalue=0.00e+00;
c96153/f59p15/1668	uncharacterized protein n 1 tax solanum lycopersicum k4buy9_sollc score=548.89 evalue=0.00e+00;
c96153/f59p15/1668	putative uncharacterized protein n 1 tax vitis vinifera f6h210_vitvi score=496.51 evalue=3.60e-168;
c96153/f59p15/1668	predicted protein n 1 tax populus trichocarpa b9i1e5_poptr score=484.18 evalue=3.46e-163;
c96604/f53p36/1578	phosphoribulokinase n 1 tax solanum lycopersicum k4cmy9_sollc score=790.41 evalue=0.00e+00;
c96604/f53p36/1578	phosphoribulokinase n 1 tax ricinus communis b9rz33_ricco score=751.12 evalue=0.00e+00;
c96604/f53p36/1578	phosphoribulokinase n 1 tax populus trichocarpa b9mua4_poptr score=744.96 evalue=0.00e+00;
c96604/f53p36/1578	phosphoribulokinase n 2 tax populus trichocarpa b9gzt5_poptr score=744.58 evalue=0.00e+00;
c96604/f53p36/1578	phosphoribulokinase n 1 tax vitis vinifera f6h7q2_vitvi score=743.81 evalue=0.00e+00;
c96641/f2p28/1554	atp synthase gamma chain n 1 tax solanum lycopersicum k4b9s5_sollc score=644.42 evalue=0.00e+00;
c96641/f2p28/1554	homoserine dehydrogenase n 1 tax bacillus sp. m 2-6 i4v9m3_9baci score=630.56 evalue=0.00e+00;
c96641/f2p28/1554	atp synthase gamma chain chloroplastic n 1 tax nicotiana tabacum atpg_tobac score=628.25 evalue=0.00e+00;
c96641/f2p28/1554	atp synthase gamma chain n 1 tax cucumis melo subsp. melo e5gc53_cucme score=583.56 evalue=0.00e+00;
c96641/f2p28/1554	atp synthase gamma chain n 3 tax populus a9pjj6_9rosi score=582.79 evalue=0.00e+00;
c96662/f5p3/1048	ubiquitin-conjugating protein-like n 1 tax solanum tuberosum q2v986_soltu score=402.90 evalue=1.61e-138;
c96662/f5p3/1048	ubiquitin conjugating enzyme-like n 1 tax solanum tuberosum q2vck7_soltu score=400.98 evalue=9.44e-138;
c96662/f5p3/1048	ubiquitin conjugating enzyme n 1 tax solanum lycopersicum q43780_sollc score=399.82 evalue=2.72e-137;
c96662/f5p3/1048	ubiquitin-conjugating enzyme e2-25kd putative n 1 tax ricinus communis b9ra92_ricco score=338.58 evalue=3.20e-113;
c96662/f5p3/1048	predicted protein n 1 tax populus trichocarpa a9p939_poptr score=336.26 evalue=1.99e-112;
c96665/f2p2/2679	hop-interacting protein thi044 n 1 tax solanum lycopersicum g8z271_sollc score=1450.26 evalue=0.00e+00;

c96665/f2p2/2679	putative uncharacterized protein n 1 tax vitis vinifera f6i050_vitvi score=1029.62 evalue=0.00e+00;
c96665/f2p2/2679	putative uncharacterized protein n 1 tax vitis vinifera a5bdq0_vitvi score=998.42 evalue=0.00e+00;
c96665/f2p2/2679	predicted protein n 1 tax populus trichocarpa b9h4j0_poptr score=966.84 evalue=0.00e+00;
c96665/f2p2/2679	putative uncharacterized protein n 1 tax medicago truncatula g7i5w7_medtr score=905.21 evalue=0.00e+00;
c96805/f2p4/1620	uncharacterized protein n 1 tax solanum lycopersicum k4cww3_sollc score=781.94 evalue=0.00e+00;
c96805/f2p4/1620	putative uncharacterized protein n 1 tax vitis vinifera d7u9k6_vitvi score=515.77 evalue=7.18e-177;
c96805/f2p4/1620	putative uncharacterized protein n 1 tax vitis vinifera a5bzi0_vitvi score=498.43 evalue=1.12e-169;
c96805/f2p4/1620	uncharacterized protein n 1 tax glycine max i1ln48_soybn score=481.10 evalue=1.91e-163;
c96805/f2p4/1620	uncharacterized protein n 1 tax glycine max k7mp69_soybn score=481.10 evalue=6.74e-163;
c96899/f54p62/1588	phosphoribulokinase n 1 tax solanum lycopersicum k4cmy9_sollc score=790.03 evalue=0.00e+00;
c96899/f54p62/1588	phosphoribulokinase n 1 tax ricinus communis b9rz33_ricco score=751.51 evalue=0.00e+00;
c96899/f54p62/1588	phosphoribulokinase n 1 tax populus trichocarpa b9mua4_poptr score=744.96 evalue=0.00e+00;
c96899/f54p62/1588	phosphoribulokinase n 1 tax vitis vinifera f6h7q2_vitvi score=744.58 evalue=0.00e+00;
c96899/f54p62/1588	phosphoribulokinase n 2 tax populus trichocarpa b9gzt5_poptr score=744.19 evalue=0.00e+00;
c97172/f2p2/1726	uncharacterized protein n 1 tax solanum lycopersicum k4bvg9_sollc score=864.76 evalue=0.00e+00;
c97172/f2p2/1726	putative uncharacterized protein n 1 tax vitis vinifera e0cpg0_vitvi score=644.04 evalue=0.00e+00;
c97172/f2p2/1726	jhl18i08.5 protein n 1 tax jatropha curcas e6nu61_9rosi score=610.14 evalue=0.00e+00;
c97172/f2p2/1726	putative uncharacterized protein n 1 tax vitis vinifera a5b1b5_vitvi score=565.07 evalue=0.00e+00;
c97172/f2p2/1726	gtp-dependent nucleic acid-binding protein engd putative n 1 tax ricinus communis b9r818_ricco score=562.38 evalue=0.00e+00;
c97196/f24p5/1776	uncharacterized protein n 1 tax solanum lycopersicum k4cee9_sollc score=865.53 evalue=0.00e+00;
c97196/f24p5/1776	uncharacterized protein n 1 tax solanum lycopersicum k4cec8_sollc score=837.02 evalue=0.00e+00;
c97196/f24p5/1776	dsk2 n 1 tax nicotiana tabacum q0z839_tobac score=779.25 evalue=0.00e+00;
c97196/f24p5/1776	putative uncharacterized protein n 2 tax vitis vinifera f6h9n7_vitvi score=749.58 evalue=0.00e+00;
c97196/f24p5/1776	uncharacterized protein n 1 tax glycine max i1kpp1_soybn score=702.98 evalue=0.00e+00;
c97199/f1p3/1532	uncharacterized protein n 1 tax solanum lycopersicum k4bvr9_sollc score=819.30 evalue=0.00e+00;
c97199/f1p3/1532	putative uncharacterized protein n 1 tax vitis vinifera f6h0e3_vitvi score=568.93 evalue=0.00e+00;
c97199/f1p3/1532	predicted protein n 1 tax populus trichocarpa b9h525_poptr score=553.52 evalue=0.00e+00;
c97199/f1p3/1532	nucleoredoxin putative n 1 tax ricinus communis b9r8f0_ricco score=520.39 evalue=3.02e-179;
c97199/f1p3/1532	uncharacterized protein n 1 tax glycine max i1jsz5_soybn score=501.90 evalue=2.00e-171;
c97211/f275p64/1834	catalase isozyme 1 n 2 tax solanum cata1_sollc score=1027.31 evalue=0.00e+00;
c97211/f275p64/1834	catalase n 1 tax solanum tuberosum q2pyw5_soltu score=1025.39 evalue=0.00e+00;

c97211/f275p64/1834	catalase isozyme 2 n 1 tax solanum tuberosum cata2_soltu score=1023.46 evalue=0.00e+00;
c97211/f275p64/1834	glutamate synthase subunit alpha n 1 tax rhodanobacter thiooxydans lcs2 i4wtb3_9gamm score=1022.69 evalue=0.00e+00;
c97211/f275p64/1834	glutamate synthase subunit alpha n 1 tax rhodanobacter thiooxydans lcs2 i4wtb3_9gamm score=775.78 evalue=0.00e+00;
c97217/f5p5/1900	uncharacterized protein n 1 tax solanum lycopersicum k4d440_sollc score=608.60 evalue=0.00e+00;
c97217/f5p5/1900	uncharacterized protein n 1 tax solanum lycopersicum k4cqd0_sollc score=493.81 evalue=1.30e-165;
c97217/f5p5/1900	uncharacterized protein n 1 tax solanum lycopersicum k4d3l4_sollc score=451.82 evalue=2.93e-149;
c97217/f5p5/1900	calmodulin binding protein putative n 1 tax ricinus communis b9sgq6_ricco score=401.75 evalue=5.37e-130;
c97217/f5p5/1900	predicted protein n 1 tax populus trichocarpa b9mt91_poptr score=385.19 evalue=2.02e-123;
c97329/f38p20/1800	uncharacterized protein n 1 tax solanum lycopersicum k4c353_sollc score=784.25 evalue=0.00e+00;
c97329/f38p20/1800	putative uncharacterized protein n 1 tax vitis vinifera f6guy5_vitvi score=471.86 evalue=5.81e-157;
c97329/f38p20/1800	uncharacterized protein n 1 tax glycine max i1ljy2_soybn score=469.54 evalue=4.73e-156;
c97329/f38p20/1800	putative uncharacterized protein n 1 tax populus trichocarpa a9pfd6_poptr score=457.99 evalue=1.39e-151;
c97329/f38p20/1800	predicted protein n 1 tax populus trichocarpa a9ph50_poptr score=456.83 evalue=4.09e-151;
c97349/f4p6/1704	uncharacterized protein n 1 tax solanum lycopersicum k4blp5_sollc score=773.85 evalue=0.00e+00;
c97349/f4p6/1704	putative uncharacterized protein n 1 tax vitis vinifera d7tza8_vitvi score=617.85 evalue=0.00e+00;
c97349/f4p6/1704	predicted protein (fragment) n 1 tax populus trichocarpa b9mwm3_poptr score=605.13 evalue=0.00e+00;
c97349/f4p6/1704	uncharacterized protein n 1 tax glycine max i1nj60_soybn score=602.82 evalue=0.00e+00;
c97349/f4p6/1704	prli-interacting factor l putative n 1 tax ricinus communis b9rvd0_ricco score=586.64 evalue=0.00e+00;
c97371/f2p9/1639	uncharacterized protein n 1 tax solanum lycopersicum k4blr2_sollc score=888.64 evalue=0.00e+00;
c97371/f2p9/1639	putative hydroxycinnamoyl transferase n 1 tax capsicum annuum b5lav0_capan score=866.68 evalue=0.00e+00;
c97371/f2p9/1639	shikimate o-hydroxycinnamoyltransferase n 1 tax nicotiana tabacum hst_tobac score=857.05 evalue=0.00e+00;
c97371/f2p9/1639	hydroxycinnamoyl transferase n 1 tax coffea arabica q05hb0_cofar score=786.18 evalue=0.00e+00;
c97371/f2p9/1639	hydroxycinnamoyl-coa shikimate/quinate hydroxycinnamoyltransferase n 1 tax coffea arabica a4zki0_cofar score=785.02 evalue=0.00e+00;
c97422/f1p6/1852	uncharacterized protein n 1 tax solanum lycopersicum k4cb65_sollc score=914.45 evalue=0.00e+00;
c97422/f1p6/1852	uncharacterized protein n 1 tax solanum lycopersicum k4dc77_sollc score=805.82 evalue=0.00e+00;
c97422/f1p6/1852	predicted protein n 1 tax populus trichocarpa b9i742_poptr score=791.19 evalue=0.00e+00;
c97422/f1p6/1852	uncharacterized protein n 1 tax glycine max k7mhb7_soybn score=786.95 evalue=0.00e+00;
c97422/f1p6/1852	putative uncharacterized protein n 1 tax vitis vinifera d7t7l1_vitvi score=781.17 evalue=0.00e+00;
c97591/f1p6/1498	uncharacterized protein n 1 tax solanum lycopersicum k4d6k3_sollc score=518.46 evalue=5.78e-179;
c97591/f1p6/1498	uncharacterized protein n 1 tax solanum lycopersicum k4c7h7_sollc score=499.59 evalue=2.95e-173;
c97591/f1p6/1498	predicted protein n 1 tax populus trichocarpa b9mw58_poptr score=459.14 evalue=4.08e-156;

c97591/f1p6/1498	protein-tyrosine phosphatase 1 plants putative n 1 tax ricinus communis b9t701_ricco score=448.74 evalue=3.32e-152;
c97591/f1p6/1498	putative uncharacterized protein n 1 tax vitis vinifera f6gyu9_vitvi score=446.05 evalue=2.60e-151;
c97630/f5p1/1629	uncharacterized protein n 1 tax solanum lycopersicum k4bpg6_sollc score=842.80 evalue=0.00e+00;
c97630/f5p1/1629	uncharacterized protein n 1 tax solanum lycopersicum k4buy7_sollc score=716.46 evalue=0.00e+00;
c97630/f5p1/1629	predicted protein n 1 tax populus trichocarpa b9i1e5_poptr score=493.04 evalue=6.98e-167;
c97630/f5p1/1629	putative uncharacterized protein n 1 tax vitis vinifera f6h201_vitvi score=489.96 evalue=1.24e-165;
c97630/f5p1/1629	udp-glucosyltransferase putative n 1 tax ricinus communis b9sb92_ricco score=488.03 evalue=5.82e-165;
c97673/f6p14/3359	uncharacterized protein n 1 tax solanum lycopersicum k4b8y8_sollc score=1848.94 evalue=0.00e+00;
c97673/f6p14/3359	uncharacterized protein n 1 tax solanum lycopersicum k4be53_sollc score=1462.97 evalue=0.00e+00;
c97673/f6p14/3359	putative uncharacterized protein n 1 tax vitis vinifera f6hm39_vitvi score=1399.80 evalue=0.00e+00;
c97673/f6p14/3359	leucine-rich repeat receptor-like protein kinase n 1 tax pyrus pyrifolia q6j331_pyrpy score=1389.79 evalue=0.00e+00;
c97673/f6p14/3359	leucine-rich repeat receptor-like protein kinase n 1 tax pyrus pyrifolia q6j332_pyrpy score=1388.63 evalue=0.00e+00;
c97697/f6p6/2838	uncharacterized protein n 1 tax solanum lycopersicum k4crn4_sollc score=1408.28 evalue=0.00e+00;
c97697/f6p6/2838	putative acetyl co-enzyme a carboxylase carboxyltransferase alpha subunit n 1 tax capsicum annuum b5las6_capan score=1382.47 evalue=0.00e+00;
c97697/f6p6/2838	putative uncharacterized protein n 1 tax vitis vinifera f6hkx6_vitvi score=1051.97 evalue=0.00e+00;
c97697/f6p6/2838	acetyl-coa carboxylase alpha-ct subunit n 1 tax jatropha curcas f2wmv2_9rosi score=1030.01 evalue=0.00e+00;
c97697/f6p6/2838	alpha-carboxyltransferase subunit n 1 tax jatropha curcas c9ei97_9rosi score=1029.24 evalue=0.00e+00;
c97753/f1p4/2303	uncharacterized protein n 1 tax solanum lycopersicum k4asj4_sollc score=1149.81 evalue=0.00e+00;
c97753/f1p4/2303	formate--tetrahydrofolate ligase n 1 tax spinacia oleracea fths_spiol score=1067.37 evalue=0.00e+00;
c97753/f1p4/2303	10-formyltetrahydrofolate synthetase n 1 tax populus trichocarpa b9glk3_poptr score=1063.91 evalue=0.00e+00;
c97753/f1p4/2303	10-formyltetrahydrofolate synthetase n 1 tax arabidopsis lyrata subsp. lyrata d7kg02_arall score=1062.37 evalue=0.00e+00;
c97753/f1p4/2303	formate--tetrahydrofolate ligase n 1 tax arabidopsis thaliana fths_arath score=1062.37 evalue=0.00e+00;
c97791/f2p7/1862	uncharacterized protein n 1 tax solanum lycopersicum k4d9q1_sollc score=961.44 evalue=0.00e+00;
c97791/f2p7/1862	lethal leaf spot 1-like protein n 1 tax solanum lycopersicum q8w5a3_sollc score=957.98 evalue=0.00e+00;
c97791/f2p7/1862	lethal leaf spot 1-like protein n 1 tax capsicum annuum k7qll5_capan score=920.23 evalue=0.00e+00;
c97791/f2p7/1862	pheophorbide a oxygenase 2 n 1 tax nicotiana tabacum a9ytw4_tobac score=914.06 evalue=0.00e+00;
c97791/f2p7/1862	pheophorbide a oxygenase 1 n 1 tax nicotiana tabacum a9ytw3_tobac score=905.59 evalue=0.00e+00;
c97917/f1p6/1336	uncharacterized protein n 1 tax solanum lycopersicum k4cp05_sollc score=521.16 evalue=0.00e+00;
c97917/f1p6/1336	uncharacterized protein n 1 tax solanum lycopersicum k4cir4_sollc score=448.36 evalue=3.24e-153;
c97917/f1p6/1336	uncharacterized protein n 1 tax lotus japonicus i3t5f6_lotja score=445.28 evalue=9.73e-152;
c97917/f1p6/1336	putative uncharacterized protein n 1 tax ricinus communis b9rbz1_ricco score=441.81 evalue=2.27e-150;

c97917/f1p6/1336	predicted protein n 1 tax populus trichocarpa b9gw41_poptr score=441.81 evalue=2.57e-150;
c97951/f3p1/1965	uncharacterized protein n 1 tax solanum lycopersicum k4bz03_sollc score=875.93 evalue=0.00e+00;
c97951/f3p1/1965	uncharacterized protein n 1 tax solanum lycopersicum k4cdu9_sollc score=803.90 evalue=0.00e+00;
c97951/f3p1/1965	casein kinase n 1 tax beta vulgaris a2i5g0_betvu score=759.21 evalue=0.00e+00;
c97951/f3p1/1965	predicted protein n 1 tax populus trichocarpa b9hdx8_poptr score=754.98 evalue=0.00e+00;
c97951/f3p1/1965	predicted protein n 1 tax populus trichocarpa b9n5f1_poptr score=745.73 evalue=0.00e+00;
c98022/f6p7/1606	uncharacterized protein n 1 tax solanum lycopersicum k4bvr9_sollc score=819.30 evalue=0.00e+00;
c98022/f6p7/1606	putative uncharacterized protein n 1 tax vitis vinifera f6h0e3_vitvi score=568.93 evalue=0.00e+00;
c98022/f6p7/1606	predicted protein n 1 tax populus trichocarpa b9h525_poptr score=553.52 evalue=0.00e+00;
c98022/f6p7/1606	nucleoredoxin putative n 1 tax ricinus communis b9r8f0_ricco score=520.39 evalue=7.34e-179;
c98022/f6p7/1606	uncharacterized protein n 1 tax glycine max i1jsz5_soybn score=501.90 evalue=4.83e-171;
c98025/f2p0/1179	uncharacterized protein n 1 tax solanum lycopersicum k4dfz4_sollc score=325.09 evalue=2.60e-107;
c98025/f2p0/1179	uncharacterized protein n 1 tax solanum lycopersicum k4bti5_sollc score=281.57 evalue=4.94e-90;
c98025/f2p0/1179	predicted protein n 1 tax populus trichocarpa b9h7w0_poptr score=254.60 evalue=1.21e-79;
c98025/f2p0/1179	putative uncharacterized protein n 1 tax vitis vinifera f6gy65_vitvi score=250.37 evalue=8.91e-78;
c98025/f2p0/1179	putative uncharacterized protein n 1 tax ricinus communis b9seb2_ricco score=241.12 evalue=1.68e-74;
c98066/f2p1/3102	uncharacterized protein n 1 tax solanum lycopersicum k4cx66_sollc score=1431.00 evalue=0.00e+00;
c98066/f2p1/3102	putative uncharacterized protein n 1 tax vitis vinifera e0cvm0_vitvi score=1215.68 evalue=0.00e+00;
c98066/f2p1/3102	putative uncharacterized protein n 1 tax vitis vinifera d7tem3_vitvi score=1160.59 evalue=0.00e+00;
c98066/f2p1/3102	hd-1d n 1 tax gossypium hirsutum i7b3v3_goshi score=1160.21 evalue=0.00e+00;
c98066/f2p1/3102	putative uncharacterized protein n 1 tax vitis vinifera a5c0j7_vitvi score=1160.21 evalue=0.00e+00;
c98100/f8p7/3139	uncharacterized protein n 1 tax solanum lycopersicum k4c523_sollc score=1056.97 evalue=0.00e+00;
c98100/f8p7/3139	putative uncharacterized protein n 1 tax vitis vinifera d7t479_vitvi score=853.97 evalue=0.00e+00;
c98100/f8p7/3139	uncharacterized protein n 1 tax glycine max k7lmh4_soybn score=772.70 evalue=0.00e+00;
c98100/f8p7/3139	uncharacterized protein n 1 tax glycine max i1jai8_soybn score=766.53 evalue=0.00e+00;
c98100/f8p7/3139	uncharacterized protein n 2 tax glycine max i1nj71_soybn score=764.22 evalue=0.00e+00;
c98106/f10p6/1960	serine hydroxymethyltransferase n 1 tax solanum lycopersicum k4clc9_sollc score=1075.46 evalue=0.00e+00;
c98106/f10p6/1960	serine hydroxymethyltransferase n 1 tax solanum lycopersicum k4dh66_sollc score=926.39 evalue=0.00e+00;
c98106/f10p6/1960	serine hydroxymethyltransferase putative n 1 tax ricinus communis b9s1d7_ricco score=902.12 evalue=0.00e+00;
c98106/f10p6/1960	serine hydroxymethyltransferase 8 n 1 tax populus trichocarpa b9hdq7_poptr score=901.74 evalue=0.00e+00;
c98106/f10p6/1960	putative uncharacterized protein n 1 tax vitis vinifera d7stm0_vitvi score=900.20 evalue=0.00e+00;

c98445/f23p4/1586	uncharacterized protein n 1 tax solanum lycopersicum k4bqx4_sollc score=843.57 evalue=0.00e+00;
c98445/f23p4/1586	putative uncharacterized protein n 1 tax vitis vinifera d7spm1_vitvi score=630.94 evalue=0.00e+00;
c98445/f23p4/1586	peptide chain release factor putative n 1 tax ricinus communis b9rm42_ricco score=622.47 evalue=0.00e+00;
c98445/f23p4/1586	uncharacterized protein n 2 tax glycine max i1l681_soybn score=616.30 evalue=0.00e+00;
c98445/f23p4/1586	putative translation releasing factor 2 n 1 tax cucumis sativus q6zy50_cucsa score=613.61 evalue=0.00e+00;
c98482/f4p1/1517	uncharacterized protein n 1 tax solanum lycopersicum k4d8e5_sollc score=783.10 evalue=0.00e+00;
c98482/f4p1/1517	predicted protein n 1 tax populus trichocarpa b9gf90_poptr score=554.67 evalue=0.00e+00;
c98482/f4p1/1517	uncharacterized protein n 2 tax glycine max i1kr42_soybn score=545.43 evalue=0.00e+00;
c98482/f4p1/1517	uncharacterized protein n 1 tax glycine max i1k2p9_soybn score=544.27 evalue=0.00e+00;
c98482/f4p1/1517	php domain-containing protein n 1 tax arabidopsis lyrata subsp. lyrata d7l064_arall score=500.75 evalue=5.74e-171;
c98588/f4p3/1477	uncharacterized protein n 1 tax solanum lycopersicum k4bdg0_sollc score=611.68 evalue=0.00e+00;
c98588/f4p3/1477	3-ketoacyl-coa reductase 1 n 1 tax gossypium hirsutum q0vh88_goshi score=549.67 evalue=0.00e+00;
c98588/f4p3/1477	predicted protein n 2 tax populus b9htf0_poptr score=526.55 evalue=0.00e+00;
c98588/f4p3/1477	steroid dehydrogenase putative n 1 tax ricinus communis b9rmr2_ricco score=523.09 evalue=0.00e+00;
c98588/f4p3/1477	uncharacterized protein n 1 tax medicago truncatula i3t5s9_medtr score=520.39 evalue=1.26e-180;
c98649/f1p5/984	proteasome subunit alpha type n 1 tax solanum lycopersicum k4cjh4_sollc score=485.72 evalue=7.08e-171;
c98649/f1p5/984	proteasome subunit alpha type n 1 tax solanum lycopersicum k4b832_sollc score=481.87 evalue=2.34e-169;
c98649/f1p5/984	proteasome subunit alpha type n 1 tax glycine max i1jbh2_soybn score=477.25 evalue=1.32e-167;
c98649/f1p5/984	proteasome subunit alpha type-5 n 1 tax glycine max psa5_soybn score=475.71 evalue=5.89e-167;
c98649/f1p5/984	proteasome subunit alpha type n 1 tax medicago truncatula i3ssx1_medtr score=475.71 evalue=6.58e-167;
c98792/f3p2/1285	uncharacterized protein n 1 tax solanum lycopersicum k4cn34_sollc score=483.41 evalue=2.66e-167;
c98792/f3p2/1285	predicted protein n 1 tax populus trichocarpa b9mu40_poptr score=221.09 evalue=2.89e-65;
c98792/f3p2/1285	putative uncharacterized protein n 1 tax ricinus communis b9snt4_ricco score=209.15 evalue=7.86e-61;
c98792/f3p2/1285	uncharacterized protein n 1 tax glycine max k7k1a3_soybn score=199.13 evalue=1.08e-56;
c98792/f3p2/1285	uncharacterized protein n 1 tax glycine max i1l4y2_soybn score=196.82 evalue=2.58e-56;
c98822/f1p1/1213	uncharacterized protein n 1 tax solanum lycopersicum k4c3b4_sollc score=634.79 evalue=0.00e+00;
c98822/f1p1/1213	putative uncharacterized protein n 1 tax vitis vinifera d7u8s7_vitvi score=550.82 evalue=0.00e+00;
c98822/f1p1/1213	uncharacterized protein n 1 tax lotus japonicus i3tak4_lotja score=533.87 evalue=0.00e+00;
c98822/f1p1/1213	uncharacterized protein n 1 tax glycine max c6tnw0_soybn score=533.49 evalue=0.00e+00;
c98822/f1p1/1213	at3g52390 n 1 tax arabidopsis thaliana q84td7_arath score=527.32 evalue=0.00e+00;
c98836/f2p4/1325	uncharacterized protein n 1 tax solanum lycopersicum k4ccf6_sollc score=605.13 evalue=0.00e+00;

c98836/f2p4/1325	uncharacterized protein n 1 tax glycine max i1k657_soybn score=451.44 evalue=2.63e-154;
c98836/f2p4/1325	uncharacterized protein n 1 tax glycine max i1kpp8_soybn score=450.67 evalue=6.07e-154;
c98836/f2p4/1325	uncharacterized protein n 1 tax lotus japonicus i3sgu9_lotja score=441.04 evalue=2.96e-150;
c98836/f2p4/1325	uncharacterized protein n 1 tax medicago truncatula i3s7e1_medtr score=435.26 evalue=4.91e-148;
c98879/f10p3/1902	uncharacterized protein n 1 tax solanum lycopersicum k4c3e5_sollc score=1020.38 evalue=0.00e+00;
c98879/f10p3/1902	putative uncharacterized protein n 1 tax solanum tuberosum q2v9c4_soltu score=1011.52 evalue=0.00e+00;
c98879/f10p3/1902	putative uncharacterized protein n 1 tax solanum tuberosum q2vci1_soltu score=967.99 evalue=0.00e+00;
c98879/f10p3/1902	putative uncharacterized protein (fragment) n 1 tax capsicum annuum a0mlw5_capan score=818.15 evalue=0.00e+00;
c98879/f10p3/1902	uncharacterized protein n 1 tax solanum lycopersicum k4cae8_sollc score=796.19 evalue=0.00e+00;
c98984/f6p7/1339	uncharacterized protein n 1 tax solanum lycopersicum k4bz89_sollc score=504.60 evalue=1.48e-174;
c98984/f6p7/1339	putative uncharacterized protein n 1 tax ricinus communis b9rkn3_ricco score=278.49 evalue=3.22e-86;
c98984/f6p7/1339	putative uncharacterized protein n 1 tax vitis vinifera f6hh13_vitvi score=265.39 evalue=1.96e-80;
c98984/f6p7/1339	uncharacterized protein n 1 tax glycine max i1l4k1_soybn score=238.42 evalue=1.33e-70;
c98984/f6p7/1339	zinc finger ran-binding domain-containing protein n 1 tax medicago truncatula g7kpf4_medtr score=222.63 evalue=1.89e-64;
c99157/f11p6/1284	uncharacterized protein n 1 tax solanum lycopersicum k4crb9_sollc score=511.53 evalue=3.73e-179;
c99157/f11p6/1284	putative uncharacterized protein n 1 tax ricinus communis b9syb8_ricco score=477.63 evalue=9.95e-165;
c99157/f11p6/1284	uncharacterized protein n 1 tax lotus japonicus i3sk84_lotja score=475.71 evalue=3.82e-164;
c99157/f11p6/1284	uncharacterized protein n 1 tax medicago truncatula i3taj6_medtr score=464.54 evalue=1.60e-159;
c99157/f11p6/1284	putative nad-dependent dehydrogenase 2 n 1 tax erythroxylum coca i6rzd4_erycb score=459.14 evalue=1.75e-158;
c99232/f24p6/1217	uncharacterized protein n 1 tax solanum lycopersicum k4ca57_sollc score=600.51 evalue=0.00e+00;
c99232/f24p6/1217	putative pyridoxine biosynthesis protein isoform a n 1 tax nicotiana tabacum q6qnd3_tobac score=596.66 evalue=0.00e+00;
c99232/f24p6/1217	pyridoxal biosynthesis protein n 1 tax cucumis melo subsp. melo e5gbf5_cucme score=569.31 evalue=0.00e+00;
c99232/f24p6/1217	uncharacterized protein n 1 tax glycine max i1m1p1_soybn score=566.23 evalue=0.00e+00;
c99232/f24p6/1217	pyridoxine biosynthesis protein n 1 tax lotus japonicus q45ff1_lotja score=565.07 evalue=0.00e+00;
c99267/f7p5/964	nadh-ubiquinone oxidoreductase subunit-like n 1 tax solanum tuberosum q38jg6_soltu score=408.30 evalue=6.45e-141;
c99267/f7p5/964	uncharacterized protein n 1 tax solanum lycopersicum k4daf9_sollc score=407.14 evalue=2.44e-140;
c99267/f7p5/964	nadh dehydrogenase [ubiquinone] iron-sulfur protein 7 mitochondrial n 1 tax solanum tuberosum ndus7_soltu score=405.99 evalue=6.67e-140;
c99267/f7p5/964	putative uncharacterized protein n 1 tax vitis vinifera f6h393_vitvi score=344.35 evalue=8.26e-116;
c99267/f7p5/964	putative uncharacterized protein n 1 tax vitis vinifera a5ay34_vitvi score=343.58 evalue=1.95e-115;
c99279/f7p3/1855	uncharacterized protein n 1 tax solanum lycopersicum k4bfe0_sollc score=787.33 evalue=0.00e+00;
c99279/f7p3/1855	uncharacterized protein n 1 tax solanum lycopersicum k4b9s1_sollc score=668.31 evalue=0.00e+00;

c99279/f7p3/1855	putative uncharacterized protein n 1 tax vitis vinifera f6h7n2_vitvi score=537.72 evalue=0.00e+00;
c99279/f7p3/1855	putative uncharacterized protein n 1 tax ricinus communis b9rxm0_ricco score=509.61 evalue=1.13e-172;
c99279/f7p3/1855	uncharacterized protein n 1 tax glycine max i1mfg9_soybn score=487.65 evalue=7.79e-164;
c99489/f2p2/1523	uncharacterized protein n 1 tax solanum lycopersicum k4buy7_sollc score=836.25 evalue=0.00e+00;
c99489/f2p2/1523	uncharacterized protein n 1 tax solanum lycopersicum k4bpg6_sollc score=739.95 evalue=0.00e+00;
c99489/f2p2/1523	uncharacterized protein n 1 tax solanum lycopersicum k4buy9_sollc score=523.86 evalue=0.00e+00;
c99489/f2p2/1523	predicted protein n 1 tax populus trichocarpa b9i1e5_poptr score=509.61 evalue=7.84e-174;
c99489/f2p2/1523	putative uncharacterized protein n 1 tax vitis vinifera f6h201_vitvi score=502.67 evalue=3.60e-171;
c99520/f7p6/1336	putative strictosidine synthase n 1 tax solanum lycopersicum q9lkw1_sollc score=622.08 evalue=0.00e+00;
c99520/f7p6/1336	uncharacterized protein n 1 tax solanum lycopersicum k4cga7_sollc score=620.16 evalue=0.00e+00;
c99520/f7p6/1336	uncharacterized protein n 1 tax solanum lycopersicum k4cga8_sollc score=480.71 evalue=2.24e-164;
c99520/f7p6/1336	uncharacterized protein n 1 tax solanum lycopersicum k4d2k2_sollc score=440.65 evalue=3.26e-149;
c99520/f7p6/1336	strictosidine synthase-like protein n 1 tax nicotiana tabacum a7wpl3_tobac score=437.57 evalue=8.51e-148;
c99608/f16p11/868	chlorophyll a-b binding protein cp24 10b chloroplastic n 1 tax solanum lycopersicum cb4b_sollc score=496.89 evalue=1.25e-175;
c99608/f16p11/868	chloroplast pigment-binding protein cp24 n 1 tax nicotiana tabacum q0pws6_tobac score=466.08 evalue=1.92e-163;
c99608/f16p11/868	poly (3-hydroxybutyrate) depolymerase n 1 tax rhodanobacter sp. 116-2 i4wva4_9gamm score=459.14 evalue=2.12e-159;
c99608/f16p11/868	chlorophyll a-b binding protein cp24 10a chloroplastic n 1 tax solanum lycopersicum cb4a_sollc score=450.28 evalue=3.18e-157;
c99608/f16p11/868	chloroplast chlorophyll a/b-binding protein cp24 n 1 tax medicago truncatula g7int9_medtr score=439.11 evalue=8.81e-153;
c99634/f13p3/1540	uncharacterized protein n 1 tax solanum lycopersicum k4bul6_sollc score=540.04 evalue=0.00e+00;
c99634/f13p3/1540	predicted protein n 1 tax populus trichocarpa b9ibr0_poptr score=519.62 evalue=3.34e-180;
c99634/f13p3/1540	uncharacterized protein n 1 tax glycine max k7ki29_soybn score=519.24 evalue=4.29e-180;
c99634/f13p3/1540	uncharacterized protein n 1 tax glycine max i1k870_soybn score=513.07 evalue=1.16e-177;
c99634/f13p3/1540	putative uncharacterized protein n 1 tax vitis vinifera a5bye8_vitvi score=513.84 evalue=1.21e-177;
c99711/f6p1/1115	uncharacterized protein n 7 tax lamiids k4asw3_sollc score=632.48 evalue=0.00e+00;
c99711/f6p1/1115	ribosomal protein l2-b n 1 tax medicago truncatula g7jh62_medtr score=529.25 evalue=0.00e+00;
c99711/f6p1/1115	ribosomal protein l2-a chloroplastic n 6 tax core eudicotyledons rk2a_atrbe score=525.01 evalue=0.00e+00;
c99711/f6p1/1115	ribosomal protein l2 chloroplastic n 1 tax saxifraga stolonifera a6ya71_9magn score=523.09 evalue=0.00e+00;
c99711/f6p1/1115	ribosomal protein l2 chloroplastic n 1 tax capsicum annuum j7hau1_capan score=522.70 evalue=0.00e+00;
c99742/f8p7/2147	granule-bound starch synthase 1 chloroplastic/amyloplastic n 11 tax solanum ssg1_soltu score=1186.40 evalue=0.00e+00;
c99742/f8p7/2147	granule-bound starch synthase n 1 tax solanum tuberosum b0zte3_soltu score=1175.61 evalue=0.00e+00;
c99742/f8p7/2147	uncharacterized protein n 4 tax solanum lycopersicum k4cpx6_sollc score=1159.05 evalue=0.00e+00;

c99742/f8p7/2147	granule-bound starch synthase 1 chloroplastic/amyloplastic n 1 tax antirrhinum majus ssg1_antma score=986.87 evalue=0.00e+00;
c99742/f8p7/2147	granule-bound starch synthase i n 3 tax ipomoea batatas d4ahs6_ipoba score=974.54 evalue=0.00e+00;
c99986/f5p4/949	uncharacterized protein n 1 tax solanum lycopersicum k4d3x7_sollc score=473.01 evalue=5.40e-165;
c99986/f5p4/949	uncharacterized protein n 1 tax solanum lycopersicum k4csx3_sollc score=281.57 evalue=1.49e-90;
c99986/f5p4/949	predicted protein n 1 tax populus trichocarpa b9hda3_poptr score=221.09 evalue=4.27e-67;
c99986/f5p4/949	putative uncharacterized protein n 1 tax ricinus communis b9t649_ricco score=207.99 evalue=1.14e-62;
c99986/f5p4/949	predicted protein n 1 tax populus trichocarpa b9igq2_poptr score=207.61 evalue=7.14e-62;
c100034/f10p30/1559	s-adenosylmethionine synthase 1 n 1 tax solanum tuberosum metk1_soltu score=776.55 evalue=0.00e+00;
c100034/f10p30/1559	s-adenosylmethionine synthase n 1 tax solanum palustre metk_solbr score=773.08 evalue=0.00e+00;
c100034/f10p30/1559	s-adenosylmethionine synthase 1 n 1 tax solanum lycopersicum metk1_sollc score=768.07 evalue=0.00e+00;
c100034/f10p30/1559	s-adenosylmethionine synthetase putative n 1 tax ricinus communis b9rfq1_ricco score=753.05 evalue=0.00e+00;
c100034/f10p30/1559	s-adenosylmethionine synthase 3 n 1 tax petunia x hybrida metk3_pethy score=749.20 evalue=0.00e+00;
c100048/f6p2/1414	uncharacterized protein n 1 tax solanum lycopersicum k4bz53_sollc score=679.48 evalue=0.00e+00;
c100048/f6p2/1414	putative anion:sodium symporter n 1 tax solanum lycopersicum q672q4_sollc score=677.17 evalue=0.00e+00;
c100048/f6p2/1414	putative uncharacterized protein n 1 tax vitis vinifera d7tbu8_vitvi score=528.48 evalue=0.00e+00;
c100048/f6p2/1414	sodium-dependent pyruvate transporter n 1 tax flaveria trinervia e0d3h5_flatr score=519.24 evalue=6.21e-179;
c100048/f6p2/1414	sodium/pyruvate cotransporter bass2 chloroplastic n 1 tax arabidopsis thaliana bass2_arath score=508.45 evalue=8.07e-175;
c100117/f3p14/909	ribosomal protein l13 n 1 tax solanum lycopersicum k4dh88_sollc score=358.99 evalue=7.28e-122;
c100117/f3p14/909	ribosomal protein l13 n 1 tax solanum lycopersicum k4cmt7_sollc score=351.29 evalue=8.33e-119;
c100117/f3p14/909	ribosomal protein l13 n 1 tax solanum tuberosum q3hry7_soltu score=349.36 evalue=5.20e-118;
c100117/f3p14/909	ribosomal protein l13 (fragment) n 1 tax solanum palustre q6tkt4_solbr score=347.82 evalue=1.43e-117;
c100117/f3p14/909	ribosomal protein l13 n 1 tax populus trichocarpa b9mud1_poptr score=329.72 evalue=2.62e-110;
c100130/f2p5/1170	annexin n 1 tax solanum lycopersicum k4buw7_sollc score=626.32 evalue=0.00e+00;
c100130/f2p5/1170	annexin n 1 tax vitis vinifera d7t8g1_vitvi score=505.37 evalue=2.42e-176;
c100130/f2p5/1170	annexin n 1 tax solanum lycopersicum k4bny3_sollc score=504.21 evalue=6.11e-176;
c100130/f2p5/1170	annexin n 1 tax glycine max c6thm2_soybn score=491.12 evalue=1.12e-170;
c100130/f2p5/1170	annexin n 2 tax glycine max c6tlc9_soybn score=489.19 evalue=5.09e-170;
c100145/f2p1/1478	branched-chain-amino-acid aminotransferase n 1 tax solanum tuberosum q9sny8_soltu score=737.26 evalue=0.00e+00;
c100145/f2p1/1478	branched-chain-amino-acid aminotransferase n 1 tax solanum lycopersicum k4bcz5_sollc score=731.87 evalue=0.00e+00;
c100145/f2p1/1478	branched-chain-amino-acid aminotransferase n 1 tax nicotiana benthamiana b6rfk8_nicbe score=719.92 evalue=0.00e+00;
c100145/f2p1/1478	branched-chain-amino-acid aminotransferase n 1 tax solanum lycopersicum k4bg08_sollc score=681.79 evalue=0.00e+00;

c100145/f2p1/1478	branched-chain amino acid aminotransferase n 1 tax solanum tuberosum q9sny9_soltu score=667.15 evalue=0.00e+00;
c100148/f2p0/1460	uncharacterized protein n 1 tax solanum lycopersicum k4bw79_sollc score=588.19 evalue=0.00e+00;
c100148/f2p0/1460	alcohol dehydrogenase putative n 1 tax ricinus communis b9shb0_ricco score=464.54 evalue=1.20e-157;
c100148/f2p0/1460	putative uncharacterized protein n 1 tax vitis vinifera f6hhu0_vitvi score=463.38 evalue=2.10e-157;
c100148/f2p0/1460	uncharacterized protein n 1 tax glycine max i1kxg0_soybn score=461.45 evalue=2.66e-156;
c100148/f2p0/1460	uncharacterized protein n 1 tax glycine max i1n1g8_soybn score=461.07 evalue=3.75e-156;
c100150/f2p6/3739	cellulose synthase n 1 tax solanum tuberosum q6xp46_soltu score=2162.11 evalue=0.00e+00;
c100150/f2p6/3739	uncharacterized protein n 1 tax solanum lycopersicum k4ayb2_sollc score=2152.10 evalue=0.00e+00;
c100150/f2p6/3739	cellulose synthase n 1 tax betula platyphylla b2lwm0_betpl score=1967.20 evalue=0.00e+00;
c100150/f2p6/3739	cellulose synthase 3 n 1 tax paeonia lactiflora i1wye4_paelc score=1950.64 evalue=0.00e+00;
c100150/f2p6/3739	cellulose synthase catalytic subunit n 1 tax gossypium gossypioides i1t895_gosgo score=1930.22 evalue=0.00e+00;
c100162/f2p0/1058	proteasome subunit beta type-6 n 1 tax nicotiana tabacum psb6_tobac score=431.80 evalue=3.12e-149;
c100162/f2p0/1058	proteasome subunit beta type n 1 tax solanum lycopersicum k4ccd7_sollc score=410.61 evalue=6.00e-141;
c100162/f2p0/1058	proteasome subunit beta type n 1 tax ricinus communis b9sps6_ricco score=400.98 evalue=3.80e-137;
c100162/f2p0/1058	proteasome subunit beta type-6 n 1 tax arabidopsis thaliana psb6_arath score=395.97 evalue=2.96e-135;
c100162/f2p0/1058	proteasome subunit beta type n 1 tax arabidopsis lyrata subsp. lyrata d7mb80_arall score=396.36 evalue=3.00e-135;
c100306/f1p9/3279	uncharacterized protein n 1 tax solanum lycopersicum k4axx8_sollc score=1652.11 evalue=0.00e+00;
c100306/f1p9/3279	putative uncharacterized protein n 1 tax vitis vinifera d7u2u3_vitvi score=1363.98 evalue=0.00e+00;
c100306/f1p9/3279	uncharacterized protein n 1 tax glycine max k7mzm9_soybn score=1354.73 evalue=0.00e+00;
c100306/f1p9/3279	uncharacterized protein n 1 tax glycine max i1jqx2_soybn score=1349.73 evalue=0.00e+00;
c100306/f1p9/3279	predicted protein n 1 tax populus trichocarpa b9gta0_poptr score=1337.40 evalue=0.00e+00;
c100360/f1p1/1261	uncharacterized protein n 1 tax solanum lycopersicum k4c3b4_sollc score=634.79 evalue=0.00e+00;
c100360/f1p1/1261	putative uncharacterized protein n 1 tax vitis vinifera d7u8s7_vitvi score=550.82 evalue=0.00e+00;
c100360/f1p1/1261	uncharacterized protein n 1 tax lotus japonicus i3tak4_lotja score=533.87 evalue=0.00e+00;
c100360/f1p1/1261	uncharacterized protein n 1 tax glycine max c6tnw0_soybn score=533.49 evalue=0.00e+00;
c100360/f1p1/1261	at3g52390 n 1 tax arabidopsis thaliana q84td7_arath score=527.32 evalue=0.00e+00;

