## Low Expression Profiles of Heat Stress-Related Genes in Capsicum annuum

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A cDNA library was constructed for hot pepper plants that had been heat-shock-treated. We used a modified differential screening method, double negative screening, to isolate 500 cDNA clones that represented genes with low expression levels under conditions of high-temperature stress. Of those 500 clones, 200 were randomly selected for singleread sequencing from the 5' ends. After annotation with Blastx, the sequence was applied to InterProScan to scan for functional motifs of proteins. Among the cDNA clones analyzed, about 41% of the ESTs could not be functionally classified. However, of those that could be, the largest portion of the ESTs (15%) were assigned to the category of cell rescue and defense; genes involved in cell cycle/DNA processing constituted the smallest group, comprising 1% of the ESTs. Genes related to energy and protein fates constituted the second (10%) and third (9%) largest groups, respectively. Finally, 3% of the ESTs were assigned to transcription, and 2% to signal transduction. The high portion of unclassified ESTs probably resulted from the screening method, which was designed for low-expression messages. Likewise, the high number of ESTs for cell rescue and defense suggests that many genes with low levels of expression are associated with the stress response.

Keywords: cDNA library, double negative screening, high-temperature stress, hot pepper (Capsicum annuum)

Drought, salinity, extreme temperatures, and oxidative stress are often interconnected, and may induce similar cellular damage (Wang et al., 2003). The ability of plants to switch on signal transduction and adaptive responses to abiotic stresses is a critical step in determining survival and reproduction in adverse environments. Numerous stress-specific reactions as well as a sophisticated and complex network of adaptation all help to protect these plants from multiple environmental stresses (Chinnusamy et al., 2004).

Gene activation depends on a distinct set of transcription factors, whose expression imparts stress tolerance while leading to various physiological and biochemical actions. These transcription factors produce multiple phenotypic alterations, many of which are involved in stress responses (Pellegrineschi et al., 2001). Although individual member of the same transcription factor family often responds differently to various stimuli, some stress-responsive genes may share the same transcription factors, as indicated by significant overlap in their induced expression profiles (Bohnert et al., 2001; Seki et al., 2001; Chen et al., 2002; Fowler and Thomashow, 2002; Kreps et al., 2002). However, another level in the hierarchy of genetic control may have important bearing in regulating stress responses, namely, the components of signal transduction. Nevertheless, studies have been limited with regard to either signal transduction mechanisms in plants or abiotic stress interactions.

Genomics approaches have greatly facilitated the discovery of relevant plant genes (Asamizu et al., 2000; Ohlrogge and Benning, 2000; van der Hoeven et al., 2002). Large-scale cDNA sequencing projects have identified expressed sequence tags (ESTs), including those from wheat, maize, barley, soybean, Arabidopsis, rice, sugarcane, potato, tomato, tobacco, and hot pepper, all of which are now catalogued in the EST division (dbEST) of GenBank (http://www.ncbi. nlm.nih.gov/dbEST/dbEST summary.html). Out of a total of 3,148,436 entries, Capsicum annuum is represented by 30,149 entries. Ideally, the ESTs generated from cDNA libraries should denote all the genes expressed in a target organ and tissue, at a particular developmental stage, and/or in a specific environment. However, variations in expression levels among genes from a given tissue type yield mRNAs that differ in their abundance, making it difficult to capture rare mRNA in cDNA libraries. Therefore, to identify those

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rare genes by this approach, it is necessary to either sequence all the clones in the library or else prepare a normalized library. In theory, the latter approach would generate uniform abundances of cDNA classes. However, this requires large-scale sequencing of total cDNA libraries, which is accompanied by high costs for both resources and labor (Bonaldo et al., 1996; Carson and Botha, 2000; Reddy et al., 2002; Fernández et al., 2003).

Heat stress is one of the most serious constraints on crop production in tropical and subtropical regions. The severity of the situation, at least locally, worsens each year, probably because of global warming. Exposure to high temperatures causes an intricate set of changes in plant gene expression that can induce thermo-tolerance and cellular survival. This is known as the heat-shock response. At the molecular level, this reaction is a temporary re-programming of cellular activities, which involves the synthesis of heatshock proteins (HSPs) and simultaneous cessation of normal protein synthesis (Chen et al., 2002).

To isolate the high-temperature stress-specific rare mRNA species in hot pepper from a relatively small number of analyzed sequences, we used a modified screening method -- double negative screening -- adopted from Cho et al. (2003). A cDNA library was constructed from hot pepper treated with physiologically high temperature. Through double negative screening of that cDNA library, we were able to isolate clones showing weak or negative signals by cDNA probes generated from heat-treated as well as normally grown plants. After the selected clones were sequenced, we used annotations of *Arabidopsis thaliana* as comparisons for putatively characterizing those rare transcript species from stressed hot pepper plants.

#### MATERIALS AND METHODS

#### **Plant Material**

Hot pepper (*C. annuum* cv. Bugang) plants were grown for 4 weeks (or to a height of 5 to 7 cm) in a chamber (16-h photoperiod, 25°C, 60% relative humidity, and 200  $\mu$ E/m<sup>2</sup>s from white fluorescent lamps). The high-temperature treatment was applied by placing the pots in an incubator at 42°C for 30 min, or 1, 2, 3, or 4 h. Control plants were maintained at 25°C. Afterward, the collected seedlings were quickly frozen in liquid nitrogen and stored at -80°C.

#### Preparation of Poly(A)<sup>+</sup> RNA, Construction of cDNA Library, and Double Negative Screening

Total RNA was extracted from the hot pepper seedlings according to the method of Sambrook et al. (1989). Poly(A)<sup>+</sup>RNA was purified via the PolyATtract mRNA isolation system (Promega, USA). From the purified poly(A)<sup>+</sup>RNA, we constructed a unidirectional EcoRI/XhoI cDNA library, using a ZAP-cDNA synthesis kit and ZAP-cDNA GigapackIII gold packaging extracts (Stratagene, USA), according to the manufacturer's instructions. This cDNA library had a complexity of  $2.2 \times 10^7$  pfu ml<sup>-1</sup>, and >95% of the phages contained cDNA inserts (data not shown). For the double negative screening, after amplification and titering, duplicate plagues were lifted onto nylon membranes (Hybond-N, Amersham, USA) from 150mm plates (about  $5 \times 10^3$  pfu per plate). The plaque lifts were denatured, neutralized, rinsed, blotted, dried, and fixed by UV cross linking. Membranes were prehybridized, then hybridized with two probes for differential screening. Those probes were made using poly(A)<sup>+</sup>RNA from either heat-shocked or unstressed hot pepper plants to the <sup>32</sup>P-labeled cDNA. The hybridized membranes were washed and exposed to X-ray film (Fuji, Japan). All the procedures described above essentially followed those of Sambrook et al (1989) and manufacturer's instructions. Five hundred clones were randomly picked up by precisely aligning both autoradiographs of the duplicate lifts that had reacted to the differential screening probes with the plate containing the original plaques. Isolated cDNA clones were in vivo-excised from the UniZAP-XR vector and subcloned into pBluescript SK(-) using the Exassist helper phage (M13, Stratagene).

# Nucleotide Sequencing, Sequence Processing, and Functional Classification

Plasmid DNA was purified with an AccuPrep plasmid extrction kit (Bioneer, Korea). Sequence reactions were run on an automated sequencer (Model 3100; Applied Biosystems, USA). The nucleic acid sequences obtained for each cDNA clone were then converted into amino acid sequences for six different reading frames. Finally, we performed database searches at the National Center of Biotechnology Information server (http://www.ncbi.nlm.nih.gov) with Entrez, BLAST (Altschul et al., 1997). Sequences smaller than 200 nucleotides were not further processed. To assign the functioning of ESTs, hot pepper sequences were aligned to the GenBank nucleotide sequence database using the BLASTX algorithm for comparison, with an E-value cut off at  $10^{-5}$  or lower.

#### **RESULTS AND DISCUSSION**

#### cDNA Library of High Temperature-Stressed Hot Pepper

While accessing the transcription factors and the components of the signal transduction pathway in hot pepper plants, we were especially interested in ESTs with low expression profiles during high-temperature stress. In all, 500 clones were selected that showed weak or negative signals by the two cDNA probes synthesized from both treated and unstressed seed-lings. From these, we randomly chose 215 single pass-sequenced cDNA clones that then gave rise to 200 high-quality ESTs. After vector-trimming and removal of low-quality sequences, the average read length of these ESTs was over 400 nucleotides; the average insert size of the corresponding ESTs was about 800 bp.

#### **Functional Categorization of Hot Pepper ESTs**

Among the 200 cDNA clones analyzed, approximately 59% of the ESTs were assigned a function by aligning them with the translated sequences of the GenBank nucleotide sequence database; the remaining 41% encoded proteins with insufficient similarity to proteins of known function for us to confidently assign any role other than "unknown". Genes of known function were sorted into 11 primary categories (Fig. 1). The largest set of genes (15%) was assigned to the category of cell defense or rescue, while those involved in cell cycling and DNA processing constituted the smallest group, or 1%. Genes that helped determine energy and protein fates formed the second (10%) and third (9%) largest groups, respectively. The fact that more genes were placed in the cell defense or rescue category suggests that hot pepper plants possess the ability to survive heat stress in their environment.

Of the 200 ESTs from the non-normalized hot pepper cDNA library, 169 were unique while 31 could be considered redundant. That is, 14 might have been represented twice and one, three times, although the redundancy here was presumptive due to the incomplete nature of the nucleotide sequences. ESTs were defined as redundant when they gave a BLASTX or BLASTN hit to the same accession number, or when



**Figure 1.** Pie chart showing fraction of high temperature stress-modulated genes in each functional category for cDNA library constructed from heat-stressed tissues of hot pepper.

they exhibited more than 95% identity over aligned regions and were assembled in a single contig. Overall, such redundancy in our cDNA library was less than about 15.5%, which is even lower than a normalized cDNA library when EST population size is considered (Carninci et al., 2000). Although oligonucleotide fingerprint (OFP) normalized cDNA library had very low redundancy and many powerful advantages, it cannot be adapted to small-scale EST research because of its high cost and technical intricacy (Clark et al., 2001). Our data also suggested that stressed plants possess a greater diversity of transcripts, likely because of the increased abundance of various transcripts that encode stress-adaptive determinants. These results are consistent with those previously reported for transcript profiling of salinity-stress responses by large-scale EST analysis (Kore-eda et al., 2004).