Appendix B *Solanum etuberosum* genes expressed in the BC_4S pool but absent from the BC_4I pool as detected by Illumina sequencing, mapped to the *S. etuberosum* 16-1 reference database, and aligned to the UNIREF100 dataset.

c1720/f5p2/1123	dehydration-induced protein erd15 n 1 tax solanum tuberosum repid k7wtw9_soltu; score=219.55; evalue=5.33e-67;
c1720/f5p2/1123	dehydration-induced protein erd15 n 1 tax solanum lycopersicum repid q9lkw3_sollc; score=217.62; evalue=2.64e-66;
c1720/f5p2/1123	early responsive to dehydration 1 protein n 1 tax nicotiana tabacum repid f2vj76_tobac; score=213.77; evalue=1.01e-64;
c1720/f5p2/1123	uncharacterized protein n 1 tax solanum lycopersicum repid k4bqg9_sollc; score=184.11; evalue=3.43e-53;
c1720/f5p2/1123	erd15 n 1 tax capsicum annuum repid a0epi4_capan; score=182.96; evalue=7.47e-53;
c1891/f9p4/1514	uncharacterized protein n 1 tax solanum lycopersicum repid k4cet1_sollc; score=373.24; evalue=1.98e-122;
c1891/f9p4/1514	g-strand specific single-stranded telomere-binding protein 2 n 1 tax nicotiana tabacum repid e2f3s9_tobac; score=346.28; evalue=6.54e-112;
c1891/f9p4/1514	g-strand specific single-stranded telomere-binding protein 3 n 1 tax nicotiana tabacum repid e2f3t0_tobac; score=331.26; evalue=4.74e-106;
c1891/f9p4/1514	g-strand specific single-stranded telomere-binding protein 1 n 1 tax nicotiana tabacum repid e2f3s8_tobac; score=322.01; evalue=2.60e-102;
c1891/f9p4/1514	uncharacterized protein n 1 tax glycine max repid i1lxp8_soybn; score=281.95; evalue=7.22e-87;
c2831/f11p1/1311	uncharacterized protein n 1 tax solanum lycopersicum repid k4axy3_sollc; score=484.95; evalue=2.26e-167;
c2831/f11p1/1311	putative uncharacterized protein n 1 tax ricinus communis repid b9scd5_ricco; score=300.83; evalue=2.48e-95;
c2831/f11p1/1311	uncharacterized protein n 1 tax solanum lycopersicum repid k4b5d0_sollc; score=294.66; evalue=5.56e-93;
c2831/f11p1/1311	putative uncharacterized protein n 1 tax vitis vinifera repid d7t9m0_vitvi; score=283.11; evalue=1.27e-88;
c2831/f11p1/1311	predicted protein n 1 tax populus trichocarpa repid b9icr7_poptr; score=282.72; evalue=2.39e-88;
c3048/f6p0/800	est4 n 2 tax rhodococcus repid i7jr78_9noca; score=426.02; evalue=3.03e-147;
c3048/f6p0/800	heat shock cognate protein 80 n 2 tax solanum lycopersicum repid hsp80_sollc; score=427.17; evalue=2.60e-142;
c3048/f6p0/800	hsp90-2-like n 1 tax solanum tuberosum repid q2xte5_soltu; score=426.02; evalue=6.62e-142;
c3048/f6p0/800	putative heat shock protein 90 n 1 tax arabidopsis thaliana repid q8gru8_arath; score=417.54; evalue=7.35e-141;
c3048/f6p0/800	early-responsive to dehydration 8 n 1 tax arabidopsis lyrata subsp. lyrata repid d7mf83_arall; score=421.01; evalue=5.35e-140;
c3054/f3p2/1051	uncharacterized protein n 1 tax solanum lycopersicum repid k4d882_sollc; score=457.60; evalue=4.42e-159;
c3054/f3p2/1051	uncharacterized protein n 1 tax solanum lycopersicum repid k4bk99_sollc; score=456.83; evalue=1.07e-158;
c3054/f3p2/1051	putative uncharacterized protein n 1 tax vitis vinifera repid d7tdj2_vitvi; score=367.85; evalue=9.09e-124;
c3054/f3p2/1051	signal recognition particle receptor subunit beta n 1 tax cucumis melo subsp. melo repid e5gbi2_cucme; score=360.92; evalue=6.79e-121;
c3054/f3p2/1051	signal recognition particle receptor subunit beta putative n 1 tax ricinus communis repid b9shc8_ricco; score=359.76; evalue=1.16e-120;
c3141/f8p3/1444	uncharacterized protein n 1 tax solanum lycopersicum repid k4dep4_sollc; score=748.81; evalue=0.00e+00;
c3141/f8p3/1444	agmatine deiminase putative n 1 tax ricinus communis repid b9re78_ricco; score=635.18; evalue=0.00e+00;
c3141/f8p3/1444	jhl10i11.8 protein n 1 tax jatropha curcas repid e6nu52_9rosi; score=632.87; evalue=0.00e+00;

c3141/f8p3/1444	putative uncharacterized protein n 1 tax vitis vinifera repid d7sir1_vitvi; score=630.56; evalue=0.00e+00;
c3141/f8p3/1444	predicted protein n 1 tax populus trichocarpa repid b9n078_poptr; score=623.24; evalue=0.00e+00;
c3570/f1p3/1059	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmv2_sollc; score=362.46; evalue=6.04e-122;
c3570/f1p3/1059	putative uncharacterized protein n 1 tax vitis vinifera repid d7tzz7_vitvi; score=273.48; evalue=3.67e-87;
c3570/f1p3/1059	rna binding protein putative n 1 tax ricinus communis repid b9sn41_ricco; score=269.63; evalue=1.82e-85;
c3570/f1p3/1059	uncharacterized protein n 1 tax glycine max repid k7m953_soybn; score=263.46; evalue=6.00e-83;
c3570/f1p3/1059	predicted protein n 1 tax populus trichocarpa repid b9n193_poptr; score=262.69; evalue=8.50e-83;
c3837/f2p1/1349	uncharacterized protein n 1 tax solanum lycopersicum repid k4c7b7_sollc; score=634.02; evalue=0.00e+00;
c3837/f2p1/1349	predicted protein n 1 tax populus trichocarpa repid b9iqd5_poptr; score=509.99; evalue=1.02e-176;
c3837/f2p1/1349	polyneuridine-aldehyde esterase putative n 1 tax ricinus communis repid b9r8x6_ricco; score=506.14; evalue=3.08e-175;
c3837/f2p1/1349	predicted protein n 1 tax populus trichocarpa repid b9mwf1_poptr; score=504.60; evalue=9.61e-175;
c3837/f2p1/1349	uncharacterized protein n 1 tax glycine max repid i1kfz3_soybn; score=494.58; evalue=1.17e-170;
c4844/f2p3/1078	ubiquitin-conjugating protein-like n 1 tax solanum tuberosum repid q2v986_soltu; score=402.52; evalue=3.15e-138;
c4844/f2p3/1078	ubiquitin conjugating enzyme-like n 1 tax solanum tuberosum repid q2vck7_soltu; score=400.98; evalue=1.31e-137;
c4844/f2p3/1078	ubiquitin conjugating enzyme n 1 tax solanum lycopersicum repid q43780_sollc; score=399.44; evalue=5.30e-137;
c4844/f2p3/1078	ubiquitin-conjugating enzyme e2-25kd putative n 1 tax ricinus communis repid b9ra92_ricco; score=338.58; evalue=4.29e-113;
c4844/f2p3/1078	predicted protein n 1 tax populus trichocarpa repid a9p939_poptr; score=335.88; evalue=4.26e-112;
c5187/f1p2/680	60s ribosomal protein l34 putative n 2 tax solanum repid q6l414_solde; score=193.74; evalue=1.67e-59;
c5187/f1p2/680	uncharacterized protein n 1 tax solanum lycopersicum repid k4bbu9_sollc; score=192.20; evalue=9.06e-59;
c5187/f1p2/680	uncharacterized protein n 1 tax solanum lycopersicum repid k4bwt1_sollc; score=191.81; evalue=1.07e-58;
c5187/f1p2/680	uncharacterized protein n 1 tax glycine max repid i1j5q7_soybn; score=191.81; evalue=1.09e-58;
c5187/f1p2/680	putative uncharacterized protein n 1 tax vitis vinifera repid a5c1j0_vitvi; score=190.27; evalue=4.80e-58;
c5392/f5p20/907	chlorophyll a b binding protein type i n 1 tax solanum tuberosum repid q41449_soltu; score=541.96; evalue=0.00e+00;
c5392/f5p20/907	chlorophyll a-b binding protein 37 chloroplastic n 1 tax petunia sp. repid cb26_petsp; score=531.56; evalue=0.00e+00;
c5392/f5p20/907	chlorophyll a-b binding protein 36 chloroplastic n 1 tax nicotiana tabacum repid cb23_tobac; score=528.48; evalue=0.00e+00;
c5392/f5p20/907	chlorophyll a-b binding protein 4 chloroplastic n 1 tax solanum lycopersicum repid cb24_sollc; score=519.62; evalue=0.00e+00;
c5392/f5p20/907	chlorophyll a/b binding protein putative n 1 tax ricinus communis repid b9t0c1_ricco; score=515.00; evalue=0.00e+00;
c5572/f7p0/1268	uncharacterized protein n 1 tax solanum lycopersicum repid k4b7j7_sollc; score=485.72; evalue=3.38e-169;
c5572/f7p0/1268	trna (guanine-n(7)-)-methyltransferase putative n 1 tax ricinus communis repid b9sug0_ricco; score=422.17; evalue=3.62e-144;
c5572/f7p0/1268	uncharacterized protein n 1 tax glycine max repid i1juq6_soybn; score=417.93; evalue=2.57e-142;
c5572/f7p0/1268	uncharacterized protein n 2 tax glycine max repid k7kts8_soybn; score=417.54; evalue=3.69e-142;

c5572/f7p0/1268	uncharacterized protein n 1 tax lotus japonicus repid i3sh34_lotja; score=413.31; evalue=1.27e-140;
c5614/f4p0/884	k4cgn0 uncharacterized protein n 1 tax solanum lycopersicum repid k4cgn0_sollc; score=171.01; evalue=9.96e-49;
c5614/f4p0/884	60s ribosomal protein l18a plant putative n 1 tax ricinus communis repid b9svw7_ricco; score=85.89; evalue=2.89e-17;
c5614/f4p0/884	60s ribosomal protein l18aa n 1 tax hevea brasiliensis repid i3nmn2_hevbr; score=84.73; evalue=4.76e-17;
c5614/f4p0/884	putative uncharacterized protein n 1 tax vitis vinifera repid a5ax92_vitvi; score=82.80; evalue=2.17e-16;
c5614/f4p0/884	uncharacterized protein n 1 tax solanum lycopersicum repid k4b844_sollc; score=77.03; evalue=2.77e-14;
c5684/f3p2/1313	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2e9_sollc; score=482.26; evalue=3.32e-167;
c5684/f3p2/1313	tic20-like protein n 1 tax solanum tuberosum repid q2v9a0_soltu; score=459.14; evalue=3.75e-158;
c5684/f3p2/1313	uncharacterized protein n 1 tax solanum lycopersicum repid k4bub2_sollc; score=444.12; evalue=3.29e-152;
c5684/f3p2/1313	predicted protein n 1 tax populus trichocarpa repid a9pad4_poptr; score=378.25; evalue=2.08e-126;
c5684/f3p2/1313	putative uncharacterized protein n 1 tax ricinus communis repid b9r7z3_ricco; score=370.16; evalue=4.10e-123;
c5835/f2p1/1415	uncharacterized protein n 1 tax solanum lycopersicum repid k4c8k0_sollc; score=513.46; evalue=1.44e-177;
c5835/f2p1/1415	putative uncharacterized protein n 1 tax solanum lycopersicum repid q0kih9_sollc; score=453.37; evalue=9.65e-155;
c5835/f2p1/1415	uncharacterized protein n 1 tax solanum lycopersicum repid k4bkm2_sollc; score=327.79; evalue=4.80e-105;
c5835/f2p1/1415	putative uncharacterized protein n 1 tax vitis vinifera repid f6gsx8_vitvi; score=224.94; evalue=2.18e-65;
c5835/f2p1/1415	putative anti-virus transcriptional factor n 1 tax vitis pseudoreticulata repid b6va58_9rosi; score=223.02; evalue=1.26e-64;
c6183/f1p0/984	uncharacterized protein n 1 tax solanum lycopersicum repid k4bu32_sollc; score=259.23; evalue=2.00e-83;
c6183/f1p0/984	putative uncharacterized protein n 1 tax vitis vinifera repid e0crs3_vitvi; score=209.53; evalue=4.42e-64;
c6183/f1p0/984	predicted protein n 1 tax populus trichocarpa repid b9h6y2_poptr; score=202.99; evalue=2.04e-61;
c6183/f1p0/984	bet1-like protein at4g14600 n 1 tax arabidopsis thaliana repid betl1_arath; score=195.67; evalue=1.39e-58;
c6183/f1p0/984	uncharacterized protein n 1 tax lotus japonicus repid i3sai6_lotja; score=194.51; evalue=3.16e-58;
c6312/f1p1/1139	uncharacterized protein n 1 tax solanum lycopersicum repid k4bwb7_sollc; score=345.51; evalue=8.48e-114;
c6312/f1p1/1139	n-acetyltransferase putative n 1 tax ricinus communis repid b9szi3_ricco; score=210.31; evalue=3.26e-61;
c6312/f1p1/1139	predicted protein n 1 tax populus trichocarpa repid b9hjr4_poptr; score=209.15; evalue=1.35e-60;
c6312/f1p1/1139	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7knl1_arall; score=205.30; evalue=2.71e-59;
c6312/f1p1/1139	uncharacterized protein n 1 tax glycine max repid i1j5c5_soybn; score=200.68; evalue=6.73e-58;
c6650/f3p1/1482	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmf8_sollc; score=612.84; evalue=0.00e+00;
c6650/f3p1/1482	pyridoxin biosynthesis protein pdx1 putative n 1 tax ricinus communis repid b9rqn9_ricco; score=475.32; evalue=4.17e-163;
c6650/f3p1/1482	predicted protein n 1 tax populus trichocarpa repid b9gfp4_poptr; score=475.32; evalue=4.75e-163;
c6650/f3p1/1482	putative uncharacterized protein n 2 tax arabidopsis lyrata subsp. lyrata repid d7my59_arall; score=467.23; evalue=1.13e-159;
c6650/f3p1/1482	probable pyridoxal biosynthesis protein pdx1.2 n 1 tax arabidopsis thaliana repid pdx12_arath; score=465.31; evalue=6.31e-159;

c6946/f12p2/1079	rwd domain-containing protein n 1 tax solanum tuberosum repid q38hu0_soltu; score=340.12; evalue=8.11e-113;
c6946/f12p2/1079	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmt0_sollc; score=307.76; evalue=3.24e-100;
c6946/f12p2/1079	rwd domain-containing protein putative n 1 tax ricinus communis repid b9rq64_ricco; score=274.63; evalue=3.07e-87;
c6946/f12p2/1079	predicted protein n 1 tax populus trichocarpa repid b9n1a1_poptr; score=271.94; evalue=3.93e-86;
c6946/f12p2/1079	predicted protein n 1 tax populus trichocarpa repid b9gh49_poptr; score=262.31; evalue=2.14e-82;
c7432/f1p29/854	putative uncharacterized protein n 1 tax medicago truncatula repid g7k0e8_medtr; score=287.73; evalue=1.25e-93;
c7432/f1p29/854	putative uncharacterized protein n 1 tax medicago truncatula repid g7k0e1_medtr; score=292.35; evalue=3.75e-93;
c7432/f1p29/854	putative uncharacterized protein n 1 tax medicago truncatula repid g7k0d0_medtr; score=278.49; evalue=5.90e-88;
c7432/f1p29/854	putative uncharacterized protein n 2 tax fabids repid g7k0e5_medtr; score=289.66; evalue=4.02e-85;
c7432/f1p29/854	putative uncharacterized protein n 1 tax medicago truncatula repid g7k0d1_medtr; score=277.71; evalue=2.79e-82;
c7512/f2p1/1296	uncharacterized protein n 1 tax solanum lycopersicum repid k4clt0_sollc; score=315.85; evalue=3.28e-96;
c7512/f2p1/1296	wd-repeat protein putative n 1 tax ricinus communis repid b9rgb3_ricco; score=260.00; evalue=1.85e-75;
c7512/f2p1/1296	putative uncharacterized protein n 1 tax vitis vinifera repid f6i5t1_vitvi; score=255.37; evalue=2.44e-73;
c7512/f2p1/1296	uncharacterized protein n 1 tax glycine max repid i1m0t4_soybn; score=243.82; evalue=1.79e-69;
c7512/f2p1/1296	uncharacterized protein n 1 tax glycine max repid k7mdg3_soybn; score=243.43; evalue=7.72e-69;
c7774/f1p3/1054	putative 7-transmembrane g-protein-coupled receptor n 1 tax solanum chacoense repid q9lkk8_solch; score=575.47; evalue=0.00e+00;
c7774/f1p3/1054	uncharacterized protein n 1 tax solanum lycopersicum repid k4d5h8_sollc; score=568.93; evalue=0.00e+00;
c7774/f1p3/1054	putative uncharacterized protein n 1 tax vitis vinifera repid a5bn66_vitvi; score=463.00; evalue=1.12e-158;
c7774/f1p3/1054	putative uncharacterized protein n 1 tax vitis vinifera repid f6hrn9_vitvi; score=462.61; evalue=1.44e-158;
c7774/f1p3/1054	predicted protein n 1 tax populus trichocarpa repid b9hfd7_poptr; score=457.22; evalue=5.68e-157;
c8025/f4p2/1031	uncharacterized protein n 1 tax solanum lycopersicum repid k4b221_sollc; score=342.81; evalue=1.63e-114;
c8025/f4p2/1031	putative uncharacterized protein n 1 tax vitis vinifera repid a5bff8_vitvi; score=198.36; evalue=3.83e-58;
c8025/f4p2/1031	putative uncharacterized protein n 1 tax ricinus communis repid b9srj9_ricco; score=196.44; evalue=4.33e-57;
c8025/f4p2/1031	putative uncharacterized protein n 1 tax populus trichocarpa repid a9ph40_poptr; score=186.81; evalue=1.19e-53;
c8025/f4p2/1031	predicted protein (fragment) n 1 tax populus trichocarpa repid b9gey4_poptr; score=173.71; evalue=5.33e-49;
c10094/f1p0/863	uncharacterized protein n 2 tax solanum repid k4bdi6_sollc; score=310.07; evalue=7.04e-102;
c10094/f1p0/863	cytochrome c1 (fragment) n 1 tax solanum tuberosum repid q41450_soltu; score=309.30; evalue=9.39e-102;
c10094/f1p0/863	imidazolonepropionase n 1 tax desulfobacter postgatei 2ac9 repid i5b2y0_9delt; score=313.92; evalue=1.71e-101;
c10094/f1p0/863	cytochrome c1-2 heme protein mitochondrial (fragment) n 1 tax solanum tuberosum repid cy12_soltu; score=307.38; evalue=4.90e-101;
c10094/f1p0/863	uncharacterized protein n 1 tax solanum lycopersicum repid k4df81_sollc; score=308.92; evalue=8.84e-101;
c10201/f4p6/1066	proteasome subunit alpha type n 1 tax solanum lycopersicum repid k4bvd8_sollc; score=505.75; evalue=2.48e-177;

c10201/f4p6/1066	proteasome subunit alpha type n 1 tax nicotiana benthamiana repid q8h1y2_nicbe; score=492.27; evalue=1.91e-172;
c10201/f4p6/1066	proteasome subunit alpha type n 2 tax populus trichocarpa repid a9p9a3_poptr; score=460.30; evalue=9.47e-160;
c10201/f4p6/1066	proteasome subunit alpha type n 1 tax ricinus communis repid b9r7x1_ricco; score=456.83; evalue=2.25e-158;
c10201/f4p6/1066	proteasome subunit alpha type n 1 tax vitis vinifera repid f6h059_vitvi; score=454.14; evalue=3.00e-157;
c10334/f1p8/1140	cellulose synthase (fragment) n 1 tax nicotiana tabacum repid i1z1w9_tobac; score=604.36; evalue=0.00e+00;
c10334/f1p8/1140	uncharacterized protein n 1 tax solanum lycopersicum repid k4cuv8_sollc; score=624.78; evalue=0.00e+00;
c10334/f1p8/1140	putative uncharacterized protein n 1 tax vitis vinifera repid f6hzp8_vitvi; score=594.73; evalue=0.00e+00;
c10334/f1p8/1140	cellulose synthase n 1 tax betula platyphylla repid b2lwm2_betpl; score=591.27; evalue=0.00e+00;
c10334/f1p8/1140	cellulose synthase a catalytic subunit 6 [udp-forming] putative n 3 tax malpighiales repid b9skp1_ricco; score=588.96; evalue=0.00e+00;
c10474/f3p8/1353	uncharacterized protein n 1 tax solanum lycopersicum repid k4d2t7_sollc; score=644.42; evalue=0.00e+00;
c10474/f3p8/1353	putative uncharacterized protein n 1 tax vitis vinifera repid f6hlk0_vitvi; score=310.07; evalue=3.53e-98;
c10474/f3p8/1353	putative uncharacterized protein n 1 tax ricinus communis repid b9sn52_ricco; score=308.53; evalue=1.36e-97;
c10474/f3p8/1353	predicted protein n 1 tax populus trichocarpa repid b9hac7_poptr; score=284.26; evalue=1.56e-88;
c10474/f3p8/1353	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7lvy7_arall; score=278.87; evalue=3.12e-86;
c10563/f1p13/1039	chlorophyll a-b binding protein 3c chloroplastic n 1 tax solanum lycopersicum repid cb2g_sollc; score=490.73; evalue=4.58e-172;
c10563/f1p13/1039	chlorophyll a-b binding protein 3c-like n 1 tax solanum tuberosum repid q2xte0_soltu; score=487.65; evalue=6.44e-171;
c10563/f1p13/1039	uncharacterized protein n 1 tax solanum lycopersicum repid k4be01_sollc; score=486.49; evalue=1.88e-170;
c10563/f1p13/1039	chlorophyll a-b binding protein 40 chloroplastic n 1 tax nicotiana tabacum repid cb24_tobac; score=486.49; evalue=2.31e-170;
c10563/f1p13/1039	light harvesting chlorophyll a/b-binding protein n 1 tax nicotiana sylvestris repid o64446_nicsy; score=486.11; evalue=3.32e-170;
c10580/f1p19/1282	glyceraldehyde 3-phosphate dehydrogenase n 1 tax solanum tuberosum repid q8lk04_soltu; score=617.85; evalue=0.00e+00;
c10580/f1p19/1282	uncharacterized protein n 2 tax solanum lycopersicum repid k4byg6_sollc; score=617.46; evalue=0.00e+00;
c10580/f1p19/1282	glyceraldehyde 3-phosphate dehydrogenase-like n 1 tax solanum tuberosum repid q2xpw9_soltu; score=616.30; evalue=0.00e+00;
c10580/f1p19/1282	glyceraldehyde 3-phosphate dehydrogenase n 4 tax solanaceae repid b3f8i0_nicls; score=592.81; evalue=0.00e+00;
c10580/f1p19/1282	glyceraldehyde-3-phosphate dehydrogenase cytosolic (fragment) n 1 tax nicotiana tabacum repid g3pc_tobac; score=592.42; evalue=0.00e+00;
c11199/f8p2/1165	uncharacterized protein n 1 tax solanum lycopersicum repid k4bj21_sollc; score=355.14; evalue=6.39e-119;
c11199/f8p2/1165	putative uncharacterized protein n 1 tax vitis vinifera repid d7t4m3_vitvi; score=206.07; evalue=2.62e-60;
c11199/f8p2/1165	predicted protein n 1 tax populus trichocarpa repid b9hsl9_poptr; score=194.13; evalue=5.51e-56;
c11199/f8p2/1165	putative uncharacterized protein n 1 tax populus trichocarpa x populus deltoides repid a9pil4_9rosi; score=189.89; evalue=2.40e-54;
c11199/f8p2/1165	putative uncharacterized protein n 1 tax ricinus communis repid b9sqp4_ricco; score=184.11; evalue=1.46e-52;
c11952/f2p0/1371	uncharacterized protein n 1 tax solanum lycopersicum repid k4cyr2_sollc; score=677.94; evalue=0.00e+00;
c11952/f2p0/1371	uncharacterized protein n 1 tax solanum lycopersicum repid k4azb1_sollc; score=459.53; evalue=2.16e-156;

c11952/f2p0/1371	uncharacterized protein n 1 tax solanum lycopersicum repid k4azb2_sollc; score=391.35; evalue=1.29e-130;
c11952/f2p0/1371	f-box family protein n 1 tax populus trichocarpa repid b9ic68_poptr; score=332.03; evalue=1.81e-106;
c11952/f2p0/1371	putative uncharacterized protein n 1 tax ricinus communis repid b9rdk7_ricco; score=324.71; evalue=7.06e-104;
c12419/f6p3/1654	uncharacterized protein n 1 tax solanum lycopersicum repid k4buk4_sollc; score=925.24; evalue=0.00e+00;
c12419/f6p3/1654	uncharacterized protein n 1 tax solanum lycopersicum repid k4dgp6_sollc; score=596.27; evalue=0.00e+00;
c12419/f6p3/1654	uncharacterized protein n 1 tax solanum lycopersicum repid k4buk2_sollc; score=501.90; evalue=2.57e-170;
c12419/f6p3/1654	uncharacterized protein n 1 tax solanum lycopersicum repid k4buz0_sollc; score=501.90; evalue=3.87e-170;
c12419/f6p3/1654	uncharacterized protein n 1 tax solanum lycopersicum repid k4buz1_sollc; score=497.66; evalue=1.13e-168;
c12558/f2p2/706	hop-interacting protein thi116 n 1 tax solanum lycopersicum repid g8z281_sollc; score=451.06; evalue=5.13e-155;
c12558/f2p2/706	uncharacterized protein n 1 tax solanum lycopersicum repid k4blm7_sollc; score=451.44; evalue=7.99e-155;
c12558/f2p2/706	putative uncharacterized protein n 2 tax vitis vinifera repid f6hxr2_vitvi; score=348.59; evalue=5.92e-115;
c12558/f2p2/706	flotillin-like protein 1 n 2 tax medicago truncatula repid flot1_medtr; score=333.95; evalue=2.75e-109;
c12558/f2p2/706	flotillin-like protein 3 n 1 tax medicago truncatula repid flot3_medtr; score=333.18; evalue=4.43e-109;
c13065/f1p2/1395	uncharacterized protein n 1 tax solanum lycopersicum repid k4dh43_sollc; score=592.04; evalue=0.00e+00;
c13065/f1p2/1395	predicted protein n 1 tax populus trichocarpa repid b9gpn9_poptr; score=306.61; evalue=5.97e-98;
c13065/f1p2/1395	putative uncharacterized protein n 1 tax vitis vinifera repid d7udf0_vitvi; score=303.14; evalue=1.45e-95;
c13065/f1p2/1395	putative uncharacterized protein n 1 tax vitis vinifera repid a5at53_vitvi; score=300.06; evalue=8.12e-94;
c13065/f1p2/1395	predicted protein n 1 tax populus trichocarpa repid b9h5w2_poptr; score=290.81; evalue=8.88e-92;
c13493/f1p0/1013	uncharacterized protein n 1 tax solanum lycopersicum repid k4azk4_sollc; score=130.18; evalue=8.55e-34;
c13493/f1p0/1013	putative uncharacterized protein n 1 tax vitis vinifera repid d7sj36_vitvi; score=96.29; evalue=4.57e-21;
c13493/f1p0/1013	putative uncharacterized protein n 1 tax medicago truncatula repid q2htj3_medtr; score=92.43; evalue=2.40e-19;
c13493/f1p0/1013	putative uncharacterized protein n 2 tax glycine max repid c6t0g9_soybn; score=90.51; evalue=4.35e-19;
c13493/f1p0/1013	uncharacterized protein n 1 tax medicago truncatula repid i3sfh2_medtr; score=89.74; evalue=8.75e-19;
c14048/f13p6/1718	uncharacterized protein n 1 tax solanum lycopersicum repid k4cf40_sollc; score=915.61; evalue=0.00e+00;
c14048/f13p6/1718	predicted protein n 1 tax populus trichocarpa repid a9p7u9_poptr; score=737.64; evalue=0.00e+00;
c14048/f13p6/1718	predicted protein n 1 tax populus trichocarpa repid b9gtt7_poptr; score=726.86; evalue=0.00e+00;
c14048/f13p6/1718	putative uncharacterized protein n 1 tax vitis vinifera repid f6hie6_vitvi; score=725.32; evalue=0.00e+00;
c14048/f13p6/1719	glucan endo-1 3-beta-glucosidase putative n 1 tax ricinus communis repid b9sh66_ricco; score=711.84; evalue=0.00e+00;
c14265/f1p0/988	uncharacterized protein n 1 tax solanum lycopersicum repid k4awu0_sollc; score=202.99; evalue=3.02e-61;
c14265/f1p0/988	putative uncharacterized protein n 1 tax vitis vinifera repid d7t6f0_vitvi; score=140.97; evalue=2.36e-37;
c14265/f1p0/988	putative uncharacterized protein n 1 tax ricinus communis repid b9rt40_ricco; score=125.95; evalue=8.30e-32;

c14265/f1p0/988	uncharacterized protein n 1 tax lotus japonicus repid i3shj2_lotja; score=122.86; evalue=1.21e-30;
c14265/f1p0/988	uncharacterized protein n 1 tax lotus japonicus repid i3sbh2_lotja; score=122.86; evalue=1.40e-30;
c14336/f1p14/1390	uncharacterized protein n 1 tax glycine max repid k7mhe5_soybn; score=629.79; evalue=0.00e+00;
c14336/f1p14/1390	putative uncharacterized protein n 1 tax vitis vinifera repid d7sh58_vitvi; score=628.25; evalue=0.00e+00;
c14336/f1p14/1390	v-type proton atpase subunit c n 1 tax medicago truncatula repid g7kw90_medtr; score=628.25; evalue=0.00e+00;
c14336/f1p14/1390	uncharacterized protein n 1 tax glycine max repid i1n7z4_soybn; score=628.25; evalue=0.00e+00;
c14336/f1p14/1390	putative uncharacterized protein n 1 tax vitis vinifera repid d7svj2_vitvi; score=626.32; evalue=0.00e+00;
c14355/f1p3/844	uncharacterized protein n 1 tax solanum lycopersicum repid k4bf68_sollc; score=317.00; evalue=2.39e-105;
c14355/f1p3/844	uncharacterized protein n 1 tax solanum lycopersicum repid k4c4v7_sollc; score=251.14; evalue=1.91e-79;
c14355/f1p3/844	steroid binding protein putative n 1 tax ricinus communis repid b9r9d3_ricco; score=232.65; evalue=3.35e-72;
c14355/f1p3/844	predicted protein n 1 tax populus trichocarpa repid a9p9z4_poptr; score=230.72; evalue=8.28e-72;
c14355/f1p3/844	predicted protein n 1 tax populus trichocarpa repid b9i4c2_poptr; score=229.95; evalue=1.63e-71;
c14388/f1p1/1011	uncharacterized protein n 1 tax solanum lycopersicum repid k4cfp5_sollc; score=445.66; evalue=3.01e-155;
c14388/f1p1/1011	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7mue9_arall; score=427.56; evalue=3.63e-148;
c14388/f1p1/1011	putative uncharacterized protein n 1 tax ricinus communis repid b9sgn4_ricco; score=427.56; evalue=4.60e-148;
c14388/f1p1/1011	ras-related protein raba1f n 1 tax arabidopsis thaliana repid raa1f_arath; score=426.02; evalue=1.93e-147;
c14388/f1p1/1011	putative uncharacterized protein n 1 tax vitis vinifera repid f6hm55_vitvi; score=425.25; evalue=3.29e-147;
c14390/f2p2/1121	atp-dependent clp protease proteolytic subunit n 1 tax solanum lycopersicum repid q93yh0_sollc; score=607.83; evalue=0.00e+00;
c14390/f2p2/1121	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7kb96_arall; score=477.25; evalue=8.72e-166;
c14390/f2p2/1121	atp-dependent clp protease proteolytic subunit 5 chloroplastic n 1 tax arabidopsis thaliana repid clpp5_arath; score=476.86; evalue=1.05e-165;
c14390/f2p2/1121	atp-dependent clp protease proteolytic subunit n 1 tax carica papaya repid b8k1w3_carpa; score=468.00; evalue=3.97e-162;
c14390/f2p2/1121	predicted protein n 2 tax populus trichocarpa repid b9gst6_poptr; score=466.08; evalue=1.88e-161;
c14413/f4p4/1734	transketolase chloroplastic n 1 tax solanum tuberosum repid tktc_soltu; score=1003.05; evalue=0.00e+00;
c14413/f4p4/1734	uncharacterized protein n 1 tax solanum lycopersicum repid k4cyv4_sollc; score=999.19; evalue=0.00e+00;
c14413/f4p4/1734	plastid transketolase n 1 tax nicotiana tabacum repid c3rxi5_tobac; score=939.49; evalue=0.00e+00;
c14413/f4p4/1734	transketolase 1 n 1 tax capsicum annuum repid o78327_capan; score=927.93; evalue=0.00e+00;
c14413/f4p4/1734	putative uncharacterized protein n 1 tax populus trichocarpa repid a9phe2_poptr; score=919.07; evalue=0.00e+00;
c15560/f1p1/1391	uncharacterized protein n 1 tax solanum lycopersicum repid k4cgt5_sollc; score=665.23; evalue=0.00e+00;
c15560/f1p1/1391	n 1 tax nicotiana tabacum repid a1xem2_tobac; score=610.14; evalue=0.00e+00;
c15560/f1p1/1391	uncharacterized protein n 1 tax solanum lycopersicum repid k4cgt3_sollc; score=606.29; evalue=0.00e+00;
c15560/f1p1/1391	uncharacterized protein n 1 tax solanum lycopersicum repid k4cgt4_sollc; score=602.05; evalue=0.00e+00;

c15560/f1p1/1391	uncharacterized protein n 1 tax solanum lycopersicum repid k4cg73_sollc; score=582.41; evalue=0.00e+00;
c16545/f1p1/1087	uncharacterized protein n 1 tax solanum lycopersicum repid k4chm7_sollc; score=228.79; evalue=2.32e-65;
c16545/f1p1/1087	putative uncharacterized protein n 1 tax vitis vinifera repid f6i550_vitvi; score=177.56; evalue=7.85e-47;
c16545/f1p1/1087	uncharacterized protein n 1 tax solanum lycopersicum repid k4cxd2_sollc; score=170.24; evalue=2.27e-44;
c16545/f1p1/1087	uncharacterized protein n 1 tax glycine max repid k7mqi7_soybn; score=169.47; evalue=9.39e-44;
c16545/f1p1/1087	uncharacterized protein n 1 tax glycine max repid k7mqi6_soybn; score=169.86; evalue=9.82e-44;
c16788/f4p3/1537	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2v2_sollc; score=559.68; evalue=0.00e+00;
c16788/f4p3/1537	uncharacterized protein n 1 tax glycine max repid i1l690_soybn; score=491.89; evalue=1.32e-167;
c16788/f4p3/1537	uncharacterized protein n 1 tax glycine max repid c6t9s5_soybn; score=482.26; evalue=7.38e-164;
c16788/f4p3/1537	putative uncharacterized protein n 1 tax vitis vinifera repid d7spm7_vitvi; score=482.26; evalue=7.78e-164;
c16788/f4p3/1537	putative uncharacterized protein n 1 tax vitis vinifera repid a5c9t9_vitvi; score=479.94; evalue=8.22e-163;
c18735/f2p16/1127	arabinogalactan n 1 tax solanum lycopersicum repid q43719_sollc; score=64.70; evalue=3.79e-09;
c18735/f2p16/1127	arabinogalactan n 1 tax solanum tuberosum repid g8z0f7_soltu; score=64.70; evalue=3.99e-09;
c18735/f2p16/1127	arabinogalactan protein n 1 tax nicotiana alata repid q9ful8_nical; score=63.54; evalue=1.02e-08;
c18920/f3p2/1674	uncharacterized protein n 1 tax solanum lycopersicum repid k4cwp4_sollc; score=732.63; evalue=0.00e+00;
c18920/f3p2/1674	putative uncharacterized protein n 1 tax vitis vinifera repid d7snp4_vitvi; score=357.07; evalue=3.83e-114;
c18920/f3p2/1674	putative uncharacterized protein n 1 tax ricinus communis repid b9rwc4_ricco; score=341.66; evalue=2.36e-108;
c18920/f3p2/1674	predicted protein n 1 tax populus trichocarpa repid b9gfu5_poptr; score=327.02; evalue=1.66e-102;
c18920/f3p2/1674	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7l461_arall; score=302.37; evalue=3.71e-93;
c19034/f5p4/1420	atp-dependent (s)-nad(p)h-hydrate dehydratase n 1 tax solanum lycopersicum repid k4axn1_sollc; score=643.27; evalue=0.00e+00;
c19034/f5p4/1420	atp-dependent (s)-nad(p)h-hydrate dehydratase n 1 tax vitis vinifera repid nnrd_vitvi; score=541.58; evalue=0.00e+00;
c19034/f5p4/1420	atp-dependent (s)-nad(p)h-hydrate dehydratase n 1 tax ricinus communis repid b9rtw2_ricco; score=530.79; evalue=0.00e+00;
c19034/f5p4/1420	atp-dependent (s)-nad(p)h-hydrate dehydratase n 1 tax glycine max repid i1kna0_soybn; score=530.02; evalue=0.00e+00;
c19034/f5p4/1420	atp-dependent (s)-nad(p)h-hydrate dehydratase n 1 tax glycine max repid i1mr81_soybn; score=524.63; evalue=0.00e+00;
c19359/f3p1/1033	uncharacterized protein n 1 tax solanum lycopersicum repid k4d4t7_sollc; score=320.47; evalue=2.64e-105;
c19359/f3p1/1033	putative uncharacterized protein n 1 tax glycine max repid c6t601_soybn; score=238.04; evalue=9.01e-74;
c19359/f3p1/1033	uncharacterized protein n 1 tax lotus japonicus repid i3t550_lotja; score=237.65; evalue=2.05e-73;
c19359/f3p1/1033	uncharacterized protein n 1 tax lotus japonicus repid i3sdn7_lotja; score=236.11; evalue=1.09e-72;
c19359/f3p1/1033	uncharacterized protein n 1 tax lotus japonicus repid i3sad7_lotja; score=234.96; evalue=2.92e-72;
c19466/f7p6/1782	uncharacterized protein n 1 tax solanum lycopersicum repid k4c6u5_sollc; score=897.12; evalue=0.00e+00;
c19466/f7p6/1782	putative uncharacterized protein n 1 tax vitis vinifera repid d7tu01_vitvi; score=878.24; evalue=0.00e+00;

c19466/f7p6/1782	predicted protein n 1 tax populus trichocarpa repid a9pdi1_poptr; score=876.70; evalue=0.00e+00;
c19466/f7p6/1782	uncharacterized protein n 1 tax solanum lycopersicum repid k4cii3_sollc; score=868.61; evalue=0.00e+00;
c19466/f7p6/1782	predicted protein n 1 tax populus trichocarpa repid b9mu07_poptr; score=867.84; evalue=0.00e+00;
c19548/f2p6/1318	uncharacterized protein n 1 tax solanum lycopersicum repid k4cae2_sollc; score=506.14; evalue=3.65e-176;
c19548/f2p6/1318	uncharacterized protein n 1 tax solanum lycopersicum repid k4c3e8_sollc; score=476.86; evalue=1.31e-164;
c19548/f2p6/1318	putative uncharacterized protein n 1 tax solanum tuberosum repid q38hu5_soltu; score=474.17; evalue=1.82e-163;
c19548/f2p6/1318	uncharacterized protein n 1 tax solanum lycopersicum repid k4csh4_sollc; score=470.70; evalue=3.36e-162;
c19548/f2p6/1318	predicted protein n 1 tax populus trichocarpa repid a9pfa8_poptr; score=449.90; evalue=5.73e-154;
c19962/f1p3/1058	uncharacterized protein n 1 tax solanum lycopersicum repid k4bbg4_sollc; score=369.01; evalue=5.76e-125;
c19962/f1p3/1058	sirohydrochlorin ferrochelatase putative n 1 tax ricinus communis repid b9sf92_ricco; score=285.42; evalue=3.20e-92;
c19962/f1p3/1058	predicted protein n 1 tax populus trichocarpa repid b9gek2_poptr; score=260.38; evalue=3.97e-83;
c19962/f1p3/1058	uncharacterized protein n 1 tax glycine max repid i1k1j6_soybn; score=259.23; evalue=7.06e-82;
c19962/f1p3/1058	uncharacterized protein n 1 tax glycine max repid i1k1j3_soybn; score=258.84; evalue=8.30e-82;
c20313/f1p1/1436	uncharacterized protein n 1 tax solanum lycopersicum repid k4d694_sollc; score=758.06; evalue=0.00e+00;
c20313/f1p1/1436	heat shock protein 70 (hsp70)-interacting protein putative n 1 tax ricinus communis repid b9rj86_ricco; score=416.00; evalue=1.45e-138;
c20313/f1p1/1436	uncharacterized protein n 1 tax glycine max repid i1lw70_soybn; score=395.20; evalue=5.97e-130;
c20313/f1p1/1436	uncharacterized protein n 1 tax glycine max repid i1lw73_soybn; score=389.42; evalue=1.01e-127;
c20313/f1p1/1436	uncharacterized protein n 1 tax glycine max repid k7m6v5_soybn; score=389.04; evalue=1.58e-127;
c20393/f3p1/1133	putative sphingolipid delta 4 desaturase des-1 n 1 tax solanum lycopersicum repid q8s459_sollc; score=340.12; evalue=1.76e-178;
c20393/f3p1/1133	putative sphingolipid delta 4 desaturase des-1 n 1 tax solanum lycopersicum repid q8s459_sollc; score=313.92; evalue=1.76e-178;
c20393/f3p1/1133	sphingolipid delta 4 desaturase/c-4 hydroxylase protein des2 putative n 1 tax ricinus communis repid b9rz74_ricco; score=301.60; evalue=7.70e-157;
c20393/f3p1/1133	sphingolipid delta 4 desaturase/c-4 hydroxylase protein des2 putative n 1 tax ricinus communis repid b9rz74_ricco; score=280.03; evalue=7.70e-157;
c20393/f3p1/1133	predicted protein n 1 tax populus trichocarpa repid a9pbg6_poptr; score=303.91; evalue=3.82e-155;
c20474/f1p0/1272	uncharacterized protein n 1 tax solanum lycopersicum repid k4bwk8_sollc; score=478.02; evalue=3.93e-165;
c20474/f1p0/1272	potyviral capsid protein interacting protein 2b n 1 tax nicotiana tabacum repid q6eix7_tobac; score=444.89; evalue=4.07e-152;
c20474/f1p0/1272	potyviral capsid protein interacting protein 2a n 1 tax nicotiana tabacum repid q6eix8_tobac; score=438.73; evalue=9.74e-150;
c20474/f1p0/1272	uncharacterized protein n 1 tax solanum lycopersicum repid k4bni8_sollc; score=405.99; evalue=1.09e-136;
c20474/f1p0/1272	potyviral capsid protein interacting protein 1 n 1 tax nicotiana tabacum repid q6eix9_tobac; score=402.52; evalue=1.85e-135;
c20601/f2p1/1858	adenylyl cyclase-associated protein n 1 tax solanum lycopersicum repid k4b3h1_sollc; score=827.01; evalue=0.00e+00;
c20601/f2p1/1858	adenylyl cyclase-associated protein n 1 tax solanum lycopersicum repid k4d0t6_sollc; score=724.55; evalue=0.00e+00;
c20601/f2p1/1858	adenylyl cyclase-associated protein n 1 tax vitis vinifera repid d7tq10_vitvi; score=670.23; evalue=0.00e+00;