Predicted gene functioning, scores, e-values, and accession numbers are summarized in Table 1. The largest group, i.e., those classified as cell rescue and defense genes, are mainly small heat-shock proteins that function as ATP-independent chaperones to prevent irreversible protein aggregation and facilitate subsequent protein renaturation in cooperation with ATPdependent chaperones (Basha et al., 2004). Plant sHSPs respond to a wide range of environmental stimuli, including heat, cold, drought, salinity, and oxidative stresses. Increasing data suggest a strong correlation between sHSP accumulation and stress tolerance (Park and Hong, 2001; Sun et al., 2002; Wang et al., 2003, 2004). These HSPs likely protect a large set of proteins, with diverse cellular functions, against heatinduced damage. Other cell defense-related proteins include the dehydrin-like protein (Borovskii et al., 2002), the Bax inhibitor (Huckelhoven, 2004), and Prf (Salmeron et al., 1996), as well as proteins for the antioxidant response (such as glutathione S-transferase), their encoding genes are also present in our collection.

Genes involved in energy functioning constitute the second largest group among our classified ESTs, and comprise those related to photosynthesis. It is well known that the photosynthetic systems in higher plants are most sensitive to high temperatures, or drought and salt treatments (Falk et al., 1996; Tezara et al., 1999; Seki et al., 2002; Kore-eda et al., 2004). Following exposure to abiotic stresses, ESTs that encode large and small subunits of rubisco, chlorophyll a/b binding proteins of the photosystem I and II lightharvesting complexes, photosystem I and II reaction center subunits, oxygen evolving complexes, and components of the mitochondrial ATP synthase and plastidic photosynthetic electron transport chain complex components showed marked declines in abundance. As our approach is designed for the detecting low-abundance genes, it seems to be reasonable to have these photosynthesis-related genes from double negative screening.

Genes in the protein fate category have a role in moving, modifying, storing, and degrading proteins; they constitute our third largest group, with nearly half of them being involved in proteolysis. This proteolysis of regulatory proteins is a key aspect of cellular regulation in eukaryotes (Wei et al., 1994; del Pozo and Estelle, 1999; Schaller, 2004). Thus, the ubiquitin-proteasome pathway is significantly implicated in the plant defense response (Azevedo et al., 2002; Liu et al., 2002). Directly related to this, we identified from our isolated cDNA collection, several regulatory subunits of that pathway (Table 1).

Genes involved in metabolism make up our smallest group of classified ESTs. These include many enzymes, especially those related to photosynthesis, e.g., rubisco activase, sedoheptulose-1,7-isophosphatase, and PEP carboxy kinase; cellular metabolism-related enzymes like malate dehydrogenase; and carbohydrate metabolism-related enzymes, such as beta-amylases, beta-galactosidases, and glyceraldehydes-3-phosphate dehydrogenase. As found while profiling via a microarray approach, most of these enzymes decrease their abundance of transcripts under abiotic stress (Seki et al., 2002). While 3% of our classified ESTs encode for elongation factors and 40S ribosomal proteins that are required for protein synthesis, 2% are considered transposable elements, including a gag-pol poly protein.

Genes for a variety of transcription factors that contain typical DNA binding motifs, such as MYB, AP2/ ERF, ring-finger protein, and zinc fingers, have been reported as stress-inducible in rice and Arabidopsis (Shinozaki and Yamaguchi-Shinozaki, 1999; Rabbani et al., 2003). We also identified ESTs that code for these putative DNA binding motifs, namely two ring zinc finger family members, one MYB family member, one AP2/ERF, one PHD finger family member, and one bromodomain-containing protein. The MYB family is one of the largest families of transcriptional factors characterized in plants. MYB-related transcriptional activators are involved in regulating secondary metabolism, cellular morphogenesis, meristem formation, and the cell cycle, especially ABA- and gibberellin (GA)-signaling during seed germination (Jin and Martin, 1999; Gubler et al., 2002). Zinc finger proteins also can act as transcription factors (Margolin et al., 1994; Cook et al., 1999). The limited data from 200 ESTs in our non-normalized high temperature-stressed cDNA library also revealed expression from one protein kinase gene, one receptor-like protein kinase gene, one adenylate protein kinase gene, and one ADP-ribosylation factor 1. These are classified as components of cellular communication and signal transduction. Regulatory proteins in rice further control various functional genes under stress conditions, for example, adenylate kinase as an abiotic stress-responsive gene, or a receptor-like protein kinase gene (Rabbani et al., 2003).

Many genes with homologues in other organisms that have not been assigned a function (designated as "unclear classification" in Table 1) and have no recognizable homologue in any other organisms (designated as "unclassified" in Table 1) were highly represented in our EST collection. Although most of their sequences currently correspond to hypothetical proteins with unknown function, it will be important to determine their potential roles because these genes may be making unique contributions to thermo-tolerance in plants.

# General Connections between Different Abiotic Stresses

Several of our ESTs show significant sequence similarity to genes affected by ABA, drought, and other environmental stresses. In fact, a significant number are up-regulated by drought, cold, or high-salinity conditions in *Arabidopsis* and rice, as demonstrated from previous microarray data (Kawasaki et al., 2001;

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Table 1. Functional annotation of 200 ESTs from heat-stressed hot	pepper.
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EST ID	Description of best data match plus database accession number for homologous gene	Score	E-value		
	Metabolism				
HTS10	gi 10720247 sp O49074 RCA_LYCPN rubisco activase	485	e-136		
HTS27	gi 3024121 sp P93254  S-adenosylmethionine synthetase	372	e-102		
HTS35	gi 22329419 ref NP_172325.2  cysteine desulfurase, putative	127	3e-28		
HTS55	gi 15229546 ref NP_189036.1  dehydratase family	393	e-10		
HTS147	gi 16950587 gb AAG01894.2  PEP carboxykinase	392	e-108		
HTS275	gi 7431231 pir  T06401 malate dehydrogenase	319	3e-86		
HTS367	gi 12081917 dbj BAB20861.1  cytosolic cysteine synthase	372	e-106		
HTS447	gi 7431231 pir  T06401 malate dehydrogenase	397	e-109		
HTS140	gi 15233426 ref NP_193819.1  fatty acid hydroxylase, putative	248	1e-64		
HTS205	gi 22329419 ref NP_172325.2  cysteine desulfurase, putative	127	2e-35		
HTS78	gi 27804768 gb AAO22558.1  sedoheptulose-1,7-isphosphatase.	405	e-112		
HT\$385	gi 120676 sp P09094 glyceraldehyde3 phosphate dehydrogenase	472	e-132		
HTS375	gi 2071947 gb AAB53629.1  beta-galactosidase	135	2e-30		
HTS390	gi 5031285 gb AAD38148.1  beta-amylase [Prunus armeniaca]	361	2e-98		
HTS217	gi 18694346 emb CAC85287.1  uroporphyrinogen III synthase	233	6e-60		
HTS255	gi 10177106 dbj BAB10440.1  pyruvate kinase [Arabidopsis thaliana]	221	3e-56		
	Energy				
HTS11	gi 34921349 sp Q9ZTS2  ferredoxin, chloroplast precursor	256	7e-67		
HTS12	gi 34921349 sp Q9ZTS2  ferredoxin, chloroplast precursor	233	4e-60		
HTS21	gi 6899972 emb CAB71293.1  chloroplast ferredoxin-NADP+	535	e-151		
HTS29	gi 34787117 emb CAD89270.1  putative PSI-D subunit precursor	369	e-101		
HTS38	gi 131166 sp P12372  PSI reaction center subunit II	348	1e-94		
HTS45	gi 28629385 gb AAO49652.1  Photosystem I-N subunit	175	1e-42		
HTS46	gi 115781 sp P27492 CB21_TOBAC CAB-16	485	e-136		
HTS47	gi 34921349 sp Q9ZTS2  ferredoxin, chloroplast precursor	246	4e-64		
HTS68	gi 100196 pir  S14305 CAB-11	454	e-126		
HTS74	gi 82078 pir  S00443 CAB-6A	433	e-120		
HTS76	gi 3036951 dbj BAA25394.1  light-harvesting CAB protein	365	e-107		
HTS177	gi 12585428 sp O82702 VAG1_TOBAC V-ATPase G subunit 1	56	2e-15		
HTS270	gi 34787117 emb CAD89270.1  PSI-D subunit precursor	383	e-105		
HTS277	gi 6093830 sp P80470 PSBY_SPIOL PSII core complex protein	110	3e-23		
HTS327	gi 7489133 pir  T01782 GDP dissociation inhibitor	442	e-129		
HTS335	gi 115803 sp P14278 CB24_LYCES CAB-4	406	e-112		
HTS410	gi 693920 gb AAA80593.1  chlorophyll a/b binding protein	424	e-117		
HTS427	gi 3036944 dbj BAA25389.1  light-harvesting CAB	424	e-117		
HTS457	gi 130271 sp P17340 PLAS_LYCES plastocyanin, chloroplast pr	222	1e-56		
HTS66	gi 48927500 emb CAA61241.2  glycogen (starch) synthase	535	e-151		
Protein synthesis					
HTS25	gi 119150 sp P17786 EF1A_LYCES elongation factor 1-alpha	412	e-121		
HTS48	gi 18391048 ref NP_563848.1  elongation factor 1B-gamma	82	1e-14		
HTS51	gi 6984222 gb AAF34799.1  40S ribosomal protein S16	270	3e-71		
HTS437	gi 20139798 sp Q9LTF2 R103_ARATH 40S ribosomal protein S	186	7e-46		
HTS357	gi 29892963 emb CAD60652.1  elongation factor	202	7e-59		
HTS227	gi 1076678 pir  S42643 40S ribosomal protein S17	149	5e-35		

### Table 1. (continued).

Protein fate (folding modification, destination)     HTS16   gi 13217581 [ref [NP_174619.1] serine carboxypeptidase \$10   310   4-83     HTS20   gi 1332579 [ref [NP_174619.1] serine carboxypeptidase \$10   343   e-127     HTS61   gi 6671192 [gb [AAF23126.1] cystalin [lycopersicon esculentum]   366   e-101     HTS170   gi 113103 [gp [27158] peptid/ poly (is-trans trans isomerase   307   2-82     HTS33   gi 1076678 [pb [ch [542643 ubiquith / riboxomal protein 527a   149   5e-35     HTS430   gi 120076 [gb [aAA72493.1] alpha peptide > gj 1501281 [gb [A   70   4e-11     HTS430   gi 113103 [gp [27156] Peptid/ poly (ic-trans-trans isomerase   307   2-82     HTS407   gi 11303 [gp [27156] Peptid/ poly (ic-trans-trans isomerase   307   2-82     HTS403   gi 1020578 [gb [abid/11] alpiquitin-coniugating enzyme   310   3-83     HTS405   gi 102058180 [gb [AS2120] (pcl [phi]   266   2-70     HTS403   gi 10305479 [emb[CAC84774.1] (P70 protein [Nicotians tabacum]   254   3-257     HTS403   gi 10305479 [emb[CAC84774.1] (P70 protein [Nicotians tabacum]   254   2-70	EST ID	Description of best data match plus database accession number for homologous gene	Score	E-value
HTS10 g) g) 15217281 [ref. [NP, 174019.1] Serine carboxypeptidase S10 310 44-83   HTS20 g) 1671192 [g) [h] Taly Depubliquitin [Phus sylvestris] 366 e-101   HTS170 g) 1178103 [s] P21561 [peptidyl-prolyl cistrans-trans isomerase 307 2e-82   HTS170 g) 1178103 [s] P212391 [RUBCS O subunit binding protein ajhha 368 e-101   HTS235 g) 109078 [g] AAA72893.1 [aph-apeptida = g] 5603281 [g] A 70 4-61   HTS245 g) 109078 [g] AAA72893.1 [aph-apeptida = g] 5603281 [g] A 70 2e-70   HTS445 g) 1020478 [g] AAA72893.1 [aph-apeptida = g] 5603281 [g] A 70 4-61   HTS445 g) 1029478 [g] AAA72893.1 [aph-apeptida = g] 5603281 [g] A 70 3e-83   HTS445 g) 1029478 [g] AAA72893.1 [aph-apeptida = g] 5603281 [g] A 70 3e-83   HTS453 g) 10206738 [g] AAA72893.1 [apt-tapida = tap-tapida = g] 5007665 [d] [ABA82328.1 [c] c>dphilin 248 3e-70   HTS433 g) 10247581 [ref. [NP_564011.1 ] ref. [Partotase, putative 437 e 121   TG213 10306456 [d] [BAB2328.1 ] cyclophilin 254 <td></td> <td>Protein fate (folding, modification, destination)</td> <td></td> <td></td>		Protein fate (folding, modification, destination)		
HTS20   gi [132279] emb[CAX66667.1] polyubiquin [Pinus sylvestris]   456   e-127     HTS101   gi [671192] gb [AX223126.1] cystatin [lycopersion esculentum]   366   e-101     HTS170   gi [13103] sp [P21368] pepidyb-probl cis-trans-trans isomerase   307   2e-82     HTS170   gi [135103] sp [P21368] pepidyb-probl cis-trans-trans isomerase   307   2e-82     HTS175   gi [2000718] gb [AXA72803.1] alpha-pepidic 2g [3603281] gb [A   70   4e-11     HTS235   gi [1381913] pre]1X968 [pepidyb-probl cis-trans-trans isomerase   307   2a-82     HTS303   gi [1381914] fef [NP_17409.1] serine carboxypepids85 10   280   2z-75     HTS459   gi [30693180] refl NP_17409.1] serine carboxypepids85 10   280   2z-70     HTS430   gi [18076667] emb[CAC84774.1] P70 protein [Neotiana tabacum]   268   2z-70     HTS433   gi [18076673] emb[CAC84774.1] P70 protein [Neotiana tabacum]   268   2z-70     HTS433   gi [18076673] emb[CAC84774.1] P70 protein [Neotiana tabacum]   268   2z-70     HTS433   gi [18076673] emb[CAC84774.1] P70 protein [Neotiana tabacum]   268   2z-70     HTS433   gi [180776673] emb[CAC	HTS16	gi 15217581 ref NP_174619.1  serine carboxypeptidase S10	310	4e-83
HTS61 gi [6771192] gb [AAF23126.11 cystatin [lycopersion esculentum] 366 e-101   HTS170 gi 118103[sp] [P1256] peptidyl-prolyl cis-trans-trans isomerase 307 22-82   HTS370 gi 1301031[sp] [P1229] [RUBISCO subunit binding protein alpha 368 e-101   HTS483 gi 1076678[pir] [S42643 ubiquitin / ribosomal protein S27a 149 55-35   HTS456 gi 1007681[pir] [S42643 ubiquitin / ribosomal protein S27a 149 55-35   HTS456 gi 1007678[pir] [AAF23031.1] phan-peptide > gi 13603281[pb] A 70 4-e-11   HTS235 gi 1007678[pir] [NP 564011.1] ubiquitin-conjugating enzyme 310 3-83   HTS467 gi 152175811 ref [NP 564011.1] rabit protease, putative 437 e-121   HTS304 gi 16076673[bir] [NP 564011.1] rabit protease, putative 437 e-121   HTS430 gi 152175811 ref [NP 174619.1] serine carboxypeptidase S10 310 3-83   HTS430 gi 152175811 ref [NP 174619.1] ref protease, putative 437 e-121   HTS303 gi 152075811 ref [NP 174619.1] serine carboxypeptidase S10 310 3-83   HTS430 gi 152075811 ref [NP 174619.1] serine carboxypeptidase S10 310 4-83   H	HTS20	gi 1332579 emb CAA66667.1  polyubiquitin [Pinus sylvestris]	435	e-127
HTS170 gi [118103]sp]P21561 peptidy-prol/ cis-trans-trans isomerase 367 2-82   HTS370 gi [1351030]sp]P21239] RUBISCO subunit binding protein sD27a 149 5e-35   HTS167 gi [2090713]ref1]S42643 ubiquitir / rbosomal protein SD7a 149 5e-35   HTS167 gi [2090713]ref1]S42643 ubiquitir / rbosomal protein SD7a 149 5e-35   HTS175 gi [2090713]ref1]S42643 ubiquitir / conjagating enzyme 310 3e-83   HTS107 gi [1380416] ref1]NP_124611.1] ubiquitir-conjagating enzyme 310 3e-83   HTS475 gi [30693180] ref1]NP_1349748.1] APE-dependent protease La 124 3-2-70   HTS453 gi [13076676] ref1]NP_1549748.1] refrie carboxypeptidase S10 280 22-75   HTS453 gi [13076665] dia [18/b62328.1] cv/dophilin 268 2-70   HTS453 gi [13076676] ref1]NP_1564971.1] ubiquitir-conjugating enzyme 310 3-83   HTS453 gi [130746661]ref1]NP_564011.1] ubiquitir-conjugating enzyme 310 3-84   HTS453 gi [130746671]ref1]NP_564071.1] ubiquitir-conjugating enzyme 310 3-84   HTS453 gi [130746761]ref1]NP_564071.1] ubiquitir-conjugating enzyme 310 4-84   HTS453 <td>HTS61</td> <td>gi 6671192 gb AAF23126.1  cystatin [Lycopersicon esculentum]</td> <td>366</td> <td>e-101</td>	HTS61	gi 6671192 gb AAF23126.1  cystatin [Lycopersicon esculentum]	366	e-101
$\begin{array}{llllllllllllllllllllllllllllllllllll$	HTS170	gi   118103   sp   P21568   peptidyl-prolyl cis-trans-trans isomerase	307	2e-82
HTSa gi 1076678 [pc] [st243 ubiquin / ribosomal protein S27a 149 5e.35   HTS167 gi 209078 [gb] [AAA72893.1] alpha-poptide > gi 3603281 [gb] [A 70 4e-11   HTS235 gi [1080713] rel [XP_465055.1 putative ubiquitin ligase SINAT5 213 2e-70   HTS407 gi [118103 [sp] [21566] peptidyl-probl cis-trans-trans isomerase 307 2e-82   HTS407 gi [15217581] ref [NP_174619.1] serine carboxypeptidase S10 280 2e-75   HTS435 gi [15076665] dbj [BAB62328.1] cyclophilin 268 2e-70   HTS435 gi [15076665] dbj [BAB62328.1] cyclophilin 268 2e-70   HTS435 gi [15076665] dbj [BAB62328.1] cyclophilin 268 2e-70   HTS435 gi [18076167] emb] [CAC8477.1] P70 protein [Nicotiana tabacum] 254 3e-66   HTS435 gi [1817611 ref [NP_174619.1] serine carboxypeptidase S10 310 4e-83   HTS43 gi [1817611 ref [NP_174619.1] serine carboxypetidase S10 310 4e-83   HTS43 gi [1817611 ref [NP_174619.1] serine carboxypetidase S10 310 4e-83   HTS43 gi [1817611 ref [NP_174619.1] serine carboxypetidase S10 310 4e-83   HTS43 gi [1817611 ref [NP_1746	HTS370	gi 1351030 sp P21239 RUBISCO subunit binding protein alpha	368	e-101