c20601/f2p1/1858	adenylyl cyclase-associated protein n 1 tax populus trichocarpa repid b9h0q2_poptr; score=659.83; evalue=0.00e+00;
c20601/f2p1/1858	adenylyl cyclase-associated protein n 1 tax populus trichocarpa repid b9hrn7_poptr; score=653.67; evalue=0.00e+00;
c20648/f1p3/435	acidic ribosomal protein p1a-like n 1 tax solanum tuberosum repid q307z7_soltu; score=94.74; evalue=2.52e-22;
c20648/f1p3/435	uncharacterized protein n 1 tax solanum lycopersicum repid k4b212_sollc; score=83.96; evalue=3.14e-18;
c20648/f1p3/435	predicted protein n 1 tax populus trichocarpa repid b9idh5_poptr; score=78.18; evalue=4.52e-16;
c20648/f1p3/435	putative uncharacterized protein n 1 tax vitis vinifera repid d7u827_vitvi; score=77.41; evalue=1.10e-15;
c20648/f1p3/435	60s acidic ribosomal protein p1 putative n 1 tax ricinus communis repid b9sej7_ricco; score=75.87; evalue=4.38e-15;
c20809/f1p4/1605	uncharacterized protein n 1 tax solanum lycopersicum repid k4crb0_sollc; score=625.55; evalue=0.00e+00;
c20809/f1p4/1605	phantastica n 1 tax solanum lycopersicum repid q9xh12_sollc; score=621.70; evalue=0.00e+00;
c20809/f1p4/1605	phantastica n 1 tax nicotiana benthamiana repid g3adu5_nicbe; score=605.52; evalue=0.00e+00;
c20809/f1p4/1605	phantastica n 1 tax nicotiana tabacum repid q6q504_tobac; score=597.82; evalue=0.00e+00;
c20809/f1p4/1605	myb family transcription factor n 1 tax castanea mollissima repid d1lxi9_9rosi; score=494.58; evalue=3.11e-169;
c21382/f2p2/1566	uncharacterized protein n 1 tax solanum lycopersicum repid k4cpx5_sollc; score=687.18; evalue=0.00e+00;
c21382/f2p2/1566	uncharacterized protein n 1 tax solanum lycopersicum repid k4dfr5_sollc; score=583.18; evalue=0.00e+00;
c21382/f2p2/1566	glucan endo-1 3-beta-glucosidase putative n 1 tax ricinus communis repid b9ryw1_ricco; score=567.00; evalue=0.00e+00;
c21382/f2p2/1566	predicted protein n 1 tax populus trichocarpa repid b9i0s4_poptr; score=553.90; evalue=0.00e+00;
c21382/f2p2/1566	1 3-beta-d-glucanase gh17_65 n 1 tax populus tremula x populus tremuloides repid e9n6u1_9rosi; score=555.44; evalue=0.00e+00;
c21814/f4p2/1436	putative uncharacterized protein n 1 tax vitis vinifera repid e0cqh3_vitvi; score=521.16; evalue=1.74e-180;
c21814/f4p2/1436	nicotiana tabacum wound inducive mrna complete cds n 1 tax nicotiana tabacum repid q9lw93_tobac; score=501.13; evalue=3.51e-173;
c21814/f4p2/1436	predicted protein n 1 tax populus trichocarpa repid b9grk6_poptr; score=497.28; evalue=1.58e-171;
c21814/f4p2/1436	putative uncharacterized protein n 1 tax ricinus communis repid b9r7y6_ricco; score=482.64; evalue=8.04e-166;
c21814/f4p2/1436	predicted protein n 1 tax populus trichocarpa repid b9h4e6_poptr; score=473.01; evalue=4.15e-162;
c21861/f1p0/977	uncharacterized protein n 1 tax solanum lycopersicum repid k4cyv4_sollc; score=511.15; evalue=1.26e-173;
c21861/f1p0/977	transketolase chloroplastic n 1 tax solanum tuberosum repid tktc_soltu; score=511.15; evalue=1.55e-173;
c21861/f1p0/977	magnesium-transporting atpase n 2 tax pseudomonas repid j0per9_9psed; score=509.99; evalue=3.95e-171;
c21861/f1p0/977	plastid transketolase n 1 tax nicotiana tabacum repid c3rxi5_tobac; score=479.94; evalue=2.04e-161;
c21861/f1p0/977	predicted protein n 2 tax populus trichocarpa repid b9iby5_poptr; score=457.22; evalue=6.23e-154;
c21909/f5p1/1661	uncharacterized protein n 1 tax solanum lycopersicum repid k4bf74_sollc; score=836.25; evalue=0.00e+00;
c21909/f5p1/1661	putative uncharacterized protein n 1 tax vitis vinifera repid a5bx53_vitvi; score=454.52; evalue=5.95e-152;
c21909/f5p1/1661	putative uncharacterized protein n 1 tax vitis vinifera repid f6hp51_vitvi; score=454.14; evalue=1.07e-151;
c21909/f5p1/1661	predicted protein n 1 tax populus trichocarpa repid b9id55_poptr; score=429.10; evalue=1.33e-141;

c21909/f5p1/1661	mrna clone: rtfl01-31-g07 n 1 tax eutrema halophilum repid e4mxd7_theha; score=417.93; evalue=2.16e-137;
c22276/f1p1/1142	uncharacterized protein n 1 tax solanum lycopersicum repid k4b7v4_sollc; score=277.33; evalue=2.80e-89;
c22276/f1p1/1142	uncharacterized protein n 1 tax lotus japonicus repid i3t8g2_lotja; score=220.71; evalue=4.31e-67;
c22276/f1p1/1142	lsd1-like protein n 2 tax medicago truncatula repid g7l9l5_medtr; score=221.86; evalue=6.77e-67;
c22276/f1p1/1142	zinc finger protein lsd1 n 1 tax pisum sativum repid f8rp38_pea; score=219.94; evalue=7.78e-67;
c22276/f1p1/1142	lsd1-like protein n 1 tax medicago truncatula repid g7l9l4_medtr; score=221.09; evalue=9.55e-67;
c22618/f1p2/1545	uncharacterized protein n 1 tax solanum lycopersicum repid k4bn81_sollc; score=915.22; evalue=0.00e+00;
c22618/f1p2/1545	putative uncharacterized protein n 1 tax vitis vinifera repid f6hbz6_vitvi; score=819.69; evalue=0.00e+00;
c22618/f1p2/1545	predicted protein n 1 tax populus trichocarpa repid b9hk69_poptr; score=817.76; evalue=0.00e+00;
c22618/f1p2/1545	phosphoglycerate dehydrogenase n 1 tax medicago truncatula repid g7jvk0_medtr; score=811.99; evalue=0.00e+00;
c22618/f1p2/1545	uncharacterized protein n 1 tax glycine max repid i1kvs6_soybn; score=811.22; evalue=0.00e+00;
c22986/f1p0/1344	uncharacterized protein n 1 tax solanum lycopersicum repid k4bbc6_sollc; score=486.11; evalue=1.40e-168;
c22986/f1p0/1344	delta(7)-sterol-c5(6)-desaturase n 1 tax nicotiana tabacum repid sc5d_tobac; score=462.61; evalue=2.54e-159;
c22986/f1p0/1344	uncharacterized protein n 1 tax solanum lycopersicum repid k4b6k9_sollc; score=447.59; evalue=2.06e-153;
c22986/f1p0/1344	sterol-c5(6)-desaturase homolog n 1 tax nicotiana tabacum repid q9xei2_tobac; score=438.34; evalue=9.23e-150;
c22986/f1p0/1344	delta7 sterol c-5 desaturase n 1 tax zinnia violacea repid q4acu1_zinel; score=419.08; evalue=3.12e-142;
c23077/f10p5/1555	putative uncharacterized protein n 1 tax vitis vinifera repid d7ubm0_vitvi; score=724.55; evalue=0.00e+00;
c23077/f10p5/1555	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2v0_sollc; score=711.06; evalue=0.00e+00;
c23077/f10p5/1555	predicted protein n 1 tax populus trichocarpa repid b9mwe6_poptr; score=711.45; evalue=0.00e+00;
c23077/f10p5/1555	uncharacterized protein n 1 tax glycine max repid k7mve7_soybn; score=699.51; evalue=0.00e+00;
c23077/f10p5/1555	uncharacterized protein n 1 tax glycine max repid i1jdn2_soybn; score=698.74; evalue=0.00e+00;
c23624/f3p0/1518	uncharacterized protein n 1 tax solanum lycopersicum repid k4b454_sollc; score=781.94; evalue=0.00e+00;
c23624/f3p0/1518	f-box family protein n 1 tax populus trichocarpa repid b9hr11_poptr; score=389.04; evalue=1.61e-127;
c23624/f3p0/1518	f-box family protein n 1 tax populus trichocarpa repid b9h1m6_poptr; score=383.26; evalue=1.53e-124;
c23624/f3p0/1518	f-box protein skip23 n 1 tax arabidopsis thaliana repid ski23_arath; score=306.22; evalue=2.02e-95;
c23624/f3p0/1518	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7l8q5_arall; score=301.60; evalue=8.96e-94;
c23718/f2p3/1480	uncharacterized protein n 1 tax solanum lycopersicum repid k4cpd0_sollc; score=596.66; evalue=0.00e+00;
c23718/f2p3/1480	predicted protein n 1 tax populus trichocarpa repid b9hx45_poptr; score=543.89; evalue=0.00e+00;
c23718/f2p3/1480	predicted protein n 1 tax populus trichocarpa repid b9hil7_poptr; score=538.88; evalue=0.00e+00;
c23718/f2p3/1480	putative uncharacterized protein n 1 tax vitis vinifera repid d7syi9_vitvi; score=535.80; evalue=0.00e+00;
c23718/f2p3/1480	putative uncharacterized protein n 1 tax vitis vinifera repid a5ay90_vitvi; score=535.80; evalue=0.00e+00;

c24112/f3p2/1740	putative uncharacterized protein n 1 tax vitis vinifera repid d7sq37_vitvi; score=837.79; evalue=0.00e+00;
c24112/f3p2/1740	xylose isomerase n 1 tax ricinus communis repid b9t2e0_ricco; score=833.56; evalue=0.00e+00;
c24112/f3p2/1740	xylose isomerase n 1 tax populus trichocarpa repid b9im30_poptr; score=831.25; evalue=0.00e+00;
c24112/f3p2/1740	putative uncharacterized protein n 1 tax vitis vinifera repid a5b1e9_vitvi; score=811.99; evalue=0.00e+00;
c24112/f3p2/1740	xylose isomerase n 2 tax glycine max repid i1msu1_soybn; score=798.12; evalue=0.00e+00;
c24244/f1p1/1436	uncharacterized protein n 1 tax solanum lycopersicum repid k4d997_sollc; score=391.35; evalue=3.79e-175;
c24244/f1p1/1436	uncharacterized protein n 1 tax solanum lycopersicum repid k4d997_sollc; score=251.91; evalue=3.79e-175;
c24244/f1p1/1436	putative uncharacterized protein n 1 tax populus trichocarpa repid a9pcp9_poptr; score=309.69; evalue=9.84e-97;
c24244/f1p1/1436	putative uncharacterized protein n 1 tax vitis vinifera repid f6ha38_vitvi; score=308.92; evalue=2.33e-96;
c24244/f1p1/1436	putative uncharacterized protein n 1 tax medicago truncatula repid g7k355_medtr; score=300.83; evalue=2.28e-93;
c24697/f44p11/1367	uncharacterized protein n 1 tax solanum lycopersicum repid k4b1y6_sollc; score=606.29; evalue=0.00e+00;
c24697/f44p11/1367	uncharacterized protein n 1 tax solanum lycopersicum repid k4b1y5_sollc; score=592.42; evalue=0.00e+00;
c24697/f44p11/1367	uncharacterized protein n 1 tax solanum lycopersicum repid k4azf2_sollc; score=461.84; evalue=1.45e-157;
c24697/f44p11/1367	putative uncharacterized protein n 1 tax vitis vinifera repid f6h8x2_vitvi; score=326.25; evalue=1.51e-104;
c24697/f44p11/1367	putative uncharacterized protein n 1 tax vitis vinifera repid d7szx9_vitvi; score=324.71; evalue=7.07e-104;
c26326/f21p7/1695	uncharacterized protein n 1 tax solanum lycopersicum repid k4da40_sollc; score=914.45; evalue=0.00e+00;
c26326/f21p7/1695	ump synthase n 1 tax nicotiana plumbaginifolia repid q9lki3_nicpl; score=884.40; evalue=0.00e+00;
c26326/f21p7/1695	uridine 5'-monophosphate synthase (fragment) n 1 tax nicotiana tabacum repid umps_tobac; score=850.89; evalue=0.00e+00;
c26326/f21p7/1695	putative uncharacterized protein n 1 tax vitis vinifera repid f6hve9_vitvi; score=760.75; evalue=0.00e+00;
c26326/f21p7/1695	putative uncharacterized protein n 1 tax vitis vinifera repid a5caj7_vitvi; score=759.60; evalue=0.00e+00;
c26426/f11p5/2073	uncharacterized protein n 1 tax solanum lycopersicum repid k4c392_sollc; score=1169.07; evalue=0.00e+00;
c26426/f11p5/2073	anthranilate synthase alpha-subunit 2 n 1 tax mitragyna speciosa repid i3znu7_9gent; score=967.99; evalue=0.00e+00;
c26426/f11p5/2073	anthranilate synthase alpha subunit n 2 tax catharanthus roseus repid q9aw95_catro; score=931.78; evalue=0.00e+00;
c26426/f11p5/2073	uncharacterized protein n 1 tax glycine max repid i1nf54_soybn; score=920.23; evalue=0.00e+00;
c26426/f11p5/2073	putative uncharacterized protein n 2 tax vitis vinifera repid f6gut2_vitvi; score=910.98; evalue=0.00e+00;
c26493/f24p8/1740	uncharacterized protein n 2 tax solanum lycopersicum repid k4d3y9_sollc; score=907.90; evalue=0.00e+00;
c26493/f24p8/1740	acetyltransferase family protein n 1 tax shigella flexneri 2850-71 repid i6bgq2_shifl; score=885.95; evalue=0.00e+00;
c26493/f24p8/1740	enolase n 1 tax solanum lycopersicum repid eno_sollc; score=882.09; evalue=0.00e+00;
c26493/f24p8/1740	enolase n 1 tax nicotiana tabacum repid c5j0g6_tobac; score=873.62; evalue=0.00e+00;
c26493/f24p8/1740	mrna clone: rtfl01-03-h18 n 1 tax eutrema halophilum repid e4mvz0_theha; score=838.57; evalue=0.00e+00;
c26647/f8p4/2196	uncharacterized protein n 1 tax solanum lycopersicum repid k4c1z0_sollc; score=1080.86; evalue=0.00e+00;

c26647/f8p4/2196	putative uncharacterized protein n 1 tax vitis vinifera repid d7sy46_vitvi; score=916.76; evalue=0.00e+00;
c26647/f8p4/2196	dihydrolipoamide dehydrogenase putative n 1 tax ricinus communis repid b9rzn2_ricco; score=911.37; evalue=0.00e+00;
c26647/f8p4/2196	precursor of dehydrogenase dihydrolipoamide dehydrogenase 4 (fragment) n 1 tax populus trichocarpa repid b9hwx7_poptr; score=889.41; evalue=0.00e+00;
c26647/f8p4/2196	dihydrolipoyl dehydrogenase n 1 tax medicago truncatula repid g7jmt6_medtr; score=886.33; evalue=0.00e+00;
c27090/f9p1/1606	2-oxoglutarate-dependent dioxygenase n 1 tax solanum chacoense repid q9zsh4_solch; score=354.37; evalue=2.28e-172;
c27090/f9p1/1606	2-oxoglutarate-dependent dioxygenase n 1 tax solanum chacoense repid q9zsh4_solch; score=162.16; evalue=2.28e-172;
c27090/f9p1/1606	2-oxoglutarate-dependent dioxygenase n 1 tax solanum chacoense repid q9zsh4_solch; score=140.20; evalue=2.28e-172;
c27090/f9p1/1606	uncharacterized protein n 1 tax solanum lycopersicum repid q40131_sollc; score=356.30; evalue=1.80e-168;
c27090/f9p1/1606	uncharacterized protein n 1 tax solanum lycopersicum repid q40131_sollc; score=151.37; evalue=1.80e-168;
c27173/f3p2/1645	uncharacterized protein n 1 tax solanum lycopersicum repid k4azg9_sollc; score=689.49; evalue=0.00e+00;
c27173/f3p2/1645	putative uncharacterized protein n 1 tax vitis vinifera repid f6i6i4_vitvi; score=521.55; evalue=3.66e-179;
c27173/f3p2/1645	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7m5l8_arall; score=519.24; evalue=1.32e-178;
c27173/f3p2/1645	amino acid dehydrogenase family protein n 1 tax arabidopsis thaliana repid o65271_arath; score=516.92; evalue=1.06e-177;
c27173/f3p2/1645	uncharacterized protein n 1 tax glycine max repid c6tnl4_soybn; score=514.61; evalue=4.50e-177;
c27469/f7p14/1730	mitochondrial protein putative n 1 tax medicago truncatula repid g7i9t8_medtr; score=168.70; evalue=2.50e-72;
c27469/f7p14/1730	mitochondrial protein putative n 1 tax medicago truncatula repid g7i9t8_medtr; score=132.11; evalue=2.50e-72;
c27469/f7p14/1730	uncharacterized protein n 1 tax solanum lycopersicum repid k4d065_sollc; score=221.86; evalue=8.13e-66;
c27469/f7p14/1730	mitochondrial protein putative n 1 tax medicago truncatula repid g7i9t8_medtr; score=176.79; evalue=2.85e-54;
c27469/f7p14/1730	mitochondrial protein putative n 1 tax medicago truncatula repid g7i9t8_medtr; score=63.93; evalue=2.85e-54;
c27583/f10p2/1962	uncharacterized protein n 1 tax solanum lycopersicum repid k4cae8_sollc; score=940.64; evalue=0.00e+00;
c27583/f10p2/1962	uncharacterized protein n 1 tax solanum lycopersicum repid k4c3e5_sollc; score=741.88; evalue=0.00e+00;
c27583/f10p2/1962	putative uncharacterized protein n 1 tax solanum tuberosum repid q2v9c4_soltu; score=700.66; evalue=0.00e+00;
c27583/f10p2/1962	putative uncharacterized protein (fragment) n 1 tax capsicum annuum repid a0mlw5_capan; score=671.77; evalue=0.00e+00;
c27583/f10p2/1962	putative uncharacterized protein n 2 tax vitis vinifera repid f6h7u7_vitvi; score=674.47; evalue=0.00e+00;
c27813/f1p4/1450	uncharacterized protein n 1 tax solanum lycopersicum repid k4bak9_sollc; score=726.09; evalue=0.00e+00;
c27813/f1p4/1450	amine oxidase putative n 1 tax ricinus communis repid b9rnm3_ricco; score=528.87; evalue=0.00e+00;
c27813/f1p4/1450	putative uncharacterized protein n 1 tax vitis vinifera repid d7st93_vitvi; score=513.84; evalue=5.80e-176;
c27813/f1p4/1450	amine oxidase family protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7l8a1_arall; score=496.51; evalue=7.23e-169;
c27813/f1p4/1450	fad/nad(p)-binding oxidoreductase domain-containing protein n 1 tax arabidopsis thaliana repid q9sf45_arath; score=494.58; evalue=4.03e-168;
c28018/f2p4/1769	uncharacterized protein n 1 tax solanum lycopersicum repid k4b0m6_sollc; score=654.44; evalue=0.00e+00;
c28018/f2p4/1769	putative uncharacterized protein n 1 tax vitis vinifera repid a5brg2_vitvi; score=556.60; evalue=0.00e+00;

c28018/f2p4/1769	n 1 tax vitis vinifera repid h9t852_vitvi; score=556.21; evalue=0.00e+00;
c28018/f2p4/1769	putative uncharacterized protein n 1 tax vitis vinifera repid f6htz8_vitvi; score=554.67; evalue=0.00e+00;
c28018/f2p4/1769	gibberellin receptor gid1 putative n 1 tax ricinus communis repid b9rez1_ricco; score=553.13; evalue=0.00e+00;
c28037/f2p2/1549	uncharacterized protein n 1 tax solanum lycopersicum repid k4bp74_sollc; score=424.48; evalue=2.30e-143;
c28037/f2p2/1549	tcp transcription factor 14 n 1 tax solanum lycopersicum repid g3bgv4_sollc; score=424.48; evalue=2.30e-143;
c28037/f2p2/1549	tcp transcription factor 15 n 1 tax solanum lycopersicum repid g3bgv5_sollc; score=293.12; evalue=2.23e-92;
c28037/f2p2/1549	putative uncharacterized protein n 1 tax vitis vinifera repid f6hin5_vitvi; score=259.23; evalue=2.93e-79;
c28037/f2p2/1549	uncharacterized protein n 1 tax glycine max repid i1lf87_soybn; score=256.14; evalue=3.09e-78;
c28144/f3p2/1408	syntaxin-like protein n 1 tax solanum tuberosum repid q3hrz4_soltu; score=452.21; evalue=6.91e-155;
c28144/f3p2/1408	uncharacterized protein n 1 tax solanum lycopersicum repid k4cn16_sollc; score=451.06; evalue=2.19e-154;
c28144/f3p2/1408	syntaxin n 1 tax nicotiana tabacum repid b7x6s8_tobac; score=427.56; evalue=3.39e-145;
c28144/f3p2/1408	uncharacterized protein n 1 tax solanum lycopersicum repid k4c6w7_sollc; score=424.48; evalue=6.01e-144;
c28144/f3p2/1408	uncharacterized protein n 1 tax solanum lycopersicum repid k4ci11_sollc; score=420.24; evalue=2.40e-142;
c28776/f2p1/1122	uncharacterized protein n 1 tax solanum lycopersicum repid k4b2y6_sollc; score=516.15; evalue=0.00e+00;
c28776/f2p1/1122	putative uncharacterized protein n 1 tax ricinus communis repid b9rya8_ricco; score=410.61; evalue=5.64e-140;
c28776/f2p1/1122	putative uncharacterized protein n 1 tax vitis vinifera repid f6i5y8_vitvi; score=409.45; evalue=1.21e-139;
c28776/f2p1/1122	at4g35220/f23e12_220 n 1 tax arabidopsis thaliana repid q94jt5_arath; score=408.68; evalue=2.94e-139;
c28776/f2p1/1122	cyclase family protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7md29_arall; score=407.91; evalue=6.81e-139;
c28861/f4p2/2025	uncharacterized protein n 1 tax solanum lycopersicum repid k4d0s3_sollc; score=1031.55; evalue=0.00e+00;
c28861/f4p2/2025	putative uncharacterized protein n 1 tax vitis vinifera repid d7tpx3_vitvi; score=781.17; evalue=0.00e+00;
c28861/f4p2/2025	uncharacterized protein n 1 tax glycine max repid i1ljh0_soybn; score=764.61; evalue=0.00e+00;
c28861/f4p2/2025	cytochrome c biogenesis protein family n 1 tax arabidopsis lyrata subsp. lyrata repid d7ke35_arall; score=759.21; evalue=0.00e+00;
c28861/f4p2/2025	cytochrome c biogenesis protein ccs1 chloroplastic n 1 tax arabidopsis thaliana repid ccs1_arath; score=754.59; evalue=0.00e+00;
c28919/f1p12/986	chlorophyll a/b binding protein n 1 tax solanum tuberosum repid q41425_soltu; score=512.30; evalue=0.00e+00;
c28919/f1p12/986	chlorophyll a-b binding protein 1b chloroplastic n 1 tax solanum lycopersicum repid cb2b_sollc; score=512.30; evalue=0.00e+00;
c28919/f1p12/986	chlorophyll a/b binding protein n 1 tax solanum tuberosum repid q41422_soltu; score=511.15; evalue=1.77e-180;
c28919/f1p12/986	chlorophyll a/b binding protein n 1 tax solanum tuberosum repid q41421_soltu; score=510.76; evalue=2.71e-180;
c28919/f1p12/986	light harvesting chlorophyll a/b-binding protein n 1 tax nicotiana sylvestris repid o64443_nicsy; score=510.38; evalue=4.33e-180;
c28984/f3p0/972	uncharacterized protein n 1 tax solanum lycopersicum repid k4c1l0_sollc; score=360.53; evalue=2.61e-122;
c28984/f3p0/972	putative uncharacterized protein n 1 tax vitis vinifera repid f6hh08_vitvi; score=350.13; evalue=4.75e-118;
c28984/f3p0/972	predicted protein n 1 tax populus trichocarpa repid b9n7d1_poptr; score=340.12; evalue=4.27e-114;

c28984/f3p0/972	uncharacterized protein n 1 tax glycine max repid c6sva4_soybn; score=336.26; evalue=1.49e-112;
c28984/f3p0/972	uncharacterized protein n 1 tax glycine max repid c6sxz4_soybn; score=333.18; evalue=2.05e-111;
c29116/f3p17/2018	uncharacterized protein n 1 tax solanum lycopersicum repid k4dex3_sollc; score=1007.28; evalue=0.00e+00;
c29116/f3p17/2018	phosphoethanolamine n-methyltransferase n 1 tax solanum lycopersicum repid q9axh3_sollc; score=900.58; evalue=0.00e+00;
c29116/f3p17/2018	phosphoethanolamine n-methyltransferase putative n 1 tax ricinus communis repid b9t1h8_ricco; score=866.68; evalue=0.00e+00;
c29116/f3p17/2018	putative uncharacterized protein n 1 tax vitis vinifera repid d7sja7_vitvi; score=858.98; evalue=0.00e+00;
c29116/f3p17/2018	putative uncharacterized protein n 1 tax vitis vinifera repid a5anl8_vitvi; score=855.90; evalue=0.00e+00;
c29195/f3p2/1667	ngmtp1 n 1 tax nicotiana glauca repid q5fb33_nicgl; score=659.06; evalue=0.00e+00;
c29195/f3p2/1667	ntmtp1a n 1 tax nicotiana tabacum repid q5fb32_tobac; score=657.14; evalue=0.00e+00;
c29195/f3p2/1667	ntmtp1b n 1 tax nicotiana tabacum repid q5fb31_tobac; score=654.44; evalue=0.00e+00;
c29195/f3p2/1667	putative zinc transporter n 1 tax nicotiana tabacum repid a7wpk9_tobac; score=642.50; evalue=0.00e+00;
c29195/f3p2/1667	uncharacterized protein n 1 tax solanum lycopersicum repid k4cbh7_sollc; score=608.99; evalue=0.00e+00;
c29277/f1p1/1626	alpha-glucosidase n 1 tax solanum tuberosum repid q9lec9_soltu; score=879.78; evalue=0.00e+00;
c29277/f1p1/1626	uncharacterized protein n 1 tax solanum lycopersicum repid k4bxc1_sollc; score=875.54; evalue=0.00e+00;
c29277/f1p1/1626	putative uncharacterized protein n 1 tax vitis vinifera repid f6hex2_vitvi; score=678.32; evalue=0.00e+00;
c29277/f1p1/1626	predicted protein n 1 tax populus trichocarpa repid b9hwi3_poptr; score=670.23; evalue=0.00e+00;
c29277/f1p1/1626	predicted protein n 1 tax populus trichocarpa repid b9hj23_poptr; score=667.54; evalue=0.00e+00;
c29542/f1p0/1359	uncharacterized protein n 1 tax solanum lycopersicum repid k4d3v7_sollc; score=770.00; evalue=0.00e+00;
c29542/f1p0/1359	uncharacterized protein n 1 tax solanum lycopersicum repid k4d3w2_sollc; score=756.90; evalue=0.00e+00;
c29542/f1p0/1359	uncharacterized protein n 1 tax solanum lycopersicum repid k4d3v8_sollc; score=705.29; evalue=0.00e+00;
c29542/f1p0/1359	uncharacterized protein n 1 tax solanum lycopersicum repid k4d3s3_sollc; score=618.23; evalue=0.00e+00;
c29542/f1p0/1359	udp-glucuronosyltransferase putative n 1 tax ricinus communis repid b9six3_ricco; score=393.66; evalue=6.27e-130;
c29798/f5p3/1630	uncharacterized protein n 1 tax solanum lycopersicum repid k4c203_sollc; score=726.09; evalue=0.00e+00;
c29798/f5p3/1630	pto-interacting protein 1 n 1 tax solanum lycopersicum repid pti1_sollc; score=661.37; evalue=0.00e+00;
c29798/f5p3/1630	pto kinase interactor 1 n 1 tax capsicum annuum repid b2czj8_capan; score=645.97; evalue=0.00e+00;
c29798/f5p3/1630	putative uncharacterized protein n 1 tax vitis vinifera repid d7t684_vitvi; score=609.76; evalue=0.00e+00;
c29798/f5p3/1630	serine/threonine-protein kinase pbs1 putative n 1 tax ricinus communis repid b9rn61_ricco; score=595.12; evalue=0.00e+00;
c30006/f2p1/1515	uncharacterized protein n 1 tax solanum lycopersicum repid k4d8c3_sollc; score=673.70; evalue=0.00e+00;
c30006/f2p1/1515	aba responsive transcription factor n 1 tax solanum lycopersicum repid g5em38_sollc; score=662.53; evalue=0.00e+00;
c30006/f2p1/1515	phi-2 n 1 tax nicotiana tabacum repid q94ib2_tobac; score=560.84; evalue=0.00e+00;
c30006/f2p1/1515	bzip n 1 tax nicotiana tabacum repid q4pkh1_tobac; score=412.54; evalue=6.56e-137;

c30006/f2p1/1515	uncharacterized protein n 1 tax solanum lycopersicum repid k4b324_sollc; score=363.61; evalue=1.25e-117;
c30177/f2p2/1715	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmz6_sollc; score=769.62; evalue=0.00e+00;
c30177/f2p2/1715	predicted protein n 1 tax populus trichocarpa repid b9gwb7_poptr; score=768.46; evalue=0.00e+00;
c30177/f2p2/1715	predicted protein n 1 tax populus trichocarpa repid b9gkv7_poptr; score=748.81; evalue=0.00e+00;
c30177/f2p2/1715	uncharacterized protein n 3 tax oryza repid i1pus7_orygl; score=746.50; evalue=0.00e+00;
c30177/f2p2/1715	uncharacterized protein n 1 tax oryza brachyantha repid j3m694_orybr; score=746.12; evalue=0.00e+00;
c30188/f1p2/1575	uncharacterized protein n 1 tax solanum lycopersicum repid k4bus0_sollc; score=774.24; evalue=0.00e+00;
c30188/f1p2/1575	cytochrome p450 n 1 tax nicotiana tabacum repid c5nm78_tobac; score=675.63; evalue=0.00e+00;
c30188/f1p2/1575	cytochrome p450 n 1 tax nicotiana tabacum repid c5nm79_tobac; score=612.84; evalue=0.00e+00;
c30188/f1p2/1575	n 1 tax nicotiana tabacum repid a1xei0_tobac; score=530.79; evalue=0.00e+00;
c30188/f1p2/1575	n 1 tax nicotiana tabacum repid a1xeh9_tobac; score=528.48; evalue=3.81e-180;
c30412/f5p2/1647	uncharacterized protein n 1 tax solanum lycopersicum repid k4cl77_sollc; score=474.55; evalue=6.70e-162;
c30412/f5p2/1647	putative uncharacterized protein n 1 tax vitis vinifera repid f6h3m5_vitvi; score=444.12; evalue=8.43e-148;
c30412/f5p2/1647	putative uncharacterized protein n 1 tax vitis vinifera repid a5bxd3_vitvi; score=442.19; evalue=1.61e-140;
c30412/f5p2/1647	calmodulin binding protein putative n 1 tax ricinus communis repid b9rqr6_ricco; score=412.92; evalue=1.34e-135;
c30412/f5p2/1647	uncharacterized protein n 1 tax glycine max repid i1jtx8_soybn; score=363.61; evalue=1.62e-116;
c30664/f1p4/1996	uncharacterized protein n 1 tax solanum lycopersicum repid k4c824_sollc; score=781.94; evalue=0.00e+00;
c30664/f1p4/1996	rna splicing protein mrs2 mitochondrial putative n 1 tax ricinus communis repid b9rgm7_ricco; score=681.40; evalue=0.00e+00;
c30664/f1p4/1996	magnesium transporter n 1 tax populus trichocarpa repid b9n9x1_poptr; score=672.16; evalue=0.00e+00;
c30664/f1p4/1996	uncharacterized protein n 1 tax glycine max repid i1m5z6_soybn; score=667.92; evalue=0.00e+00;
c30664/f1p4/1996	uncharacterized protein n 1 tax glycine max repid i1mc99_soybn; score=667.15; evalue=0.00e+00;
c31744/f1p3/1600	uncharacterized protein n 1 tax solanum lycopersicum repid k4b937_sollc; score=897.89; evalue=0.00e+00;
c31744/f1p3/1600	eukaryotic translation initiation factor 3 subunit putative n 1 tax ricinus communis repid b9rbd0_ricco; score=820.85; evalue=0.00e+00;
c31744/f1p3/1600	putative uncharacterized protein n 1 tax vitis vinifera repid f6hju0_vitvi; score=807.75; evalue=0.00e+00;
c31744/f1p3/1600	uncharacterized protein n 1 tax glycine max repid i1m228_soybn; score=802.36; evalue=0.00e+00;
c31744/f1p3/1600	eukaryotic translation initiation factor 3 subunit d n 1 tax arabidopsis thaliana repid eif3d_arath; score=790.41; evalue=0.00e+00;
c32141/f7p5/1872	uncharacterized protein n 1 tax solanum lycopersicum repid k4cpa1_sollc; score=738.41; evalue=0.00e+00;
c32141/f7p5/1872	putative uncharacterized protein n 1 tax vitis vinifera repid a5b9n8_vitvi; score=541.19; evalue=0.00e+00;
c32141/f7p5/1872	putative uncharacterized protein n 1 tax vitis vinifera repid d7tvz6_vitvi; score=540.42; evalue=0.00e+00;
c32141/f7p5/1872	predicted protein n 1 tax populus trichocarpa repid b9gkh9_poptr; score=528.87; evalue=0.00e+00;
c32141/f7p5/1872	2-deoxyglucose-6-phosphate phosphatase putative n 1 tax ricinus communis repid b9rcb5_ricco; score=527.71; evalue=1.41e-180;

c32356/f2p3/1763	uncharacterized protein n 1 tax solanum lycopersicum repid k4ayl5_sollc; score=809.29; evalue=0.00e+00;
c32356/f2p3/1763	putative uncharacterized protein n 1 tax vitis vinifera repid f6gxa0_vitvi; score=340.89; evalue=5.79e-107;
c32356/f2p3/1763	putative uncharacterized protein n 1 tax vitis vinifera repid a5bsr2_vitvi; score=320.09; evalue=1.07e-98;
c32356/f2p3/1763	putative uncharacterized protein n 1 tax ricinus communis repid b9rgg5_ricco; score=307.76; evalue=9.71e-94;
c32356/f2p3/1763	predicted protein n 1 tax populus trichocarpa repid b9nay7_poptr; score=293.12; evalue=1.10e-88;
c32362/f1p4/2029	3-ketoacyl-coa synthase n 1 tax solanum lycopersicum repid k4bvc4_sollc; score=1062.75; evalue=0.00e+00;
c32362/f1p4/2029	3-ketoacyl-coa synthase n 1 tax vitis vinifera repid f6hqm8_vitvi; score=943.34; evalue=0.00e+00;
c32362/f1p4/2029	3-ketoacyl-coa synthase n 1 tax ricinus communis repid b9r7v1_ricco; score=936.41; evalue=0.00e+00;
c32362/f1p4/2029	3-ketoacyl-coa synthase n 1 tax camellia oleifera repid c3vpa4_9eric; score=924.85; evalue=0.00e+00;
c32362/f1p4/2029	3-ketoacyl-coa synthase 4 n 1 tax arabidopsis thaliana repid kcs4_arath; score=913.68; evalue=0.00e+00;
c32680/f4p17/1703	hop-interacting protein thi041 n 1 tax solanum lycopersicum repid g8z269_sollc; score=635.95; evalue=0.00e+00;
c32680/f4p17/1703	homeobox protein knotted-1-like let12 n 1 tax solanum lycopersicum repid k4cbi3_sollc; score=635.57; evalue=0.00e+00;
c32680/f4p17/1703	homeobox protein knotted-1-like let12 n 1 tax solanum lycopersicum repid let12_sollc; score=629.79; evalue=0.00e+00;
c32680/f4p17/1703	homeobox 1 protein (fragment) n 1 tax solanum lycopersicum repid q9zrb9_sollc; score=584.72; evalue=0.00e+00;
c32680/f4p17/1703	class 2 knotted1-like protein n 1 tax nicotiana tabacum repid a9cr84_tobac; score=544.66; evalue=0.00e+00;
c32941/f1p0/1766	putative uncharacterized protein n 1 tax vitis vinifera repid d7u595_vitvi; score=493.04; evalue=3.73e-168;
c32941/f1p0/1766	uncharacterized protein n 1 tax solanum lycopersicum repid k4d186_sollc; score=493.04; evalue=4.47e-168;
c32941/f1p0/1766	uncharacterized protein n 1 tax glycine max repid i1lpm9_soybn; score=478.02; evalue=2.83e-162;
c32941/f1p0/1766	non-imprinted in prader-willi/angelman syndrome region protein putative n 1 tax ricinus communis repid b9sqj1_ricco; score=459.14; evalue=4.26e-155;
c32941/f1p0/1766	uncharacterized protein n 1 tax glycine max repid i1lpn0_soybn; score=459.53; evalue=4.75e-155;
c32942/f2p3/1171	uncharacterized protein n 1 tax solanum lycopersicum repid k4cwa1_sollc; score=449.51; evalue=2.05e-155;
c32942/f2p3/1171	haloacid dehalogenase-like hydrolase n 3 tax arabidopsis thaliana repid q8rye9_arath; score=350.90; evalue=1.13e-116;
c32942/f2p3/1171	hydrolase n 1 tax arabidopsis lyrata subsp. lyrata repid d7lfr9_arall; score=350.90; evalue=1.13e-116;
c32942/f2p3/1171	phosphoglycolate phosphatase putative n 1 tax ricinus communis repid b9rwt6_ricco; score=346.67; evalue=5.41e-115;
c32942/f2p3/1171	phosphoglycolate phosphatase n 1 tax medicago truncatula repid g7i2p1_medtr; score=345.12; evalue=7.61e-115;
c33142/f1p3/1528	uncharacterized protein n 1 tax solanum lycopersicum repid k4bpm2_sollc; score=890.57; evalue=0.00e+00;
c33142/f1p3/1528	cytochrome p450 cyp736a54 n 1 tax bupleurum chinense repid i3vi25_bupch; score=637.11; evalue=0.00e+00;
c33142/f1p3/1528	putative uncharacterized protein n 1 tax vitis vinifera repid f6h499_vitvi; score=632.48; evalue=0.00e+00;
c33142/f1p3/1528	flavonoid 3-hydroxylase putative n 1 tax ricinus communis repid b9t1c6_ricco; score=626.71; evalue=0.00e+00;
c33142/f1p3/1528	uncharacterized protein n 1 tax solanum lycopersicum repid k4bsi0_sollc; score=613.99; evalue=0.00e+00;
c33647/f2p4/1439	uncharacterized protein n 1 tax solanum lycopersicum repid k4b972_sollc; score=731.87; evalue=0.00e+00;

c33647/f2p4/1439	uncharacterized protein n 1 tax solanum lycopersicum repid k4be70_sollc; score=515.38; evalue=1.70e-177;
c33647/f2p4/1439	uncharacterized protein n 1 tax solanum lycopersicum repid k4cy77_sollc; score=493.43; evalue=4.16e-169;
c33647/f2p4/1439	putative uncharacterized protein n 1 tax vitis vinifera repid f6hd56_vitvi; score=441.04; evalue=1.29e-148;
c33647/f2p4/1439	uncharacterized protein n 1 tax glycine max repid i1luy9_soybn; score=400.59; evalue=1.06e-132;
c35598/f44p18/1698	elongation factor tub chloroplastic n 2 tax nicotiana repid eftub_nicsy; score=741.11; evalue=0.00e+00;
c35598/f44p18/1698	elongation factor tua chloroplastic n 2 tax nicotiana repid eftua_nicsy; score=737.26; evalue=0.00e+00;
c35598/f44p18/1698	elongation factor tu n 1 tax solanum lycopersicum repid k4bk69_sollc; score=728.78; evalue=0.00e+00;
c35598/f44p18/1698	elongation factor tu chloroplastic n 1 tax glycine max repid eftu2_soybn; score=719.54; evalue=0.00e+00;
c35598/f44p18/1698	uncharacterized protein n 1 tax solanum lycopersicum repid k4c8q1_sollc; score=716.84; evalue=0.00e+00;
c36190/f214p189/1636	uncharacterized protein n 2 tax magnoliophyta repid k3yr52_setit; score=890.18; evalue=0.00e+00;
c36190/f214p189/1636	uncharacterized protein n 2 tax magnoliophyta repid k3yr52_setit; score=754.98; evalue=0.00e+00;
c36190/f214p189/1636	multidrug resistance protein abc transporter family n 2 tax medicago truncatula repid g7jdw8_medtr; score=889.41; evalue=0.00e+00;
c36190/f214p189/1636	multidrug resistance protein abc transporter family n 2 tax medicago truncatula repid g7jdw8_medtr; score=885.56; evalue=0.00e+00;
c36190/f214p189/1636	multidrug resistance protein abc transporter family n 2 tax medicago truncatula repid g7jdw8_medtr; score=751.51; evalue=0.00e+00;
c36402/f7p4/2055	uncharacterized protein n 1 tax solanum lycopersicum repid k4bc27_sollc; score=1040.41; evalue=0.00e+00;
c36402/f7p4/2055	uncharacterized protein n 1 tax brachypodium distachyon repid i1ih73_bradi; score=424.86; evalue=1.32e-131;
c36402/f7p4/2055	uncharacterized protein n 1 tax oryza brachyantha repid j3nef2_orybr; score=394.81; evalue=1.85e-124;
c36402/f7p4/2055	uncharacterized protein n 1 tax zea mays repid b4faj8_maize; score=385.96; evalue=2.16e-121;
c36402/f7p4/2055	putative uncharacterized protein sb08g019140 n 1 tax sorghum bicolor repid c5yqd2_sorbi; score=235.34; evalue=2.38e-66;
c36494/f6p20/930	photosystem ii oxygen-evolving complex protein 3 n 1 tax solanum lycopersicum repid q672q6_sollc; score=367.47; evalue=1.04e-124;
c36494/f6p20/930	chloroplast psbq2 n 1 tax nicotiana benthamiana repid i0b7k0_nicbe; score=332.80; evalue=3.75e-111;
c36494/f6p20/930	chloroplast oxygen-evolving protein 16 kda subunit n 1 tax nicotiana benthamiana repid q5efr5_nicbe; score=331.26; evalue=1.53e-110;
c36494/f6p20/930	chloroplast psbq1 n 1 tax nicotiana benthamiana repid i0b7j9_nicbe; score=331.26; evalue=1.68e-110;
c36494/f6p20/930	chloroplast oxygen-evolving protein 16 kda subunit n 2 tax nicotiana repid q5efr4_tobac; score=331.26; evalue=1.76e-110;
c36931/f3p2/1315	calcineurin b-like molecule n 1 tax solanum lycopersicum repid g5em34_sollc; score=448.36; evalue=1.29e-154;
c36931/f3p2/1315	uncharacterized protein n 1 tax solanum lycopersicum repid k4dd22_sollc; score=417.93; evalue=1.21e-142;
c36931/f3p2/1315	calcineurin b n 1 tax pisum sativum repid q8l7f6_pea; score=416.00; evalue=6.80e-142;
c36931/f3p2/1315	calcineurin b-like protein 02 n 1 tax vitis vinifera repid a5bys8_vitvi; score=412.54; evalue=1.62e-140;
c36931/f3p2/1315	calcineurin b putative n 1 tax ricinus communis repid b9t1q9_ricco; score=412.15; evalue=2.02e-140;
c36990/f1p6/2168	3-hydroxy-3-methylglutaryl coenzyme a reductase 1 n 1 tax solanum tuberosum repid h2bnm0_soltu; score=1158.28; evalue=0.00e+00;
c36990/f1p6/2168	3-hydroxy-3-methylglutaryl coenzyme a reductase 1 n 1 tax solanum chacoense repid h2bnm1_solch; score=1156.74; evalue=0.00e+00;