HTS167 gi [200078] gb [AAA7299.11 alpha-peptide >gi [3603281 [gb]A 70 4=11   HTS235 gi [50907133] ref[XP_465055.1 putative ubiquitin ligase SINAT5 213 2=-70   HTS450 gi [181034] sp[P21568] peptidyl-prolyl cis-tans-trans isomerase 307 3=-83   HTS477 gi [181934] for [NP_564011.1] ubiquitin-coniugating enzyme 310 3=-83   HTS478 gi [15217581] ref [NP_76401.1] ATP-dependent protease Ia 124 3=-27   HTS435 gi [150766651 [db [BA862328.1] cyclophiln 266 2=-70   HTS435 gi [150766651 [db [BA862328.1] cyclophiln 266 2=-70   HTS435 gi [181394416] ref [NP_568311.1] Est Protease, putative 437 e-121   HTS435 gi [1817671] ref [NP_568311.1] Est Protease, putative 437 e-121   UTS475 gi [1834416] ref [NP_568311.1] Est Protease, putative 437 e-121   UTS41 gi [3341464] emb [CA12367.1] Hsp20.1 protein 92 2=-17   HTS43 gi [341464] emb [CA12387.1] GT [Ab protein 33 444 e-126   UTS4157 gi [3341464] emb [CA12387.1] GT [Ab protein 33 444 e-126   HTS4 gi [340597614] ref [NP_7178110.2] HSP 70, putative	HTS83	gi 1076678 pir   S42643 ubiquitin / ribosomal protein S27a	149	5e-35
HTS235 gi J0907133 [ref] KP_465005.1 putative ubiquitin ligase SINAT5 21.3 2e-70   HTS450 gi 118103 [sp[P21568] (peptidy) prolyl cis-trans-trans isomerase 310 3e-83   HTS467 gi 115217581 [ref] NP_174619.1] serine carboxypeptidaes S10 280 2e-75   HTS467 gi 115217581 [ref] NP_174619.1] serine carboxypeptidaes S10 280 2e-75   HTS306 gi 118417611 [ref] NP_568311.1] FIsH protease, putative 437 e-121   HTS435 gi 115076665 [db] (BA62328.1] (pc)optidin 268 2e-70   HTS430 gi 115217581 [ref] NP_174619.1] serine carboxypeptidaes S10 310 3e-83   HTS475 gi 13804416 [ref] NP_564011.1] ubiquitin-conjugating enzyme 310 3e-83   HTS475 gi 13417611 [ref] NP_174619.1] serine carboxypeptidaes S10 310 4e-83   HTS47 gi 1341461 [ref] NP_2002.1 protein 42 0.027   HTS3 gi 3341461 [ref] NP_2103.2] heat-shock factor protein, putative 42 0.027   HTS4 gi 17083141 sp[P51819] H583.7] H582.01 protein 311 e.104   HTS5 gi 331544851 [gb] AA32823.1] molecular chaperone Hs90-2 431 e.104   HTS5 gi 30699461 [ref] NP_1710.3]	HTS167	gi 209078 gb AAA72893.1  alpha-peptide >gi 3603281 gb A	70	4e-11
HTS40 gil118103  splP21568  peptidyl-proble distrans-trans isomerase 307 22-82   HTS307 gil18394416  ref NP_174619.1] serine carboxypeptidaes S10 280 22-75   HTS467 gil15217581  ref NP_174619.1] serine carboxypeptidaes S10 280 22-775   HTS495 gil30693180  ref NP_849748.1  ATP-dependent protease La 124 32-27   HTS403 gil18076679  emb CAC84774.1  P70 protein [Nicotiana tabacum] 254 3-e63   HTS435 gil18076679  emb CAC84774.1  P70 protein [Nicotiana tabacum] 310 4-e33   HTS47 gil18074416  ref NP_564011.1] ubiquitin-conjugating enzyme 310 4-e33   HTS47 gil3041461  ref NP_564011.1] ubiquitin-conjugating enzyme 310 4-e33   HTS47 gil3041461  ref NP_201008.2] heat-shock factor protein, putative 42 0.27   HTS47 gil30497614  ref NP_201008.2] heat-shock protein 63 444 e-126   HTS4 gil3044581 jblAA1297.1 HS47 gil1708314 jblA1297.1 E-17   HTS4 gil304967  ref NP_178110.3] HSP 70, putative 381 e-104   HTS5 gil31544851 jblAA1297.1 Incoler charge charg	HTS235	gi 50907133 ref XP_465055.1 putative ubiquitin ligase SINAT5	213	2e-70
HTS307 gi [18394416] ref [NP, 564011.1] ubiquitin-conjugating enzyme 310 3-e83   HTS467 gi [31521788] ref [NP, 349748.1] ATP-dependent protease ta 124 3-227   HTS300 gi [1807679] emb[AC&A8774.1] (PTO protein [Nicotiana tabacum] 254 3-e66   HTS435 gi [1807667] emb[AC&A8774.1] (PTO protein [Nicotiana tabacum] 254 3-e66   HTS430 gi [1807679] emb[AC&A8774.1] (PTO protein [Nicotiana tabacum] 254 3-e66   HTS475 gi [1807679] emb[AC&A8774.1] (PTO protein [Nicotiana tabacum] 254 3-e66   HTS475 gi [1807679] emb[AC&A8774.1] (PTO protein [Nicotiana tabacum] 254 3-e66   HTS475 gi [1807671] ref [NP_564011.1] [bk] protease, putative 437 e-121   Cell rescue, defense, and virulence   HTS1 gi [341464] emb[CAA12387.1] Fbk] protein 92 2-e17   HTS1 gi [341464] emb[CAA12387.1] Fbk] protein 381 e-104   HTS1 gi [341464] emb[CAA12387.1] Fbk] protein 381 e-104   HTS1 gi [341464] emb[CAA12387.1] Fbk] protein 381 e-104   HTS1 gi [3415448149] gi [34134130] pri	HTS450	gi   118103   sp   P21568   peptidyl-prolyl cis-trans-trans isomerase	307	2e-82
HTS467 gi [15217581   ref  NP_174619.1   serine carboxypeptidase \$10 280 22-75   HTS495 gi [30693180   ref  NP_849748.1   ATP-dependent protease 1 124 32-27   HTS435 gi [18076675] [emb]CAC84774.1   P70 protein [Nicotiana tabacum] 254 32-66   HTS435 gi [18076679] [emb]CAC84774.1   P70 protein [Nicotiana tabacum] 254 32-66   HTS430 gi [182766176] [emb]CAC84774.1   P70 protein [Nicotiana tabacum] 254 32-66   HTS430 gi [18217581   ref  NP_568311.1 ] FisH protease, putative 437 e-121   Cell rescue, defense, and virulence   Tell rescue, defense, and virulence   HTS1 gi [3341464] emb]CAA12387.1   H5920.1 protein 92 22-17   HTS3 gi [30694671   ref  NP_201008.2] heat-shock factor protein, putative 42 0.027   HTS4 gi [170831418.9] P18310   H838.9 HAN Ih heat-shock protein 83 444 e-126   HTS5 gi [34474206] gb] AA129287.1   SP70, putative 391 e-108   HTS5 gi [3414861] gi [3412481] [107602 heat-shock protein 17.6 tomato 262 7e-e69   HTS1 gi [341741310 [pir] [1704316 heat-shock protein 70 190 1e-6	HTS307	gi 18394416   ref   NP_564011.1   ubiquitin-conjugating enzyme	310	3 <b>≘-8</b> 3
HT395 gi [30693180] ref [NP_849748.1] ATP-dependent protease La 124 3=27   HTS300 gi [18417611] ref [NP_568311.1] FISH protease, putative 437 e-121   HTS303 gi [18076679] emb [CAC84774.1] P70 protein [ <i>Nicotiana tabacum</i> ] 254 3>-66   HTS475 gi [1837976616] db] [BAB6328.1] cyclophilin 254 3>-66   HTS475 gi [15217581] ref [NP_17419.1] serine carboxypeptidase S10 310 4>-83   HTS67 gi [15217581] ref [NP_17419.1] serine carboxypeptidase S10 310 4>-83   HTS67 gi [15217581] ref [NP_17419.1] serine carboxypeptidase S10 310 4>-83   HTS67 gi [13417611] ref [NP_17610.1] ref recue, defense, and virulence 422 0.027   HTS1 gi [30697614] ref [NP_178110.3] HSP 70, putative 42 0.027   HTS5 gi [27447206 [gb] AA12987.1] GST-like protein 381 e-104   HTS18 gi [381544831[gb] AA812194.1] molecular chaperone Hsp0-2 431 e-119   HTS18 gi [37904866] gb] AA812194.1] molecular chaperone Hsp0-2 431 e-119   HTS19 gi [37904866] gb] AA87347.1] small heat-shock protein T.6 376 e-100   HTS39 gi [2441730 [db] [BA822699.	HTS467	gi 15217581 ref NP_174619.1 serine carboxypeptidase \$10	280	2e-75
HTS300 g  18417611   ref  NP_568311.1   FsH protease, putative 437 e-121   HTS335 g  18076652   db] [BAB62328.1   cyclophilin 268 2e-70   HTS435 g  18076679   emb CAS4774.1   70 protein [Nicotiana tabacum] 254 3:-66   HTS430 g  12217581   ref  NP_564011.1   ubiquitin-conjugating enzyme 310 3:-83   HTS430 g  1217581   ref  NP_568311.1   FsH protease, putative 437 e-121   Cell rescue, defense, and virulence   HTS1 g  30697614   ref  NP_20100.21 heat-shock factor protein nutative 42 0.027   HTS4 g  30697614   ref  NP_20108.21 heat-shock protein 83 444 e-126   HTS4 g  30697614   ref  NP_178110.3   HSP 70, putative 391 e-104   HTS5 g  30699467   ref  NP_178110.3   HSP 70, putative 391 e-108   HTS5 g  38154485   gb   AAR12194.1   molecular chaperone Hsp0-2 431 e-119   HTS13 g  32094866   gb   AAP5747.7   small heat-shock protein 17.6 formato 262 7:-69   HTS14 g  104716 heat-shock protein 70 190 1:e-6   HTS33 g  12071947   gb   AAP57427.1   small heat-shock protein 70 <td>HTS495</td> <td>gi 30693180 ref NP_849748.1 ATP-dependent protease La</td> <td>124</td> <td>3-2-27</td>	HTS495	gi 30693180 ref NP_849748.1 ATP-dependent protease La	124	3-2-27