c36990/f1p6/2168	uncharacterized protein n 4 tax solanum lycopersicum repid k4ba96_sollc; score=1154.43; evalue=0.00e+00;
c36990/f1p6/2168	3-hydroxy-3-methylglutaryl-coenzyme a reductase 1 n 1 tax solanum tuberosum repid hmdh1_soltu; score=1146.72; evalue=0.00e+00;
c36990/f1p6/2168	hydroxy-methylglutaryl-coenzyme a reductase n 1 tax nicotiana tabacum repid o48624_tobac; score=1087.79; evalue=0.00e+00;
c37219/f5p7/1466	uncharacterized protein n 1 tax solanum lycopersicum repid k4cvt4_sollc; score=889.80; evalue=0.00e+00;
c37219/f5p7/1466	mar-binding protein n 1 tax nicotiana tabacum repid q9av96_tobac; score=864.37; evalue=0.00e+00;
c37219/f5p7/1466	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2r3_sollc; score=828.93; evalue=0.00e+00;
c37219/f5p7/1466	putative uncharacterized protein n 1 tax vitis vinifera repid a5arv8_vitvi; score=817.76; evalue=0.00e+00;
c37219/f5p7/1466	putative uncharacterized protein n 1 tax vitis vinifera repid f6htw5_vitvi; score=819.69; evalue=0.00e+00;
c37455/f1p3/2078	mid1-complementing activity 1 n 1 tax nicotiana tabacum repid f5hs57_tobac; score=764.22; evalue=0.00e+00;
c37455/f1p3/2078	mid1-complementing activity 2 n 1 tax nicotiana tabacum repid f5hs58_tobac; score=679.09; evalue=0.00e+00;
c37455/f1p3/2078	uncharacterized protein n 1 tax solanum lycopersicum repid k4bam2_sollc; score=674.09; evalue=0.00e+00;
c37455/f1p3/2078	putative uncharacterized protein n 1 tax vitis vinifera repid f6h5i8_vitvi; score=650.97; evalue=0.00e+00;
c37455/f1p3/2078	uncharacterized protein n 1 tax glycine max repid i1li39_soybn; score=621.70; evalue=0.00e+00;
c37705/f1p1/1921	uncharacterized protein n 1 tax solanum lycopersicum repid k4bcx1_sollc; score=432.56; evalue=1.65e-143;
c37705/f1p1/1921	uncharacterized protein n 1 tax solanum lycopersicum repid k4bfz7_sollc; score=309.69; evalue=2.70e-93;
c37705/f1p1/1921	putative uncharacterized protein n 1 tax vitis vinifera repid d7ssi3_vitvi; score=294.28; evalue=1.43e-88;
c37705/f1p1/1921	predicted protein n 1 tax populus trichocarpa repid b9hfs4_poptr; score=261.92; evalue=1.68e-76;
c37705/f1p1/1921	putative uncharacterized protein n 2 tax ricinus communis repid b9ssd7_ricco; score=244.20; evalue=7.15e-70;
c37834/f1p0/2115	uncharacterized protein n 1 tax solanum lycopersicum repid k4ayy9_sollc; score=756.52; evalue=0.00e+00;
c37834/f1p0/2115	putative uncharacterized protein n 1 tax vitis vinifera repid d7slw0_vitvi; score=457.60; evalue=1.49e-152;
c37834/f1p0/2115	uncharacterized protein (fragment) n 2 tax glycine max repid k7lfx1_soybn; score=453.37; evalue=1.03e-149;
c37834/f1p0/2115	uncharacterized protein n 2 tax glycine max repid k7mui8_soybn; score=447.97; evalue=1.45e-148;
c37834/f1p0/2115	putative uncharacterized protein n 1 tax ricinus communis repid b9rd21_ricco; score=447.59; evalue=2.80e-148;
c37861/f1p1/1876	uncharacterized protein n 1 tax solanum lycopersicum repid k4c3f9_sollc; score=568.54; evalue=0.00e+00;
c37861/f1p1/1876	uncharacterized protein n 1 tax solanum lycopersicum repid k4c3f9_sollc; score=158.30; evalue=0.00e+00;
c37861/f1p1/1876	uncharacterized protein n 1 tax solanum lycopersicum repid k4ctl7_sollc; score=317.00; evalue=2.70e-122;
c37861/f1p1/1876	uncharacterized protein n 1 tax solanum lycopersicum repid k4ctl7_sollc; score=150.60; evalue=2.70e-122;
c37861/f1p1/1876	uncharacterized protein n 1 tax solanum lycopersicum repid k4cai5_sollc; score=322.40; evalue=2.86e-122;
c37952/f1p3/1651	h(+)-transporting atpase n 1 tax solanum tuberosum repid q43178_soltu; score=799.27; evalue=0.00e+00;
c37952/f1p3/1651	uncharacterized protein n 1 tax solanum lycopersicum repid k4ccj2_sollc; score=797.73; evalue=0.00e+00;
c37952/f1p3/1651	plasma membrane h+-atpase n 1 tax solanum lycopersicum repid q96578_sollc; score=796.96; evalue=0.00e+00;

c37952/f1p3/1651	plasma membrane atpase 4 n 1 tax nicotiana plumbaginifolia repid pma4_nicpl; score=776.93; evalue=0.00e+00;
c37952/f1p3/1651	autoinhibited h+ atpase n 1 tax populus trichocarpa repid b9n321_poptr; score=737.26; evalue=0.00e+00;
c38354/f1p2/626	uncharacterized protein n 1 tax solanum lycopersicum repid k4ax99_sollc; score=304.29; evalue=1.17e-102;
c38354/f1p2/626	uncharacterized protein n 1 tax solanum lycopersicum repid k4br52_sollc; score=288.50; evalue=1.44e-96;
c38354/f1p2/626	uncharacterized protein n 1 tax solanum lycopersicum repid k4bw97_sollc; score=286.19; evalue=1.32e-95;
c38354/f1p2/626	40s ribosomal protein s16b n 1 tax hevea brasiliensis repid i3nmp7_hevbr; score=275.40; evalue=2.18e-91;
c38354/f1p2/626	40s ribosomal protein s16 (fragment) n 1 tax euphorbia esula repid q9m5l1_eupes; score=275.02; evalue=3.34e-91;
c38441/f2p4/1466	uncharacterized protein n 1 tax solanum lycopersicum repid k4bsy0_sollc; score=547.35; evalue=0.00e+00;
c38441/f2p4/1466	protein n 1 tax jatropha curcas repid e6nu80_9rosi; score=432.95; evalue=3.77e-146;
c38441/f2p4/1466	putative uncharacterized protein n 1 tax ricinus communis repid b9s2u0_ricco; score=418.31; evalue=1.92e-140;
c38441/f2p4/1466	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7kk29_arall; score=405.60; evalue=2.01e-135;
c38441/f2p4/1466	predicted protein n 1 tax populus trichocarpa repid b9gu02_poptr; score=402.13; evalue=3.46e-134;
c38540/f1p0/1290	gaga-binding transcriptional activator n 1 tax solanum tuberosum repid h1zn95_soltu; score=546.58; evalue=0.00e+00;
c38540/f1p0/1290	gaga-binding transcriptional activator n 1 tax solanum lycopersicum repid h1zn86_sollc; score=543.50; evalue=0.00e+00;
c38540/f1p0/1290	uncharacterized protein n 1 tax solanum lycopersicum repid k4bnz4_sollc; score=527.71; evalue=0.00e+00;
c38540/f1p0/1290	gaga-binding transcriptional activator n 1 tax nicotiana tabacum repid h1zn83_tobac; score=509.22; evalue=8.41e-178;
c38540/f1p0/1290	putative uncharacterized protein n 1 tax vitis vinifera repid f6hfa4_vitvi; score=398.28; evalue=2.70e-133;
c38624/f1p1/1760	s-adenosylmethionine decarboxylase proenzyme n 1 tax solanum lycopersicum repid k4bcb2_sollc; score=539.65; evalue=0.00e+00;
c38624/f1p1/1760	s-adenosylmethionine decarboxylase proenzyme n 1 tax solanum lycopersicum repid b0f6u7_sollc; score=535.41; evalue=0.00e+00;
c38624/f1p1/1760	s-adenosylmethionine decarboxylase n 1 tax capsicum annuum repid k7r0t7_capan; score=518.46; evalue=1.17e-177;
c38624/f1p1/1760	s-adenosylmethionine decarboxylase proenzyme n 1 tax ipomoea nil repid dcam_iponi; score=421.78; evalue=6.26e-140;
c38624/f1p1/1760	s-adenosylmethionine decarboxylase proenzyme n 2 tax ipomoea batatas repid dcam_ipoba; score=416.39; evalue=9.77e-138;
c38962/f2p0/1719	uncharacterized protein n 4 tax zea mays repid b4f923_maize; score=348.21; evalue=1.02e-161;
c38962/f2p0/1719	uncharacterized protein n 4 tax zea mays repid b4f923_maize; score=250.75; evalue=1.02e-161;
c38962/f2p0/1719	uncharacterized protein n 1 tax oryza brachyantha repid j3nbx3_orybr; score=348.21; evalue=2.37e-161;
c38962/f2p0/1719	uncharacterized protein n 1 tax oryza brachyantha repid j3nbx3_orybr; score=249.59; evalue=2.37e-161;
c38962/f2p0/1719	uncharacterized protein n 1 tax oryza glaberrima repid i1r4l9_orygl; score=345.51; evalue=2.83e-160;
c39151/f1p2/1488	uncharacterized protein n 1 tax solanum lycopersicum repid k4b419_sollc; score=875.93; evalue=0.00e+00;
c39151/f1p2/1488	putative uncharacterized protein n 1 tax vitis vinifera repid f6i104_vitvi; score=509.99; evalue=3.84e-171;
c39151/f1p2/1488	putative uncharacterized protein n 1 tax vitis vinifera repid a5ap74_vitvi; score=509.61; evalue=7.21e-171;
c39151/f1p2/1488	atp binding protein putative n 1 tax ricinus communis repid b9t7d3_ricco; score=489.19; evalue=8.66e-164;

c39151/f1p2/1488	predicted protein n 1 tax populus trichocarpa repid b9h1a0_poptr; score=488.03; evalue=1.45e-162;
c39304/f3p1/1657	uncharacterized protein n 1 tax solanum lycopersicum repid k4c266_sollc; score=731.10; evalue=0.00e+00;
c39304/f3p1/1657	predicted protein n 1 tax populus trichocarpa repid b9hyc3_poptr; score=597.43; evalue=0.00e+00;
c39304/f3p1/1657	uncharacterized protein n 1 tax glycine max repid i1ktv7_soybn; score=568.15; evalue=0.00e+00;
c39304/f3p1/1657	putative uncharacterized protein n 1 tax vitis vinifera repid f6h9s8_vitvi; score=561.99; evalue=0.00e+00;
c39304/f3p1/1657	uncharacterized protein n 1 tax glycine max repid k7mcz5_soybn; score=559.30; evalue=0.00e+00;
c39331/f2p1/2088	importin subunit alpha n 1 tax solanum lycopersicum repid k4awf0_sollc; score=1043.88; evalue=0.00e+00;
c39331/f2p1/2088	importin subunit alpha n 1 tax capsicum annuum repid q94ka9_capan; score=1010.36; evalue=0.00e+00;
c39331/f2p1/2088	importin subunit alpha n 1 tax nicotiana benthamiana repid a1yul9_nicbe; score=1007.67; evalue=0.00e+00;
c39331/f2p1/2088	importin subunit alpha n 1 tax vitis vinifera repid d7sy66_vitvi; score=944.11; evalue=0.00e+00;
c39331/f2p1/2088	importin subunit alpha n 1 tax glycine max repid i1mrn6_soybn; score=943.73; evalue=0.00e+00;
c40086/f1p3/1777	uncharacterized protein n 1 tax solanum lycopersicum repid k4bw48_sollc; score=895.58; evalue=0.00e+00;
c40086/f1p3/1777	predicted protein n 2 tax populus trichocarpa repid b9hlt0_poptr; score=680.63; evalue=0.00e+00;
c40086/f1p3/1777	putative uncharacterized protein n 1 tax vitis vinifera repid f6hhv8_vitvi; score=667.54; evalue=0.00e+00;
c40086/f1p3/1777	uncharacterized protein n 2 tax glycine max repid i1kxe1_soybn; score=664.46; evalue=0.00e+00;
c40086/f1p3/1777	polygalacturonase putative n 1 tax ricinus communis repid b9sh92_ricco; score=661.76; evalue=0.00e+00;
c40308/f1p1/1800	uncharacterized protein n 1 tax solanum lycopersicum repid k4bb52_sollc; score=759.60; evalue=0.00e+00;
c40308/f1p1/1800	uncharacterized protein n 1 tax coffea canephora repid i6m4g8_cofca; score=551.59; evalue=0.00e+00;
c40308/f1p1/1800	putative uncharacterized protein n 1 tax vitis vinifera repid d7spf5_vitvi; score=551.21; evalue=0.00e+00;
c40308/f1p1/1800	putative uncharacterized protein n 1 tax ricinus communis repid b9s6i8_ricco; score=527.71; evalue=1.96e-179;
c40308/f1p1/1800	predicted protein (fragment) n 1 tax populus trichocarpa repid b9hev9_poptr; score=523.47; evalue=4.27e-178;
c40432/f1p2/1687	uncharacterized protein n 1 tax solanum lycopersicum repid k4bzn9_sollc; score=852.82; evalue=0.00e+00;
c40432/f1p2/1687	putative uncharacterized protein n 1 tax vitis vinifera repid f6i1p2_vitvi; score=458.76; evalue=4.86e-153;
c40432/f1p2/1687	putative uncharacterized protein n 1 tax ricinus communis repid b9rfw9_ricco; score=423.70; evalue=2.35e-139;
c40432/f1p2/1687	col domain class transcription factor n 1 tax malus x domestica repid d9ziw6_maldo; score=404.06; evalue=1.48e-131;
c40432/f1p2/1687	predicted protein n 1 tax populus trichocarpa repid b9gzb7_poptr; score=389.42; evalue=9.64e-127;
c41074/f1p4/2236	putative uncharacterized protein n 1 tax vitis vinifera repid d7tfc0_vitvi; score=1188.71; evalue=0.00e+00;
c41074/f1p4/2236	uncharacterized protein n 1 tax solanum lycopersicum repid k4cmq3_sollc; score=1183.70; evalue=0.00e+00;
c41074/f1p4/2236	abc transporter e family member 2 n 1 tax arabidopsis thaliana repid ab2e_arath; score=1175.23; evalue=0.00e+00;
c41074/f1p4/2236	putative uncharacterized protein n 1 tax picea sitchensis repid b8lr96_picsi; score=1174.46; evalue=0.00e+00;
c41074/f1p4/2236	putative uncharacterized protein n 1 tax vitis vinifera repid a5bqn0_vitvi; score=1172.53; evalue=0.00e+00;

c41097/f4p4/1989	uncharacterized protein n 1 tax solanum lycopersicum repid k4bdc5_sollc; score=1146.34; evalue=0.00e+00;
c41097/f4p4/1989	uncharacterized protein n 1 tax solanum lycopersicum repid k4bg62_sollc; score=1011.52; evalue=0.00e+00;
c41097/f4p4/1989	predicted protein n 1 tax populus trichocarpa repid b9h6h6_poptr; score=1010.75; evalue=0.00e+00;
c41097/f4p4/1989	putative uncharacterized protein n 1 tax vitis vinifera repid f6h4j6_vitvi; score=993.80; evalue=0.00e+00;
c41097/f4p4/1989	predicted protein n 1 tax populus trichocarpa repid b9hha8_poptr; score=993.42; evalue=0.00e+00;
c41377/f3p5/2058	isoform 2 of serine/threonine-protein phosphatase 5 n 1 tax solanum lycopersicum repid q84k11-2; score=1001.12; evalue=0.00e+00;
c41377/f3p5/2058	serine/threonine protein phosphatase 5 n 1 tax solanum torvum repid g1aqh6_9soln; score=986.87; evalue=0.00e+00;
c41377/f3p5/2058	uncharacterized protein n 1 tax solanum lycopersicum repid k4cgb9_sollc; score=976.47; evalue=0.00e+00;
c41377/f3p5/2058	serine/threonine-protein phosphatase 5 n 1 tax nicotiana tabacum repid g5elz4_tobac; score=971.46; evalue=0.00e+00;
c41377/f3p5/2058	predicted protein n 1 tax populus trichocarpa repid b9ia45_poptr; score=915.99; evalue=0.00e+00;
c41883/f3p0/1898	3-ketoacyl-coa synthase n 1 tax solanum tuberosum repid b7ssk0_soltu; score=1026.54; evalue=0.00e+00;
c41883/f3p0/1898	3-ketoacyl-coa synthase n 1 tax solanum lycopersicum repid k4bb98_sollc; score=1020.76; evalue=0.00e+00;
c41883/f3p0/1898	3-ketoacyl-coa synthase n 1 tax solanum lycopersicum repid c6kh60_sollc; score=1008.44; evalue=0.00e+00;
c41883/f3p0/1898	3-ketoacyl-coa synthase n 1 tax solanum lycopersicum repid k4b6k1_sollc; score=921.77; evalue=0.00e+00;
c41883/f3p0/1898	3-ketoacyl-coa synthase n 1 tax arachis hypogaea repid i1e3d2_arahy; score=909.83; evalue=0.00e+00;
c42234/f1p0/1859	uncharacterized protein n 1 tax solanum lycopersicum repid k4c1t2_sollc; score=922.54; evalue=0.00e+00;
c42234/f1p0/1859	uncharacterized protein n 1 tax solanum lycopersicum repid k4c5s4_sollc; score=907.90; evalue=0.00e+00;
c42234/f1p0/1859	uncharacterized protein n 1 tax solanum lycopersicum repid k4bj22_sollc; score=898.27; evalue=0.00e+00;
c42234/f1p0/1859	methylcrotonyl-coa carboxylase alpha-subunit liud n 1 tax pseudomonas chlororaphis o6 repid i4y340_9psed; score=863.99; evalue=0.00e+00;
c42234/f1p0/1859	clathrin heavy chain (fragment) n 1 tax leucaena leucocephala repid k4pbu4_leule; score=865.91; evalue=0.00e+00;
c42786/f5p3/1724	uncharacterized protein n 1 tax solanum lycopersicum repid k4asc1_sollc; score=848.20; evalue=0.00e+00;
c42786/f5p3/1724	predicted protein n 2 tax populus trichocarpa repid b9gy58_poptr; score=715.30; evalue=0.00e+00;
c42786/f5p3/1724	predicted protein (fragment) n 1 tax populus trichocarpa repid b9gld1_poptr; score=713.76; evalue=0.00e+00;
c42786/f5p3/1724	putative uncharacterized protein n 2 tax vitis vinifera repid a5bph6_vitvi; score=713.76; evalue=0.00e+00;
c42786/f5p3/1724	uncharacterized protein n 1 tax glycine max repid i1ksp0_soybn; score=711.45; evalue=0.00e+00;
c42799/f2p2/940	uncharacterized protein n 1 tax solanum lycopersicum repid k4bcj1_sollc; score=468.00; evalue=5.52e-164;
c42799/f2p2/940	uncharacterized protein n 1 tax glycine max repid i1k1r5_soybn; score=315.08; evalue=7.21e-104;
c42799/f2p2/940	50s ribosomal protein l25 putative n 1 tax ricinus communis repid b9s8k5_ricco; score=313.54; evalue=4.00e-103;
c42799/f2p2/940	putative uncharacterized protein (fragment) n 1 tax vitis vinifera repid f6hju4_vitvi; score=305.83; evalue=3.31e-100;
c42799/f2p2/940	50s ribosomal protein l25 n 1 tax medicago truncatula repid g7lgd1_medtr; score=305.06; evalue=9.13e-100;
c42892/f2p2/1777	uncharacterized protein n 1 tax solanum lycopersicum repid k4cf87_sollc; score=947.19; evalue=0.00e+00;

c42892/f2p2/1777	aspartic protease n 1 tax nicotiana tabacum repid c3pts5_tobac; score=882.48; evalue=0.00e+00;
c42892/f2p2/1777	predicted protein n 1 tax populus trichocarpa repid b9gje2_poptr; score=743.42; evalue=0.00e+00;
c42892/f2p2/1777	cyprosin n 2 tax cynara cardunculus repid q39476_cynca; score=738.80; evalue=0.00e+00;
c42892/f2p2/1777	preprocirsin n 1 tax cirsium vulgare repid h6uwy9_cirvu; score=737.64; evalue=0.00e+00;
c44609/f29p37/1701	uncharacterized protein n 1 tax solanum lycopersicum repid k4dh64_sollc; score=918.30; evalue=0.00e+00;
c44609/f29p37/1701	cysteine protease n 1 tax solanum lycopersicum repid q18lc4_sollc; score=916.38; evalue=0.00e+00;
c44609/f29p37/1701	vascular processing enzyme-3 n 1 tax capsicum annuum repid b2czk0_capan; score=870.54; evalue=0.00e+00;
c44609/f29p37/1701	vacuolar processing enzyme-3 n 1 tax nicotiana tabacum repid q852t0_tobac; score=866.68; evalue=0.00e+00;
c44609/f29p37/1701	vacuolar processing enzyme-1b n 1 tax nicotiana tabacum repid q852t2_tobac; score=798.89; evalue=0.00e+00;
c45508/f9p9/3337	putative uncharacterized protein n 1 tax vitis vinifera repid f6huc5_vitvi; score=1053.89; evalue=0.00e+00;
c45508/f9p9/3337	uncharacterized protein n 1 tax glycine max repid i1k6i4_soybn; score=1006.13; evalue=0.00e+00;
c45508/f9p9/3337	uncharacterized protein n 1 tax glycine max repid k7l4e7_soybn; score=991.88; evalue=0.00e+00;
c45508/f9p9/3337	putative uncharacterized protein n 1 tax vitis vinifera repid a5bh78_vitvi; score=968.38; evalue=0.00e+00;
c45508/f9p9/3337	predicted protein (fragment) n 1 tax populus trichocarpa repid b9gkh5_poptr; score=960.67; evalue=0.00e+00;
c45730/f29p10/1449	uncharacterized protein n 1 tax solanum lycopersicum repid k4azn5_sollc; score=648.66; evalue=0.00e+00;
c45730/f29p10/1449	bypass1 n 1 tax nicotiana benthamiana repid a9lm04_nicbe; score=644.04; evalue=0.00e+00;
c45730/f29p10/1449	putative uncharacterized protein n 1 tax solanum tuberosum repid q38hv7_soltu; score=562.76; evalue=0.00e+00;
c45730/f29p10/1449	bypass2 n 1 tax nicotiana benthamiana repid a9lm03_nicbe; score=516.92; evalue=6.46e-179;
c45730/f29p10/1449	putative uncharacterized protein in35 n 1 tax ipomoea nil repid a2pzf0_iponi; score=452.21; evalue=1.82e-153;
c45746/f8p7/2965	alpha-glucan phosphorylase h isozyme n 2 tax solanum tuberosum repid phsh_soltu; score=1659.81; evalue=0.00e+00;
c45746/f8p7/2965	phosphorylase n 1 tax solanum lycopersicum repid k4csq2_sollc; score=1617.05; evalue=0.00e+00;
c45746/f8p7/2965	phosphorylase n 1 tax populus trichocarpa repid b9hp81_poptr; score=1462.20; evalue=0.00e+00;
c45746/f8p7/2965	phosphorylase n 1 tax ricinus communis repid b9s366_ricco; score=1457.58; evalue=0.00e+00;
c45746/f8p7/2965	phosphorylase n 1 tax vitis vinifera repid d7sk33_vitvi; score=1457.20; evalue=0.00e+00;
c45766/f9p7/3503	uncharacterized protein n 1 tax solanum lycopersicum repid k4bnn5_sollc; score=1381.70; evalue=0.00e+00;
c45766/f9p7/3503	putative uncharacterized protein n 1 tax vitis vinifera repid f6hua4_vitvi; score=986.48; evalue=0.00e+00;
c45766/f9p7/3503	nucleoporin 98 n 1 tax daucus carota repid a9zp15_dauca; score=907.13; evalue=0.00e+00;
c45766/f9p7/3503	predicted protein n 1 tax populus trichocarpa repid b9i0p2_poptr; score=793.50; evalue=0.00e+00;
c45766/f9p7/3503	uncharacterized protein n 1 tax glycine max repid i1lvb2_soybn; score=770.00; evalue=0.00e+00;
c45970/f11p7/3645	uncharacterized protein n 1 tax solanum lycopersicum repid k4c245_sollc; score=1819.28; evalue=0.00e+00;
c45970/f11p7/3645	uncharacterized protein n 1 tax solanum lycopersicum repid k4cwk1_sollc; score=1654.42; evalue=0.00e+00;

c45970/f11p7/3645	putative 26s proteasome subunit rpn2a n 1 tax capsicum chinense repid b1q487_capch; score=1624.37; evalue=0.00e+00;
c45970/f11p7/3645	putative uncharacterized protein n 1 tax vitis vinifera repid d7tew7_vitvi; score=1558.89; evalue=0.00e+00;
c45970/f11p7/3645	putative uncharacterized protein n 2 tax vitis vinifera repid a5bg30_vitvi; score=1527.69; evalue=0.00e+00;
c46146/f4p5/3202	uncharacterized protein n 1 tax solanum lycopersicum repid k4bvn8_sollc; score=1735.31; evalue=0.00e+00;
c46146/f4p5/3202	putative uncharacterized protein n 1 tax vitis vinifera repid f6h1m3_vitvi; score=1241.48; evalue=0.00e+00;
c46146/f4p5/3202	predicted protein n 1 tax populus trichocarpa repid b9h500_poptr; score=1205.28; evalue=0.00e+00;
c46146/f4p5/3202	receptor protein kinase clavata1 putative n 1 tax ricinus communis repid b9r8b4_ricco; score=1198.34; evalue=0.00e+00;
c46146/f4p5/3202	clavata1 n 2 tax brassica napus repid d4nzh8_brana; score=1164.44; evalue=0.00e+00;
c46263/f6p5/3286	uncharacterized protein n 1 tax solanum lycopersicum repid k4bp20_sollc; score=1539.24; evalue=0.00e+00;
c46263/f6p5/3286	putative uncharacterized protein n 1 tax vitis vinifera repid d7tc86_vitvi; score=1303.50; evalue=0.00e+00;
c46263/f6p5/3286	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7kri4_arall; score=1232.24; evalue=0.00e+00;
c46263/f6p5/3286	sec34-like protein n 1 tax arabidopsis thaliana repid f4hq84_arath; score=1230.31; evalue=0.00e+00;
c46263/f6p5/3286	at1g73430/t9l24_16 n 1 tax arabidopsis thaliana repid q8l744_arath; score=1227.23; evalue=0.00e+00;
c46664/f3p3/3573	uncharacterized protein n 1 tax solanum lycopersicum repid k4bjd6_sollc; score=963.37; evalue=0.00e+00;
c46664/f3p3/3573	putative uncharacterized protein n 1 tax vitis vinifera repid f6hee0_vitvi; score=310.07; evalue=2.14e-144;
c46664/f3p3/3573	putative uncharacterized protein n 1 tax vitis vinifera repid f6hee0_vitvi; score=232.26; evalue=2.14e-144;
c46664/f3p3/3573	atp binding protein putative n 1 tax ricinus communis repid b9s250_ricco; score=283.49; evalue=5.96e-131;
c46664/f3p3/3573	atp binding protein putative n 1 tax ricinus communis repid b9s250_ricco; score=214.16; evalue=5.96e-131;
c46744/f4p2/3377	uncharacterized protein n 1 tax solanum lycopersicum repid k4ddz1_sollc; score=1534.62; evalue=0.00e+00;
c46744/f4p2/3377	uncharacterized protein n 1 tax solanum lycopersicum repid k4bbf9_sollc; score=956.05; evalue=0.00e+00;
c46744/f4p2/3377	putative uncharacterized protein n 1 tax vitis vinifera repid f6hux2_vitvi; score=799.27; evalue=0.00e+00;
c46744/f4p2/3377	rrm/rnp domain putative n 1 tax ricinus communis repid b9sf86_ricco; score=762.68; evalue=0.00e+00;
c46744/f4p2/3377	predicted protein n 1 tax populus trichocarpa repid b9ijm5_poptr; score=731.48; evalue=0.00e+00;
c46775/f4p2/2623	uncharacterized protein n 1 tax solanum lycopersicum repid k4asg2_sollc; score=909.44; evalue=0.00e+00;
c46775/f4p2/2623	putative uncharacterized protein n 1 tax vitis vinifera repid f6hlf4_vitvi; score=855.51; evalue=0.00e+00;
c46775/f4p2/2623	putative uncharacterized protein n 1 tax vitis vinifera repid a5b299_vitvi; score=854.36; evalue=0.00e+00;
c46775/f4p2/2623	uncharacterized protein n 1 tax solanum lycopersicum repid k4bgk0_sollc; score=809.29; evalue=0.00e+00;
c46775/f4p2/2623	predicted protein (fragment) n 1 tax populus trichocarpa repid b9glh4_poptr; score=801.97; evalue=0.00e+00;
c46812/f4p3/3611	ethylene receptor homolog n 1 tax solanum lycopersicum repid q9xet9_sollc; score=1447.18; evalue=0.00e+00;
c46812/f4p3/3611	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2i4_sollc; score=1180.24; evalue=0.00e+00;
c46812/f4p3/3611	putative ethylene receptor n 1 tax nicotiana tabacum repid q9sdy2_tobac; score=1160.21; evalue=0.00e+00;

c46812/f4p3/3611	ethylene receptor n 2 tax coffea repid c0iln8_cofca; score=1129.39; evalue=0.00e+00;
c46812/f4p3/3611	ethylene receptor n 1 tax coffea canephora repid d7ric8_cofca; score=1122.46; evalue=0.00e+00;
c46840/f2p0/1469	uncharacterized protein n 1 tax solanum lycopersicum repid k4cxw2_sollc; score=610.91; evalue=0.00e+00;
c46840/f2p0/1469	predicted protein (fragment) n 1 tax populus trichocarpa repid b9n011_poptr; score=401.36; evalue=8.49e-133;
c46840/f2p0/1469	putative uncharacterized protein n 1 tax vitis vinifera repid a5cbp2_vitvi; score=396.74; evalue=1.43e-130;
c46840/f2p0/1469	leucine-rich repeat family protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7ljd1_arall; score=382.49; evalue=2.33e-124;
c46840/f2p0/1469	n 1 tax arabidopsis thaliana repid q9sjh6_arath; score=379.41; evalue=2.93e-123;
c46961/f2p1/1547	uncharacterized protein n 1 tax solanum lycopersicum repid k4bxy4_sollc; score=680.63; evalue=0.00e+00;
c46961/f2p1/1547	dna binding protein putative n 1 tax ricinus communis repid b9rcx3_ricco; score=478.40; evalue=1.63e-163;
c46961/f2p1/1547	putative uncharacterized protein n 1 tax vitis vinifera repid d7t9t0_vitvi; score=459.91; evalue=4.27e-156;
c46961/f2p1/1547	uncharacterized protein n 1 tax glycine max repid i1jeb0_soybn; score=441.81; evalue=3.10e-149;
c46961/f2p1/1547	putative uncharacterized protein n 1 tax vitis vinifera repid a5ay99_vitvi; score=464.92; evalue=7.73e-149;
c47073/f2p0/2747	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmh6_sollc; score=1578.53; evalue=0.00e+00;
c47073/f2p0/2747	uncharacterized protein n 1 tax solanum lycopersicum repid k4c7u7_sollc; score=1466.83; evalue=0.00e+00;
c47073/f2p0/2747	uncharacterized protein n 1 tax solanum lycopersicum repid k4df88_sollc; score=1435.62; evalue=0.00e+00;
c47073/f2p0/2747	coatomer beta subunit putative n 1 tax ricinus communis repid b9sqc0_ricco; score=1390.56; evalue=0.00e+00;
c47073/f2p0/2747	uncharacterized protein n 1 tax glycine max repid k7m8y1_soybn; score=1387.47; evalue=0.00e+00;
c47179/f2p2/2784	uncharacterized protein n 1 tax solanum lycopersicum repid k4csi8_sollc; score=1372.45; evalue=0.00e+00;
c47179/f2p2/2784	putative uncharacterized protein n 1 tax vitis vinifera repid f6hzl0_vitvi; score=831.63; evalue=0.00e+00;
c47179/f2p2/2784	predicted protein n 1 tax populus trichocarpa repid b9gs07_poptr; score=765.38; evalue=0.00e+00;
c47179/f2p2/2784	predicted protein n 1 tax populus trichocarpa repid b9h8n4_poptr; score=764.99; evalue=0.00e+00;
c47179/f2p2/2784	ubiquitin-protein ligase putative n 1 tax ricinus communis repid b9t1b5_ricco; score=743.42; evalue=0.00e+00;
c47714/f2p1/1629	uncharacterized protein n 1 tax solanum lycopersicum repid k4axl6_sollc; score=673.32; evalue=0.00e+00;
c47714/f2p1/1629	protein c9orf114 putative n 1 tax ricinus communis repid b9rty3_ricco; score=494.97; evalue=4.11e-169;
c47714/f2p1/1629	predicted protein n 1 tax populus trichocarpa repid b9hju9_poptr; score=494.20; evalue=8.92e-169;
c47714/f2p1/1629	putative uncharacterized protein n 1 tax vitis vinifera repid d7t6u1_vitvi; score=491.89; evalue=5.26e-168;
c47714/f2p1/1629	putative uncharacterized protein n 1 tax vitis vinifera repid a5asc7_vitvi; score=491.50; evalue=8.49e-168;
c47941/f1p5/3889	uncharacterized protein n 1 tax solanum lycopersicum repid k4b8r1_sollc; score=1202.96; evalue=0.00e+00;
c47941/f1p5/3889	uncharacterized protein n 1 tax solanum lycopersicum repid k4b8r1_sollc; score=749.58; evalue=0.00e+00;
c47941/f1p5/3889	putative uncharacterized protein n 1 tax ricinus communis repid b9s9b2_ricco; score=218.01; evalue=1.62e-73;
c47941/f1p5/3889	putative uncharacterized protein n 1 tax ricinus communis repid b9s9b2_ricco; score=88.58; evalue=1.62e-73;

c47941/f1p5/3889	uncharacterized protein n 1 tax glycine max repid i1k3z5_soybn; score=159.84; evalue=2.72e-57;
c48221/f4p5/3334	trehalose-phosphate synthase 1 n 1 tax solanum lycopersicum repid a6miz0_sollc; score=1842.01; evalue=0.00e+00;
c48221/f4p5/3334	trehalose 6-phosphate synthase n 1 tax nicotiana tabacum repid d4qak4_tobac; score=1741.86; evalue=0.00e+00;
c48221/f4p5/3334	trehalose-6-phosphate synthase n 1 tax petunia x hybrida repid e2jjg8_pethy; score=1737.24; evalue=0.00e+00;
c48221/f4p5/3334	trehalose-6-phosphate synthase n 1 tax camellia sinensis repid i1yp72_camsi; score=1566.59; evalue=0.00e+00;
c48221/f4p5/3334	predicted protein n 2 tax populus trichocarpa repid b9n7r9_poptr; score=1516.90; evalue=0.00e+00;
c48257/f5p2/3093	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmw0_sollc; score=1455.27; evalue=0.00e+00;
c48257/f5p2/3093	putative uncharacterized protein n 1 tax vitis vinifera repid f6hy19_vitvi; score=877.09; evalue=0.00e+00;
c48257/f5p2/3093	putative uncharacterized protein n 1 tax vitis vinifera repid f6hgv9_vitvi; score=816.99; evalue=0.00e+00;
c48257/f5p2/3093	protein kinase n 1 tax cucumis melo subsp. melo repid e5gcb1_cucme; score=796.96; evalue=0.00e+00;
c48257/f5p2/3093	predicted protein n 1 tax populus trichocarpa repid b9mws7_poptr; score=785.02; evalue=0.00e+00;
c48425/f1p3/2021	uncharacterized protein n 1 tax solanum lycopersicum repid k4bn60_sollc; score=929.09; evalue=0.00e+00;
c48425/f1p3/2021	alanine aminotransferase n 1 tax capsicum annuum repid q6vej5_capan; score=893.65; evalue=0.00e+00;
c48425/f1p3/2021	uncharacterized protein n 1 tax solanum lycopersicum repid k4c740_sollc; score=890.18; evalue=0.00e+00;
c48425/f1p3/2021	uncharacterized protein n 1 tax solanum lycopersicum repid k4bn59_sollc; score=865.53; evalue=0.00e+00;
c48425/f1p3/2021	predicted protein n 1 tax populus trichocarpa repid b9gxz6_poptr; score=861.29; evalue=0.00e+00;
c48679/f1p3/2943	uncharacterized protein n 1 tax solanum lycopersicum repid k4cnj1_sollc; score=1741.86; evalue=0.00e+00;
c48679/f1p3/2943	putative uncharacterized protein n 1 tax ricinus communis repid b9szp1_ricco; score=996.88; evalue=0.00e+00;
c48679/f1p3/2943	predicted protein n 1 tax populus trichocarpa repid b9gyl7_poptr; score=984.94; evalue=0.00e+00;
c48679/f1p3/2943	hos1 n 1 tax citrus trifoliata repid d6bp27_pontr; score=956.05; evalue=0.00e+00;
c48679/f1p3/2943	putative uncharacterized protein n 1 tax vitis vinifera repid f6hjp8_vitvi; score=953.36; evalue=0.00e+00;
c48912/f2p2/3193	uncharacterized protein n 1 tax solanum lycopersicum repid k4ch16_sollc; score=1330.85; evalue=0.00e+00;
c48912/f2p2/3193	wd-repeat protein putative n 1 tax ricinus communis repid b9t7m5_ricco; score=933.32; evalue=0.00e+00;
c48912/f2p2/3193	predicted protein n 1 tax populus trichocarpa repid b9hzx5_poptr; score=924.47; evalue=0.00e+00;
c48912/f2p2/3193	predicted protein n 1 tax populus trichocarpa repid b9n1k2_poptr; score=920.61; evalue=0.00e+00;
c48912/f2p2/3193	putative uncharacterized protein n 1 tax vitis vinifera repid f6h267_vitvi; score=910.21; evalue=0.00e+00;
c49136/f2p7/3222	uncharacterized protein n 1 tax solanum lycopersicum repid k4dd60_sollc; score=1434.47; evalue=0.00e+00;
c49136/f2p7/3222	putative uncharacterized protein n 1 tax ricinus communis repid b9ri49_ricco; score=807.75; evalue=0.00e+00;
c49136/f2p7/3222	predicted protein n 1 tax populus trichocarpa repid b9i0j7_poptr; score=803.13; evalue=0.00e+00;
c49136/f2p7/3222	putative uncharacterized protein n 1 tax vitis vinifera repid a5c725_vitvi; score=787.72; evalue=0.00e+00;
c49136/f2p7/3222	putative uncharacterized protein n 1 tax vitis vinifera repid f6htj0_vitvi; score=783.48; evalue=0.00e+00;

c49316/f1p5/3068	dnaj-like protein n 1 tax solanum tuberosum repid q38ht9_soltu; score=666.38; evalue=0.00e+00;
c49316/f1p5/3068	dnaj-like protein n 1 tax solanum tuberosum repid q38ht9_soltu; score=665.23; evalue=0.00e+00;
c49316/f1p5/3068	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2j3_sollc; score=659.45; evalue=0.00e+00;
c49316/f1p5/3068	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2j3_sollc; score=658.29; evalue=0.00e+00;
c49316/f1p5/3068	dnaj-like protein n 1 tax solanum tuberosum repid q38hu8_soltu; score=659.45; evalue=0.00e+00;
c49351/f1p3/3402	uncharacterized protein n 1 tax solanum lycopersicum repid k4d5q0_sollc; score=1052.35; evalue=0.00e+00;
c49351/f1p3/3402	uncharacterized protein n 1 tax solanum lycopersicum repid k4d5q0_sollc; score=580.48; evalue=0.00e+00;
c49351/f1p3/3402	uncharacterized protein n 1 tax solanum lycopersicum repid k4d5q0_sollc; score=289.66; evalue=0.00e+00;
c49351/f1p3/3402	atp binding protein putative n 1 tax ricinus communis repid b9t2b2_ricco; score=750.36; evalue=0.00e+00;
c49351/f1p3/3402	atp binding protein putative n 1 tax ricinus communis repid b9t2b2_ricco; score=261.54; evalue=0.00e+00;
c49642/f1p2/1326	uncharacterized protein n 1 tax solanum lycopersicum repid k4cv23_sollc; score=439.50; evalue=1.10e-148;
c49642/f1p2/1326	uncharacterized protein n 1 tax glycine max repid i1lf96_soybn; score=226.10; evalue=2.38e-66;
c49642/f1p2/1326	uncharacterized protein n 1 tax glycine max repid i1nf47_soybn; score=224.17; evalue=1.21e-65;
c49642/f1p2/1326	zinc finger protein putative n 1 tax ricinus communis repid b9r8b0_ricco; score=224.17; evalue=2.42e-65;
c49642/f1p2/1326	putative uncharacterized protein n 1 tax vitis vinifera repid a5bx64_vitvi; score=218.39; evalue=2.23e-63;
c49795/f1p2/2980	uncharacterized protein n 1 tax solanum lycopersicum repid k4cn26_sollc; score=1706.03; evalue=0.00e+00;
c49795/f1p2/2980	putative uncharacterized protein n 1 tax vitis vinifera repid f6ht67_vitvi; score=1513.05; evalue=0.00e+00;
c49795/f1p2/2980	predicted protein n 1 tax populus trichocarpa repid b9gza1_poptr; score=1501.49; evalue=0.00e+00;
c49795/f1p2/2980	putative uncharacterized protein n 1 tax vitis vinifera repid a5c0j5_vitvi; score=1488.01; evalue=0.00e+00;
c49795/f1p2/2980	uncharacterized protein n 1 tax glycine max repid i1nfn9_soybn; score=1443.33; evalue=0.00e+00;
c49919/f4p2/2276	uncharacterized protein n 1 tax solanum lycopersicum repid k4cf51_sollc; score=1423.30; evalue=0.00e+00;
c49919/f4p2/2276	putative uncharacterized protein n 1 tax vitis vinifera repid f6hk83_vitvi; score=1226.85; evalue=0.00e+00;
c49919/f4p2/2276	putative uncharacterized protein n 1 tax vitis vinifera repid a5ak91_vitvi; score=1217.60; evalue=0.00e+00;
c49919/f4p2/2276	putative uncharacterized protein n 1 tax vitis vinifera repid f6hk91_vitvi; score=1201.81; evalue=0.00e+00;
c49919/f4p2/2276	predicted protein n 1 tax populus trichocarpa repid b9ijr9_poptr; score=1172.92; evalue=0.00e+00;
c49931/f1p0/3378	uncharacterized protein n 1 tax solanum lycopersicum repid k4d2f8_sollc; score=1372.84; evalue=0.00e+00;
c49931/f1p0/3378	uncharacterized protein n 1 tax solanum lycopersicum repid k4bq62_sollc; score=1135.17; evalue=0.00e+00;
c49931/f1p0/3378	predicted protein n 1 tax populus trichocarpa repid b9ii76_poptr; score=1079.70; evalue=0.00e+00;
c49931/f1p0/3378	putative uncharacterized protein n 1 tax vitis vinifera repid a5aj32_vitvi; score=1074.69; evalue=0.00e+00;
c49931/f1p0/3378	predicted protein n 1 tax populus trichocarpa repid b9h9v2_poptr; score=1061.21; evalue=0.00e+00;
c49947/f1p1/3478	uncharacterized protein n 1 tax solanum lycopersicum repid k4cms0_sollc; score=1145.57; evalue=0.00e+00;

c49947/f1p1/3478	uncharacterized protein n 1 tax solanum lycopersicum repid k4cms0_sollc; score=926.01; evalue=0.00e+00;
c49947/f1p1/3478	putative uncharacterized protein n 1 tax vitis vinifera repid d7u407_vitvi; score=930.63; evalue=0.00e+00;
c49947/f1p1/3478	putative uncharacterized protein n 1 tax vitis vinifera repid d7u407_vitvi; score=733.41; evalue=0.00e+00;
c49947/f1p1/3478	neutral alpha-glucosidase ab putative n 1 tax ricinus communis repid b9s1m1_ricco; score=883.63; evalue=0.00e+00;
c49993/f2p2/2345	uncharacterized protein n 1 tax solanum lycopersicum repid k4bi85_sollc; score=1253.81; evalue=0.00e+00;
c49993/f2p2/2345	soluble starch synthase 1 chloroplastic/amyloplastic n 1 tax solanum tuberosum repid ssy1_soltu; score=1218.37; evalue=0.00e+00;
c49993/f2p2/2345	single-stranded-dna-specific exonuclease recj n 1 tax helicobacter pylori hp a-9 repid j0jxm0_helpx; score=1036.94; evalue=0.00e+00;
c49993/f2p2/2345	predicted protein n 1 tax populus trichocarpa repid b9idq2_poptr; score=902.51; evalue=0.00e+00;
c49993/f2p2/2345	starch synthase isoform i n 1 tax manihot esculenta repid b3srp2_manes; score=887.49; evalue=0.00e+00;
c50001/f3p9/3254	uncharacterized protein n 1 tax solanum lycopersicum repid k4b7r1_sollc; score=1698.72; evalue=0.00e+00;
c50001/f3p9/3254	putative uncharacterized protein n 1 tax vitis vinifera repid f6hit8_vitvi; score=954.12; evalue=0.00e+00;
c50001/f3p9/3254	putative uncharacterized protein n 1 tax vitis vinifera repid a5asg4_vitvi; score=947.96; evalue=0.00e+00;
c50001/f3p9/3254	predicted protein n 1 tax populus trichocarpa repid b9icj7_poptr; score=826.62; evalue=0.00e+00;
c50001/f3p9/3254	predicted protein n 1 tax populus trichocarpa repid b9na50_poptr; score=823.54; evalue=0.00e+00;
c50039/f1p8/3464	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmh6_sollc; score=1828.53; evalue=0.00e+00;
c50039/f1p8/3464	uncharacterized protein n 1 tax solanum lycopersicum repid k4c7u7_sollc; score=1703.72; evalue=0.00e+00;
c50039/f1p8/3464	uncharacterized protein n 1 tax solanum lycopersicum repid k4df88_sollc; score=1670.21; evalue=0.00e+00;
c50039/f1p8/3464	coatomer beta subunit putative n 1 tax ricinus communis repid b9sqc0_ricco; score=1628.22; evalue=0.00e+00;
c50039/f1p8/3464	uncharacterized protein n 1 tax glycine max repid k7m8y1_soybn; score=1627.45; evalue=0.00e+00;
c50115/f1p6/3204	uncharacterized protein n 1 tax solanum lycopersicum repid k4cmv1_sollc; score=1606.65; evalue=0.00e+00;
c50115/f1p6/3204	putative uncharacterized protein n 1 tax vitis vinifera repid f6i092_vitvi; score=1043.11; evalue=0.00e+00;
c50115/f1p6/3204	putative uncharacterized protein n 1 tax vitis vinifera repid a5aqn6_vitvi; score=1036.56; evalue=0.00e+00;
c50115/f1p6/3204	replication factor a 1 rfa1 putative n 1 tax ricinus communis repid b9s1l9_ricco; score=904.05; evalue=0.00e+00;
c50115/f1p6/3204	predicted protein n 1 tax populus trichocarpa repid b9gzw2_poptr; score=860.14; evalue=0.00e+00;
c50178/f2p3/2436	translation elongation factor 2 n 1 tax prunus persica repid i3uih9_prupe; score=1463.74; evalue=0.00e+00;
c50178/f2p3/2436	uncharacterized protein n 2 tax glycine max repid i1ku21_soybn; score=1454.88; evalue=0.00e+00;
c50178/f2p3/2436	uncharacterized protein n 1 tax glycine max repid i1mj86_soybn; score=1454.11; evalue=0.00e+00;
c50178/f2p3/2436	eukaryotic translation elongation factor putative n 1 tax ricinus communis repid b9ri35_ricco; score=1453.73; evalue=0.00e+00;
c50178/f2p3/2436	putative uncharacterized protein n 1 tax vitis vinifera repid f6h4t7_vitvi; score=1453.34; evalue=0.00e+00;
c50284/f2p8/3597	uncharacterized protein n 1 tax solanum lycopersicum repid k4bjd6_sollc; score=1368.99; evalue=0.00e+00;
c50284/f2p8/3597	putative uncharacterized protein n 1 tax vitis vinifera repid f6hee0_vitvi; score=543.50; evalue=8.78e-173;

c50284/f2p8/3597	atp binding protein putative n 1 tax ricinus communis repid b9s250_ricco; score=501.52; evalue=5.98e-157;
c50284/f2p8/3597	predicted protein n 1 tax populus trichocarpa repid b9iph4_poptr; score=486.11; evalue=1.42e-153;
c50284/f2p8/3597	uncharacterized protein n 1 tax solanum lycopersicum repid k4c8z3_sollc; score=456.06; evalue=4.25e-140;
c50695/f2p0/1946	uncharacterized protein n 1 tax solanum lycopersicum repid k4b9i2_sollc; score=646.74; evalue=0.00e+00;
c50695/f2p0/1946	kinase putative n 1 tax ricinus communis repid b9rij8_ricco; score=528.09; evalue=5.24e-177;
c50695/f2p0/1946	putative uncharacterized protein n 1 tax vitis vinifera repid f6h837_vitvi; score=517.31; evalue=1.95e-172;
c50695/f2p0/1946	putative uncharacterized protein n 1 tax vitis vinifera repid f6hal7_vitvi; score=511.15; evalue=2.09e-170;
c50695/f2p0/1946	kinase putative n 1 tax ricinus communis repid b9rij6_ricco; score=511.15; evalue=1.65e-169;
c50766/f2p3/3052	uncharacterized protein n 1 tax solanum lycopersicum repid k4b092_sollc; score=1542.71; evalue=0.00e+00;
c50766/f2p3/3052	uncharacterized protein n 1 tax glycine max repid i1jrq3_soybn; score=573.16; evalue=0.00e+00;
c50766/f2p3/3052	predicted protein n 1 tax populus trichocarpa repid b9n9u6_poptr; score=570.85; evalue=0.00e+00;
c50766/f2p3/3052	predicted protein n 1 tax populus trichocarpa repid b9i5l1_poptr; score=560.84; evalue=3.41e-180;
c50766/f2p3/3052	uncharacterized protein n 1 tax glycine max repid k7n054_soybn; score=533.10; evalue=1.01e-170;
c51164/f1p2/1742	uncharacterized protein n 1 tax solanum lycopersicum repid k4ckq2_sollc; score=1023.46; evalue=0.00e+00;
c51164/f1p2/1742	cellulose synthase (fragment) n 1 tax solanum tuberosum repid q6xp44_soltu; score=1015.37; evalue=0.00e+00;
c51164/f1p2/1742	putative uncharacterized protein n 1 tax vitis vinifera repid f6h311_vitvi; score=963.75; evalue=0.00e+00;
c51164/f1p2/1742	putative uncharacterized protein n 1 tax vitis vinifera repid a5avi5_vitvi; score=962.60; evalue=0.00e+00;
c51164/f1p2/1742	cellulose synthase n 1 tax populus trichocarpa repid b9ikv7_poptr; score=961.06; evalue=0.00e+00;
c51358/f3p5/3513	uncharacterized protein n 1 tax solanum lycopersicum repid k4c9c5_sollc; score=1690.63; evalue=0.00e+00;
c51358/f3p5/3513	putative uncharacterized protein n 1 tax vitis vinifera repid f6hab9_vitvi; score=1111.29; evalue=0.00e+00;
c51358/f3p5/3513	predicted protein n 1 tax populus trichocarpa repid b9ghz6_poptr; score=1074.31; evalue=0.00e+00;
c51358/f3p5/3513	putative uncharacterized protein n 1 tax vitis vinifera repid f6hks3_vitvi; score=1035.40; evalue=0.00e+00;
c51358/f3p5/3513	uncharacterized protein n 1 tax glycine max repid k7lq39_soybn; score=1030.78; evalue=0.00e+00;
c51431/f1p1/2942	uncharacterized protein n 1 tax solanum lycopersicum repid k4dgc9_sollc; score=583.18; evalue=0.00e+00;
c51431/f1p1/2942	uncharacterized protein n 1 tax solanum lycopersicum repid k4dgc9_sollc; score=581.64; evalue=0.00e+00;
c51431/f1p1/2942	putative uncharacterized protein n 1 tax vitis vinifera repid f6h4f3_vitvi; score=300.06; evalue=8.81e-90;
c51431/f1p1/2942	putative uncharacterized protein n 1 tax vitis vinifera repid f6h4f3_vitvi; score=60.08; evalue=8.81e-90;
c51431/f1p1/2942	predicted protein n 1 tax populus trichocarpa repid b9h7f1_poptr; score=295.82; evalue=1.81e-84;
c51758/f2p3/2841	uncharacterized protein n 1 tax solanum lycopersicum repid k4d2w0_sollc; score=1335.86; evalue=0.00e+00;
c51758/f2p3/2841	putative uncharacterized protein n 1 tax vitis vinifera repid a5c016_vitvi; score=1202.96; evalue=0.00e+00;
c51758/f2p3/2841	putative uncharacterized protein n 1 tax vitis vinifera repid f6hlb3_vitvi; score=1198.73; evalue=0.00e+00;

c51758/f2p3/2841	casein kinase putative n 1 tax ricinus communis repid b9shg2_ricco; score=1197.57; evalue=0.00e+00;
c51758/f2p3/2841	uncharacterized protein n 1 tax glycine max repid i1ml29_soybn; score=1173.69; evalue=0.00e+00;
c51816/f1p0/1575	uncharacterized protein n 1 tax solanum lycopersicum repid k4b172_sollc; score=626.32; evalue=0.00e+00;
c51816/f1p0/1575	nad(p) transhydrogenase subunit alpha protein n 2 tax rhodanobacter repid i4wh70_9gamm; score=610.91; evalue=0.00e+00;
c51816/f1p0/1575	calreticulin n 1 tax nicotiana plumbaginifolia repid calr_nicpl; score=611.68; evalue=0.00e+00;
c51816/f1p0/1575	calreticulin n 1 tax nicotiana tabacum repid b5m6x8_tobac; score=607.06; evalue=0.00e+00;
c51816/f1p0/1575	tobacco calretulin (fragment) n 1 tax nicotiana tabacum repid q40567_tobac; score=598.59; evalue=0.00e+00;
c51862/f1p3/3285	uncharacterized protein n 1 tax solanum lycopersicum repid k4cpp9_sollc; score=1409.82; evalue=0.00e+00;
c51862/f1p3/3285	putative uncharacterized protein n 1 tax vitis vinifera repid d7ub46_vitvi; score=1146.34; evalue=0.00e+00;
c51862/f1p3/3285	cell division protein isolog n 1 tax arabidopsis thaliana repid o22993_arath; score=1139.79; evalue=0.00e+00;
c51862/f1p3/3285	predicted protein n 1 tax populus trichocarpa repid b9gl42_poptr; score=1137.09; evalue=0.00e+00;
c51862/f1p3/3285	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7m8z5_arall; score=1130.93; evalue=0.00e+00;
c52106/f3p7/2725	uncharacterized protein n 1 tax solanum lycopersicum repid k4d808_sollc; score=1230.31; evalue=0.00e+00;
c52106/f3p7/2725	putative uncharacterized protein n 1 tax vitis vinifera repid f6hn29_vitvi; score=599.74; evalue=0.00e+00;
c52106/f3p7/2725	uncharacterized protein n 1 tax glycine max repid k7k5e5_soybn; score=535.80; evalue=6.19e-174;
c52106/f3p7/2725	uncharacterized protein n 1 tax glycine max repid k7k5e4_soybn; score=531.18; evalue=3.82e-172;
c52106/f3p7/2725	nucleic acid binding protein putative n 1 tax ricinus communis repid b9shq3_ricco; score=522.70; evalue=9.91e-169;
c52122/f1p2/1361	uncharacterized protein n 1 tax solanum lycopersicum repid k4btt5_sollc; score=516.92; evalue=2.75e-180;
c52122/f1p2/1361	predicted protein n 1 tax populus trichocarpa repid b9h739_poptr; score=391.35; evalue=5.88e-131;
c52122/f1p2/1361	predicted protein n 1 tax populus trichocarpa repid a9p8j2_poptr; score=387.88; evalue=1.72e-129;
c52122/f1p2/1361	putative uncharacterized protein n 1 tax vitis vinifera repid a5btz9_vitvi; score=372.47; evalue=1.44e-123;
c52122/f1p2/1361	putative uncharacterized protein n 1 tax vitis vinifera repid f6h0p5_vitvi; score=370.16; evalue=1.87e-122;
c52384/f1p1/3305	uncharacterized protein n 1 tax solanum lycopersicum repid k4b440_sollc; score=1538.86; evalue=0.00e+00;
c52384/f1p1/3305	uncharacterized protein n 1 tax glycine max repid i1lf63_soybn; score=1283.09; evalue=0.00e+00;
c52384/f1p1/3305	uncharacterized protein n 1 tax glycine max repid i1nf81_soybn; score=1274.23; evalue=0.00e+00;
c52384/f1p1/3305	putative uncharacterized protein n 1 tax vitis vinifera repid d7u509_vitvi; score=1269.60; evalue=0.00e+00;
c52384/f1p1/3305	predicted protein n 1 tax populus trichocarpa repid b9h1l0_poptr; score=1249.57; evalue=0.00e+00;
c52449/f1p4/2743	uncharacterized protein n 1 tax solanum lycopersicum repid k4bd90_sollc; score=1369.76; evalue=0.00e+00;
c52449/f1p4/2743	lim domain kinase putative n 1 tax ricinus communis repid b9sg04_ricco; score=893.26; evalue=0.00e+00;
c52449/f1p4/2743	putative uncharacterized protein n 1 tax vitis vinifera repid f6hsy9_vitvi; score=889.03; evalue=0.00e+00;
c52449/f1p4/2743	predicted protein n 1 tax populus trichocarpa repid b9hh81_poptr; score=884.40; evalue=0.00e+00;

c52449/f1p4/2743	predicted protein n 1 tax populus trichocarpa repid b9h6k2_poptr; score=883.63; evalue=0.00e+00;
c52600/f1p4/3171	uncharacterized protein n 1 tax solanum lycopersicum repid k4b8i9_sollc; score=1705.26; evalue=0.00e+00;
c52600/f1p4/3171	trehalose-6-phosphate synthase putative n 1 tax ricinus communis repid b9s8d6_ricco; score=1477.61; evalue=0.00e+00;
c52600/f1p4/3171	putative uncharacterized protein n 1 tax vitis vinifera repid f6hmb8_vitvi; score=1471.45; evalue=0.00e+00;
c52600/f1p4/3171	trehalose-6-phosphate synthase n 1 tax cucumis melo subsp. melo repid e5gc29_cucme; score=1446.41; evalue=0.00e+00;
c52600/f1p4/3171	predicted protein n 1 tax populus trichocarpa repid b9h2e7_poptr; score=1441.79; evalue=0.00e+00;
c53095/f1p2/2026	uncharacterized protein n 1 tax solanum lycopersicum repid k4d3l4_sollc; score=358.99; evalue=8.94e-113;
c53095/f1p2/2026	uncharacterized protein n 1 tax solanum lycopersicum repid k4d3l4_sollc; score=330.87; evalue=6.07e-102;
c53095/f1p2/2026	uncharacterized protein n 2 tax glycine max repid k7lzm0_soybn; score=208.76; evalue=2.43e-91;
c53095/f1p2/2026	uncharacterized protein n 2 tax glycine max repid k7lzm0_soybn; score=155.99; evalue=2.43e-91;
c53095/f1p2/2026	uncharacterized protein n 1 tax glycine max repid i1na64_soybn; score=213.00; evalue=6.97e-90;
c53182/f1p15/3237	alpha-1 4 glucan phosphorylase l-2 isozyme chloroplastic/amyloplastic n 1 tax solanum tuberosum repid phsl2_soltu; score=1463.74; evalue=0.00e+00;
c53182/f1p15/3237	phosphorylase n 1 tax solanum lycopersicum repid k4bxx3_sollc; score=1447.57; evalue=0.00e+00;
c53182/f1p15/3237	phosphorylase n 1 tax vitis vinifera repid f6hf78_vitvi; score=1270.76; evalue=0.00e+00;
c53182/f1p15/3237	phosphorylase n 1 tax populus trichocarpa repid b9hxl0_poptr; score=1234.94; evalue=0.00e+00;
c53182/f1p15/3237	phosphorylase n 1 tax ricinus communis repid b9rcw0_ricco; score=1228.00; evalue=0.00e+00;
c53686/f1p2/1572	uncharacterized protein n 1 tax solanum lycopersicum repid k4b820_sollc; score=716.46; evalue=0.00e+00;
c53686/f1p2/1572	hop-interacting protein thi030 n 1 tax solanum lycopersicum repid g8z259_sollc; score=714.53; evalue=0.00e+00;
c53686/f1p2/1572	putative uncharacterized protein n 1 tax ricinus communis repid b9syi2_ricco; score=553.90; evalue=0.00e+00;
c53686/f1p2/1572	predicted protein n 1 tax populus trichocarpa repid b9gjg1_poptr; score=547.35; evalue=0.00e+00;
c53686/f1p2/1572	uncharacterized protein n 1 tax glycine max repid i1m1j3_soybn; score=511.53; evalue=1.38e-173;
c54587/f3p4/2967	uncharacterized protein n 1 tax solanum lycopersicum repid k4ct32_sollc; score=1407.12; evalue=0.00e+00;
c54587/f3p4/2967	transporter atm1 mitochondrial putative n 1 tax ricinus communis repid b9t3v9_ricco; score=1064.68; evalue=0.00e+00;
c54587/f3p4/2967	abc transporter family of the mitochondria family n 1 tax populus trichocarpa repid b9i784_poptr; score=1043.49; evalue=0.00e+00;
c54587/f3p4/2967	abc superfamily atp binding cassette transporter abc protein n 1 tax medicago truncatula repid g7k5w0_medtr; score=1024.62; evalue=0.00e+00;
c54587/f3p4/2967	abc superfamily atp binding cassette transporter abc protein n 1 tax medicago truncatula repid g7k5w0_medtr; score=981.09; evalue=0.00e+00;
c54759/f1p2/2638	alpha-glucan water dikinase n 1 tax solanum tuberosum repid i0dfj7_soltu; score=1536.16; evalue=0.00e+00;
c54759/f1p2/2638	alpha-glucan water dikinase chloroplastic n 1 tax solanum tuberosum repid gwd1_soltu; score=1533.08; evalue=0.00e+00;
c54759/f1p2/2638	dna-directed rna polymerase subunit beta/beta n 1 tax helicobacter cinaedi atcc baa-847 repid i7hdr5_9heli; score=1529.23; evalue=0.00e+00;
c54759/f1p2/2638	dna-directed rna polymerase subunit beta/beta n 1 tax helicobacter cinaedi atcc baa-847 repid i7hdr5_9heli; score=862.06; evalue=0.00e+00;
c54759/f1p2/2638	uncharacterized protein n 1 tax solanum lycopersicum repid k4bw33_sollc; score=1527.69; evalue=0.00e+00;

c55491/f2p6/1893	uncharacterized protein n 1 tax solanum lycopersicum repid k4cbc3_sollc; score=946.42; evalue=0.00e+00;
c55491/f2p6/1893	protein translocase secy subunit putative n 1 tax ricinus communis repid b9t4l2_ricco; score=749.20; evalue=0.00e+00;
c55491/f2p6/1893	putative uncharacterized protein n 1 tax vitis vinifera repid f6h9m6_vitvi; score=741.88; evalue=0.00e+00;
c55491/f2p6/1893	uncharacterized protein n 1 tax glycine max repid i1kdg6_soybn; score=732.63; evalue=0.00e+00;
c55491/f2p6/1893	uncharacterized protein n 1 tax glycine max repid k7kwm1_soybn; score=732.25; evalue=0.00e+00;
c57469/f46p19/3316	auxin response factor 2 n 1 tax solanum lycopersicum repid q2laj3_sollc; score=1589.70; evalue=0.00e+00;
c57469/f46p19/3316	uncharacterized protein n 1 tax solanum lycopersicum repid k4df01_sollc; score=1210.67; evalue=0.00e+00;
c57469/f46p19/3316	putative uncharacterized protein n 1 tax vitis vinifera repid d7sh69_vitvi; score=1109.36; evalue=0.00e+00;
c57469/f46p19/3316	putative uncharacterized protein n 1 tax vitis vinifera repid a5bg94_vitvi; score=1081.63; evalue=0.00e+00;
c57469/f46p19/3316	auxin-response factor n 1 tax citrus sinensis repid g9i820_citsi; score=1066.22; evalue=0.00e+00;
c57897/f36p12/1764	uncharacterized protein n 1 tax solanum lycopersicum repid k4b0s5_sollc; score=874.77; evalue=0.00e+00;
c57897/f36p12/1764	putative uncharacterized protein n 1 tax vitis vinifera repid d7u1z6_vitvi; score=792.73; evalue=0.00e+00;
c57897/f36p12/1764	seryl-trna synthetase putative n 1 tax ricinus communis repid b9rkx9_ricco; score=778.09; evalue=0.00e+00;
c57897/f36p12/1764	serine--trna ligase n 1 tax helianthus annuus repid sys_helan; score=766.15; evalue=0.00e+00;
c57897/f36p12/1764	atp-dependent rna helicase dead n 1 tax enterobacter sp. ag1 repid j0meh6_9entr; score=770.77; evalue=0.00e+00;
c58088/f7p9/3247	uncharacterized protein n 1 tax solanum lycopersicum repid k4bt68_sollc; score=1194.87; evalue=0.00e+00;
c58088/f7p9/3247	uncharacterized protein n 1 tax solanum lycopersicum repid k4bt71_sollc; score=464.15; evalue=9.84e-147;
c58088/f7p9/3247	uncharacterized protein n 1 tax solanum lycopersicum repid k4bt71_sollc; score=407.53; evalue=2.79e-125;
c58088/f7p9/3247	putative uncharacterized protein n 1 tax vitis vinifera repid f6h0a2_vitvi; score=353.98; evalue=3.22e-102;
c58088/f7p9/3247	putative uncharacterized protein n 1 tax vitis vinifera repid a5bl82_vitvi; score=347.05; evalue=9.44e-100;
c58225/f1p5/1645	uncharacterized protein n 1 tax solanum lycopersicum repid k4cc33_sollc; score=759.99; evalue=0.00e+00;
c58225/f1p5/1645	26s proteasome subunit rpn7 n 1 tax capsicum annuum repid a0mkc7_capan; score=717.23; evalue=0.00e+00;
c58225/f1p5/1645	26s proteasome non-atpase regulatory subunit putative n 1 tax ricinus communis repid b9ram4_ricco; score=672.54; evalue=0.00e+00;
c58225/f1p5/1645	predicted protein n 1 tax populus trichocarpa repid b9if58_poptr; score=669.08; evalue=0.00e+00;
c58225/f1p5/1645	26s proteasome non-atpase regulatory subunit n 1 tax cucumis melo subsp. melo repid e5gbw6_cucme; score=666.38; evalue=0.00e+00;
c58503/f2p4/3411	uncharacterized protein n 1 tax solanum lycopersicum repid k4bi70_sollc; score=1651.72; evalue=0.00e+00;
c58503/f2p4/3411	putative uncharacterized protein n 1 tax vitis vinifera repid e0cv68_vitvi; score=1644.79; evalue=0.00e+00;
c58503/f2p4/3411	importin beta-1 putative n 1 tax ricinus communis repid b9sjt7_ricco; score=1623.99; evalue=0.00e+00;
c58503/f2p4/3411	predicted protein n 1 tax populus trichocarpa repid b9i1y1_poptr; score=1595.48; evalue=0.00e+00;
c58503/f2p4/3411	importin beta-1 putative n 1 tax ricinus communis repid b9rq34_ricco; score=1587.78; evalue=0.00e+00;
c58621/f2p36/3166	alpha-1 4 glucan phosphorylase l-2 isozyme chloroplastic/amyloplastic n 1 tax solanum tuberosum repid phsl2_soltu; score=1689.47; evalue=0.00e+00;

c58621/f2p36/3166	phosphorylase n 1 tax solanum lycopersicum repid k4bxx3_sollc; score=1665.97; evalue=0.00e+00;
c58621/f2p36/3166	phosphorylase n 1 tax vitis vinifera repid f6hf78_vitvi; score=1468.75; evalue=0.00e+00;
c58621/f2p36/3166	phosphorylase n 1 tax populus trichocarpa repid b9hxl0_poptr; score=1434.85; evalue=0.00e+00;
c58621/f2p36/3166	phosphorylase n 1 tax ricinus communis repid b9rcw0_ricco; score=1427.54; evalue=0.00e+00;
c58746/f2p1/2387	putative uncharacterized protein n 1 tax vitis vinifera repid d7sxr1_vitvi; score=537.72; evalue=0.00e+00;
c58746/f2p1/2387	putative uncharacterized protein n 1 tax vitis vinifera repid d7sxr1_vitvi; score=318.55; evalue=0.00e+00;
c58746/f2p1/2387	putative uncharacterized protein n 1 tax vitis vinifera repid d7sxr1_vitvi; score=133.26; evalue=0.00e+00;
c58746/f2p1/2387	putative uncharacterized protein n 1 tax vitis vinifera repid d7sxr1_vitvi; score=97.44; evalue=0.00e+00;
c58746/f2p1/2387	predicted protein n 1 tax populus trichocarpa repid b9gi91_poptr; score=542.73; evalue=0.00e+00;
c58818/f2p4/3356	uncharacterized protein n 1 tax solanum lycopersicum repid k4cr73_sollc; score=1486.86; evalue=0.00e+00;
c58818/f2p4/3356	eukaryotic translation initiation factor 3 subunit a n 1 tax nicotiana tabacum repid eif3a_tobac; score=1373.99; evalue=0.00e+00;
c58818/f2p4/3356	uncharacterized protein n 1 tax solanum lycopersicum repid k4d3q1_sollc; score=1248.03; evalue=0.00e+00;
c58818/f2p4/3356	putative uncharacterized protein n 1 tax vitis vinifera repid f6i4q7_vitvi; score=1160.59; evalue=0.00e+00;
c58818/f2p4/3356	eukaryotic translation initiation factor 3 subunit putative n 1 tax ricinus communis repid b9rff6_ricco; score=1125.15; evalue=0.00e+00;
c58915/f2p1/2935	uncharacterized protein n 1 tax solanum lycopersicum repid k4bdz9_sollc; score=1358.97; evalue=0.00e+00;
c58915/f2p1/2935	uncharacterized protein n 1 tax solanum lycopersicum repid k4b894_sollc; score=910.21; evalue=0.00e+00;
c58915/f2p1/2935	putative uncharacterized protein n 1 tax vitis vinifera repid f6hmg9_vitvi; score=678.71; evalue=0.00e+00;
c58915/f2p1/2935	putative uncharacterized protein n 1 tax ricinus communis repid b9s173_ricco; score=657.52; evalue=0.00e+00;
c58915/f2p1/2935	predicted protein n 1 tax populus trichocarpa repid b9i113_poptr; score=654.05; evalue=0.00e+00;
c58927/f2p1/2768	uncharacterized protein n 1 tax solanum lycopersicum repid k4bvw0_sollc; score=1621.68; evalue=0.00e+00;
c58927/f2p1/2768	putative uncharacterized protein n 1 tax vitis vinifera repid d7ud95_vitvi; score=1214.52; evalue=0.00e+00;
c58927/f2p1/2768	ribosome biogenesis protein tsr1 putative n 1 tax ricinus communis repid b9r8l9_ricco; score=1212.98; evalue=0.00e+00;
c58927/f2p1/2768	predicted protein n 1 tax populus trichocarpa repid b9h5g6_poptr; score=1170.99; evalue=0.00e+00;
c58927/f2p1/2768	at1g42440/f7f22_7 n 1 tax arabidopsis thaliana repid q9asu6_arath; score=1146.72; evalue=0.00e+00;
c59147/f1p3/3451	uncharacterized protein n 1 tax solanum lycopersicum repid k4dbh9_sollc; score=1412.51; evalue=0.00e+00;
c59147/f1p3/3451	uncharacterized protein n 1 tax solanum lycopersicum repid k4byy8_sollc; score=1009.21; evalue=0.00e+00;
c59147/f1p3/3451	putative uncharacterized protein n 1 tax vitis vinifera repid a5c725_vitvi; score=936.02; evalue=0.00e+00;
c59147/f1p3/3451	putative uncharacterized protein n 1 tax vitis vinifera repid f6htj0_vitvi; score=927.93; evalue=0.00e+00;
c59147/f1p3/3451	predicted protein n 1 tax populus trichocarpa repid b9hd71_poptr; score=807.75; evalue=0.00e+00;
c59277/f1p6/2958	uncharacterized protein n 1 tax solanum lycopersicum repid k4byw8_sollc; score=1157.13; evalue=0.00e+00;
c59277/f1p6/2958	putative uncharacterized protein n 1 tax vitis vinifera repid f6htm7_vitvi; score=897.50; evalue=0.00e+00;

c59277/f1p6/2958	predicted protein n 1 tax populus trichocarpa repid b9ihb8_poptr; score=828.16; evalue=0.00e+00;
c59277/f1p6/2958	predicted protein n 1 tax populus trichocarpa repid b9hd61_poptr; score=815.07; evalue=0.00e+00;
c59277/f1p6/2958	zinc finger protein putative n 1 tax ricinus communis repid b9s4y7_ricco; score=782.33; evalue=0.00e+00;
c59475/f1p1/2965	uncharacterized protein n 1 tax solanum lycopersicum repid k4c7s2_sollc; score=918.30; evalue=0.00e+00;
c59475/f1p1/2965	putative uncharacterized protein n 1 tax vitis vinifera repid f6hy92_vitvi; score=841.65; evalue=0.00e+00;
c59475/f1p1/2965	uncharacterized protein n 1 tax glycine max repid i1k9h7_soybn; score=814.30; evalue=0.00e+00;
c59475/f1p1/2965	uncharacterized protein n 1 tax glycine max repid i1k9h6_soybn; score=816.61; evalue=0.00e+00;
c59475/f1p1/2965	uncharacterized protein n 1 tax glycine max repid i1k9h4_soybn; score=816.61; evalue=0.00e+00;
c59543/f1p2/2713	uncharacterized protein n 1 tax solanum lycopersicum repid k4ciw9_sollc; score=160.61; evalue=9.70e-42;
c59543/f1p2/2713	uncharacterized protein n 1 tax solanum lycopersicum repid k4ciw9_sollc; score=143.66; evalue=1.16e-35;
c59543/f1p2/2713	uncharacterized protein n 1 tax glycine max repid i1lg91_soybn; score=135.19; evalue=1.90e-32;
c59543/f1p2/2713	uncharacterized protein n 2 tax glycine max repid i1lg92_soybn; score=135.19; evalue=1.91e-32;
c59543/f1p2/2713	uncharacterized protein n 1 tax glycine max repid i1jad7_soybn; score=132.11; evalue=2.38e-31;
c59609/f1p2/3138	uncharacterized protein n 1 tax solanum lycopersicum repid k4csj6_sollc; score=423.70; evalue=8.27e-149;
c59609/f1p2/3138	uncharacterized protein n 1 tax solanum lycopersicum repid k4csj6_sollc; score=133.26; evalue=8.27e-149;
c59609/f1p2/3138	uncharacterized protein n 1 tax solanum lycopersicum repid k4csj6_sollc; score=434.49; evalue=3.72e-132;
c59609/f1p2/3138	sr-rich pre-mrna splicing activator n 1 tax oryza sativa japonica group repid q84jx7_orysj; score=273.09; evalue=2.27e-81;
c59609/f1p2/3138	putative uncharacterized protein n 1 tax oryza sativa indica group repid b8akp6_orysi; score=272.71; evalue=3.44e-81;
c59752/f1p5/3263	uncharacterized protein n 1 tax solanum lycopersicum repid k4bkw8_sollc; score=1696.40; evalue=0.00e+00;
c59752/f1p5/3263	putative uncharacterized protein n 1 tax vitis vinifera repid f6gtf8_vitvi; score=1002.28; evalue=0.00e+00;
c59752/f1p5/3263	predicted protein (fragment) n 1 tax populus trichocarpa repid b9ie27_poptr; score=924.08; evalue=0.00e+00;
c59752/f1p5/3263	pentatricopeptide repeat protein n 1 tax medicago truncatula repid g7isz5_medtr; score=894.42; evalue=0.00e+00;
c59752/f1p5/3263	uncharacterized protein n 1 tax glycine max repid i1kd47_soybn; score=873.23; evalue=0.00e+00;
c59760/f1p4/2664	uncharacterized protein n 1 tax solanum lycopersicum repid k4cbn5_sollc; score=810.06; evalue=0.00e+00;
c59760/f1p4/2664	uncharacterized protein n 1 tax solanum lycopersicum repid k4cbn5_sollc; score=221.48; evalue=0.00e+00;
c59760/f1p4/2664	putative uncharacterized protein n 1 tax vitis vinifera repid f6hcg5_vitvi; score=820.46; evalue=0.00e+00;
c59760/f1p4/2664	putative uncharacterized protein n 1 tax vitis vinifera repid a5apz2_vitvi; score=819.30; evalue=0.00e+00;
c59760/f1p4/2664	predicted protein n 1 tax populus trichocarpa repid b9n715_poptr; score=782.71; evalue=0.00e+00;
c59806/f1p17/3405	uncharacterized protein n 1 tax solanum lycopersicum repid k4cfd4_sollc; score=1941.01; evalue=0.00e+00;
c59806/f1p17/3405	putative aconitase n 1 tax capsicum chinense repid b1q486_capch; score=1884.77; evalue=0.00e+00;
c59806/f1p17/3405	aconitase (fragment) n 1 tax solanum pennellii repid q84ni5_solpn; score=1798.10; evalue=0.00e+00;

c59806/f1p17/3405	aconitase (fragment) n 1 tax solanum pennellii repid q84tr4_solpn; score=1781.92; evalue=0.00e+00;
c59806/f1p17/3405	uncharacterized protein n 1 tax solanum lycopersicum repid k4dbc4_sollc; score=1757.65; evalue=0.00e+00;
c60009/f1p1/1483	uncharacterized protein n 1 tax solanum lycopersicum repid k4bwk8_sollc; score=542.35; evalue=0.00e+00;
c60009/f1p1/1483	potyviral capsid protein interacting protein 2b n 1 tax nicotiana tabacum repid q6eix7_tobac; score=502.29; evalue=1.41e-173;
c60009/f1p1/1483	potyviral capsid protein interacting protein 2a n 1 tax nicotiana tabacum repid q6eix8_tobac; score=497.66; evalue=7.59e-172;
c60009/f1p1/1483	uncharacterized protein n 1 tax solanum lycopersicum repid k4bni8_sollc; score=454.14; evalue=1.45e-154;
c60009/f1p1/1483	potyviral capsid protein interacting protein 1 n 1 tax nicotiana tabacum repid q6eix9_tobac; score=451.06; evalue=1.75e-153;
c60057/f1p5/2934	uncharacterized protein n 1 tax solanum lycopersicum repid k4csj6_sollc; score=553.90; evalue=2.44e-178;
c60057/f1p5/2934	uncharacterized protein n 1 tax solanum lycopersicum repid k4csj6_sollc; score=434.11; evalue=8.17e-133;
c60057/f1p5/2934	sr-rich pre-mrna splicing activator n 1 tax oryza sativa japonica group repid q84jx7_orysj; score=273.48; evalue=9.31e-82;
c60057/f1p5/2934	putative uncharacterized protein n 1 tax oryza sativa indica group repid b8akp6_orysi; score=273.09; evalue=1.29e-81;
c60057/f1p5/2934	predicted protein n 1 tax populus trichocarpa repid b9hpd0_poptr; score=270.01; evalue=8.49e-81;
c60300/f1p1/3492	uncharacterized protein n 1 tax solanum lycopersicum repid k4df88_sollc; score=1697.95; evalue=0.00e+00;
c60300/f1p1/3492	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmh6_sollc; score=1690.63; evalue=0.00e+00;
c60300/f1p1/3492	uncharacterized protein n 1 tax solanum lycopersicum repid k4c7u7_sollc; score=1657.50; evalue=0.00e+00;
c60300/f1p1/3492	coatomer beta subunit putative n 1 tax ricinus communis repid b9sqc0_ricco; score=1585.08; evalue=0.00e+00;
c60300/f1p1/3492	uncharacterized protein n 1 tax glycine max repid k7m8y1_soybn; score=1581.62; evalue=0.00e+00;
c61066/f1p3/4098	uncharacterized protein n 1 tax solanum lycopersicum repid k4apw5_sollc; score=1345.49; evalue=0.00e+00;
c61066/f1p3/4098	uncharacterized protein n 1 tax solanum lycopersicum repid k4bac4_sollc; score=1316.98; evalue=0.00e+00;
c61066/f1p3/4098	predicted protein n 1 tax populus trichocarpa repid b9h680_poptr; score=783.10; evalue=0.00e+00;
c61066/f1p3/4098	putative uncharacterized protein n 1 tax vitis vinifera repid f6i0r5_vitvi; score=773.47; evalue=0.00e+00;
c61066/f1p3/4098	uncharacterized protein n 1 tax glycine max repid i1m635_soybn; score=761.14; evalue=0.00e+00;
c61268/f1p5/2470	uncharacterized protein n 2 tax solanum lycopersicum repid k4c390_sollc; score=1354.35; evalue=0.00e+00;
c61268/f1p5/2470	thiamine biosynthesis protein thic variant l1 n 1 tax solanum lycopersicum repid b9tu32_sollc; score=1347.80; evalue=0.00e+00;
c61268/f1p5/2470	uncharacterized protein n 1 tax glycine max repid i1n019_soybn; score=1163.67; evalue=0.00e+00;
c61268/f1p5/2470	putative uncharacterized protein n 1 tax vitis vinifera repid f6guu1_vitvi; score=1160.21; evalue=0.00e+00;
c61268/f1p5/2470	mrna clone: rtfl01-17-g05 n 1 tax eutrema halophilum repid e4mx93_theha; score=1159.05; evalue=0.00e+00;
c61309/f1p6/3183	non-lysosomal glucosylceramidase n 1 tax solanum lycopersicum repid k4b1p9_sollc; score=1855.88; evalue=0.00e+00;
c61309/f1p6/3183	non-lysosomal glucosylceramidase n 1 tax vitis vinifera repid d7tgq9_vitvi; score=1340.10; evalue=0.00e+00;
c61309/f1p6/3183	non-lysosomal glucosylceramidase n 1 tax ricinus communis repid b9ss77_ricco; score=1326.23; evalue=0.00e+00;
c61309/f1p6/3183	non-lysosomal glucosylceramidase n 1 tax populus trichocarpa repid b9n7a1_poptr; score=1288.09; evalue=0.00e+00;

c61309/f1p6/3183	non-lysosomal glucosylceramidase n 1 tax arabidopsis lyrata subsp. lyrata repid d7mpg2_arall; score=1283.09; evalue=0.00e+00;
c61904/f1p11/3285	uncharacterized protein n 1 tax solanum lycopersicum repid k4dfg9_sollc; score=1347.41; evalue=0.00e+00;
c61904/f1p11/3285	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmu3_sollc; score=1141.72; evalue=0.00e+00;
c61904/f1p11/3285	putative uncharacterized protein n 1 tax vitis vinifera repid f6hy31_vitvi; score=1034.63; evalue=0.00e+00;
c61904/f1p11/3285	uncharacterized protein n 1 tax glycine max repid i1kge2_soybn; score=1010.75; evalue=0.00e+00;
c61904/f1p11/3285	uncharacterized protein n 1 tax glycine max repid k7l7n3_soybn; score=1008.82; evalue=0.00e+00;
c61957/f1p1/2699	auxin efflux facilitator slpin4 n 1 tax solanum lycopersicum repid e5kgd4_sollc; score=1111.29; evalue=0.00e+00;
c61957/f1p1/2699	auxin efflux carrier n 1 tax solanum lycopersicum repid d6rt10_sollc; score=1108.98; evalue=0.00e+00;
c61957/f1p1/2699	auxin efflux carrier component n 1 tax populus trichocarpa repid b9hja9_poptr; score=967.22; evalue=0.00e+00;
c61957/f1p1/2699	auxin efflux carrier component (fragment) n 1 tax populus trichocarpa repid b9hw69_poptr; score=954.51; evalue=0.00e+00;
c61957/f1p1/2699	pin1-like auxin transport protein n 1 tax populus tremula x populus tremuloides repid q8lkh1_9rosi; score=952.20; evalue=0.00e+00;
c62117/f1p12/3137	ago4a n 1 tax solanum lycopersicum repid k4at92_sollc; score=1770.36; evalue=0.00e+00;
c62117/f1p12/3137	ago4-2 (fragment) n 1 tax nicotiana benthamiana repid q2lfc1_nicbe; score=1703.72; evalue=0.00e+00;
c62117/f1p12/3137	uncharacterized protein n 1 tax solanum lycopersicum repid k4c973_sollc; score=1605.50; evalue=0.00e+00;
c62117/f1p12/3137	ago4b n 1 tax solanum lycopersicum repid k4lp77_sollc; score=1603.19; evalue=0.00e+00;
c62117/f1p12/3137	ago4-1 (fragment) n 1 tax nicotiana benthamiana repid q2lfc2_nicbe; score=1593.17; evalue=0.00e+00;
c62205/f1p0/2428	malic enzyme n 1 tax solanum lycopersicum repid k4cj21_sollc; score=1169.84; evalue=0.00e+00;
c62205/f1p0/2428	nad-dependent malic enzyme 62 kda isoform mitochondrial n 1 tax solanum tuberosum repid maom_soltu; score=1138.25; evalue=0.00e+00;
c62205/f1p0/2428	malic enzyme n 1 tax populus trichocarpa repid b9gp43_poptr; score=1052.35; evalue=0.00e+00;
c62205/f1p0/2428	malic enzyme n 1 tax populus trichocarpa repid b9mvc4_poptr; score=1040.80; evalue=0.00e+00;
c62205/f1p0/2428	malic enzyme n 1 tax ricinus communis repid b9skh7_ricco; score=1038.10; evalue=0.00e+00;
c62323/f1p1/2462	uncharacterized protein n 1 tax solanum lycopersicum repid k4cjm3_sollc; score=1233.78; evalue=0.00e+00;
c62323/f1p1/2462	putative uncharacterized protein n 1 tax vitis vinifera repid d7suv8_vitvi; score=696.81; evalue=0.00e+00;
c62323/f1p1/2462	ubiquitin-protein ligase bre1a putative n 1 tax ricinus communis repid b9rp29_ricco; score=666.38; evalue=0.00e+00;
c62323/f1p1/2462	predicted protein n 1 tax populus trichocarpa repid b9haf6_poptr; score=628.25; evalue=0.00e+00;
c62323/f1p1/2462	uncharacterized protein n 1 tax glycine max repid i1mwt3_soybn; score=583.18; evalue=0.00e+00;
c62508/f1p4/2296	uncharacterized protein n 1 tax solanum lycopersicum repid k4dax8_sollc; score=1339.32; evalue=0.00e+00;
c62508/f1p4/2296	phototropin-1 n 1 tax solanum lycopersicum repid a3ex92_sollc; score=1334.70; evalue=0.00e+00;
c62508/f1p4/2296	putative uncharacterized protein n 1 tax vitis vinifera repid f6gtw2_vitvi; score=1086.25; evalue=0.00e+00;
c62508/f1p4/2296	phototropin 1 n 1 tax fragaria x ananassa repid j7m8m9_fraan; score=1066.60; evalue=0.00e+00;
c62508/f1p4/2296	blue light photoreceptor (fragment) n 1 tax fragaria x ananassa repid c3vp55_fraan; score=1054.66; evalue=0.00e+00;