HTS355 gl 15076665 dbj 82.8-70   HTS3250 gj 18076679 emb[CAC84774.1] P70 protein ( <i>Nicotaina tabacum</i> ] 25.4 3:-66   HTS4755 gj 183944161 (refl NP_564011.1] ubiquitin-conjugating enzyme 310 3:-83   HTS475 gj 182147611 (refl NP_56411.1] ubiquitin-conjugating enzyme 310 4:-83   HTS67 gj 13414461 (refl NP_56411.1] ubiquitin-conjugating enzyme 32 e-121   Cell rescue, defense, and virulence   V 2:-77   HTS4 gj 30341461 (refl NP_201008.2] heat-shock factor protein, putative 42 0.027   HTS5 gj 324747206 [gb JAN12827.1] GST gj e-104   HTS5 gj 7441328 [pir] Tof020 teat-shock protein 17.6 tomato 262 7:e-69   HTS19 gj 32904866 [gb AAR2194.1] molecular chaperone Hsp0-2 431 e-103   HTS19 gj 32904486 [gb AAR2194.1] molecular chaperone Hsp0-2 431 e-103   HTS18 gj 7441328 [	HT\$300	gi 18417611 ref NP_568311.1  FtsH protease, putative	437	e-121
HTS230 g  18076679 emb CAC84774.1   P70 protein [Nicotiana tabacum] 254 32-66   HTS475 g  18394116 ref NP_564011.1   ubiquitin-conjugating enzyme 310 32-83   HTS430 g  12175811   ref NP_174619.1   serine carboxypeptidase S10 310 42-83   HTS67 g  18417611   ref NP_568311.1   FtsH protease, putative 437 e-121   Cell rescue, defense, and virulence   HTS1 g  3141464   emb CAA12387.1   Hsp20.1 protein 92 2-r17   HTS4 g  1708314   sp  P51819   Hs83_PHANI heat-shock forcein 83 444 e-126   HTS5 g  27447206   gb   AA192873.1   CST-like protein 381 e-104   HTS5 g  34744864   gb   AA192873.1   CST-like protein 17.6 tomato 262 72-69   HTS18 g  38154485   gb   AA1719.4   Jb   Dr, putative 391 e-100   HTS19 g  37904866   gb   AAP5747.1   small heat-shock protein 367 e-100   HTS39 g  271471   gb   AAB53629.1   beta-shock protein 70 190 1e-56   HTS39 g  7441328   pri   T07602 heat-shock protein 70 190 1e-56   HTS39 g  7441310   pri   F104316 heat-shock protein 70 190 1e-56	HTS435	gi 15076665 dbj BAB62328.1  cyclophilin	268	2-2-70
HTS475 g  18394416 ref NP_564011.1  ubiquitin-conjugating enzyme 310 3-e83   HTS430 g  15217581  ref NP_174619.1] serine carboxypeptidase 510 310 4-e83   HTS67 g  18417611  ref NP_568311.1  FsH protease, putative 427 e-121   Cell rescue, defense, and virulence   HTS1 g  3041464]emb CAA12387.1  Hsp20.1 protein 92 2e-17   HTS4 g  1708314 sp]P51819 HS83 PHANh heat-shock factor protein, putative 42 0.027   HTS4 g  1708314 sp]P51819 HS83 PHANh heat-shock protein 83 444 e-126   HTS5 g  3041464 emb CAA12387.1  GST-like protein 381 e-104   HTS5 g  31744815 g  AR1294.1  molecular chaperone Hsp90-2 431 e-118   HTS19 g  327904866 gb AAP57477.1  small heat-shock protein 367 e-100   HTS39 g  7441310 pir  1704316 heat-shock protein 70 190 1-e   HTS53 g  48474196 db] BAD22699.1  heat-shock protein 70 190 1-e   HTS54 g  1079648 emb CAC12824.1  putative DNA] protein 233 5e-61   HTS55 g  744328 pir  107703 chaperonin 60 beta chain precursor 217 e-155	HTS230	gi 18076679 emb CAC84774.1 P70 protein [Nicotiana tabacum]	254	3·e-66
HTS430 gi [15217581]ref]NP_174619.1] serine carboxypeptidase S10 310 4-e-83   HTS67 gi [18417611]ref]NP_568311.1] FtsH protease, putative 437 e-121   Cell rescue, defense, and virulence   HTS1 gi [3341464]emb]CAX12387.1] Hsp20.1 protein 92 2-s-17   HTS3 gi [30697614]ref]NP_201008.2] heat-shock factor protein, putative 42 0.027   HTS4 gi [708314]sp]P51819]HS83.PHANI heat-shock protein 83 444 e-126   HTS5 gi [27447206]gb]AAL32873.1] CST-like protein 381 e-104   HTS7 gi [30699467]ref]NP_178110.3] HSP 70, putative 391 e-108   HTS15 gi [27447206]gb]AAL32873.1] CST-like protein 367 e-100   HTS13 gi [38154485]gb]AAR12194.1] molecular chaperone Hsp90-2 431 e-119   HTS39 gi [2071947]gb]AAB53629.1] beta-galactosidase 135 2-30   HTS50 gi [2071947]gb]AAF3612.1] Prif [Vopcersicon esculentum] 377 e-103   HTS53 gi [4474196]db]BAD22699.1] heat-shock protein 70 190 1e-6   HTS54 gi [107732 chaperonin 60 beta chain precursor 217 e-15   HTS55 gi [27447206]gb]AA	HTS475	gi 18394416 ref NP_564011.1  ubiquitin-conjugating enzyme	310	3e-83
HTS67 gi 18417611  ref  NP_568311.1   FtsH protease, putative 437 e-121   Cell rescue, defense, and virulence   HTS1 gi 3341464  emb   CAA12387.1   Hsp20.1 protein 92 22-17   HTS3 gi 30697614  ref  NP_201008.2   heat-shock factor protein, putative 42 0.027   HTS4 gi 1708314  sp  P51819  HS83_PHANI heat-shock protein 83 444 e-126   HTS5 gi 27447206 [gb  AAL92873.1   CST-like protein 381 e-104   HTS7 gi 30699671 [ref  NP_178110.3   HSP 70, putative 391 e-108   HTS15 gi 7441328  pir   T07602 heat-shock protein 17.6 tomato 262 7>-69   HTS18 gi 38154485  gb  AAR12194.1   molecular chaperone Hsp90-2 431 e-119   HTS19 gi 7904866 [gb  AAP57477.1   small heat-shock protein 367 e-100   HTS33 gi 4847196 [db]  BAD22699.1   beta-glactosidase 135 2e-30   HTS54 gi 10498648  emb  CAC12824.1   putative DNA protein 233 5e-61   HTS55 gi 12447310   pir   T04316 heat-shock protein 70 190 1e-6   HTS54 gi 17447206   gb  AAP5373.1   CST-like protein 335 5e-61   HTS55 <	HTS430	gi 15217581 ref NP_174619.1 serine carboxypeptidase S10	310	4e-83
Cell rescue, defense, and virulenceHTS1gi ] 3491464] emb CAA12387.1]Hsp20.1 protein922+17HTS3gi ] 30697614[ref NP_201008.2]heat-shock factor protein, putative420.027HTS4gi ] 1708314[sp]P51819]HS83_PHANI heat-shock protein 8344e-126HTS5gi ] 27447206[gb]AAL92873.1]CST-like protein381e-104HTS7gi ] 30699467 [ref NP_178110.3]HSP 70, putative391e-108HTS15gi [ 7441328 [pir] [170702 heat-shock protein 17.6 tomato2627-e-69HTS18gi [ 38154485 [gb]AAR12194.1]molecular chaperone Hsp90-2431e-119HTS19gi ] 37094866 [gb]AAP57477.1]small heat-shock protein367e-100HTS33gi [ 2071947 [gb] AAB53629.1]beta-galactosidase13520-30HTS39gi [ 241310] pir ] [T04316 heat-shock protein MTSHP precursor2212e-56HTS50gi [ 84473196 [db] BAD22699.1]heat-shock protein 701901e-6HTS54gi [ 10798648] emb[CAC12824.1]putative DNAJ protein2335e-61HTS57gi [ 27447206 [gb]AAL92873.1]CST-like protein3356e-91HTS58gi [ 7443855 ] pir   [ 107733 chaperonin 60 beta chain precursor417e-115HTS19gi ] 305316 [gb]AAQ23059.1]heat-shock factor RHSF53228e-60HTS19gi ] 33591104 [gb]AAQ23059.1]heat-shock factor RHSF53238e-61HTS29gi [ 1067384 [db] BAB16318.1]chaperone Hsp90-1419	HTS67	gi 18417611 ref NP_568311.1  FtsH protease, putative	437	e-121
HTS1gi3341464embCAA12387.1Hsp20.1 protein922e-17HTS3gi30697614IrefNP_201008.2heat-shock factor protein, putative420.027HTS4gi1708314lspP51819HAN1 heat-shock factor protein83444e-126HTS5gi27447206gbAA.192873.1CST-like protein331e-104HTS7gi30699467refNP_178110.3HSP 70, putative391ee108HTS15gi27441328pirl170602heat-shock protein70.670.660.670.660.670.660.670.660.670.660.670.660.670.660.670.660.670.6 <td>10.0 6</td> <td>Cell rescue, defense, and virulence</td> <td></td> <td></td>	10.0 6	Cell rescue, defense, and virulence		
HTS3 gi 30697614  ref  NP_201008.2   heat-shock factor protein, putative 42 0 027   HTS4 gi 1708314  sp  P51819  HS83_PHANI heat-shock protein 83 444 e-126   HTS5 gi 27447206  gb  AAL92873.1   GST-like protein 381 e-104   HTS7 gi 30699467  ref  NP_178110.3   HSP 70, putative 391 e-108   HTS15 gi 7441328  pir   T07602 heat-shock protein 17.6 tomato 262 7e-69   HTS18 gi 38154485  gb  AAR12194.1   molecular chaperone Hsp90-2 431 e-119   HTS33 gi 2071947  gb  AAB53629.1   beta-galactosidase 135 2e-30   HTS33 gi 7441310  pir   T04316 heat-shock protein MTSHP precursor 221 2e-56   HTS50 gi 8547237  gb  AAF76312.1   Pf [ <i>lycopersicon esculentum</i> ] 377 e-103   HTS53 gi 44741328  pir   T07702 heat-shock protein 70 190 1e-6   HTS54 gi 10798648  emb   CAC12824.1   putative DNAJ protein 233 5e-61   HTS55 gi 7444328  pir   T07733 chaperonin 60 beta chain precursor 417 e-115   HTS76 gi 74443855  pir   T07733 chaperonin 60 beta chain precursor 279 2e-76   HTS82 gi 100335  pir   S18181 dnaK-type molec	HTS1	gi 3341464 emb CAA12387.1  Hsp20.1 protein	92	2e-17