c62793/f1p1/1162	uncharacterized protein n 1 tax solanum lycopersicum repid k4cw92_sollc; score=531.18; evalue=0.00e+00;
c62793/f1p1/1162	putative uncharacterized protein n 1 tax vitis vinifera repid d7szn5_vitvi; score=470.31; evalue=1.90e-159;
c62793/f1p1/1162	predicted protein n 1 tax populus trichocarpa repid b9hku6_poptr; score=468.39; evalue=9.56e-159;
c62793/f1p1/1162	uncharacterized protein n 1 tax glycine max repid i1nen5_soybn; score=459.14; evalue=4.22e-155;
c62793/f1p1/1162	predicted protein n 1 tax populus trichocarpa repid b9hst8_poptr; score=457.60; evalue=1.47e-154;
c62798/f1p21/3215	uncharacterized protein n 1 tax solanum lycopersicum repid k4ckq2_sollc; score=1945.24; evalue=0.00e+00;
c62798/f1p21/3215	putative uncharacterized protein n 1 tax vitis vinifera repid f6h311_vitvi; score=1806.96; evalue=0.00e+00;
c62798/f1p21/3215	cellulose synthase a catalytic subunit 6 [udp-forming] putative n 1 tax ricinus communis repid b9rp67_ricco; score=1793.09; evalue=0.00e+00;
c62798/f1p21/3215	cellulose synthase n 1 tax populus trichocarpa repid b9ikv7_poptr; score=1774.60; evalue=0.00e+00;
c62798/f1p21/3215	cellulose synthase a n 1 tax eucalyptus camaldulensis repid g0z2c3_eucca; score=1764.59; evalue=0.00e+00;
c62895/f1p1/3243	uncharacterized protein n 1 tax solanum lycopersicum repid k4d1n9_sollc; score=1109.75; evalue=0.00e+00;
c62895/f1p1/3243	uncharacterized protein n 1 tax solanum lycopersicum repid k4b466_sollc; score=813.91; evalue=0.00e+00;
c62895/f1p1/3243	putative uncharacterized protein n 1 tax vitis vinifera repid f6i0v6_vitvi; score=640.57; evalue=0.00e+00;
c62895/f1p1/3243	predicted protein n 1 tax populus trichocarpa repid b9hqy0_poptr; score=616.30; evalue=0.00e+00;
c62895/f1p1/3243	putative uncharacterized protein n 1 tax ricinus communis repid b9sid1_ricco; score=608.60; evalue=0.00e+00;
c63260/f1p4/3429	uncharacterized protein n 1 tax solanum lycopersicum repid k4b2j0_sollc; score=1935.61; evalue=0.00e+00;
c63260/f1p4/3429	putative uncharacterized protein n 1 tax vitis vinifera repid f6hw57_vitvi; score=1365.13; evalue=0.00e+00;
c63260/f1p4/3429	uncharacterized protein n 1 tax glycine max repid i1me27_soybn; score=1266.14; evalue=0.00e+00;
c63260/f1p4/3429	uncharacterized protein n 1 tax glycine max repid i1m2k6_soybn; score=1257.28; evalue=0.00e+00;
c63260/f1p4/3429	dna polymerase v n 1 tax medicago truncatula repid g7isa4_medtr; score=1249.96; evalue=0.00e+00;
c63822/f1p6/3552	uncharacterized protein n 1 tax solanum lycopersicum repid k4bpj0_sollc; score=1920.21; evalue=0.00e+00;
c63822/f1p6/3552	2-oxoglutarate dehydrogenase putative n 1 tax ricinus communis repid b9sr46_ricco; score=1862.43; evalue=0.00e+00;
c63822/f1p6/3552	predicted protein n 1 tax populus trichocarpa repid b9hm58_poptr; score=1861.66; evalue=0.00e+00;
c63822/f1p6/3552	predicted protein n 1 tax populus trichocarpa repid b9htm3_poptr; score=1859.73; evalue=0.00e+00;
c63822/f1p6/3552	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2e1_sollc; score=1859.34; evalue=0.00e+00;
c63985/f1p2/3649	uncharacterized protein n 1 tax solanum lycopersicum repid k4df36_sollc; score=700.66; evalue=0.00e+00;
c63985/f1p2/3649	inositol polyphosphate multikinase n 1 tax solanum tuberosum repid a4h2j1_soltu; score=614.38; evalue=0.00e+00;
c63985/f1p2/3649	uncharacterized protein n 1 tax solanum lycopersicum repid k4blv1_sollc; score=490.35; evalue=3.68e-160;
c63985/f1p2/3649	ipk2 protein n 1 tax vitis vinifera repid h6x2p5_vitvi; score=434.11; evalue=1.61e-138;
c63985/f1p2/3649	inositol hexaphosphate kinase putative n 1 tax ricinus communis repid b9ra37_ricco; score=431.41; evalue=1.70e-137;
c64133/f1p1/2392	uncharacterized protein n 1 tax solanum lycopersicum repid k4cw45_sollc; score=715.30; evalue=0.00e+00;

c64133/f1p1/2392	uncharacterized protein n 1 tax solanum lycopersicum repid k4cw45_sollc; score=469.54; evalue=0.00e+00;
c64133/f1p1/2392	uncharacterized protein n 1 tax solanum lycopersicum repid k4bdy4_sollc; score=641.73; evalue=0.00e+00;
c64133/f1p1/2392	uncharacterized protein n 1 tax solanum lycopersicum repid k4bdy4_sollc; score=439.50; evalue=0.00e+00;
c64133/f1p1/2392	probable methyltransferase pmt8 n 1 tax arabidopsis thaliana repid pmt8_arath; score=568.54; evalue=0.00e+00;
c65336/f1p2/2929	uncharacterized protein n 1 tax solanum lycopersicum repid k4bp28_sollc; score=944.88; evalue=0.00e+00;
c65336/f1p2/2929	uncharacterized protein n 1 tax solanum lycopersicum repid k4b4y6_sollc; score=592.81; evalue=0.00e+00;
c65336/f1p2/2929	uncharacterized protein n 1 tax solanum lycopersicum repid k4bp28_sollc; score=458.37; evalue=4.06e-143;
c65336/f1p2/2929	putative uncharacterized protein n 1 tax vitis vinifera repid f6hvx7_vitvi; score=445.66; evalue=1.88e-138;
c65336/f1p2/2929	uncharacterized protein n 1 tax solanum lycopersicum repid k4b4y6_sollc; score=444.51; evalue=3.91e-138;
c65442/f1p2/2690	auxin response factor 2 n 1 tax solanum lycopersicum repid q2laj3_sollc; score=1315.06; evalue=0.00e+00;
c65442/f1p2/2690	uncharacterized protein n 1 tax solanum lycopersicum repid k4df01_sollc; score=1004.59; evalue=0.00e+00;
c65442/f1p2/2690	putative uncharacterized protein n 1 tax vitis vinifera repid d7sh69_vitvi; score=923.31; evalue=0.00e+00;
c65442/f1p2/2690	putative uncharacterized protein n 1 tax vitis vinifera repid a5bg94_vitvi; score=895.58; evalue=0.00e+00;
c65442/f1p2/2690	auxin-response factor n 1 tax citrus sinensis repid g9i820_citsi; score=887.87; evalue=0.00e+00;
c65822/f1p3/2884	uncharacterized protein n 1 tax solanum lycopersicum repid k4byn8_sollc; score=1470.68; evalue=0.00e+00;
c65822/f1p3/2884	putative uncharacterized protein n 1 tax vitis vinifera repid d7tav0_vitvi; score=1227.23; evalue=0.00e+00;
c65822/f1p3/2884	mannosyl-oligosaccharide glucosidase putative n 1 tax ricinus communis repid b9rmg4_ricco; score=1197.19; evalue=0.00e+00;
c65822/f1p3/2884	predicted protein n 1 tax populus trichocarpa repid b9ht87_poptr; score=1182.93; evalue=0.00e+00;
c65822/f1p3/2884	uncharacterized protein n 1 tax glycine max repid i1k3k8_soybn; score=1124.77; evalue=0.00e+00;
c66237/f2p19/2839	arginine decarboxylase n 2 tax solanum lycopersicum repid g8z275_sollc; score=1261.90; evalue=0.00e+00;
c66237/f2p19/2839	arginine decarboxylase n 1 tax datura stramonium repid q9scf0_datst; score=1234.94; evalue=0.00e+00;
c66237/f2p19/2839	arginine decarboxylase n 1 tax nicotiana tabacum repid q9ldm9_tobac; score=1148.65; evalue=0.00e+00;
c66237/f2p19/2839	arginine decarboxylase n 1 tax nicotiana tabacum repid q71s28_tobac; score=1145.57; evalue=0.00e+00;
c66237/f2p19/2839	arginine decarboxylase n 1 tax nicotiana tabacum repid q9m7k9_tobac; score=1140.95; evalue=0.00e+00;
c66541/f1p0/3105	uncharacterized protein n 1 tax solanum lycopersicum repid k4bkf9_sollc; score=1561.97; evalue=0.00e+00;
c66541/f1p0/3105	uncharacterized protein n 1 tax solanum lycopersicum repid k4bkf7_sollc; score=1417.14; evalue=0.00e+00;
c66541/f1p0/3105	putative uncharacterized protein n 1 tax vitis vinifera repid f6gt97_vitvi; score=1217.60; evalue=0.00e+00;
c66541/f1p0/3105	uncharacterized protein n 1 tax glycine max repid i1jwx7_soybn; score=1185.24; evalue=0.00e+00;
c66541/f1p0/3105	uncharacterized protein n 1 tax glycine max repid k7kvx1_soybn; score=1170.99; evalue=0.00e+00;
c67485/f9p9/1443	uncharacterized protein n 1 tax solanum lycopersicum repid k4cg45_sollc; score=620.93; evalue=0.00e+00;
c67485/f9p9/1443	uncharacterized protein n 1 tax solanum lycopersicum repid k4dch3_sollc; score=434.49; evalue=1.31e-146;

c67485/f9p9/1443	putative uncharacterized protein n 1 tax vitis vinifera repid e0ctr9_vitvi; score=389.81; evalue=3.11e-129;
c67485/f9p9/1443	putative uncharacterized protein n 1 tax vitis vinifera repid a5ah71_vitvi; score=388.65; evalue=7.48e-129;
c67485/f9p9/1443	putative uncharacterized protein n 1 tax ricinus communis repid b9src2_ricco; score=385.19; evalue=4.97e-127;
c70048/f3p1/1214	uncharacterized protein n 1 tax solanum lycopersicum repid k4c841_sollc; score=557.75; evalue=0.00e+00;
c70048/f3p1/1214	uncharacterized protein n 1 tax solanum lycopersicum repid k4blu0_sollc; score=452.98; evalue=5.31e-156;
c70048/f3p1/1214	amino acid binding protein putative n 1 tax ricinus communis repid b9sak5_ricco; score=394.43; evalue=4.24e-133;
c70048/f3p1/1214	uncharacterized protein n 1 tax glycine max repid i1kgs6_soybn; score=388.65; evalue=1.50e-130;
c70048/f3p1/1214	uncharacterized protein n 1 tax glycine max repid c6tik4_soybn; score=386.73; evalue=7.54e-130;
c70575/f1p6/3002	uncharacterized protein n 1 tax solanum lycopersicum repid k4b3g4_sollc; score=1592.02; evalue=0.00e+00;
c70575/f1p6/3002	putative uncharacterized protein n 1 tax vitis vinifera repid f6hql6_vitvi; score=700.66; evalue=0.00e+00;
c70575/f1p6/3002	chromatin remodeling complex subunit n 1 tax populus trichocarpa repid b9hrp3_poptr; score=679.48; evalue=0.00e+00;
c70575/f1p6/3002	chromatin remodeling complex subunit n 1 tax populus trichocarpa repid b9h0p7_poptr; score=676.40; evalue=0.00e+00;
c70575/f1p6/3002	putative uncharacterized protein n 1 tax vitis vinifera repid a5bfl4_vitvi; score=657.14; evalue=0.00e+00;
c70907/f1p5/1857	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2z8_sollc; score=956.44; evalue=0.00e+00;
c70907/f1p5/1857	putative uncharacterized protein n 1 tax vitis vinifera repid f6hei3_vitvi; score=671.39; evalue=0.00e+00;
c70907/f1p5/1857	putative uncharacterized protein n 1 tax vitis vinifera repid a5alw8_vitvi; score=664.84; evalue=0.00e+00;
c70907/f1p5/1857	predicted protein n 1 tax populus trichocarpa repid b9h877_poptr; score=634.02; evalue=0.00e+00;
c70907/f1p5/1857	uncharacterized protein n 1 tax glycine max repid k7lh18_soybn; score=620.93; evalue=0.00e+00;
c71051/f1p0/1365	uncharacterized protein n 1 tax solanum lycopersicum repid k4buc1_sollc; score=572.39; evalue=0.00e+00;
c71051/f1p0/1365	putative uncharacterized protein n 1 tax vitis vinifera repid f6gzk9_vitvi; score=446.05; evalue=9.02e-151;
c71051/f1p0/1365	putative uncharacterized protein n 1 tax vitis vinifera repid a5bds3_vitvi; score=440.65; evalue=2.08e-150;
c71051/f1p0/1365	catalytic putative n 1 tax ricinus communis repid b9smx1_ricco; score=435.65; evalue=1.47e-148;
c71051/f1p0/1365	phosphoglycerate mutase-like protein n 1 tax glycine max repid q8lgt8_soybn; score=424.48; evalue=4.61e-144;
c71520/f1p0/2146	uncharacterized protein n 1 tax solanum lycopersicum repid k4b2d7_sollc; score=626.32; evalue=0.00e+00;
c71520/f1p0/2146	uncharacterized protein n 1 tax solanum lycopersicum repid k4b2d7_sollc; score=201.44; evalue=0.00e+00;
c71520/f1p0/2146	calcium-dependent protein kinase n 1 tax hevea brasiliensis repid g3m0d5_hevbr; score=456.06; evalue=2.35e-151;
c71520/f1p0/2146	calcium-dependent protein kinase n 1 tax hevea brasiliensis repid g3m0d5_hevbr; score=109.00; evalue=2.35e-151;
c71520/f1p0/2146	putative uncharacterized protein n 2 tax populus trichocarpa repid a9pfi3_poptr; score=447.59; evalue=4.51e-149;
c71572/f1p1/1475	uncharacterized protein n 1 tax solanum lycopersicum repid k4bxb3_sollc; score=754.59; evalue=0.00e+00;
c71572/f1p1/1475	putative uncharacterized protein n 2 tax vitis vinifera repid d7t940_vitvi; score=521.55; evalue=1.42e-179;
c71572/f1p1/1475	monoglyceride lipase putative n 1 tax ricinus communis repid b9t6u9_ricco; score=478.40; evalue=1.13e-163;

c71572/f1p1/1475	monoglyceride lipase n 1 tax medicago truncatula repid g7k1k2_medtr; score=479.17; evalue=3.22e-163;
c71572/f1p1/1475	uncharacterized protein n 1 tax lotus japonicus repid i3s4t0_lotja; score=472.63; evalue=8.60e-161;
c71624/f1p1/1232	uncharacterized protein n 1 tax solanum lycopersicum repid k4ayw9_sollc; score=514.23; evalue=3.90e-179;
c71624/f1p1/1232	putative uncharacterized protein n 1 tax vitis vinifera repid d7sly5_vitvi; score=428.71; evalue=1.35e-145;
c71624/f1p1/1232	leucine carboxyl methyltransferase putative n 1 tax ricinus communis repid b9rcz7_ricco; score=425.63; evalue=3.19e-144;
c71624/f1p1/1232	uncharacterized protein n 1 tax glycine max repid k7mum8_soybn; score=415.62; evalue=1.85e-140;
c71624/f1p1/1232	putative uncharacterized protein n 1 tax vitis vinifera repid a5b6p8_vitvi; score=414.85; evalue=3.19e-140;
c71891/f2p8/1223	probable xyloglucan endotransglucosylase/hydrolase 1 n 1 tax solanum lycopersicum repid xth1_sollc; score=612.07; evalue=0.00e+00;
c71891/f2p8/1223	heavy metal translocating p-type atpase family protein n 1 tax streptococcus pneumoniae 2071004 repid j0wbg5_stree; score=613.61; evalue=0.00e+00;
c71891/f2p8/1223	endo-xyloglucan transferase (exgt) n 1 tax nicotiana tabacum repid o80431_tobac; score=588.57; evalue=0.00e+00;
c71891/f2p8/1223	probable xyloglucan endotransglucosylase/hydrolase protein n 1 tax nicotiana tabacum repid xth_tobac; score=585.10; evalue=0.00e+00;
c71891/f2p8/1223	flagellar biosynthesis protein flha n 1 tax rhizobium leguminosarum bv. trifolii wsm2297 repid j0wbj7_rhilt; score=585.10; evalue=0.00e+00;
c71979/f1p9/1245	uncharacterized protein n 1 tax solanum lycopersicum repid k4cgi6_sollc; score=679.48; evalue=0.00e+00;
c71979/f1p9/1245	glycolate oxidase n 1 tax nicotiana benthamiana repid e1axt8_nicbe; score=661.76; evalue=0.00e+00;
c71979/f1p9/1245	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7kva4_arall; score=652.51; evalue=0.00e+00;
c71979/f1p9/1245	glycolate oxidase n 1 tax gossypium hirsutum repid h2d5s6_goshi; score=651.36; evalue=0.00e+00;
c71979/f1p9/1245	glycolate oxidase n 1 tax mikania micrantha repid d7ezn6_9astr; score=649.05; evalue=0.00e+00;
c72158/f1p4/1238	udp-glucuronate decarboxylase 1 n 1 tax nicotiana tabacum repid q6ivk5_tobac; score=686.41; evalue=0.00e+00;
c72158/f1p4/1238	uncharacterized protein n 1 tax solanum lycopersicum repid k4bpj4_sollc; score=670.23; evalue=0.00e+00;
c72158/f1p4/1238	predicted protein n 1 tax populus trichocarpa repid a9pbp7_poptr; score=662.14; evalue=0.00e+00;
c72158/f1p4/1238	udp-glucuronate decarboxylase n 1 tax camellia oleifera repid f8v2y4_9eric; score=659.83; evalue=0.00e+00;
c72158/f1p4/1238	predicted protein n 1 tax populus trichocarpa repid a9pgd5_poptr; score=657.14; evalue=0.00e+00;
c72352/f1p5/2098	uncharacterized protein n 1 tax solanum lycopersicum repid k4bxn9_sollc; score=1075.85; evalue=0.00e+00;
c72352/f1p5/2098	heat shock protein 90 n 1 tax ipomoea nil repid d0ewd6_iponi; score=1009.98; evalue=0.00e+00;
c72352/f1p5/2098	putative uncharacterized protein n 1 tax vitis vinifera repid f6hgf1_vitvi; score=993.80; evalue=0.00e+00;
c72352/f1p5/2098	uncharacterized protein n 1 tax glycine max repid i1jel6_soybn; score=991.88; evalue=0.00e+00;
c72352/f1p5/2098	predicted protein n 1 tax populus trichocarpa repid b9hiv4_poptr; score=991.10; evalue=0.00e+00;
c72574/f1p6/1240	betaine aldehyde dehydrogenase n 1 tax solanum torvum repid h6v8t9_9soln; score=687.18; evalue=0.00e+00;
c72574/f1p6/1240	aminoaldehyde dehydrogenase 2 n 1 tax solanum lycopersicum repid b6ecn9_sollc; score=685.26; evalue=0.00e+00;
c72574/f1p6/1240	uncharacterized protein n 1 tax solanum lycopersicum repid k4bkn2_sollc; score=682.95; evalue=0.00e+00;
c72574/f1p6/1240	betaine aldehyde dehydrogenase n 1 tax lycium barbarum repid d2dek8_lycba; score=593.19; evalue=0.00e+00;

c72574/f1p6/1240	betaine-aldehyde dehydrogenase chloroplast putative n 1 tax solanum lycopersicum repid q53j19_sollc; score=585.87; evalue=0.00e+00;
c72708/f1p1/1918	glutamyl-trna reductase (fragment) n 1 tax nicotiana tabacum repid a6q0f0_tobac; score=902.89; evalue=0.00e+00;
c72708/f1p1/1918	glutamyl-trna reductase n 1 tax vitis vinifera repid a5bzy3_vitvi; score=839.72; evalue=0.00e+00;
c72708/f1p1/1918	glutamyl-trna reductase 1 chloroplastic n 2 tax cucumis sativus repid hem11_cucsa; score=823.54; evalue=0.00e+00;
c72708/f1p1/1918	glutamyl-trna reductase 1 chloroplast putative n 1 tax ricinus communis repid b9r6q2_ricco; score=808.90; evalue=0.00e+00;
c72708/f1p1/1918	glutamyl-trna reductase n 2 tax medicago truncatula repid g7j442_medtr; score=790.41; evalue=0.00e+00;
c72767/f1p1/1659	uncharacterized protein n 1 tax solanum lycopersicum repid k4b0p3_sollc; score=517.69; evalue=0.00e+00;
c72767/f1p1/1659	uncharacterized protein n 1 tax solanum lycopersicum repid k4b0p3_sollc; score=357.45; evalue=0.00e+00;
c72767/f1p1/1659	sugar transporter putative n 1 tax ricinus communis repid b9rf04_ricco; score=357.84; evalue=4.05e-178;
c72767/f1p1/1659	sugar transporter putative n 1 tax ricinus communis repid b9rf04_ricco; score=295.82; evalue=4.05e-178;
c72767/f1p1/1659	putative erd6-like transporter n 1 tax vitis vinifera repid e3vww6_vitvi; score=347.82; evalue=2.01e-174;
c73008/f2p0/1414	uncharacterized protein n 1 tax solanum lycopersicum repid k4atj2_sollc; score=681.79; evalue=0.00e+00;
c73008/f2p0/1414	putative uncharacterized protein n 1 tax vitis vinifera repid f6i1n0_vitvi; score=487.26; evalue=1.29e-167;
c73008/f2p0/1414	predicted protein n 1 tax populus trichocarpa repid a9pgt3_poptr; score=484.95; evalue=3.12e-167;
c73008/f2p0/1414	aminocarboxymuconate-semialdehyde decarboxylase putative n 1 tax ricinus communis repid b9rma4_ricco; score=472.24; evalue=1.30e-161;
c73008/f2p0/1414	n 1 tax arabidopsis lyrata subsp. lyrata repid d7lhw4_arall; score=469.54; evalue=3.30e-161;
c73404/f2p6/1609	uncharacterized protein n 1 tax solanum lycopersicum repid k4cek4_sollc; score=937.18; evalue=0.00e+00;
c73404/f2p6/1609	putative cytochrome p-450 n 1 tax nicotiana plumbaginifolia repid q40411_nicpl; score=560.07; evalue=0.00e+00;
c73404/f2p6/1609	putative cytochrome p450 n 1 tax solanum tuberosum repid q8s9c0_soltu; score=558.52; evalue=0.00e+00;
c73404/f2p6/1609	putative cytochrome p450 n 1 tax solanum lycopersicum repid q9m4x2_sollc; score=519.62; evalue=8.10e-177;
c73404/f2p6/1609	cytochrome p450 putative n 1 tax ricinus communis repid b9rvu1_ricco; score=495.74; evalue=2.05e-167;
c73412/f2p4/2100	uncharacterized protein n 1 tax solanum lycopersicum repid k4cq45_sollc; score=1085.86; evalue=0.00e+00;
c73412/f2p4/2100	putative uncharacterized protein n 1 tax vitis vinifera repid f6h6t5_vitvi; score=989.95; evalue=0.00e+00;
c73412/f2p4/2100	calcium-dependent protein kinase putative n 1 tax ricinus communis repid b9t5w7_ricco; score=988.79; evalue=0.00e+00;
c73412/f2p4/2100	calcium dependent protein kinase 13 n 1 tax populus trichocarpa repid b9iga3_poptr; score=984.94; evalue=0.00e+00;
c73412/f2p4/2100	calcium-dependent protein kinase n 1 tax cucumis melo subsp. melo repid e5gbe9_cucme; score=978.39; evalue=0.00e+00;
c75213/f1p5/1601	serine hydroxymethyltransferase mitochondrial n 1 tax solanum tuberosum repid glym_soltu; score=926.78; evalue=0.00e+00;
c75213/f1p5/1601	serine hydroxymethyltransferase n 1 tax solanum lycopersicum repid k4bcv4_sollc; score=922.15; evalue=0.00e+00;
c75213/f1p5/1601	serine hydroxymethyltransferase n 1 tax glycine max repid c6zjz0_soybn; score=892.88; evalue=0.00e+00;
c75213/f1p5/1601	mrna clone: rtfl01-07-d21 n 1 tax eutrema halophilum repid e4mw05_theha; score=885.17; evalue=0.00e+00;
c75213/f1p5/1601	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7m9m1_arall; score=882.09; evalue=0.00e+00;

c76031/f1p17/2065	atp synthase subunit beta n 1 tax solanum lycopersicum repid k4bnr2_sollc; score=1004.59; evalue=0.00e+00;
c76031/f1p17/2065	atp synthase subunit beta mitochondrial n 1 tax nicotiana plumbaginifolia repid atpbm_nicpl; score=991.88; evalue=0.00e+00;
c76031/f1p17/2065	atp synthase subunit beta n 1 tax solanum lycopersicum repid k4bx20_sollc; score=988.79; evalue=0.00e+00;
c76031/f1p17/2065	atp synthase subunit beta n 1 tax nicotiana sylvestris repid o82721_nicsy; score=971.07; evalue=0.00e+00;
c76031/f1p17/2065	atp synthase subunit beta n 1 tax nicotiana sylvestris repid o82722_nicsy; score=969.53; evalue=0.00e+00;
c76662/f24p11/3155	cytosine-specific methyltransferase n 1 tax solanum lycopersicum repid k4di54_sollc; score=1667.90; evalue=0.00e+00;
c76662/f24p11/3155	chromomethylase n 2 tax nicotiana sylvestris repid b1gyh3_nicsy; score=1089.33; evalue=0.00e+00;
c76662/f24p11/3155	chromomethylase-like protein n 1 tax nicotiana tabacum repid q8h0h2_tobac; score=1071.23; evalue=0.00e+00;
c76662/f24p11/3155	chromomethylase 3 n 1 tax nicotiana benthamiana repid i3vkd1_nicbe; score=1056.20; evalue=0.00e+00;
c76662/f24p11/3155	cytosine-specific methyltransferase n 1 tax solanum lycopersicum repid k4ash6_sollc; score=986.87; evalue=0.00e+00;
c79304/f3p6/1415	uncharacterized protein n 1 tax solanum lycopersicum repid k4byc1_sollc; score=719.92; evalue=0.00e+00;
c79304/f3p6/1415	uncharacterized protein n 1 tax glycine max repid i1k070_soybn; score=646.74; evalue=0.00e+00;
c79304/f3p6/1415	putative uncharacterized protein n 1 tax glycine max repid c6the5_soybn; score=642.11; evalue=0.00e+00;
c79304/f3p6/1415	putative uncharacterized protein n 1 tax vitis vinifera repid d7smf7_vitvi; score=640.57; evalue=0.00e+00;
c79304/f3p6/1415	pectate lyase n 1 tax gossypium herbaceum repid d3izz1_goshe; score=640.19; evalue=0.00e+00;
c79371/f32p5/1182	uncharacterized protein n 11 tax solanum repid k4axb5_sollc; score=464.92; evalue=1.75e-161;
c79371/f32p5/1182	putative uncharacterized protein n 1 tax vitis vinifera repid f6h560_vitvi; score=449.51; evalue=1.24e-154;
c79371/f32p5/1182	atp synthase subunit d putative n 1 tax ricinus communis repid b9sal7_ricco; score=447.59; evalue=2.17e-154;
c79371/f32p5/1182	atp synthase subunit d putative n 1 tax ricinus communis repid b9t370_ricco; score=446.43; evalue=6.17e-154;
c79371/f32p5/1182	predicted protein n 2 tax populus trichocarpa repid b9gjs3_poptr; score=437.19; evalue=2.91e-150;
c79498/f649p50/1039	chlorophyll a-b binding protein 3c chloroplastic n 1 tax solanum lycopersicum repid cb2g_sollc; score=490.73; evalue=4.58e-172;
c79498/f649p50/1039	chlorophyll a-b binding protein 3c-like n 1 tax solanum tuberosum repid q2xte0_soltu; score=487.65; evalue=6.44e-171;
c79498/f649p50/1039	uncharacterized protein n 1 tax solanum lycopersicum repid k4be01_sollc; score=486.49; evalue=1.88e-170;
c79498/f649p50/1039	chlorophyll a-b binding protein 40 chloroplastic n 1 tax nicotiana tabacum repid cb24_tobac; score=486.49; evalue=2.31e-170;
c79498/f649p50/1039	light harvesting chlorophyll a/b-binding protein n 1 tax nicotiana sylvestris repid o64446_nicsy; score=486.11; evalue=3.32e-170;
c80287/f2p4/1996	uncharacterized protein n 1 tax solanum lycopersicum repid k4aw47_sollc; score=1008.05; evalue=0.00e+00;
c80287/f2p4/1996	galactokinase putative n 1 tax ricinus communis repid b9rzt4_ricco; score=871.69; evalue=0.00e+00;
c80287/f2p4/1996	uncharacterized protein n 2 tax glycine max repid i1kmp3_soybn; score=867.84; evalue=0.00e+00;
c80287/f2p4/1996	uncharacterized protein n 2 tax glycine max repid i1mrt3_soybn; score=867.07; evalue=0.00e+00;
c80287/f2p4/1996	putative uncharacterized protein n 1 tax vitis vinifera repid f6h710_vitvi; score=866.30; evalue=0.00e+00;
c80533/f2p1/1899	elongation factor ts n 1 tax solanum lycopersicum repid k4ccp7_sollc; score=905.59; evalue=0.00e+00;

c80533/f2p1/1899	elongation factor ts n 1 tax vitis vinifera repid f6hh07_vitvi; score=498.05; evalue=3.67e-159;
c80533/f2p1/1899	elongation factor ts n 1 tax ricinus communis repid b9rkl9_ricco; score=416.77; evalue=8.24e-130;
c80533/f2p1/1899	elongation factor ts (fragment) n 1 tax populus trichocarpa repid b9ilq4_poptr; score=409.07; evalue=8.65e-127;
c80533/f2p1/1899	at4g29060/f19b15_90 n 1 tax arabidopsis thaliana repid q93zg6_arath; score=360.53; evalue=3.36e-114;
c81527/f1p2/1633	uncharacterized protein n 1 tax solanum lycopersicum repid k4ct72_sollc; score=758.06; evalue=0.00e+00;
c81527/f1p2/1633	putative uncharacterized protein n 1 tax vitis vinifera repid d7sk79_vitvi; score=520.78; evalue=5.98e-178;
c81527/f1p2/1633	putative uncharacterized protein n 1 tax ricinus communis repid b9s3d3_ricco; score=515.38; evalue=7.26e-176;
c81527/f1p2/1633	predicted protein n 1 tax populus trichocarpa repid b9gj76_poptr; score=499.20; evalue=1.78e-169;
c81527/f1p2/1633	uncharacterized protein n 1 tax glycine max repid i1m4z3_soybn; score=489.19; evalue=8.29e-166;
c81589/f1p0/1558	uncharacterized protein n 1 tax solanum lycopersicum repid k4bs54_sollc; score=322.01; evalue=4.51e-117;
c81589/f1p0/1558	uncharacterized protein n 1 tax solanum lycopersicum repid k4bs54_sollc; score=128.26; evalue=4.51e-117;
c81589/f1p0/1558	uncharacterized protein n 1 tax solanum lycopersicum repid k4bs53_sollc; score=312.00; evalue=1.65e-99;
c81589/f1p0/1558	putative uncharacterized protein n 1 tax ricinus communis repid b9shk8_ricco; score=226.48; evalue=1.36e-87;
c81589/f1p0/1558	putative uncharacterized protein n 1 tax ricinus communis repid b9shk8_ricco; score=125.18; evalue=1.36e-87;
c82131/f1p1/1776	putative transcription factor n 1 tax solanum tuberosum repid q70mt1_soltu; score=533.10; evalue=0.00e+00;
c82131/f1p1/1776	tcp transcription factor 24 n 1 tax solanum lycopersicum repid g3bgw3_sollc; score=468.00; evalue=2.43e-157;
c82131/f1p1/1776	uncharacterized protein n 1 tax solanum lycopersicum repid k4ckj0_sollc; score=462.23; evalue=3.54e-155;
c82131/f1p1/1776	uncharacterized protein n 1 tax solanum lycopersicum repid k4cki9_sollc; score=368.62; evalue=1.49e-119;
c82131/f1p1/1776	tcp transcription factor n 1 tax camellia sinensis repid j7f3k5_camsi; score=254.22; evalue=6.87e-74;
c82398/f2p0/2116	uncharacterized protein n 1 tax solanum lycopersicum repid k4da23_sollc; score=766.92; evalue=0.00e+00;
c82398/f2p0/2116	uncharacterized protein n 1 tax solanum lycopersicum repid k4c9e0_sollc; score=565.46; evalue=0.00e+00;
c82398/f2p0/2116	expressed protein putative n 1 tax ricinus communis repid b9scx1_ricco; score=537.34; evalue=0.00e+00;
c82398/f2p0/2116	putative uncharacterized protein n 1 tax vitis vinifera repid f6hhd7_vitvi; score=522.70; evalue=4.13e-175;
c82398/f2p0/2116	predicted protein n 1 tax populus trichocarpa repid b9hq41_poptr; score=512.69; evalue=3.65e-171;
c82425/f1p2/2211	uncharacterized protein n 1 tax solanum lycopersicum repid q93x45_sollc; score=1325.46; evalue=0.00e+00;
c82425/f1p2/2211	uncharacterized protein n 1 tax solanum lycopersicum repid q93x46_sollc; score=1109.36; evalue=0.00e+00;
c82425/f1p2/2211	putative uncharacterized protein n 1 tax vitis vinifera repid d7spi5_vitvi; score=1044.65; evalue=0.00e+00;
c82425/f1p2/2211	uncharacterized protein n 1 tax glycine max repid i1lhn4_soybn; score=1041.95; evalue=0.00e+00;
c82425/f1p2/2211	xaa-pro aminopeptidase putative n 1 tax ricinus communis repid b9sgi3_ricco; score=1035.79; evalue=0.00e+00;
c82776/f1p2/1327	putative 1-deoxy-d-xylulose 5-phosphate synthase 2 n 1 tax solanum habrochaites repid q68ip4_solha; score=749.20; evalue=0.00e+00;
c82776/f1p2/1327	uncharacterized protein n 1 tax solanum lycopersicum repid k4d5p3_sollc; score=747.66; evalue=0.00e+00;

c82776/f1p2/1327	1-deoxy-d-xylulose 5-phosphate synthase 2 n 1 tax solanum lycopersicum repid c7u111_sollc; score=742.65; evalue=0.00e+00;
c82776/f1p2/1327	chloroplast 1-deoxy-d-xylulose-5-phosphate synthase n 1 tax eucommia ulmoides repid k4k2d9_eucul; score=671.77; evalue=0.00e+00;
c82776/f1p2/1327	1-deoxyxylulose 5-phosphate synthase n 1 tax catharanthus roseus repid o82676_catro; score=671.39; evalue=0.00e+00;
c83471/f1p6/2009	uncharacterized protein n 1 tax solanum lycopersicum repid k4b9y6_sollc; score=1131.32; evalue=0.00e+00;
c83471/f1p6/2009	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta n 2 tax solanaceae repid pfpb_soltu; score=1080.86; evalue=0.00e+00;
c83471/f1p6/2009	predicted protein n 2 tax populus trichocarpa repid b9hze4_poptr; score=941.03; evalue=0.00e+00;
c83471/f1p6/2009	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta n 1 tax ricinus communis repid pfpb_ricco; score=934.87; evalue=0.00e+00;
c83471/f1p6/2009	phosphofructokinase putative n 1 tax ricinus communis repid b9rxe7_ricco; score=934.48; evalue=0.00e+00;
c83562/f1p16/1838	isph protein n 1 tax solanum lycopersicum repid d0vny3_sollc; score=926.78; evalue=0.00e+00;
c83562/f1p16/1838	lytb-like protein-like n 1 tax solanum tuberosum repid q2xtb5_soltu; score=901.35; evalue=0.00e+00;
c83562/f1p16/1838	1-hydroxy-2-methyl-2-(e)-butenyl 4-diphosphate reductase n 1 tax nicotiana langsdorffii x nicotiana sanderae repid b3f8g9_nicls; score=881.32; evalue=0.00e+00;
c83562/f1p16/1838	1-hydroxy-2-methyl-butenyl 4-diphosphate reductase n 2 tax nicotiana benthamiana repid g0t511_nicbe; score=879.40; evalue=0.00e+00;
c83562/f1p16/1838	chloroplast 1-hydroxy-2-methyl-butenyl 4-diphosphate reductase n 1 tax nicotiana tabacum repid q9spl9_tobac; score=872.08; evalue=0.00e+00;
c83775/f1p1/1830	uncharacterized protein n 1 tax solanum lycopersicum repid k4clq3_sollc; score=983.01; evalue=0.00e+00;
c83775/f1p1/1830	putative uncharacterized protein n 1 tax vitis vinifera repid f6h3e4_vitvi; score=655.60; evalue=0.00e+00;
c83775/f1p1/1830	ankyrin repeat-containing protein putative n 1 tax ricinus communis repid b9rs18_ricco; score=653.28; evalue=0.00e+00;
c83775/f1p1/1830	predicted protein n 1 tax populus trichocarpa repid b9ikj8_poptr; score=650.97; evalue=0.00e+00;
c83775/f1p1/1830	putative uncharacterized protein n 1 tax vitis vinifera repid a5ank4_vitvi; score=643.65; evalue=0.00e+00;
c84258/f1p0/1412	mads16 n 1 tax solanum tuberosum repid q537g4_soltu; score=417.93; evalue=6.43e-142;
c84258/f1p0/1412	mads transcriptional factor n 1 tax solanum tuberosum repid o48871_soltu; score=412.54; evalue=7.77e-140;
c84258/f1p0/1412	mads domain mpf2-like transcription factor n 6 tax withania repid c9wxv0_9sola; score=375.17; evalue=4.85e-125;
c84258/f1p0/1412	mpf2-like n 1 tax vassobia breviflora repid a8qyw3_9sola; score=373.63; evalue=4.18e-124;
c84258/f1p0/1412	msm2 n 1 tax solanum macrocarpon repid q537h0_solma; score=371.70; evalue=7.63e-124;
c85030/f2p3/1754	ubiquitin c variant n 9 tax eukaryota repid e7raa7_picad; score=766.15; evalue=0.00e+00;
c85030/f2p3/1754	ubiquitin c variant n 9 tax eukaryota repid e7raa7_picad; score=260.00; evalue=0.00e+00;
c85030/f2p3/1754	ubiquitin c variant n 9 tax eukaryota repid e7raa7_picad; score=766.92; evalue=0.00e+00;
c85030/f2p3/1754	ubiquitin c variant n 9 tax eukaryota repid e7raa7_picad; score=766.92; evalue=0.00e+00;
c85030/f2p3/1754	ubiquitin c variant n 9 tax eukaryota repid e7raa7_picad; score=766.92; evalue=0.00e+00;
c85610/f4p2/1330	uncharacterized protein n 1 tax solanum lycopersicum repid k4bf65_sollc; score=568.15; evalue=0.00e+00;
c85610/f4p2/1330	putative uncharacterized protein n 1 tax ricinus communis repid b9r9d1_ricco; score=461.07; evalue=5.01e-158;
c85610/f4p2/1330	putative uncharacterized protein n 2 tax vitis vinifera repid a5c998_vitvi; score=439.11; evalue=2.25e-149;

c85610/f4p2/1330	uncharacterized protein n 1 tax glycine max repid i1ngs2_soybn; score=432.95; evalue=3.88e-147;
c85610/f4p2/1330	uncharacterized protein n 1 tax glycine max repid k7ll39_soybn; score=424.86; evalue=4.32e-144;
c85832/f1p1/1887	predicted protein n 1 tax populus trichocarpa repid b9hnj6_poptr; score=774.24; evalue=0.00e+00;
c85832/f1p1/1887	putative uncharacterized protein n 1 tax vitis vinifera repid f6hag4_vitvi; score=770.00; evalue=0.00e+00;
c85832/f1p1/1887	transcription factor putative n 1 tax ricinus communis repid b9sb74_ricco; score=766.92; evalue=0.00e+00;
c85832/f1p1/1887	predicted protein n 1 tax populus trichocarpa repid b9gfs8_poptr; score=766.53; evalue=0.00e+00;
c85832/f1p1/1887	uncharacterized protein n 1 tax glycine max repid i1m771_soybn; score=760.75; evalue=0.00e+00;
c86413/f2p5/3088	uncharacterized protein n 1 tax solanum lycopersicum repid k4d6k8_sollc; score=1570.06; evalue=0.00e+00;
c86413/f2p5/3088	predicted protein n 1 tax populus trichocarpa repid b9gn40_poptr; score=476.48; evalue=5.56e-147;
c86413/f2p5/3088	sentrin/sumo-specific protease putative n 1 tax ricinus communis repid b9s9i8_ricco; score=439.50; evalue=1.09e-134;
c86413/f2p5/3088	predicted protein n 1 tax populus trichocarpa repid b9h6v2_poptr; score=423.70; evalue=3.08e-131;
c86413/f2p5/3088	uncharacterized protein n 1 tax glycine max repid k7kj36_soybn; score=427.94; evalue=5.55e-130;
c86733/f3p3/1993	uncharacterized protein n 1 tax solanum lycopersicum repid k4b202_sollc; score=705.29; evalue=0.00e+00;
c86733/f3p3/1993	putative uncharacterized protein n 1 tax vitis vinifera repid f6h966_vitvi; score=672.54; evalue=0.00e+00;
c86733/f3p3/1993	uncharacterized protein n 1 tax glycine max repid i1kuk8_soybn; score=648.28; evalue=0.00e+00;
c86733/f3p3/1993	uncharacterized protein n 1 tax glycine max repid i1mdp6_soybn; score=645.58; evalue=0.00e+00;
c86733/f3p3/1993	predicted protein n 1 tax populus trichocarpa repid b9gzf9_poptr; score=645.20; evalue=0.00e+00;
c87049/f30p7/1554	uncharacterized protein n 1 tax solanum lycopersicum repid k4b3y2_sollc; score=542.35; evalue=0.00e+00;
c87049/f30p7/1554	putative uncharacterized protein n 1 tax vitis vinifera repid f6i126_vitvi; score=246.13; evalue=2.94e-72;
c87049/f30p7/1554	putative uncharacterized protein n 1 tax vitis vinifera repid a5bqn4_vitvi; score=246.51; evalue=1.91e-67;
c87049/f30p7/1554	uncharacterized protein n 1 tax glycine max repid i1lpn1_soybn; score=201.44; evalue=8.90e-56;
c87049/f30p7/1554	translation initiation factor n 1 tax cucumis melo subsp. melo repid e5gc13_cucme; score=201.06; evalue=2.37e-55;
c88309/f32p20/1684	uncharacterized protein n 1 tax solanum lycopersicum repid k4d9s4_sollc; score=895.58; evalue=0.00e+00;
c88309/f32p20/1684	uncharacterized protein n 1 tax solanum lycopersicum repid k4d9s5_sollc; score=767.69; evalue=0.00e+00;
c88309/f32p20/1684	putative glucosyltransferase n 1 tax solanum lycopersicum repid q8rxa4_sollc; score=491.12; evalue=4.35e-166;
c88309/f32p20/1684	putative uncharacterized protein n 1 tax vitis vinifera repid f6hku5_vitvi; score=493.43; evalue=1.33e-165;
c88309/f32p20/1684	udp-glucose glucosyltransferase n 1 tax gardenia jasminoides repid f8wkw6_9gent; score=489.57; evalue=6.10e-165;
c88381/f24p7/1076	uncharacterized protein n 1 tax solanum lycopersicum repid k4axn3_sollc; score=479.94; evalue=4.53e-168;
c88381/f24p7/1076	aluminum-induced protein n 1 tax codonopsis lanceolata repid q5mcr8_9astr; score=433.72; evalue=6.34e-150;
c88381/f24p7/1076	al-induced protein n 1 tax gossypium hirsutum repid q6uk15_goshi; score=426.02; evalue=6.13e-147;
c88381/f24p7/1076	putative uncharacterized protein n 1 tax solanum tuberosum repid q3hrw3_soltu; score=424.09; evalue=7.37e-146;

c88381/f24p7/1076	predicted protein n 1 tax populus trichocarpa repid a9pef3_poptr; score=418.31; evalue=7.44e-144;
c88578/f33p22/1616	uncharacterized protein n 1 tax solanum lycopersicum repid k4b825_sollc; score=714.92; evalue=0.00e+00;
c88578/f33p22/1616	putative uncharacterized protein n 1 tax vitis vinifera repid d7tk66_vitvi; score=587.41; evalue=0.00e+00;
c88578/f33p22/1616	katanin p60 atpase-containing subunit putative n 1 tax ricinus communis repid b9s114_ricco; score=587.03; evalue=0.00e+00;
c88578/f33p22/1616	uncharacterized protein n 1 tax lotus japonicus repid i3shp0_lotja; score=572.78; evalue=0.00e+00;
c88578/f33p22/1616	uncharacterized protein n 1 tax glycine max repid i1k345_soybn; score=568.54; evalue=0.00e+00;
c89021/f21p40/1688	uncharacterized protein n 1 tax solanum lycopersicum repid k4c9c7_sollc; score=831.63; evalue=0.00e+00;
c89021/f21p40/1688	uncharacterized protein n 1 tax solanum lycopersicum repid k4atc7_sollc; score=739.18; evalue=0.00e+00;
c89021/f21p40/1688	putative uncharacterized protein n 1 tax vitis vinifera repid f6gyl5_vitvi; score=712.61; evalue=0.00e+00;
c89021/f21p40/1688	predicted protein n 2 tax populus trichocarpa repid b9hv17_poptr; score=704.90; evalue=0.00e+00;
c89021/f21p40/1688	sterol delta-7 reductase dwf5 n 1 tax gossypium hirsutum repid q2qcx7_goshi; score=699.12; evalue=0.00e+00;
c89023/f5p1/2181	proton pump interactor 1 n 1 tax solanum tuberosum repid d5l6g0_soltu; score=979.16; evalue=0.00e+00;
c89023/f5p1/2181	uncharacterized protein n 1 tax solanum lycopersicum repid k4cgz3_sollc; score=957.21; evalue=0.00e+00;
c89023/f5p1/2181	predicted protein n 1 tax populus trichocarpa repid b9hzv0_poptr; score=487.65; evalue=5.42e-160;
c89023/f5p1/2181	putative uncharacterized protein n 1 tax vitis vinifera repid a5c436_vitvi; score=482.64; evalue=4.51e-159;
c89023/f5p1/2181	putative uncharacterized protein n 1 tax vitis vinifera repid f6h241_vitvi; score=483.03; evalue=7.34e-159;
c89330/f1p4/1712	uncharacterized protein n 1 tax solanum lycopersicum repid k4cwq9_sollc; score=865.14; evalue=0.00e+00;
c89330/f1p4/1712	putative uncharacterized protein n 1 tax vitis vinifera repid f6gwe5_vitvi; score=755.75; evalue=0.00e+00;
c89330/f1p4/1712	putative uncharacterized protein n 1 tax vitis vinifera repid a5bn70_vitvi; score=747.27; evalue=0.00e+00;
c89330/f1p4/1712	predicted protein n 1 tax populus trichocarpa repid a9p9k8_poptr; score=729.55; evalue=0.00e+00;
c89330/f1p4/1712	udp-d-glucuronic acid 4-epimerase n 1 tax medicago truncatula repid g7ja85_medtr; score=727.24; evalue=0.00e+00;
c89498/f2p2/3374	uncharacterized protein n 1 tax solanum lycopersicum repid k4b147_sollc; score=1333.55; evalue=0.00e+00;
c89498/f2p2/3374	putative uncharacterized protein n 1 tax vitis vinifera repid f6i4r0_vitvi; score=358.99; evalue=1.78e-105;
c89498/f2p2/3374	uncharacterized protein n 1 tax glycine max repid i1lb70_soybn; score=326.63; evalue=3.22e-93;
c89498/f2p2/3374	uncharacterized protein n 1 tax glycine max repid k7n5b7_soybn; score=320.47; evalue=1.88e-90;
c89498/f2p2/3374	splicing factor arginine/serine-rich 2 rnap interacting protein putative n 1 tax ricinus communis repid b9rfg0_ricco; score=301.98; evalue=1.67e-84;
c90279/f4p1/2218	uncharacterized protein n 1 tax solanum lycopersicum repid k4bwe4_sollc; score=1058.51; evalue=0.00e+00;
c90279/f4p1/2218	chloroplast envelope protein 1 n 1 tax nicotiana benthamiana repid c9e9w2_nicbe; score=978.39; evalue=0.00e+00;
c90279/f4p1/2218	leucine rich repeat-containing protein putative n 1 tax ricinus communis repid b9s2j9_ricco; score=803.13; evalue=0.00e+00;
c90279/f4p1/2218	uncharacterized protein n 1 tax glycine max repid k7k653_soybn; score=793.88; evalue=0.00e+00;
c90279/f4p1/2218	nucleotide-binding oligomerization domain-containing protein n 2 tax medicago truncatula repid g7k465_medtr; score=781.17; evalue=0.00e+00;

c90393/f1p0/1551	uncharacterized protein n 1 tax solanum lycopersicum repid k4d645_sollc; score=326.25; evalue=6.72e-171;
c90393/f1p0/1551	uncharacterized protein n 1 tax solanum lycopersicum repid k4d645_sollc; score=302.75; evalue=6.72e-171;
c90393/f1p0/1551	putative uncharacterized protein n 1 tax vitis vinifera repid e0cnn9_vitvi; score=283.49; evalue=1.82e-149;
c90393/f1p0/1551	putative uncharacterized protein n 1 tax vitis vinifera repid e0cnn9_vitvi; score=274.63; evalue=1.82e-149;
c90393/f1p0/1551	uncharacterized protein n 1 tax solanum lycopersicum repid k4c292_sollc; score=279.64; evalue=4.48e-148;
c90492/f1p0/1724	uncharacterized protein n 1 tax solanum lycopersicum repid k4bk48_sollc; score=724.55; evalue=0.00e+00;
c90492/f1p0/1724	putative uncharacterized protein n 1 tax vitis vinifera repid d7shf5_vitvi; score=625.93; evalue=0.00e+00;
c90492/f1p0/1724	predicted protein n 1 tax populus trichocarpa repid b9i3i7_poptr; score=619.39; evalue=0.00e+00;
c90492/f1p0/1724	copine putative n 1 tax ricinus communis repid b9rar5_ricco; score=618.23; evalue=0.00e+00;
c90492/f1p0/1724	uncharacterized protein n 1 tax glycine max repid i1kc97_soybn; score=605.13; evalue=0.00e+00;
c90718/f1p0/1855	uncharacterized protein n 1 tax solanum lycopersicum repid k4bfk6_sollc; score=677.94; evalue=0.00e+00;
c90718/f1p0/1855	uncharacterized protein n 1 tax solanum lycopersicum repid k4bal0_sollc; score=593.58; evalue=0.00e+00;
c90718/f1p0/1855	predicted protein n 1 tax populus trichocarpa repid a9pfh7_poptr; score=592.04; evalue=0.00e+00;
c90718/f1p0/1855	protein phosphatase 2c putative n 1 tax ricinus communis repid b9sxa9_ricco; score=588.96; evalue=0.00e+00;
c90718/f1p0/1855	protein phosphatase 2c homolog n 1 tax mesembryanthemum crystallinum repid q9zsq7_mescr; score=588.96; evalue=0.00e+00;
c90719/f1p2/1581	uncharacterized protein n 1 tax solanum lycopersicum repid k4cuf5_sollc; score=689.88; evalue=0.00e+00;
c90719/f1p2/1581	potassium channel regulatory factor putative n 1 tax ricinus communis repid b9s407_ricco; score=551.59; evalue=0.00e+00;
c90719/f1p2/1581	uncharacterized protein n 1 tax glycine max repid i1n9i5_soybn; score=550.05; evalue=0.00e+00;
c90719/f1p2/1581	putative uncharacterized protein n 1 tax vitis vinifera repid f6hi43_vitvi; score=550.05; evalue=0.00e+00;
c90719/f1p2/1581	uncharacterized protein n 1 tax glycine max repid i1jnv3_soybn; score=544.27; evalue=0.00e+00;
c90751/f1p0/1492	uncharacterized protein n 1 tax solanum lycopersicum repid k4c8n1_sollc; score=808.13; evalue=0.00e+00;
c90751/f1p0/1492	uncharacterized protein n 1 tax solanum lycopersicum repid k4bkb5_sollc; score=696.81; evalue=0.00e+00;
c90751/f1p0/1492	putative uncharacterized protein n 1 tax ricinus communis repid b9ray3_ricco; score=639.03; evalue=0.00e+00;
c90751/f1p0/1492	putative uncharacterized protein n 1 tax vitis vinifera repid f6gsl1_vitvi; score=635.95; evalue=0.00e+00;
c90751/f1p0/1492	uncharacterized protein n 1 tax glycine max repid i1k029_soybn; score=635.95; evalue=0.00e+00;
c91427/f1p3/1299	uncharacterized protein n 1 tax solanum lycopersicum repid k4bdg0_sollc; score=611.68; evalue=0.00e+00;
c91427/f1p3/1299	3-ketoacyl-coa reductase 1 n 1 tax gossypium hirsutum repid q0vh88_goshi; score=549.67; evalue=0.00e+00;
c91427/f1p3/1299	predicted protein n 2 tax populus repid b9htf0_poptr; score=526.55; evalue=0.00e+00;
c91427/f1p3/1299	steroid dehydrogenase putative n 1 tax ricinus communis repid b9rmr2_ricco; score=523.09; evalue=0.00e+00;
c91427/f1p3/1299	uncharacterized protein n 1 tax medicago truncatula repid i3t5s9_medtr; score=520.39; evalue=0.00e+00;
c91471/f1p1/1873	uncharacterized protein n 1 tax solanum lycopersicum repid k4czr5_sollc; score=750.36; evalue=0.00e+00;

c91471/f1p1/1873	emb1692 n 1 tax arabidopsis lyrata subsp. lyrata repid d7mnd5_arall; score=461.07; evalue=7.73e-153;
c91471/f1p1/1873	putative uncharacterized protein n 1 tax ricinus communis repid b9sb45_ricco; score=447.97; evalue=5.78e-148;
c91471/f1p1/1873	predicted protein n 1 tax populus trichocarpa repid b9gua5_poptr; score=447.20; evalue=1.60e-147;
c91471/f1p1/1873	uncharacterized protein n 1 tax glycine max repid k7lvz7_soybn; score=446.82; evalue=3.03e-147;
c91557/f1p0/1982	uncharacterized protein n 1 tax solanum lycopersicum repid k4d2e2_sollc; score=897.12; evalue=0.00e+00;
c91557/f1p0/1982	putative uncharacterized protein n 1 tax vitis vinifera repid f6hlh3_vitvi; score=737.64; evalue=0.00e+00;
c91557/f1p0/1982	predicted protein n 1 tax populus trichocarpa repid b9iib4_poptr; score=718.38; evalue=0.00e+00;
c91557/f1p0/1982	uncharacterized protein n 1 tax glycine max repid k7kf34_soybn; score=690.65; evalue=0.00e+00;
c91557/f1p0/1982	uncharacterized protein n 1 tax glycine max repid k7kf34_soybn; score=142.90; evalue=0.00e+00;
c91588/f1p9/1655	uncharacterized protein n 1 tax solanum lycopersicum repid k4bl24_sollc; score=921.38; evalue=0.00e+00;
c91588/f1p9/1655	flavonoid 3'-monooxygenase n 1 tax petunia x hybrida repid f3ph_pethy; score=835.10; evalue=0.00e+00;
c91588/f1p9/1655	flavonoid-3'-hydroxylase n 1 tax vitis vinifera repid q2uyu6_vitvi; score=762.30; evalue=0.00e+00;
c91588/f1p9/1655	flavonoid 3'-hydroxylase n 1 tax vitis vinifera repid q3c212_vitvi; score=761.91; evalue=0.00e+00;
c91588/f1p9/1655	putative uncharacterized protein n 1 tax vitis vinifera repid a5bu46_vitvi; score=760.75; evalue=0.00e+00;
c92166/f1p3/1533	uncharacterized protein n 1 tax solanum lycopersicum repid k4c190_sollc; score=637.88; evalue=0.00e+00;
c92166/f1p3/1533	uncharacterized protein n 1 tax solanum lycopersicum repid k4azz1_sollc; score=582.41; evalue=0.00e+00;
c92166/f1p3/1533	ubiquitin ligase n 1 tax lotus japonicus repid h8wvc6_lotja; score=563.53; evalue=0.00e+00;
c92166/f1p3/1533	uncharacterized protein n 1 tax glycine max repid i1kas8_soybn; score=552.75; evalue=0.00e+00;
c92166/f1p3/1533	sina1 n 1 tax medicago truncatula repid a8w460_medtr; score=549.67; evalue=0.00e+00;
c92192/f1p3/2013	uncharacterized protein n 1 tax solanum lycopersicum repid k4c227_sollc; score=1122.07; evalue=0.00e+00;
c92192/f1p3/2013	chaperonin-60kd ch60 putative n 1 tax ricinus communis repid b9rwq2_ricco; score=1040.80; evalue=0.00e+00;
c92192/f1p3/2013	putative uncharacterized protein n 1 tax vitis vinifera repid d7ts57_vitvi; score=1030.39; evalue=0.00e+00;
c92192/f1p3/2013	putative uncharacterized protein n 1 tax arabidopsis lyrata subsp. lyrata repid d7l4a9_arall; score=1030.39; evalue=0.00e+00;
c92192/f1p3/2013	chaperonin cpn60 mitochondrial n 2 tax brassicaceae repid ch60a_arath; score=1030.01; evalue=0.00e+00;
c92241/f1p5/1406	uncharacterized protein n 1 tax solanum lycopersicum repid k4bam6_sollc; score=372.47; evalue=1.07e-124;
c92241/f1p5/1406	rac-like gtpase 1 n 1 tax nicotiana tabacum repid q93x84_tobac; score=368.62; evalue=2.75e-123;
c92241/f1p5/1406	rac/rop-like small gtpase n 1 tax scoparia dulcis repid b9vi82_scodu; score=366.70; evalue=1.58e-122;
c92241/f1p5/1406	ntgp2 n 1 tax nicotiana tabacum repid q9s820_tobac; score=365.93; evalue=3.34e-122;
c92241/f1p5/1406	gtp-binding rop/rac gtpase n 1 tax petunia integrifolia subsp. inflata repid q06e27_petin; score=365.54; evalue=4.67e-122;
c92361/f1p6/1705	uncharacterized protein n 1 tax solanum lycopersicum repid k4cek4_sollc; score=1043.11; evalue=0.00e+00;
c92361/f1p6/1705	putative cytochrome p-450 n 1 tax nicotiana plumbaginifolia repid q40411_nicpl; score=612.07; evalue=0.00e+00;

c92361/f1p6/1705	putative cytochrome p450 n 1 tax solanum tuberosum repid q8s9c0_soltu; score=609.37; evalue=0.00e+00;
c92361/f1p6/1705	putative cytochrome p450 n 1 tax solanum lycopersicum repid q9m4x2_sollc; score=569.31; evalue=0.00e+00;
c92361/f1p6/1705	cytochrome p450 putative n 1 tax ricinus communis repid b9rvu1_ricco; score=533.87; evalue=0.00e+00;
c92610/f1p2/1569	uncharacterized protein n 1 tax solanum lycopersicum repid k4b3p3_sollc; score=684.10; evalue=0.00e+00;
c92610/f1p2/1569	uncharacterized protein n 1 tax glycine max repid i1k731_soybn; score=583.95; evalue=0.00e+00;
c92610/f1p2/1569	uncharacterized protein n 1 tax glycine max repid i1jsk3_soybn; score=578.56; evalue=0.00e+00;
c92610/f1p2/1569	clathrin binding protein putative n 1 tax ricinus communis repid b9rhc4_ricco; score=577.40; evalue=0.00e+00;
c92610/f1p2/1569	neutrophil cytosol factor n 2 tax medicago truncatula repid g7j7r7_medtr; score=575.47; evalue=0.00e+00;
c92637/f4p0/1458	uncharacterized protein n 1 tax solanum lycopersicum repid k4cw98_sollc; score=718.38; evalue=0.00e+00;
c92637/f4p0/1458	predicted protein n 1 tax populus trichocarpa repid b9mu88_poptr; score=657.14; evalue=0.00e+00;
c92637/f4p0/1458	putative uncharacterized protein n 1 tax vitis vinifera repid f6ht17_vitvi; score=656.75; evalue=0.00e+00;
c92637/f4p0/1458	uncharacterized protein n 1 tax glycine max repid c6tjl2_soybn; score=655.60; evalue=0.00e+00;
c92637/f4p0/1458	uncharacterized protein n 1 tax solanum lycopersicum repid k4c1z4_sollc; score=650.97; evalue=0.00e+00;
c92692/f1p0/1916	uncharacterized protein n 1 tax solanum lycopersicum repid k4b251_sollc; score=793.50; evalue=0.00e+00;
c92692/f1p0/1916	predicted protein n 1 tax populus trichocarpa repid b9idl6_poptr; score=145.21; evalue=1.80e-34;
c92692/f1p0/1916	uncharacterized protein n 1 tax glycine max repid k7m9p6_soybn; score=132.11; evalue=5.08e-30;
c92692/f1p0/1916	putative uncharacterized protein n 1 tax medicago truncatula repid g7il94_medtr; score=129.41; evalue=2.32e-29;
c92692/f1p0/1916	putative uncharacterized protein n 1 tax ricinus communis repid b9scp8_ricco; score=125.18; evalue=1.12e-27;
c92829/f1p3/2095	uncharacterized protein n 1 tax solanum lycopersicum repid k4b170_sollc; score=1046.57; evalue=0.00e+00;
c92829/f1p3/2095	putative pyruvate dehydrogenase e3 subunit n 1 tax capsicum annuum repid b5law5_capan; score=1005.36; evalue=0.00e+00;
c92829/f1p3/2095	dihydrolipoyl dehydrogenase n 1 tax arabidopsis thaliana repid q9m5k5_arath; score=911.75; evalue=0.00e+00;
c92829/f1p3/2095	dihydrolipoyl dehydrogenase n 1 tax arabidopsis thaliana repid a8ms68_arath; score=911.37; evalue=0.00e+00;
c92829/f1p3/2095	dihydrolipoamide dehydrogenase putative n 1 tax ricinus communis repid b9rzn2_ricco; score=910.60; evalue=0.00e+00;
c92850/f1p3/1914	putative 1-deoxy-d-xylulose 5-phosphate synthase 2 n 1 tax solanum habrochaites repid q68ip4_solha; score=1060.83; evalue=0.00e+00;
c92850/f1p3/1914	uncharacterized protein n 1 tax solanum lycopersicum repid k4d5p3_sollc; score=1059.28; evalue=0.00e+00;
c92850/f1p3/1914	1-deoxy-d-xylulose 5-phosphate synthase 2 n 1 tax solanum lycopersicum repid c7u111_sollc; score=1053.89; evalue=0.00e+00;
c92850/f1p3/1914	1-deoxyxylulose 5-phosphate synthase n 1 tax catharanthus roseus repid o82676_catro; score=971.46; evalue=0.00e+00;
c92850/f1p3/1914	chloroplast 1-deoxy-d-xylulose-5-phosphate synthase n 1 tax eucommia ulmoides repid k4k2d9_eucul; score=969.53; evalue=0.00e+00;
c93064/f1p1/1913	uncharacterized protein n 1 tax solanum lycopersicum repid k4bd33_sollc; score=824.31; evalue=0.00e+00;
c93064/f1p1/1913	putative uncharacterized protein n 1 tax vitis vinifera repid f6hss8_vitvi; score=688.34; evalue=0.00e+00;
c93064/f1p1/1913	putative short-root protein n 1 tax ipomoea nil repid a8r3j0_iponi; score=687.57; evalue=0.00e+00;

c93064/f1p1/1913	chitin-inducible gibberellin-responsive protein putative n 1 tax ricinus communis repid b9sh07_ricco; score=673.70; evalue=0.00e+00;
c93064/f1p1/1913	putative uncharacterized protein n 1 tax vitis vinifera repid a5aq59_vitvi; score=659.45; evalue=0.00e+00;
c93544/f1p2/2147	proton pump interactor 1 n 1 tax solanum tuberosum repid d5l6g0_soltu; score=979.16; evalue=0.00e+00;
c93544/f1p2/2147	uncharacterized protein n 1 tax solanum lycopersicum repid k4cgz3_sollc; score=957.21; evalue=0.00e+00;
c93544/f1p2/2147	putative uncharacterized protein n 1 tax vitis vinifera repid f6h241_vitvi; score=487.26; evalue=1.00e-160;
c93544/f1p2/2147	predicted protein n 1 tax populus trichocarpa repid b9hzv0_poptr; score=487.65; evalue=3.85e-160;
c93544/f1p2/2147	putative uncharacterized protein n 1 tax vitis vinifera repid a5c436_vitvi; score=482.64; evalue=3.20e-159;
c93980/f5p4/1244	uncharacterized protein n 1 tax solanum lycopersicum repid k4be74_sollc; score=430.64; evalue=1.02e-146;
c93980/f5p4/1244	uncharacterized protein n 1 tax solanum lycopersicum repid k4b978_sollc; score=305.83; evalue=1.66e-97;
c93980/f5p4/1244	putative uncharacterized protein n 1 tax vitis vinifera repid a5bxh1_vitvi; score=259.61; evalue=1.21e-79;
c93980/f5p4/1244	putative uncharacterized protein n 1 tax vitis vinifera repid f6hws4_vitvi; score=260.77; evalue=1.62e-79;
c93980/f5p4/1244	uncharacterized protein n 1 tax medicago truncatula repid i3s047_medtr; score=207.22; evalue=1.01e-59;
c93997/f10p13/1645	uncharacterized protein n 9 tax solanum repid k4by24_sollc; score=811.22; evalue=0.00e+00;
c93997/f10p13/1645	putative uncharacterized protein n 2 tax vitis vinifera repid f6htu0_vitvi; score=722.24; evalue=0.00e+00;
c93997/f10p13/1645	putative uncharacterized protein n 1 tax vitis vinifera repid a5aeb0_vitvi; score=714.92; evalue=0.00e+00;
c93997/f10p13/1645	predicted protein n 1 tax populus trichocarpa repid b9i7r0_poptr; score=707.21; evalue=0.00e+00;
c93997/f10p13/1645	predicted protein n 2 tax populus trichocarpa repid b9hxp3_poptr; score=706.44; evalue=0.00e+00;
c94022/f1p3/1071	uncharacterized protein n 2 tax solanum lycopersicum repid k4cfj6_sollc; score=607.83; evalue=0.00e+00;
c94022/f1p3/1071	predicted protein n 2 tax populus trichocarpa repid b9inr2_poptr; score=509.99; evalue=3.98e-179;
c94022/f1p3/1071	xyloglucan endotransglycosylase n 1 tax populus tremula x populus tremuloides repid a1yz21_9rosi; score=509.61; evalue=8.11e-179;
c94022/f1p3/1071	predicted protein n 1 tax populus trichocarpa repid a9pc40_poptr; score=506.91; evalue=8.62e-178;
c94022/f1p3/1071	putative uncharacterized protein n 1 tax vitis vinifera repid a5bhg3_vitvi; score=506.14; evalue=1.71e-177;
c94239/f1p1/1108	uncharacterized protein n 1 tax solanum lycopersicum repid k4bq05_sollc; score=270.78; evalue=1.76e-85;
c94239/f1p1/1108	putative uncharacterized protein n 1 tax solanum tuberosum repid q2xtd1_soltu; score=104.38; evalue=9.33e-43;
c94239/f1p1/1108	putative uncharacterized protein n 1 tax solanum tuberosum repid q2xtd1_soltu; score=97.06; evalue=9.33e-43;
c94239/f1p1/1108	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2a0_sollc; score=126.72; evalue=4.05e-30;
c94239/f1p1/1108	uncharacterized protein n 1 tax solanum lycopersicum repid k4d672_sollc; score=117.47; evalue=4.60e-27;
c94301/f5p0/1458	uncharacterized protein n 1 tax solanum lycopersicum repid k4cw98_sollc; score=718.77; evalue=0.00e+00;
c94301/f5p0/1458	predicted protein n 1 tax populus trichocarpa repid b9mu88_poptr; score=657.52; evalue=0.00e+00;
c94301/f5p0/1458	putative uncharacterized protein n 1 tax vitis vinifera repid f6ht17_vitvi; score=657.14; evalue=0.00e+00;
c94301/f5p0/1458	uncharacterized protein n 1 tax glycine max repid c6tjl2_soybn; score=655.60; evalue=0.00e+00;

c94301/f5p0/1458	uncharacterized protein n 1 tax solanum lycopersicum repid k4c1z4_sollc; score=651.36; evalue=0.00e+00;
c94313/f2p2/1459	uncharacterized protein n 1 tax solanum lycopersicum repid k4crb0_sollc; score=625.55; evalue=0.00e+00;
c94313/f2p2/1459	phantastica n 1 tax solanum lycopersicum repid q9xh12_sollc; score=621.70; evalue=0.00e+00;
c94313/f2p2/1459	phantastica n 1 tax nicotiana benthamiana repid g3adu5_nicbe; score=605.52; evalue=0.00e+00;
c94313/f2p2/1459	phantastica n 1 tax nicotiana tabacum repid q6q504_tobac; score=597.82; evalue=0.00e+00;
c94313/f2p2/1459	myb family transcription factor n 1 tax castanea mollissima repid d1lxi9_9rosi; score=494.58; evalue=5.52e-170;
c94500/f1p24/1018	uncharacterized protein n 1 tax solanum lycopersicum repid k4btw8_sollc; score=476.86; evalue=1.55e-166;
c94500/f1p24/1018	uncharacterized protein n 2 tax solanum repid k4bt19_sollc; score=476.48; evalue=2.02e-166;
c94500/f1p24/1018	40s ribosomal protein s2 n 1 tax medicago truncatula repid g7lal7_medtr; score=434.49; evalue=6.46e-150;
c94500/f1p24/1018	uncharacterized protein n 1 tax glycine max repid i1k5k3_soybn; score=431.80; evalue=5.87e-149;
c94500/f1p24/1018	40s ribosomal protein s2 n 1 tax cucumis melo subsp. melo repid e5gby7_cucme; score=431.41; evalue=1.00e-148;
c94508/f3p3/2952	uncharacterized protein n 1 tax solanum lycopersicum repid k4cl50_sollc; score=1753.41; evalue=0.00e+00;
c94508/f3p3/2952	putative uncharacterized protein n 1 tax vitis vinifera repid d7stt1_vitvi; score=1433.70; evalue=0.00e+00;
c94508/f3p3/2952	putative uncharacterized protein n 1 tax vitis vinifera repid a5aq52_vitvi; score=1429.46; evalue=0.00e+00;
c94508/f3p3/2952	puromycin-sensitive aminopeptidase putative n 1 tax ricinus communis repid b9rqt2_ricco; score=1391.33; evalue=0.00e+00;
c94508/f3p3/2952	uncharacterized protein n 1 tax glycine max repid k7ki86_soybn; score=1385.16; evalue=0.00e+00;
c94681/f15p19/1502	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2q2_sollc; score=763.84; evalue=0.00e+00;
c94681/f15p19/1502	putative uncharacterized protein n 1 tax vitis vinifera repid d7spn8_vitvi; score=683.33; evalue=0.00e+00;
c94681/f15p19/1502	predicted protein n 1 tax populus trichocarpa repid a9pdx0_poptr; score=680.25; evalue=0.00e+00;
c94681/f15p19/1502	predicted protein n 1 tax populus trichocarpa repid a9p9k5_poptr; score=678.71; evalue=0.00e+00;
c94681/f15p19/1502	translation initiation factor n 1 tax elaeis guineensis repid b3tm17_elagv; score=675.24; evalue=0.00e+00;
c94740/f9p9/1130	uncharacterized protein n 1 tax solanum lycopersicum repid k4b778_sollc; score=559.68; evalue=0.00e+00;
c94740/f9p9/1130	mitochondrial outer membrane protein porin of 34 kda n 1 tax solanum tuberosum repid vdac1_soltu; score=559.68; evalue=0.00e+00;
c94740/f9p9/1130	voltage-dependent anion channel n 1 tax nicotiana tabacum repid a9cm22_tobac; score=532.72; evalue=0.00e+00;
c94740/f9p9/1130	34 kda outer mitochondrial membrane protein porin-like protein n 1 tax solanum tuberosum repid q2pyx4_soltu; score=496.51; evalue=8.76e-174;
c94740/f9p9/1130	uncharacterized protein n 2 tax magnoliophyta repid k4bgt9_sollc; score=493.81; evalue=1.15e-171;
c94839/f1p10/1645	uncharacterized protein n 1 tax solanum lycopersicum repid k4b3f4_sollc; score=821.23; evalue=0.00e+00;
c94839/f1p10/1645	putative uncharacterized protein n 1 tax vitis vinifera repid d7tpx8_vitvi; score=712.99; evalue=0.00e+00;
c94839/f1p10/1645	uncharacterized protein n 1 tax medicago truncatula repid i3t0q3_medtr; score=687.57; evalue=0.00e+00;
c94839/f1p10/1645	uncharacterized protein n 1 tax glycine max repid i1lq57_soybn; score=684.10; evalue=0.00e+00;
c94839/f1p10/1645	uncharacterized protein n 1 tax glycine max repid i1lq58_soybn; score=682.17; evalue=0.00e+00;

c95105/f14p8/1625	uncharacterized protein n 1 tax solanum lycopersicum repid k4cc33_sollc; score=759.99; evalue=0.00e+00;
c95105/f14p8/1625	26s proteasome subunit rpn7 n 1 tax capsicum annuum repid a0mkc7_capan; score=717.23; evalue=0.00e+00;
c95105/f14p8/1625	26s proteasome non-atpase regulatory subunit putative n 1 tax ricinus communis repid b9ram4_ricco; score=672.54; evalue=0.00e+00;
c95105/f14p8/1625	predicted protein n 1 tax populus trichocarpa repid b9if58_poptr; score=669.08; evalue=0.00e+00;
c95105/f14p8/1625	26s proteasome non-atpase regulatory subunit n 1 tax cucumis melo subsp. melo repid e5gbw6_cucme; score=666.38; evalue=0.00e+00;
c95175/f1p7/2725	transketolase 1 n 1 tax capsicum annuum repid o78327_capan; score=1348.95; evalue=0.00e+00;
c95175/f1p7/2725	uncharacterized protein n 1 tax solanum lycopersicum repid k4cyv4_sollc; score=1304.27; evalue=0.00e+00;
c95175/f1p7/2725	plastid transketolase n 1 tax nicotiana tabacum repid c3rxi5_tobac; score=1301.96; evalue=0.00e+00;
c95175/f1p7/2725	transketolase chloroplastic n 1 tax solanum tuberosum repid tktc_soltu; score=1296.57; evalue=0.00e+00;
c95175/f1p7/2725	transketolase putative n 1 tax ricinus communis repid b9rda1_ricco; score=1259.20; evalue=0.00e+00;
c95462/f3p9/1927	uncharacterized protein n 1 tax solanum lycopersicum repid k4cd52_sollc; score=888.64; evalue=0.00e+00;
c95462/f3p9/1927	putative chlorophyll b reductase n 1 tax nicotiana tabacum repid b5m0y6_tobac; score=882.86; evalue=0.00e+00;
c95462/f3p9/1927	uncharacterized protein n 1 tax glycine max repid i1kiq4_soybn; score=692.96; evalue=0.00e+00;
c95462/f3p9/1927	uncharacterized protein n 1 tax glycine max repid i1l4i7_soybn; score=686.41; evalue=0.00e+00;
c95462/f3p9/1927	oxidoreductase n 1 tax medicago truncatula repid g7kpv9_medtr; score=673.32; evalue=0.00e+00;
c95491/f3p4/3212	auxin response factor 4 n 1 tax solanum lycopersicum repid q2lai9_sollc; score=1580.07; evalue=0.00e+00;
c95491/f3p4/3212	putative arf4 protein n 1 tax petunia x hybrida repid c9e9n5_pethy; score=1378.23; evalue=0.00e+00;
c95491/f3p4/3212	putative uncharacterized protein n 1 tax vitis vinifera repid d7skv9_vitvi; score=1113.60; evalue=0.00e+00;
c95491/f3p4/3212	auxin response factor putative n 1 tax ricinus communis repid b9sk50_ricco; score=1075.85; evalue=0.00e+00;
c95491/f3p4/3212	uncharacterized protein n 1 tax glycine max repid k7lvf7_soybn; score=1006.51; evalue=0.00e+00;
c95548/f1p1/1525	tyrosyl-trna synthetase n 1 tax nicotiana tabacum repid p93363_tobac; score=733.02; evalue=0.00e+00;
c95548/f1p1/1525	uncharacterized protein n 1 tax solanum lycopersicum repid k4b3e9_sollc; score=681.79; evalue=0.00e+00;
c95548/f1p1/1525	putative uncharacterized protein n 1 tax vitis vinifera repid d7tvz2_vitvi; score=646.35; evalue=0.00e+00;
c95548/f1p1/1525	putative uncharacterized protein n 1 tax vitis vinifera repid a5bh76_vitvi; score=645.20; evalue=0.00e+00;
c95548/f1p1/1525	tyrosyl-trna synthetase putative n 1 tax ricinus communis repid b9rup0_ricco; score=637.49; evalue=0.00e+00;
c95570/f5p3/1870	uncharacterized protein n 1 tax solanum lycopersicum repid k4d413_sollc; score=977.62; evalue=0.00e+00;
c95570/f5p3/1870	uncharacterized protein n 1 tax solanum lycopersicum repid k4bw06_sollc; score=969.15; evalue=0.00e+00;
c95570/f5p3/1870	rna helicase-like protein n 1 tax gossypium hirsutum repid d6n3h0_goshi; score=719.15; evalue=0.00e+00;
c95570/f5p3/1870	putative uncharacterized protein n 1 tax vitis vinifera repid f6hkf1_vitvi; score=704.90; evalue=0.00e+00;
c95570/f5p3/1870	dead box rna helicase n 1 tax populus alba x populus tremula var. glandulosa repid d9ilu3_9rosi; score=685.64; evalue=0.00e+00;
c95587/f4p9/3179	uncharacterized protein n 1 tax solanum lycopersicum repid k4d2t3_sollc; score=1447.95; evalue=0.00e+00;

c95587/f4p9/3179	anthranilate phosphoribosyltransferase-like protein n 1 tax arabidopsis thaliana repid q9m2r0_arath; score=1394.02; evalue=0.00e+00;
c95587/f4p9/3179	anthranilate phosphoribosyltransferase-like protein n 2 tax arabidopsis thaliana repid q0tv71_arath; score=1393.25; evalue=0.00e+00;
c95587/f4p9/3179	at3g57880/t10k17_90 n 1 tax arabidopsis thaliana repid q94jq8_arath; score=1392.48; evalue=0.00e+00;
c95587/f4p9/3179	anthranilate phosphoribosyltransferase-like protein n 1 tax medicago truncatula repid a2q4u9_medtr; score=1390.94; evalue=0.00e+00;
c95814/f11p6/1376	putative strictosidine synthase n 1 tax solanum lycopersicum repid q9lkw1_sollc; score=626.32; evalue=0.00e+00;
c95814/f11p6/1376	uncharacterized protein n 1 tax solanum lycopersicum repid k4cga7_sollc; score=624.78; evalue=0.00e+00;
c95814/f11p6/1376	uncharacterized protein n 1 tax solanum lycopersicum repid k4cga8_sollc; score=485.34; evalue=5.05e-166;
c95814/f11p6/1376	uncharacterized protein n 1 tax solanum lycopersicum repid k4d2k2_sollc; score=442.19; evalue=1.63e-149;
c95814/f11p6/1376	strictosidine synthase-like protein n 1 tax nicotiana tabacum repid a7wpl3_tobac; score=435.65; evalue=7.90e-147;
c96055/f24p12/2017	uncharacterized protein n 1 tax solanum lycopersicum repid k4b438_sollc; score=982.25; evalue=0.00e+00;
c96055/f24p12/2017	vacuolar atpase subunit b n 1 tax mesembryanthemum crystallinum repid q8gub5_mescr; score=975.31; evalue=0.00e+00;
c96055/f24p12/2017	predicted protein n 1 tax populus trichocarpa repid a9pck1_poptr; score=972.23; evalue=0.00e+00;
c96055/f24p12/2017	v-type atp synthase beta chain n 1 tax medicago truncatula repid g7ksi7_medtr; score=969.53; evalue=0.00e+00;
c96055/f24p12/2017	uncharacterized protein n 1 tax solanum lycopersicum repid k4d1f7_sollc; score=967.61; evalue=0.00e+00;
c96178/f3p1/1662	uncharacterized protein n 1 tax solanum lycopersicum repid k4ayr4_sollc; score=488.03; evalue=2.04e-167;
c96178/f3p1/1662	protein kinase ck2 regulatory subunit 2 n 1 tax nicotiana tabacum repid q8lpd2_tobac; score=474.55; evalue=3.28e-162;
c96178/f3p1/1662	predicted protein n 1 tax populus trichocarpa repid b9mv44_poptr; score=458.76; evalue=8.04e-156;
c96178/f3p1/1662	predicted protein n 2 tax populus repid b9gp84_poptr; score=437.96; evalue=1.47e-147;
c96178/f3p1/1662	uncharacterized protein n 1 tax solanum lycopersicum repid k4c1a0_sollc; score=433.33; evalue=5.52e-146;
c96184/f9p7/1542	uncharacterized protein n 1 tax solanum lycopersicum repid k4cnb0_sollc; score=800.04; evalue=0.00e+00;
c96184/f9p7/1542	putative uncharacterized protein n 1 tax vitis vinifera repid d7ttj6_vitvi; score=596.27; evalue=0.00e+00;
c96184/f9p7/1542	putative uncharacterized protein n 1 tax vitis vinifera repid a5agj0_vitvi; score=575.47; evalue=0.00e+00;
c96184/f9p7/1542	placental protein 11 putative n 1 tax ricinus communis repid b9rur9_ricco; score=543.89; evalue=0.00e+00;
c96184/f9p7/1542	uncharacterized protein n 1 tax glycine max repid i1mva1_soybn; score=525.40; evalue=0.00e+00;
c96202/f10p2/1621	putative uncharacterized protein n 1 tax solanum tuberosum repid q3hrx8_soltu; score=876.32; evalue=0.00e+00;
c96202/f10p2/1621	uncharacterized protein n 1 tax solanum lycopersicum repid k4c4w6_sollc; score=875.16; evalue=0.00e+00;
c96202/f10p2/1621	putative uncharacterized protein n 1 tax solanum tuberosum repid q3hrz9_soltu; score=874.00; evalue=0.00e+00;
c96202/f10p2/1621	oligoendopeptidase f n 1 tax helicobacter pylori hp h-4 repid j0n5l2_helpx; score=869.77; evalue=0.00e+00;
c96202/f10p2/1621	tubulin beta chain putative n 1 tax ricinus communis repid b9r9a9_ricco; score=869.77; evalue=0.00e+00;
c96384/f13p8/1394	uncharacterized protein n 1 tax solanum lycopersicum repid k4c2c7_sollc; score=630.94; evalue=0.00e+00;
c96384/f13p8/1394	tsc13 protein n 1 tax nicotiana benthamiana repid q3iaa0_nicbe; score=609.76; evalue=0.00e+00;