HTS4 gi   7708314   sp   P51819   HS83_PHAN heat-shock protein 83 444 e-126   HTS5 gi   27447206   gb   AAL92873.1   CST-like protein 381 e-104   HTS7 gi   30699467   ref   NP_178110.3   HSP 70, putative 391 e-108   HTS15 gi   741328   pir   107602 heat-shock protein 17.6 tomato 262 7:e-69   HTS18 gi   38154485   gb   AAR12194.1   molecular chaperone Hsp90-2 431 e-119   HTS19 gi   37904866   gb   AAP57477.1   small heat-shock protein 367 e-100   HTS33 gi   7041310   pir   104316 heat-shock protein 70 211 2e-56   HTS50 gi   847237   gb   AAF76312.1   Prf lLycopersicon esculentum] 377 e-103   HTS53 gi   48474196   db   BAD22699.1   heat-shock protein 70 190 1e-6   HTS54 gi   10798648   emb  CAC12824.1   putative DNAJ protein 233 5e-61   HTS57 gi   7443855   pir   107733 chaperonin 60 beta chain precursor 417 e-115   HTS64 gi   10033   pir   18181 dnak-type molecular chaperone Nthsp70 350 3e-95   HTS82 gi   100335   pir   107733 chaperonin 60 beta chain precursor 279 2e-76   HTS55 gi   3	HTS3	gi 30697614 ref NP_201008.2  heat-shock factor protein, putative	42	0 027
HTS5 gi   27447206   gb   AAL92873.1   GST-like protein 381 e-104   HTS7 gi   3069467   ref   NP_178110.3   HSP 70, putative 391 e-108   HTS15 gi   7441328   pir     T07602 heat-shock protein 17.6 tomato 262 7e-69   HTS18 gi   38154485   gb   AAR12194.1   molecular chaperone Hsp90-2 431 e-119   HTS19 gi   37904866   gb   AAP57477.1   small heat-shock protein 367 e-100   HTS33 gi   2071947   gb   AAB53629.1   beta-galactosidase 135 2e-30   HTS39 gi   7441310   pir   104316 heat-shock protein MTSHP precursor 221 2e-56   HTS53 gi   847237   gb   AAF76312.1   Prf   Lycopersicon esculentum] 377 e-103   HTS54 gi   10798648   emb   CAC12824.1   putative DNAJ protein 233 5e-61   HTS57 gi   7443855   pir   107733 chaperonin 60 beta chain precursor 417 e-115   HTS58 gi   100335   pir   158181 dnaK-type molecular chaperone Nthsp70 350 3e-95   HTS19 gi   33591104   gb   AAQ23059.1   heat-shock factor RHSF5 232 8e-60   HTS250 gi   10697184   dbj   BAB16318.1   chaperonin-60 alpha subunit 367 e-101   HTS250	HTS4	gi 1708314 sp P51819 HS83_PHANI heat-shock protein 83	444	e-126
HTS7 gi 30699467  ref  NP_178110.3   HSP 70, putative 391 e-108   HTS15 gi 7441328  pri   107602 heat-shock protein 17.6 tomato 262 7e-69   HTS18 gi 38154485  gb   AAR12194.1   molecular chaperone Hsp90-2 431 e-119   HTS19 gi 38154485  gb   AAR12194.1   molecular chaperone Hsp90-2 431 e-100   HTS33 gi 2071947  gb   AAB53629.1   beta-galactosidase 135 2e-30   HTS39 gi 7441310  pir   104316 heat-shock protein MTSHP precursor 221 2e-56   HTS50 gi 8547237  gb   AAF76312.1   Prf ( <i>lycopersicon esculentum</i> ) 377 e-103   HTS53 gi 48474196   db   BAD26699.1   heat-shock protein 70 190 1e-6   HTS54 gi 10798648  emb   CAC12824.1   putative DNA  protein 233 5e-61   HTS57 gi 7441328  pir   107733 chaperonin 60 beta chain precursor 417 e-115   HTS58 gi 7443855  pir   107733 chaperonin 60 beta chain precursor 279 2e-76   HTS19 gi 303591104  gb   AAQ23059.1   heat-shock factor RHSF5 232 8e-60   HTS297 gi 7447806  gb   AAQ23059.1   heat-shock factor RHSF5 232 8e-60   HTS250 gi 1003718   dbj   BAR16318	HTS5	gi 27447206 gb AAL92873.1  GST-like protein	381	e-104
HTS15gi  7441328  pir   107602 heat-shock protein 17.6 tomato2627e-69HTS18gi  38154485  gb   AAR12194.1   molecular chaperone Hsp90-2431e-119HTS19gi  37904866  gb   AAP57477.1   small heat-shock protein367e-100HTS33gi  2071947  gb   AAB53629.1   beta-galactosidase1352e-30HTS39gi  7441310   pir    T04316 heat-shock protein MTSHP precursor2212e-56HTS50gi  8547237  gb   AAF76312.1   Pf [ <i>Lycopersicon esculentum</i> ]377e-103HTS53gi  48474196   dbj  BAD22699.1   heat-shock protein 701901e-6HTS54gi  10798648   emb  CAC12824.1   putative DNA) protein2335e-61HTS57gi  7441328   pir   107702 heat-shock protein 17.62296e-59HTS58gi  10798648   emb  CAC12824.1   putative DNA) protein3356e-91HTS57gi  27447206   gb   AAL92873.1   CST-like protein3356e-91HTS82gi  100335   pir    518181 dnaK-type molecular chaperone Nthsp703503e-95HTS190gi  7443855   pir    107733 chaperonin 60 beta chain precursor2792e-76HTS195gi  325917.04   gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS297gi  28973653   gb   AAO64147.1   putative TPR-repeat protein3028e-81HTS207gi  28973653   gb   AAO64147.1   putative TPR-repeat protein3028e-81HTS337gi  3314164   emb  CAA12387.1   Hsp20.1 protein2681e-70HTS337gi  3341464   emb  CAA12387.1   Hsp20.1 protein365e-1	HTS7	gi 30699467 ref NP_178110.3  HSP 70, putative	391	e-108
HTS18gi   38154485   gb   AAR12194.1   molecular chaperone Hsp90-2431e-119HTS19gi   37904866   gb   AAP57477.1   small heat-shock protein367e-100HTS33gi   2071947   gb   AAB53629.1   beta-galactosidase1352e-30HTS39gi /7441310   pir   T04316 heat-shock protein MTSHP precursor2212e-56HTS50gi   8547237   gb   AAF76312.1   Prf [ <i>Lycopersicon esculentum</i> ]377e-103HTS53gi   44474196   db   BAD22699.1   heat-shock protein 701901.e-6HTS54gi   10798648   emb   CAC12824.1   putative DNAJ protein2335e-61HTS57gi /7441328   pir   T07602 heat-shock protein 17.62296e-59HTS58gi /7443855   pir   T07733 chaperonin 60 beta chain precursor417e-115HTS70gi   27447206   gb   AAL92873.1   CST-like protein3503e-95HTS19gi   100335   pir   S18181 dnaK-type molecular chaperone Nthsp703503e-95HTS19gi   10697184   db   BAB16318.1   chaperonin-60 alpha subunit367e-101HTS20gi   10697184   db   BAB16318.1   chaperone Hsp90-1419e-116HTS317gi   3351104   gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS20gi   10697184   db   BAB16318.1   chaperone Hsp90-1419e-116HTS320gi   341464   emb   CAA12387.1   BAZ 10   protein3628e-81HTS317gi   3351104   gb   AAR28754.1   Bax inhibitor385e-106HTS320gi   1291028   ref   NP_175665.1   26.5 kDa class   sHSP1728e-4	HTS15	gi 7441328 pir  T07602 heat-shock protein 17.6 tomato	262	7e-69
HTS19gi   37904866   gb   AAP57477.1   small heat-shock protein367e-100HTS33gi   2071947   gb   AAB53629.1   beta-galactosidase1352e-30HTS39gi   7441310   pir   T04316 heat-shock protein MTSHP precursor2212e-56HTS50gi   8547237   gb   AAF76312.1   Prf ( <i>lycopersicon esculentum</i> ]377e-103HTS53gi   48474196   db   BAD22699.1   heat-shock protein 701901e-6HTS57gi   10798648   emb   CAC12824.1   putative DNAJ protein2335e-61HTS57gi   7441328   pir   T07602 heat-shock protein 17.62296e-59HTS58gi   7443855   pir   107733 chaperonin 60 beta chain precursor417e-115HTS70gi   27447206   gb   AAL92873.1   CST-like protein3356e-91HTS82gi   100335   pir   S18181 dnak-type molecular chaperone Nthsp703503e-95HTS190gi   7443855   pir   T07733 chaperonin 60 beta chain precursor2792e-76HTS19gi   3591104   gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS20gi   10697184   db   BAB16318.1   chaperonin-60 alpha subunit367e-101HTS20gi   7441310   pir   T04316 heat-shock protein MTSHP precursor2073e-52HTS317gi   3341464   emb   CAA12387.1   Hsp20.1 protein368e-106HTS320gi   7441310   pir   T04216 heat-shock protein (BiP)2763e-91HTS400gi   15219028   ref   NP_175665.1   26.5 kDa class I sHSP1728e-42HTS450gi   10697184   db   BAB16318.1   chaperonin-60 alpha	HTS18	gi 38154485 gb AAR12194.1  molecular chaperone Hsp90-2	431	e-119
HTS33gi   2071947   gb   AAB53629.1   beta-galactosidase1352e-30HTS39gi   7441310   pir    T04316 heat-shock protein MTSHP precursor2212e-56HTS50gi   8547237   gb   AAF76312.1   Prf   <i>Lycopersicon esculentum</i> ]377e-103HTS53gi   48474196   db   BAD22699.1   heat-shock protein 701901e-6HTS54gi   10798648   emb   CAC12824.1   putative DNAJ protein2335e-61HTS57gi   744328   pir     T07602 heat-shock protein 17.62296e-59HTS58gi / 7443855   pir     T07733 chaperonin 60 beta chain precursor417e-115HTS2gi   100335   pir   518181 dnaK-type molecular chaperone Nthsp703503e-95HTS19gi   33591104   gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS20gi   10697184   db   BAB16318.1   chaperonin-60 alpha subunit367e-101HTS217gi   28973653   gb   AAO64147.1   putative TPR-repeat protein3028e-81HTS37gi   33514489   gb   AAR12195.1   molecular chaperone Hsp90-1419e-116HTS320gi   7441310   pir     T04316 heat-shock protein MTSHP precursor2073e-52HTS337gi   39579116   gb   AAR28754.1   Bax inhibitor385e-106HTS377gi   19813   emb   CAA12387.1   Hsp20.1 protein2681e-70HTS337gi   39579116   gb   AAR28754.1   Bax inhibitor385e-106HTS377gi   19813   emb   CAA42660.1   luminal binding protein (BiP)2763e-91HTS400gi   15219028   ref   NP_175665.1   26.5 kDa clas	HTS19	gi 37904866 gb AAP57477.1  small heat-shock protein	367	e-100
HTS39gi  7441310   pir    T04316 heat-shock protein MTSHP precursor2212e-56HTS50gi  8547237   gb  AAF76312.1   Pf [Lycopersicon esculentum]377e-103HTS53gi  48474196   db   BAD22699.1   heat-shock protein 701901e-6HTS54gi  10798648   emb   CAC12824.1   putative DNAJ protein2335e-61HTS57gi /7441328   pir   1707602 heat-shock protein 17.62296e-59HTS58gi /7443855   pir   107733 chaperonin 60 beta chain precursor417e-115HTS70gi  27447206   gb   AAL92873.1   GST-like protein3356e-91HTS82gi  100335   pir   IS18181 dnaK-type molecular chaperone Nthsp703503e-95HTS190gi  7443855   pir    T07733 chaperonin 60 beta chain precursor2792e-76HTS195gi  33591104   gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS207gi  28973653   gb   AAO64147.1   putative TPR-repeat protein3028e-81HTS317gi  38154489   gb   AAR12195.1   molecular chaperone Hsp90-1419e-116HTS320gi  39579116   gb   AAR28754.1   Bax inhibitor385e-106HTS377gi  39579116   gb   AAR28754.1   Bax inhibitor385e-106HTS377gi  15219028   ref   NP_175665.1   26.5 kDa class I sHSP1728e-42HTS400gi  16097184   db   BAB16318.1   chaperonin-60 alpha subunit3595e-91HTS400gi  16097184   db   BAB16318.1   chaperonin-60 alpha subunit359se-91HTS400gi  39579116   gb   AAR28754.1   Bax inhibitor385 </td <td>HTS33</td> <td>gi 2071947 gb AAB53629.1  beta-galactosidase</td> <td>135</td> <td>2e-30</td>	HTS33	gi 2071947 gb AAB53629.1  beta-galactosidase	135	2e-30
HTS50gi  8547237  gb  AAF76312.1   Pf [Lycopersicon esculentum]377e-103HTS53gi  48474196  db  BAD22699.1   heat-shock protein 701901e-6HTS54gi  10798648   emb  CAC12824.1   putative DNAJ protein2335e-61HTS57gi  7441328   pir    T07602 heat-shock protein 17.62296e-59HTS58gi  7443855   pir    T07733 chaperonin 60 beta chain precursor417e-115HTS70gi  27447206   gb   AAL92873.1   GST-like protein3356e-91HTS82gi   100335   pir    S18181 dnaK-type molecular chaperone Nthsp703503e-95HTS19gi   3591104   gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS20gi   10697184   db   BAB16318.1   chaperonin-60 alpha subunit367e-101HTS20gi   28973653   gb   AAO64147.1   putative TPR-repeat protein3028e-81HTS317gi   38154489   gb   AAR12195.1   molecular chaperone Hsp90-1419e-116HTS323gi   7441310   pir   T04316 heat-shock protein MTSHP precursor2073e-52HTS337gi   39579116   gb   AAR28754.1   Bax inhibitor385e-106HTS377gi   19813   emb   CAA12387.1   Hsp20.1 protein2681e-70HTS435gi   7447302   pir   170639 probable glutathione transferase3281e-88HTS40gi   15219028   ref   NP_175665.1   26.5 kDa class   sHSP1728e-42HTS45gi   704466   gb   AAP57477.1   small heat-shock protein3595e-98HTS460gi   10697184   db   BAB16318.1   chaperonin-60 alpha subunit	HTS39	gi 7441310 pir  T04316 heat-shock protein MTSHP precursor	221	2e-56
HTS53gi  48474196 dbj  BAD22699.1  heat-shock protein 701901e-6HTS54gi  10798648 emb CAC12824.1  putative DNAJ protein2335e-61HTS57gi  7441328 pir  T07602 heat-shock protein 17.62296e-59HTS58gi  7443855 pir  T07733 chaperonin 60 beta chain precursor417e-115HTS70gi  27447206 gb AAL92873.1  CST-like protein3356e-91HTS82gi  100335 pir  S18181 dnak-type molecular chaperone Nthsp703503e-95HTS190gi  7443855 pir  T07733 chaperonin 60 beta chain precursor2792e-76HTS195gi  3591104 gb AAQ23059.1  heat-shock factor RHSF52328e-60HTS207gi  28973653 gb AAO64147.1  putative TPR-repeat protein3028e-81HTS317gi  38154489 gb AAR12195.1  molecular chaperone Hsp90-1419e-116HTS320gi  7441310 pir  T04316 heat-shock protein MTSHP precursor2073e-52HTS337gi  39579116 gb AAR28754.1  Bax inhibitor385e-106HTS377gi  9813 emb CAA42660.1  luminal binding protein (BiP)2763e-91HTS400gi  7447302 pir  T06239 probable glutathione transferase3281e-88HTS400gi  709088 c AAP57477.1  small heat-shock protein3595e-98HTS460gi  700846 gb AAP57477.1  small heat-shock protein3595e-98HTS470gi  2790846 gb AAP57477.1  small heat-shock protein3595e-98HTS470gi  2790846 gb AAP57477.1  small heat-shock protein3595e-98	HTS50	gi   8547237   gb   AAF76312.1   Prf [Lycopersicon esculentum]	377	e-103
HTS54gi   10798648   emb   CAC12824.1   putative DNAJ protein2335e-61HTS57gi   7441328   pir     T07602 heat-shock protein 17.62296e-59HTS58gi   7443855   pir     T07733 chaperonin 60 beta chain precursor417e-115HTS70gi   27447206   gb   AAL92873.1   CST-like protein3356e-91HTS82gi   100335   pir     518181 dnaK-type molecular chaperone Nthsp703503e-95HTS190gi   7443855   pir   T07733 chaperonin 60 beta chain precursor2792e-76HTS195gi   33591104   gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS250gi   10697184   db   BAB16318.1   chaperonin-60 alpha subunit367e-101HTS297gi   28973653   gb   AAC64147.1   putative TPR-repeat protein3028e-81HTS317gi   33154489   gb   AAR12195.1   molecular chaperone Hsp90-1419e-116HTS320gi   7441310   pir   T04316 heat-shock protein MTSHP precursor2073e-52HTS337gi   39579116   gb   AAR28754.1   Bax inhibitor385e-106HTS377gi   19813   emb   CAA42660.1   luminal binding protein (BiP)2763e-91HTS400gi   7447302   pir   T06239 probable glutathione transferase3281e-88HTS400gi   10697184   db   BAB16318.1   chaperonin-60 alpha subunit3595e-98HTS400gi   7441302   pir   T06239 probable glutathione transferase3281e-88HTS400gi   7447302   pir   T06239 probable glutathione transferase3281e-88HTS460gi   37904866	HTS53	gi 48474196 dbj BAD22699.1  heat-shock protein 70	190	1e-6
HTS57g  7441328 pir  107602 heat-shock protein 17.62296e-59HTS58g  7443855 pir  107733 chaperonin 60 beta chain precursor417e-115HTS70g  27447206 gb AAL92873.1  GST-like protein3356e-91HTS82g  100335 pir  S18181 dnaK-type molecular chaperone Nthsp703503e-95HTS190g  7443855 pir  T07733 chaperonin 60 beta chain precursor2792e-76HTS195g  33591104 gb AAQ23059.1  heat-shock factor RHSF52328e-60HTS250g  10697184 dbj BAB16318.1  chaperonin-60 alpha subunit367e-101HTS297g  28973653 gb AAO64147.1  putative TPR-repeat protein3028e-81HTS317g  38154489 gb AAR12195.1  molecular chaperone Hsp90-1419e-116HTS320g  7441310 pir  T04316 heat-shock protein MTSHP precursor2073e-52HTS337g  39579116 gb AAR28754.1  Bax inhibitor385e-106HTS377g  19813 emb CAA42660.1  luminal binding protein (BiP)2763e-91HTS400g  15219028 ref NP_175665.1  26.5 kDa class I sHSP1728e-42HTS45g  7447302 pir  T06239 probable glutathione transferase3281e-88HTS400g  10697184 dbj BAB16318.1  chaperonin-60 alpha subunit3595e-98HTS47g  37904866 gb AAP57477.1  small heat-shock protein3602e-98	HTS54	gi 10798648 emb CAC12824.1  putative DNAJ protein	233	5e-61