c96384/f13p8/1394	enoyl-coa reductase n 1 tax nicotiana tabacum repid h9cci1_tobac; score=605.90; evalue=0.00e+00;
c96384/f13p8/1394	synaptic glycoprotein sc2 putative n 1 tax ricinus communis repid b9sxz3_ricco; score=577.01; evalue=0.00e+00;
c96384/f13p8/1394	trans-2-enoyl-coa reductase n 1 tax gossypium hirsutum repid a9xug8_goshi; score=573.16; evalue=0.00e+00;
c96413/f1p64/1104	chlorophyll a-b binding protein 7 chloroplastic n 1 tax solanum lycopersicum repid cb12_sollc; score=544.66; evalue=0.00e+00;
c96413/f1p64/1104	lysr family transcriptional regulator n 1 tax rhodanobacter thiooxydans lcs2 repid i4wv39_9gamm; score=529.25; evalue=0.00e+00;
c96413/f1p64/1104	chlorophyll a-b binding protein chloroplastic n 1 tax petunia x hybrida repid cb12_pethy; score=508.83; evalue=7.22e-179;
c96413/f1p64/1104	sss sodium solute transporter superfamily protein n 1 tax rhodanobacter thiooxydans lcs2 repid i4wv38_9gamm; score=509.99; evalue=1.76e-171;
c96413/f1p64/1104	light-harvesting complex i protein lhca2 n 1 tax populus trichocarpa repid b9gml1_poptr; score=483.80; evalue=5.83e-169;
c96443/f6p2/1338	uncharacterized protein n 1 tax solanum lycopersicum repid k4axy3_sollc; score=484.95; evalue=3.02e-167;
c96443/f6p2/1338	putative uncharacterized protein n 1 tax ricinus communis repid b9scd5_ricco; score=300.83; evalue=3.18e-95;
c96443/f6p2/1338	uncharacterized protein n 1 tax solanum lycopersicum repid k4b5d0_sollc; score=294.66; evalue=7.12e-93;
c96443/f6p2/1338	putative uncharacterized protein n 1 tax vitis vinifera repid d7t9m0_vitvi; score=283.11; evalue=1.62e-88;
c96443/f6p2/1338	predicted protein n 1 tax populus trichocarpa repid b9icr7_poptr; score=282.72; evalue=3.05e-88;
c96512/f2p4/1396	uncharacterized protein n 1 tax solanum lycopersicum repid k4bh21_sollc; score=663.30; evalue=0.00e+00;
c96512/f2p4/1396	putative uncharacterized protein n 1 tax vitis vinifera repid d7ti59_vitvi; score=475.32; evalue=9.96e-163;
c96512/f2p4/1396	putative uncharacterized protein n 1 tax ricinus communis repid b9shg7_ricco; score=466.85; evalue=1.77e-159;
c96512/f2p4/1396	predicted protein n 1 tax populus trichocarpa repid b9ipp5_poptr; score=462.61; evalue=1.11e-157;
c96512/f2p4/1396	galactose mutarotase-like n 1 tax medicago truncatula repid a2q5n9_medtr; score=459.53; evalue=1.56e-156;
c96528/f11p11/2202	granule-bound starch synthase 1 chloroplastic/amyloplastic n 11 tax solanum repid ssg1_soltu; score=1186.40; evalue=0.00e+00;
c96528/f11p11/2202	granule-bound starch synthase n 1 tax solanum tuberosum repid b0zte3_soltu; score=1175.61; evalue=0.00e+00;
c96528/f11p11/2202	uncharacterized protein n 4 tax solanum lycopersicum repid k4cpx6_sollc; score=1159.05; evalue=0.00e+00;
c96528/f11p11/2202	granule-bound starch synthase 1 chloroplastic/amyloplastic n 1 tax antirrhinum majus repid ssg1_antma; score=986.87; evalue=0.00e+00;
c96528/f11p11/2202	granule-bound starch synthase i n 3 tax ipomoea batatas repid d4ahs6_ipoba; score=974.54; evalue=0.00e+00;
c96711/f1p4/3125	uncharacterized protein n 1 tax solanum lycopersicum repid k4cwj1_sollc; score=1708.35; evalue=0.00e+00;
c96711/f1p4/3125	chromosome transmission fidelity factor putative n 1 tax ricinus communis repid b9rwk5_ricco; score=948.35; evalue=0.00e+00;
c96711/f1p4/3125	chromosome transmission fidelity protein 18 n 1 tax arabidopsis thaliana repid f4i5s3_arath; score=917.92; evalue=0.00e+00;
c96711/f1p4/3125	uncharacterized protein n 1 tax glycine max repid k7n258_soybn; score=911.37; evalue=0.00e+00;
c96711/f1p4/3125	uncharacterized protein n 1 tax glycine max repid k7liz1_soybn; score=909.83; evalue=0.00e+00;
c96804/f1p8/3314	uncharacterized protein n 1 tax solanum lycopersicum repid k4b991_sollc; score=1465.29; evalue=0.00e+00;
c96804/f1p8/3314	putative uncharacterized protein n 1 tax vitis vinifera repid f6gzf1_vitvi; score=630.94; evalue=0.00e+00;
c96804/f1p8/3314	putative uncharacterized protein n 1 tax ricinus communis repid b9rz42_ricco; score=569.70; evalue=0.00e+00;

c96804/f1p8/3314	uncharacterized protein n 1 tax glycine max repid i1m287_soybn; score=477.63; evalue=6.82e-148;
c96804/f1p8/3314	uncharacterized protein n 2 tax glycine max repid k7ma29_soybn; score=466.85; evalue=1.41e-143;
c96874/f42p7/1740	uncharacterized protein n 1 tax solanum lycopersicum repid k4cc33_sollc; score=759.99; evalue=0.00e+00;
c96874/f42p7/1740	26s proteasome subunit rpn7 n 1 tax capsicum annuum repid a0mkc7_capan; score=717.23; evalue=0.00e+00;
c96874/f42p7/1740	26s proteasome non-atpase regulatory subunit putative n 1 tax ricinus communis repid b9ram4_ricco; score=672.54; evalue=0.00e+00;
c96874/f42p7/1740	predicted protein n 1 tax populus trichocarpa repid b9if58_poptr; score=669.08; evalue=0.00e+00;
c96874/f42p7/1740	26s proteasome non-atpase regulatory subunit n 1 tax cucumis melo subsp. melo repid e5gbw6_cucme; score=666.38; evalue=0.00e+00;
c96875/f1p7/1928	uncharacterized protein n 1 tax solanum lycopersicum repid k4b8i7_sollc; score=961.06; evalue=0.00e+00;
c96875/f1p7/1928	at2g34250 protein n 2 tax arabidopsis repid o80774_arath; score=892.11; evalue=0.00e+00;
c96875/f1p7/1928	sec61 transport protein n 1 tax populus trichocarpa repid b9n8w6_poptr; score=891.34; evalue=0.00e+00;
c96875/f1p7/1928	putative uncharacterized protein at1g29310 n 1 tax arabidopsis thaliana repid q8rwj5_arath; score=890.57; evalue=0.00e+00;
c96875/f1p7/1928	sec61 transport protein n 1 tax populus trichocarpa repid a9pg45_poptr; score=890.18; evalue=0.00e+00;
c96917/f1p4/1191	uncharacterized protein n 1 tax solanum lycopersicum repid k4b778_sollc; score=559.68; evalue=0.00e+00;
c96917/f1p4/1191	mitochondrial outer membrane protein porin of 34 kda n 1 tax solanum tuberosum repid vdac1_soltu; score=559.68; evalue=0.00e+00;
c96917/f1p4/1191	voltage-dependent anion channel n 1 tax nicotiana tabacum repid a9cm22_tobac; score=532.72; evalue=0.00e+00;
c96917/f1p4/1191	kda outer mitochondrial membrane protein porin-like protein n 1 tax solanum tuberosum repid q2pyx4_soltu; score=496.51; evalue=1.93e-173;
c96917/f1p4/1191	uncharacterized protein n 2 tax magnoliophyta repid k4bgt9_sollc; score=493.81; evalue=2.52e-171;
c97395/f5p3/1468	uncharacterized protein n 1 tax solanum lycopersicum repid k4cg27_sollc; score=583.56; evalue=0.00e+00;
c97395/f5p3/1468	putative uncharacterized protein n 1 tax vitis vinifera repid f6gxr6_vitvi; score=469.54; evalue=1.66e-160;
c97395/f5p3/1468	putative uncharacterized protein n 1 tax ricinus communis repid b9rw84_ricco; score=436.80; evalue=7.48e-148;
c97395/f5p3/1468	uncharacterized protein n 1 tax glycine max repid k7ky75_soybn; score=414.07; evalue=7.15e-139;
c97395/f5p3/1468	predicted protein (fragment) n 1 tax populus trichocarpa repid b9i6h4_poptr; score=412.92; evalue=8.51e-139;
c97406/f20p8/2309	3-hydroxy-3-methylglutaryl coenzyme a reductase 1 n 1 tax solanum tuberosum repid h2bnm0_soltu; score=1154.81; evalue=0.00e+00;
c97406/f20p8/2309	3-hydroxy-3-methylglutaryl coenzyme a reductase 1 n 1 tax solanum chacoense repid h2bnm1_solch; score=1154.04; evalue=0.00e+00;
c97406/f20p8/2309	uncharacterized protein n 4 tax solanum lycopersicum repid k4ba96_sollc; score=1152.50; evalue=0.00e+00;
c97406/f20p8/2309	3-hydroxy-3-methylglutaryl-coenzyme a reductase 1 n 1 tax solanum tuberosum repid hmdh1_soltu; score=1145.95; evalue=0.00e+00;
c97406/f20p8/2309	hydroxy-methylglutaryl-coenzyme a reductase n 1 tax nicotiana tabacum repid o48624_tobac; score=1087.79; evalue=0.00e+00;
c97482/f4p37/1477	uncharacterized protein n 1 tax solanum lycopersicum repid k4dcq6_sollc; score=766.92; evalue=0.00e+00;
c97482/f4p37/1477	nadph:protochlorophyllide oxidoreductase n 1 tax nicotiana tabacum repid q8lsz3_tobac; score=674.47; evalue=0.00e+00;
c97482/f4p37/1477	uncharacterized protein n 3 tax solanum lycopersicum repid k4cxm0_sollc; score=661.37; evalue=0.00e+00;
c97482/f4p37/1477	putative uncharacterized protein n 1 tax vitis vinifera repid e0csp0_vitvi; score=649.43; evalue=0.00e+00;

c97482/f4p37/1477	predicted protein n 1 tax populus trichocarpa repid b9hzx4_poptr; score=636.72; evalue=0.00e+00;
c97498/f4p12/2157	heat shock cognate 70 kda protein 2 n 1 tax solanum lycopersicum repid k4d473_sollc; score=1234.94; evalue=0.00e+00;
c97498/f4p12/2157	heat shock cognate 70 kda protein 2 n 1 tax solanum lycopersicum repid hsp72_sollc; score=1230.31; evalue=0.00e+00;
c97498/f4p12/2157	heat shock protein 70 isoform 2 n 1 tax solanum lycopersicum repid h1zxa8_sollc; score=1228.00; evalue=0.00e+00;
c97498/f4p12/2157	uncharacterized protein n 5 tax magnoliophyta repid k4d9l5_sollc; score=1208.36; evalue=0.00e+00;
c97498/f4p12/2157	heat shock protein 70-3 n 1 tax nicotiana tabacum repid q67bd0_tobac; score=1207.59; evalue=0.00e+00;
c97524/f13p1/1284	uncharacterized protein n 1 tax solanum lycopersicum repid k4by04_sollc; score=226.10; evalue=1.42e-66;
c97524/f13p1/1284	uncharacterized protein n 1 tax solanum lycopersicum repid k4by07_sollc; score=187.19; evalue=1.84e-52;
c97524/f13p1/1284	uncharacterized protein n 1 tax solanum lycopersicum repid k4by08_sollc; score=171.78; evalue=3.99e-47;
c97524/f13p1/1284	uncharacterized protein n 1 tax solanum lycopersicum repid k4by03_sollc; score=160.23; evalue=9.30e-43;
c97524/f13p1/1284	uncharacterized protein n 1 tax solanum lycopersicum repid k4bnf9_sollc; score=112.85; evalue=4.41e-25;
c97526/f9p9/1620	uncharacterized protein n 1 tax solanum lycopersicum repid k4blr2_sollc; score=888.64; evalue=0.00e+00;
c97526/f9p9/1620	putative hydroxycinnamoyl transferase n 1 tax capsicum annuum repid b5lav0_capan; score=866.68; evalue=0.00e+00;
c97526/f9p9/1620	shikimate o-hydroxycinnamoyltransferase n 1 tax nicotiana tabacum repid hst_tobac; score=857.05; evalue=0.00e+00;
c97526/f9p9/1620	hydroxycinnamoyl transferase n 1 tax coffea arabica repid q05hb0_cofar; score=786.18; evalue=0.00e+00;
c97526/f9p9/1620	hydroxycinnamoyl-coa shikimate/quinate hydroxycinnamoyltransferase n 1 tax coffea arabica repid a4zki0_cofar; score=785.02; evalue=0.00e+00;
c97530/f1p18/1812	fatty acid hydroperoxide lyase n 1 tax solanum tuberosum repid c7enw3_soltu; score=926.39; evalue=0.00e+00;
c97530/f1p18/1812	fatty acid hydroperoxide lyase n 1 tax solanum tuberosum repid q93x18_soltu; score=924.08; evalue=0.00e+00;
c97530/f1p18/1812	uncharacterized protein n 1 tax solanum lycopersicum repid k4cf70_sollc; score=909.83; evalue=0.00e+00;
c97530/f1p18/1812	fatty acid hydroperoxide lyase n 1 tax solanum lycopersicum repid q9arh8_sollc; score=907.52; evalue=0.00e+00;
c97530/f1p18/1812	fatty acid hydroperoxide lyase n 1 tax solanum lycopersicum repid q9lla9_sollc; score=907.13; evalue=0.00e+00;
c97540/f6p36/3264	uncharacterized protein n 1 tax solanum lycopersicum repid k4cfr0_sollc; score=1536.55; evalue=0.00e+00;
c97540/f6p36/3264	putative uncharacterized protein n 1 tax vitis vinifera repid e0cti4_vitvi; score=1430.23; evalue=0.00e+00;
c97540/f6p36/3264	26s proteasome regulatory subunit rpn1 putative n 1 tax ricinus communis repid b9rvt9_ricco; score=1429.46; evalue=0.00e+00;
c97540/f6p36/3264	uncharacterized protein n 1 tax glycine max repid i1ls70_soybn; score=1405.58; evalue=0.00e+00;
c97540/f6p36/3264	uncharacterized protein n 2 tax papilionoideae repid i1key6_soybn; score=1405.19; evalue=0.00e+00;
c97586/f6p14/1304	nad-dependent glyceraldehyde 3-p dehydrogenase n 1 tax solanum chacoense repid c9drq8_solch; score=620.93; evalue=0.00e+00;
c97586/f6p14/1304	uncharacterized protein n 1 tax solanum lycopersicum repid k4c8r4_sollc; score=620.16; evalue=0.00e+00;
c97586/f6p14/1304	glyceraldehyde-3-phosphate dehydrogenase n 1 tax nicotiana tabacum repid q9xg67_tobac; score=592.04; evalue=0.00e+00;
c97586/f6p14/1304	glyceraldehyde 3-phosphate dehydrogenase n 1 tax solanum tuberosum repid k7wny2_soltu; score=588.57; evalue=0.00e+00;
c97586/f6p14/1304	glyceraldehyde-3-phosphate dehydrogenase cytosolic n 1 tax petunia x hybrida repid g3pc_pethy; score=587.80; evalue=0.00e+00;

c97807/f19p57/1863	s-adenosylmethionine decarboxylase proenzyme n 1 tax solanum tuberosum repid dcam_soltu; score=669.46; evalue=0.00e+00;
c97807/f19p57/1863	s-adenosylmethionine decarboxylase proenzyme (fragment) n 1 tax solanum peruvianum repid a8him6_solpe; score=660.22; evalue=0.00e+00;
c97807/f19p57/1863	s-adenosylmethionine decarboxylase proenzyme (fragment) n 4 tax lycopersicon repid e7cd00_9soln; score=660.22; evalue=0.00e+00;
c97807/f19p57/1863	s-adenosylmethionine decarboxylase proenzyme (fragment) n 1 tax solanum chilense repid a8hiq1_solci; score=659.83; evalue=0.00e+00;
c97807/f19p57/1863	s-adenosylmethionine decarboxylase proenzyme n 1 tax solanum lycopersicum repid a5jme7_sollc; score=660.60; evalue=0.00e+00;
c97858/f5p4/1223	uncharacterized protein n 1 tax solanum lycopersicum repid k4cff0_sollc; score=659.45; evalue=0.00e+00;
c97858/f5p4/1223	peroxidase n 1 tax solanum lycopersicum repid q07446_sollc; score=654.05; evalue=0.00e+00;
c97858/f5p4/1223	uncharacterized protein n 1 tax solanum lycopersicum repid k4cff3_sollc; score=529.63; evalue=0.00e+00;
c97858/f5p4/1223	uncharacterized protein n 1 tax solanum lycopersicum repid k4cff2_sollc; score=527.71; evalue=0.00e+00;
c97858/f5p4/1223	uncharacterized protein n 1 tax solanum lycopersicum repid k4c0t4_sollc; score=521.93; evalue=0.00e+00;
c97859/f3p3/1857	uncharacterized protein n 1 tax solanum lycopersicum repid k4bfe0_sollc; score=787.33; evalue=0.00e+00;
c97859/f3p3/1857	uncharacterized protein n 1 tax solanum lycopersicum repid k4b9s1_sollc; score=668.31; evalue=0.00e+00;
c97859/f3p3/1857	putative uncharacterized protein n 1 tax vitis vinifera repid f6h7n2_vitvi; score=537.72; evalue=0.00e+00;
c97859/f3p3/1857	putative uncharacterized protein n 1 tax ricinus communis repid b9rxm0_ricco; score=509.61; evalue=1.17e-172;
c97859/f3p3/1857	uncharacterized protein n 1 tax glycine max repid i1mfg9_soybn; score=487.65; evalue=8.05e-164;
c97968/f3p3/3092	uncharacterized protein n 2 tax magnoliophyta repid k4cqu8_sollc; score=1693.71; evalue=0.00e+00;
c97968/f3p3/3092	starch branching enzyme ii n 1 tax solanum tuberosum repid q9xga6_soltu; score=1691.78; evalue=0.00e+00;
c97968/f3p3/3092	starch branching enzyme ii n 1 tax solanum tuberosum repid q9xga5_soltu; score=1683.31; evalue=0.00e+00;
c97968/f3p3/3092	starch branching enzyme ii n 1 tax solanum tuberosum repid q9xga8_soltu; score=1677.53; evalue=0.00e+00;
c97968/f3p3/3092	starch branching enzyme ii (fragment) n 1 tax solanum tuberosum repid q9xga7_soltu; score=1610.89; evalue=0.00e+00;
c98026/f2p16/1145	1-aminocyclopropane-1-carboxylate oxidase n 2 tax core eudicotyledons repid a4zyq6_sollc; score=583.18; evalue=0.00e+00;
c98026/f2p16/1145	1-aminocyclopropane-1-carboxylate oxidase n 1 tax solanum tuberosum repid q94f65_soltu; score=581.25; evalue=0.00e+00;
c98026/f2p16/1145	acc oxidase aco3 n 1 tax nicotiana attenuata repid a7kav4_nicat; score=548.89; evalue=0.00e+00;
c98026/f2p16/1145	1-amniocyclopropane-1-carboxylate oxidase n 1 tax nicotiana tabacum repid q43590_tobac; score=532.72; evalue=0.00e+00;
c98026/f2p16/1145	acc oxidase 2 isoform a n 1 tax nicotiana tabacum repid e5lcn0_tobac; score=531.18; evalue=0.00e+00;
c98056/f11p3/1412	putative uncharacterized protein n 1 tax solanum tuberosum repid q38hw1_soltu; score=559.68; evalue=0.00e+00;
c98056/f11p3/1412	uncharacterized protein n 1 tax solanum lycopersicum repid k4bdk8_sollc; score=483.41; evalue=2.72e-167;
c98056/f11p3/1412	predicted protein n 1 tax populus trichocarpa repid b9n102_poptr; score=450.28; evalue=1.05e-153;
c98056/f11p3/1412	b2 protein putative n 1 tax ricinus communis repid b9rbi2_ricco; score=444.12; evalue=3.83e-151;
c98056/f11p3/1412	uncharacterized protein n 1 tax lotus japonicus repid i3shh8_lotja; score=439.11; evalue=2.64e-149;
c98096/f2p1/1273	uncharacterized protein n 1 tax solanum lycopersicum repid k4bvx2_sollc; score=504.98; evalue=5.42e-176;

c98096/f2p1/1273	putative uncharacterized protein n 1 tax vitis vinifera repid f6h085_vitvi; score=182.57; evalue=1.42e-50;
c98096/f2p1/1273	putative uncharacterized protein n 1 tax vitis vinifera repid a5c7c8_vitvi; score=185.27; evalue=1.88e-49;
c98096/f2p1/1273	uncharacterized protein n 1 tax glycine max repid i1jsa6_soybn; score=115.55; evalue=4.69e-26;
c98096/f2p1/1273	uncharacterized protein n 1 tax glycine max repid i1k6v1_soybn; score=115.16; evalue=5.68e-26;
c98334/f2p7/1127	uncharacterized protein n 1 tax solanum lycopersicum repid k4b0q1_sollc; score=577.01; evalue=0.00e+00;
c98334/f2p7/1127	putative uncharacterized protein n 1 tax vitis vinifera repid d7u1w8_vitvi; score=441.43; evalue=8.41e-152;
c98334/f2p7/1127	putative uncharacterized protein n 1 tax ricinus communis repid b9rf18_ricco; score=416.77; evalue=4.89e-142;
c98334/f2p7/1127	uncharacterized protein n 1 tax glycine max repid i1niw9_soybn; score=414.85; evalue=2.74e-141;
c98334/f2p7/1127	uncharacterized protein n 1 tax glycine max repid c6tm31_soybn; score=414.46; evalue=3.84e-141;
c98343/f4p4/1588	sucrose-phosphatase n 1 tax solanum lycopersicum repid q84zx6_sollc; score=872.08; evalue=0.00e+00;
c98343/f4p4/1588	sucrose-phosphatase n 1 tax solanum tuberosum repid a7lh87_soltu; score=869.77; evalue=0.00e+00;
c98343/f4p4/1588	sucrose-phosphatase 2 n 1 tax nicotiana tabacum repid spp2_tobac; score=849.35; evalue=0.00e+00;
c98343/f4p4/1588	sucrose-phosphatase 1 n 1 tax nicotiana tabacum repid spp1_tobac; score=804.28; evalue=0.00e+00;
c98343/f4p4/1588	uncharacterized protein n 1 tax solanum lycopersicum repid k4asp0_sollc; score=788.49; evalue=0.00e+00;
c98344/f6p7/1753	mitogen-activated protein kinase 9 n 1 tax solanum lycopersicum repid d9j1y9_sollc; score=714.92; evalue=0.00e+00;
c98344/f6p7/1753	mitogen-activated protein kinase homolog ntf3 n 1 tax nicotiana tabacum repid ntf3_tobac; score=701.82; evalue=0.00e+00;
c98344/f6p7/1753	mitogen-activated protein kinase homolog 1 n 1 tax petunia x hybrida repid mapk_pethy; score=695.66; evalue=0.00e+00;
c98344/f6p7/1753	putative mapk2 n 1 tax catharanthus roseus repid b8lfe1_catro; score=670.62; evalue=0.00e+00;
c98344/f6p7/1753	putative uncharacterized protein n 2 tax vitis vinifera repid f6h1j2_vitvi; score=667.54; evalue=0.00e+00;
c98430/f1p0/1655	uncharacterized protein n 1 tax solanum lycopersicum repid k4bdz2_sollc; score=427.17; evalue=1.46e-141;
c98430/f1p0/1655	uncharacterized protein n 1 tax solanum lycopersicum repid k4cw78_sollc; score=397.51; evalue=2.93e-129;
c98430/f1p0/1655	putative uncharacterized protein n 1 tax vitis vinifera repid a5bk88_vitvi; score=347.05; evalue=6.84e-110;
c98430/f1p0/1655	putative uncharacterized protein n 1 tax vitis vinifera repid f6h8s2_vitvi; score=347.05; evalue=7.21e-110;
c98430/f1p0/1655	uncharacterized protein n 2 tax glycine max repid i1ni06_soybn; score=331.64; evalue=7.81e-104;
c98523/f1p2/2060	uncharacterized protein n 1 tax solanum lycopersicum repid k4b7g9_sollc; score=1016.91; evalue=0.00e+00;
c98523/f1p2/2060	putative uncharacterized protein n 1 tax vitis vinifera repid f6i2v0_vitvi; score=775.39; evalue=0.00e+00;
c98523/f1p2/2060	kinase putative n 1 tax ricinus communis repid b9s040_ricco; score=770.77; evalue=0.00e+00;
c98523/f1p2/2060	predicted protein n 1 tax populus trichocarpa repid b9mum1_poptr; score=756.13; evalue=0.00e+00;
c98523/f1p2/2060	uncharacterized protein n 1 tax setaria italica repid k3xg65_setit; score=696.04; evalue=0.00e+00;
c98561/f4p6/1414	uncharacterized protein n 1 tax solanum lycopersicum repid k4atu6_sollc; score=603.59; evalue=0.00e+00;
c98561/f4p6/1414	uncharacterized protein n 1 tax glycine max repid k7k7s2_soybn; score=512.30; evalue=1.21e-177;

c98561/f4p6/1414	putative uncharacterized protein n 1 tax vitis vinifera repid d7t9v3_vitvi; score=512.30; evalue=1.63e-177;
c98561/f4p6/1414	uncharacterized protein n 1 tax lotus japonicus repid i3sut2_lotja; score=507.29; evalue=1.18e-175;
c98561/f4p6/1414	leucine-rich repeat receptor protein kinase exs n 2 tax medicago truncatula repid g7jxx6_medtr; score=506.91; evalue=1.63e-175;
c98594/f1p5/2831	uncharacterized protein n 1 tax solanum lycopersicum repid k4cns6_sollc; score=1556.58; evalue=0.00e+00;
c98594/f1p5/2831	atsco1/atsco1/cpef-g n 1 tax arabidopsis lyrata subsp. lyrata repid d7ku74_arall; score=1328.54; evalue=0.00e+00;
c98594/f1p5/2831	putative uncharacterized protein n 2 tax vitis vinifera repid f6hhs2_vitvi; score=1318.14; evalue=0.00e+00;
c98594/f1p5/2831	translation elongation factor g putative n 1 tax ricinus communis repid b9rbp7_ricco; score=1317.37; evalue=0.00e+00;
c98594/f1p5/2831	elongation factor ef-g n 2 tax arabidopsis thaliana repid q9si75_arath; score=1314.67; evalue=0.00e+00;
c98617/f2p3/1238	uncharacterized protein n 1 tax solanum lycopersicum repid k4bk45_sollc; score=458.76; evalue=6.02e-158;
c98617/f2p3/1238	28 kda ribonucleoprotein chloroplastic n 1 tax nicotiana sylvestris repid roc3_nicsy; score=372.47; evalue=1.99e-124;
c98617/f2p3/1238	mnos-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase n 1 tax helicobacter pylori hp p-26 repid j0aaf0_helpx; score=373.24; evalue=6.53e-122;
c98617/f2p3/1238	kda ribonucleoprotein chloroplastic n 1 tax nicotiana sylvestris repid roc4_nicsy; score=348.21; evalue=2.27e-114;
c98617/f2p3/1238	uncharacterized protein n 2 tax helicobacter pylori repid j0aag7_helpx; score=320.09; evalue=3.31e-105;
c98631/f2p9/1098	cutin-deficient 1 protein n 1 tax solanum lycopersicum repid g1dex3_sollc; score=544.66; evalue=0.00e+00;
c98631/f2p9/1098	uncharacterized protein n 1 tax solanum lycopersicum repid k4bs37_sollc; score=461.84; evalue=8.41e-159;
c98631/f2p9/1098	putative uncharacterized protein n 1 tax glycine max repid c6tl20_soybn; score=455.29; evalue=2.11e-156;
c98631/f2p9/1098	zinc finger protein putative n 1 tax ricinus communis repid b9s7q1_ricco; score=454.14; evalue=6.30e-156;
c98631/f2p9/1098	putative tea geometrid larvae-inducible protein n 1 tax camellia sinensis repid c4pg05_camsi; score=450.67; evalue=2.12e-154;
c98658/f2p1/1836	uncharacterized protein n 1 tax solanum lycopersicum repid k4d2u2_sollc; score=766.53; evalue=0.00e+00;
c98658/f2p1/1836	putative uncharacterized protein n 1 tax vitis vinifera repid f6hiw7_vitvi; score=516.15; evalue=3.16e-175;
c98658/f2p1/1836	uncharacterized protein n 1 tax glycine max repid k7kjr6_soybn; score=501.52; evalue=1.37e-170;
c98658/f2p1/1836	uncharacterized protein n 1 tax glycine max repid i1kfl7_soybn; score=492.66; evalue=4.37e-167;
c98658/f2p1/1836	ubiquitin-protein ligase putative n 1 tax ricinus communis repid b9shw0_ricco; score=488.80; evalue=3.03e-165;
c98672/f6p2/821	uncharacterized protein n 1 tax solanum lycopersicum repid k4c155_sollc; score=308.53; evalue=2.78e-103;
c98672/f6p2/821	predicted protein n 3 tax fabids repid b9hdk6_poptr; score=308.53; evalue=3.35e-102;
c98672/f6p2/821	uncharacterized protein n 2 tax solanoideae repid k4civ6_sollc; score=303.91; evalue=1.52e-101;
c98672/f6p2/821	ubiquitin-conjugating enzyme ubc2 n 1 tax mesembryanthemum crystallinum repid q9spf9_mescr; score=303.14; evalue=2.92e-101;
c98672/f6p2/821	predicted protein n 1 tax populus trichocarpa repid a9pgm5_poptr; score=302.37; evalue=5.61e-101;
c98744/f5p18/1418	cysteine proteinase 3 n 1 tax solanum lycopersicum repid cysp3_sollc; score=626.71; evalue=0.00e+00;
c98744/f5p18/1418	cysteine protease n 1 tax nicotiana tabacum repid q9lri2_tobac; score=596.27; evalue=0.00e+00;
c98744/f5p18/1418	cysteine protease n 2 tax nicotiana tabacum repid c3rsf4_tobac; score=595.89; evalue=0.00e+00;

c98744/f5p18/1418	cysteine proteinase aleuran type n 1 tax nicotiana benthamiana repid q2qfr3_nicbe; score=593.19; evalue=0.00e+00;
c98744/f5p18/1418	ntcp23-like cysteine proteinase n 1 tax nicotiana tabacum repid q84yh8_tobac; score=589.73; evalue=0.00e+00;
c98844/f9p12/1139	uncharacterized protein n 1 tax solanum lycopersicum repid k4b9t4_sollc; score=573.93; evalue=0.00e+00;
c98844/f9p12/1139	lactoylglutathione lyase n 1 tax gossypium hirsutum repid d2d330_goshi; score=518.46; evalue=0.00e+00;
c98844/f9p12/1139	uncharacterized protein n 1 tax glycine max repid i1mfh9_soybn; score=512.30; evalue=1.20e-179;
c98844/f9p12/1139	uncharacterized protein n 1 tax glycine max repid i1kzt2_soybn; score=511.15; evalue=2.58e-179;
c98844/f9p12/1139	putative uncharacterized protein n 1 tax vitis vinifera repid f6h7l5_vitvi; score=513.84; evalue=1.55e-178;
c99030/f17p2/2176	uncharacterized protein n 1 tax solanum lycopersicum repid k4ces8_sollc; score=1139.02; evalue=0.00e+00;
c99030/f17p2/2176	uncharacterized protein n 1 tax solanum lycopersicum repid k4dbf7_sollc; score=971.46; evalue=0.00e+00;
c99030/f17p2/2176	putative uncharacterized protein n 1 tax vitis vinifera repid f6hhq8_vitvi; score=900.58; evalue=0.00e+00;
c99030/f17p2/2176	uncharacterized protein n 1 tax glycine max repid i1mb76_soybn; score=894.03; evalue=0.00e+00;
c99030/f17p2/2176	uncharacterized protein n 1 tax glycine max repid i1jh95_soybn; score=889.41; evalue=0.00e+00;
c99071/f6p35/1614	s-adenosylmethionine synthase 1 n 1 tax solanum tuberosum repid metk1_soltu; score=776.55; evalue=0.00e+00;
c99071/f6p35/1614	s-adenosylmethionine synthase n 1 tax solanum palustre repid metk_solbr; score=773.08; evalue=0.00e+00;
c99071/f6p35/1614	s-adenosylmethionine synthase 1 n 1 tax solanum lycopersicum repid metk1_sollc; score=768.07; evalue=0.00e+00;
c99071/f6p35/1614	s-adenosylmethionine synthetase putative n 1 tax ricinus communis repid b9rfq1_ricco; score=753.05; evalue=0.00e+00;
c99071/f6p35/1614	s-adenosylmethionine synthase 3 n 1 tax petunia x hybrida repid metk3_pethy; score=749.20; evalue=0.00e+00;
c99100/f7p5/2190	polygalacturonase-1 non-catalytic subunit beta n 1 tax solanum lycopersicum repid gp1_sollc; score=1201.04; evalue=0.00e+00;
c99100/f7p5/2190	sulfatase n 1 tax pseudomonas putida dot-t1e repid i7b5d6_psepu; score=1175.23; evalue=0.00e+00;
c99100/f7p5/2190	polygalacturonase non-catalytic subunit arogp2 n 1 tax solanum lycopersicum repid gp2_sollc; score=1087.40; evalue=0.00e+00;
c99100/f7p5/2190	polygalacturonase non-catalytic subunit arogp3 n 1 tax solanum lycopersicum repid gp3_sollc; score=1055.05; evalue=0.00e+00;
c99100/f7p5/2190	putative uncharacterized protein n 1 tax vitis vinifera repid f6hht6_vitvi; score=807.36; evalue=0.00e+00;
c99188/f3p2/1985	uncharacterized protein n 1 tax solanum lycopersicum repid k4b8m7_sollc; score=918.69; evalue=0.00e+00;
c99188/f3p2/1985	protein kinase srk n 1 tax nicotiana tabacum repid q2lag3_tobac; score=838.18; evalue=0.00e+00;
c99188/f3p2/1985	putative uncharacterized protein n 1 tax vitis vinifera repid f6hma5_vitvi; score=733.79; evalue=0.00e+00;
c99188/f3p2/1985	putative serine-threonine kinase n 1 tax gossypioides kirkii repid b2zat7_9rosi; score=730.71; evalue=0.00e+00;
c99188/f3p2/1985	cbl-interacting protein kinase 01 n 1 tax vitis vinifera repid a5bkh1_vitvi; score=726.09; evalue=0.00e+00;
c99230/f16p4/1337	uncharacterized protein n 1 tax solanum lycopersicum repid k4c3f2_sollc; score=647.12; evalue=0.00e+00;
c99230/f16p4/1337	uncharacterized protein n 1 tax solanum lycopersicum repid k4cad5_sollc; score=595.50; evalue=0.00e+00;
c99230/f16p4/1337	putative uncharacterized protein n 1 tax vitis vinifera repid d7ty71_vitvi; score=558.91; evalue=0.00e+00;
c99230/f16p4/1337	putative uncharacterized protein n 1 tax vitis vinifera repid a5asv4_vitvi; score=558.91; evalue=0.00e+00;

c99230/f16p4/1337	mitochondrial import receptor subunit tom40 putative n 1 tax ricinus communis repid b9rgh8_ricco; score=544.66; evalue=0.00e+00;
c99413/f8p3/1523	uncharacterized protein n 1 tax solanum lycopersicum repid k4b0s1_sollc; score=637.49; evalue=0.00e+00;
c99413/f8p3/1523	mevalonate kinase n 1 tax catharanthus roseus repid f6k7j9_catro; score=508.06; evalue=1.91e-174;
c99413/f8p3/1523	mevalonate kinase n 1 tax salvia miltiorrhiza repid h6vlf0_salmi; score=484.95; evalue=1.89e-165;
c99413/f8p3/1523	mevalonate kinase n 1 tax hevea brasiliensis repid q944g2_hevbr; score=481.49; evalue=4.22e-164;
c99413/f8p3/1523	putative mevalonate kinase (fragment) n 1 tax olea europaea repid j9xnf4_oleeu; score=479.94; evalue=4.27e-164;
c99451/f8p0/1632	uncharacterized protein n 1 tax solanum lycopersicum repid k4c755_sollc; score=812.37; evalue=0.00e+00;
c99451/f8p0/1632	putative uncharacterized protein n 1 tax ricinus communis repid b9sql9_ricco; score=605.52; evalue=0.00e+00;
c99451/f8p0/1632	predicted protein n 1 tax populus trichocarpa repid b9hv39_poptr; score=603.59; evalue=0.00e+00;
c99451/f8p0/1632	putative uncharacterized protein n 1 tax populus trichocarpa repid a9p9s5_poptr; score=602.44; evalue=0.00e+00;
c99451/f8p0/1632	uncharacterized protein n 1 tax glycine max repid i1kg57_soybn; score=586.64; evalue=0.00e+00;
c99522/f16p8/1679	uncharacterized protein n 1 tax solanum lycopersicum repid k4bmh7_sollc; score=662.53; evalue=0.00e+00;
c99522/f16p8/1679	uncharacterized protein n 1 tax solanum lycopersicum repid k4c7u8_sollc; score=388.65; evalue=3.86e-126;
c99522/f16p8/1679	putative uncharacterized protein n 1 tax vitis vinifera repid a5awp1_vitvi; score=330.49; evalue=1.26e-103;
c99522/f16p8/1679	putative uncharacterized protein n 1 tax vitis vinifera repid f6hx24_vitvi; score=325.87; evalue=7.18e-102;
c99522/f16p8/1679	ran-binding protein putative n 1 tax ricinus communis repid b9sqb9_ricco; score=323.55; evalue=5.16e-101;
c99569/f11p4/1945	uncharacterized protein n 1 tax solanum lycopersicum repid k4bz03_sollc; score=875.93; evalue=0.00e+00;
c99569/f11p4/1945	uncharacterized protein n 1 tax solanum lycopersicum repid k4cdu9_sollc; score=803.90; evalue=0.00e+00;
c99569/f11p4/1945	casein kinase n 1 tax beta vulgaris repid a2i5g0_betvu; score=759.21; evalue=0.00e+00;
c99569/f11p4/1945	predicted protein n 1 tax populus trichocarpa repid b9hdx8_poptr; score=754.98; evalue=0.00e+00;
c99569/f11p4/1945	predicted protein n 1 tax populus trichocarpa repid b9n5f1_poptr; score=745.73; evalue=0.00e+00;
c99607/f12p2/1619	trna-dihydrouridine synthase n 1 tax solanum lycopersicum repid k4bda2_sollc; score=789.26; evalue=0.00e+00;
c99607/f12p2/1619	uncharacterized protein n 1 tax solanum lycopersicum repid k4bg46_sollc; score=669.46; evalue=0.00e+00;
c99607/f12p2/1619	putative uncharacterized protein n 1 tax vitis vinifera repid f6h4g1_vitvi; score=623.62; evalue=0.00e+00;
c99607/f12p2/1619	trna-dihydrouridine synthase putative n 1 tax ricinus communis repid b9t4u6_ricco; score=607.83; evalue=0.00e+00;
c99607/f12p2/1619	uncharacterized protein n 1 tax glycine max repid i1k265_soybn; score=577.40; evalue=0.00e+00;
c99622/f11p3/2016	uncharacterized protein n 1 tax solanum lycopersicum repid k4dca0_sollc; score=864.37; evalue=0.00e+00;
c99622/f11p3/2016	cbl-interacting protein kinase 6 n 1 tax solanum lycopersicum repid g4xmx2_sollc; score=863.99; evalue=0.00e+00;
c99622/f11p3/2016	uncharacterized protein n 1 tax solanum lycopersicum repid k4cb16_sollc; score=711.06; evalue=0.00e+00;
c99622/f11p3/2016	cbl-interacting protein kinase 7 n 1 tax populus trichocarpa repid a0mnj4_poptr; score=697.58; evalue=0.00e+00;
c99622/f11p3/2016	cbl-interacting protein kinase 9 n 2 tax populus trichocarpa repid a0mnj6_poptr; score=692.58; evalue=0.00e+00;

c99669/f3p4/2048	uncharacterized protein n 1 tax solanum lycopersicum repid k4c7c4_sollc; score=875.54; evalue=0.00e+00;
c99669/f3p4/2048	uncharacterized protein n 1 tax solanum lycopersicum repid k4d8s6_sollc; score=614.76; evalue=0.00e+00;
c99669/f3p4/2048	putative uncharacterized protein (fragment) n 1 tax cicer arietinum repid q9len5_cicar; score=527.71; evalue=4.03e-178;
c99669/f3p4/2048	putative cytosolic factor n 1 tax trifolium pratense repid q2pf01_tripr; score=524.24; evalue=7.18e-175;
c99669/f3p4/2048	predicted protein n 1 tax populus trichocarpa repid b9n5a9_poptr; score=513.46; evalue=4.16e-172;
c99730/f5p28/1698	obtusifoliol 14alpha-demethylase n 1 tax solanum chacoense repid q673e9_solch; score=934.10; evalue=0.00e+00;
c99730/f5p28/1698	uncharacterized protein n 1 tax solanum lycopersicum repid k4at09_sollc; score=931.40; evalue=0.00e+00;
c99730/f5p28/1698	obtusifoliol 14alpha-demethylase n 1 tax solanum lycopersicum repid d9j0a9_sollc; score=929.47; evalue=0.00e+00;
c99730/f5p28/1698	obtusifoliol-14-demethylase n 1 tax nicotiana tabacum repid q8gzv0_tobac; score=907.90; evalue=0.00e+00;
c99730/f5p28/1698	obtusifoliol-14-demethylase n 1 tax petunia x hybrida repid a0pfu3_pethy; score=903.28; evalue=0.00e+00;
c99844/f3p2/1459	wd-repeat protein putative n 1 tax ricinus communis repid b9scc1_ricco; score=624.39; evalue=0.00e+00;
c99844/f3p2/1459	uncharacterized protein n 1 tax glycine max repid i1mev0_soybn; score=622.08; evalue=0.00e+00;
c99844/f3p2/1459	putative uncharacterized protein n 1 tax glycine max repid c6td87_soybn; score=620.54; evalue=0.00e+00;
c99844/f3p2/1459	uncharacterized protein n 1 tax glycine max repid i1m1r3_soybn; score=619.77; evalue=0.00e+00;
c99844/f3p2/1459	uncharacterized protein n 1 tax lotus japonicus repid i3s6v4_lotja; score=616.69; evalue=0.00e+00;
c99983/f4p3/1559	uncharacterized protein n 1 tax solanum lycopersicum repid k4cww3_sollc; score=781.94; evalue=0.00e+00;
c99983/f4p3/1559	putative uncharacterized protein n 1 tax vitis vinifera repid d7u9k6_vitvi; score=515.77; evalue=3.39e-177;
c99983/f4p3/1559	putative uncharacterized protein n 1 tax vitis vinifera repid a5bzi0_vitvi; score=498.43; evalue=4.91e-170;
c99983/f4p3/1559	uncharacterized protein n 1 tax glycine max repid i1ln48_soybn; score=481.10; evalue=8.11e-164;
c99983/f4p3/1559	uncharacterized protein n 1 tax glycine max repid k7mp69_soybn; score=481.10; evalue=3.34e-163;
c100049/f6p33/1950	catechol oxidase b chloroplastic (fragment) n 1 tax solanum tuberosum repid ppob_soltu; score=1017.68; evalue=0.00e+00;
c100049/f6p33/1950	propolyphenol oxidase (fragment) n 1 tax solanum tuberosum repid q41486_soltu; score=1010.75; evalue=0.00e+00;
c100049/f6p33/1950	uncharacterized protein n 1 tax solanum lycopersicum repid k4cmi0_sollc; score=1005.36; evalue=0.00e+00;
c100049/f6p33/1950	polyphenol oxidase e chloroplastic n 1 tax solanum lycopersicum repid ppoe_sollc; score=1003.82; evalue=0.00e+00;
c100049/f6p33/1950	uncharacterized protein n 1 tax solanum lycopersicum repid k4cmi1_sollc; score=988.79; evalue=0.00e+00;
c100339/f1p2/1631	uncharacterized protein n 1 tax solanum lycopersicum repid k4bu65_sollc; score=543.50; evalue=0.00e+00;
c100339/f1p2/1631	putative uncharacterized protein n 1 tax vitis vinifera repid f6h128_vitvi; score=323.17; evalue=1.01e-102;
c100339/f1p2/1631	dnajc14 protein putative n 1 tax ricinus communis repid b9rjw9_ricco; score=312.77; evalue=4.62e-98;
c100339/f1p2/1631	putative uncharacterized protein n 1 tax prunus persica repid a6xn08_prupe; score=306.99; evalue=2.03e-96;
c100339/f1p2/1631	Predicted protein n 1 tax populous trichocarpa repid b9gn38_poptr; score=304.68; evalue=1.41e-95