HTS58gi   7443855   pir   107733 chaperonin 60 beta chain precursor417e-115HTS70gi   27447206   gb   AAL92873.1   GST-like protein3356e-91HTS82gi   100335   pir    518181 dnaK-type molecular chaperone Nthsp703503e-95HTS190gi   7443855   pir    T07733 chaperonin 60 beta chain precursor2792e-76HTS195gi   33591104   gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS250gi   10697184   dbj   BAB16318.1   chaperonin-60 alpha subunit367e-101HTS297gi   28973653   gb   AAO64147.1   putative TPR-repeat protein3028e-81HTS317gi   38154489   gb   AAR12195.1   molecular chaperone Hsp90-1419e-116HTS320gi   7441310   pir     T04316 heat-shock protein MTSHP precursor2073e-52HTS337gi   39579116   gb   AAR28754.1   Bax inhibitor385e-106HTS377gi   19813   emb   CAA42660.1   luminal binding protein (BiP)2763e-91HTS400gi   15219028   ref   NP_175665.1   26.5 kDa class I sHSP1728e-42HTS45gi   7447302   pir     T06239 probable glutathione transferase3281e-88HTS460gi   37904866   gb   AAP57477.1   small heat-shock protein3602e-98HTS470gi   37904866   gb   AAP57477.1   small heat-shock protein3602e-98	HTS57	gi   7441328   pir     T07602 heat-shock protein 17.6	229	6e-59
H1S/0gi  2/44/206 gb  AAL928/3.1   GS1-like protein3356e-91HTS82gi  100335 pir  S18181 dnaK-type molecular chaperone Nthsp703503e-95HTS190gi  7443855 pir  T07733 chaperonin 60 beta chain precursor2792e-76HTS195gi  35591104 gb  AAQ23059.1  heat-shock factor RHSF52328e-60HTS250gi  10697184 dbj  BAB16318.1  chaperonin-60 alpha subunit367e-101HTS297gi  28973653 gb  AAO64147.1  putative TPR-repeat protein3028e-81HTS317gi  38154489 gb  AAR12195.1  molecular chaperone Hsp90-1419e-116HTS320gi  7441310 pir  T04316 heat-shock protein MTSHP precursor2073e-52HTS337gi  39579116 gb  AAR28754.1  Bax inhibitor385e-106HTS377gi  19813 emb CAA42660.1  luminal binding protein (BiP)2763e-91HTS400gi  15219028 ref NP_175665.1  26.5 kDa class I sHSP1728e-42HTS45gi  10697184 dbj  BAB16318.1  chaperonin-60 alpha subunit3595e-98HTS470gi  37904866 gb  AAP57477.1  small heat-shock protein3602e-98	HIS58	gi 7443855   pir   107733 chaperonin 60 beta chain precursor	41/	e-115
H1S82g  100335  pir   S18181 dnak-type molecular chaperone Nthsp7035036e-95HTS190g  7443855  pir   T07733 chaperonin 60 beta chain precursor2792e-76HTS195g  33591104  gb  AAQ23059.1   heat-shock factor RHSF52328e-60HTS250g  10697184  dbj  BAB16318.1   chaperonin-60 alpha subunit367e-101HTS297g  28973653  gb  AAO64147.1   putative TPR-repeat protein3028e-81HTS17g  38154489  gb  AAR12195.1   molecular chaperone Hsp90-1419e-116HTS320g  7441310   pir   T04316 heat-shock protein MTSHP precursor2073e-52HTS337g  39579116  gb  AAR28754.1   Bax inhibitor385e-106HTS377g  19813   emb   CAA42660.1   luminal binding protein (BiP)2763e-91HTS400g  15219028   ref   NP_175665.1   26.5 kDa class I sHSP1728e-42HTS450g  10697184   dbj   BAB16318.1   chaperonin-60 alpha subunit3595e-98HTS470g  37904866   gb   AAP57477.1   small heat-shock protein3602e-98HTS470g  37904866   gb   AAP57477.1   small heat-shock protein3602e-98	HIS/U	gi   27447206   gb   AAL92873.1   GS1-like protein	335	6e-91
H1S190gi   7443855  pir   107733 chaperonin 60 beta chain precursor2792e-76HTS195gi   33591104  gb   AAQ23059.1   heat-shock factor RHSF52328e-60HTS250gi   10697184  dbj   BAB16318.1   chaperonin-60 alpha subunit367e-101HTS297gi   28973653  gb   AAO64147.1   putative TPR-repeat protein3028e-81HTS17gi   38154489  gb   AAR12195.1   molecular chaperone Hsp90-1419e-116HTS320gi   7441310   pir   T04316 heat-shock protein MTSHP precursor2073e-52HTS337gi   3341464   emb   CAA12387.1   Hsp20.1 protein2681e-70HTS135gi   39579116  gb   AAR28754.1   Bax inhibitor385e-106HTS377gi   19813   emb   CAA42660.1   luminal binding protein (BiP)2763e-91HTS400gi   15219028   ref   NP_175665.1   26.5 kDa class   sHSP1728e-42HTS455gi   37904866  gb   AAP57477.1   small heat-shock protein3602e-98HTS470gi   37904866  gb   AAP57477.1   small heat-shock protein3602e-98HTS477gi   37904866  gb   AAP57477.1   small heat-shock protein3602e-98	H1582	gi 100335 [pir] [ST8T8T dnak-type molecular chaperone (Nthsp70	350	3e-95
H15195 gi 33591104  g0 AAQ25059.1   heat-shock factor KH5F5 252 66-60   HTS250 gi 10697184  dbj BAB16318.1   chaperonin-60 alpha subunit 367 e-101   HTS297 gi 28973653  gb AAO64147.1   putative TPR-repeat protein 302 8e-81   HTS317 gi 38154489  gb AAR12195.1   molecular chaperone Hsp90-1 419 e-116   HTS320 gi 7441310  pir   T04316 heat-shock protein MTSHP precursor 207 3e-52   HTS337 gi 3341464  emb CAA12387.1   Hsp20.1 protein 268 1e-70   HTS135 gi 39579116  gb AAR28754.1   Bax inhibitor 385 e-106   HTS377 gi 19813  emb CAA42660.1   luminal binding protein (BiP) 276 3e-91   HTS400 gi 15219028  ref  NP_175665.1   26.5 kDa class I sHSP 172 8e-42   HTS45 gi 10697184  dbj BAB16318.1   chaperonin-60 alpha subunit 359 5e-98   HTS470 gi 37904866  gb AAP57477.1   small heat-shock protein 360 2e-98   HTS477 gi 37904866  gb AAP57477.1   small heat-shock protein 360 2e-98	HTS190	gi / 443855 pir [ 10/ / 33 chaperonin 60 beta chain precursor	279	2e-76
H15250gi [10697184 [db]] BAB16318.1]Chaperonin-bot alpha subulit3676-101HTS297gi [28973653 ]gb [AAO64147.1]putative TPR-repeat protein3028e-81HTS317gi [38154489 ]gb [AAR12195.1]molecular chaperone Hsp90-1419e-116HTS320gi [7441310  pir   T04316 heat-shock protein MTSHP precursor2073e-52HTS337gi [3341464   emb] CAA12387.1]Hsp20.1 protein2681e-70HTS135gi [39579116  gb   AAR28754.1]Bax inhibitor385e-106HTS377gi [19813   emb   CAA42660.1]luminal binding protein (BiP)2763e-91HTS400gi [15219028   ref   NP_175665.1]26.5 kDa class I sHSP1728e-42HTS45gi [10697184   db]   BAB16318.1]chaperonin-60 alpha subunit3595e-98HTS470gi [37904866   gb   AAP57477.1]small heat-shock protein3602e-98HTS487gi [37904866   gb   AAP57477.1]small heat-shock protein3602e-98		gi 33591104 go AAQ23059.1 neal-shock lactor KEISES	232	00-00
H15297 gi [28973633]gb [AAO64147.1] putative TrA-lepeat protein 362 362-81   HTS317 gi [38154489]gb [AAR12195.1] molecular chaperone Hsp90-1 419 e-116   HTS320 gi [7441310]pir] [T04316 heat-shock protein MTSHP precursor 207 3e-52   HTS337 gi [3341464]emb [CAA12387.1] Hsp20.1 protein 268 1e-70   HTS135 gi [39579116]gb [AAR28754.1] Bax inhibitor 385 e-106   HTS377 gi [19813]emb [CAA42660.1] luminal binding protein (BiP) 276 3e-91   HTS400 gi [15219028]ref [NP_175665.1] 26.5 kDa class I sHSP 172 8e-42   HTS455 gi [10697184]dbj [BAB16318.1] chaperonin-60 alpha subunit 359 5e-98   HTS470 gi [37904866]gb [AAP57477.1] small heat-shock protein 360 2e-98   HTS487 gi [37904866]gb [AAP57477.1] small heat-shock protein 360 2e-98	HI5250	gi 10097104 [ub] DAD 10310.1 [ Chaperonin-ou alpha subunit	202	e-101
HTS317 gi [38134489]gb [AAR12195.1] molecular chaperone risp90-1 419 6-110   HTS320 gi [7441310]pir] [T04316 heat-shock protein MTSHP precursor 207 3e-52   HTS337 gi [3341464]emb [CAA12387.1] Hsp20.1 protein 268 1e-70   HTS135 gi [39579116]gb [AAR28754.1] Bax inhibitor 385 e-106   HTS377 gi [19813]emb [CAA42660.1] luminal binding protein (BiP) 276 3e-91   HTS400 gi [15219028]ref [NP_175665.1] 26.5 kDa class I sHSP 172 8e-42   HTS345 gi [7447302]pir] [T06239 probable glutathione transferase 328 1e-88   HTS460 gi [37904866]gb [AAP57477.1] small heat-shock protein 360 2e-98   HTS470 gi [37904866]gb [AAP57477.1] small heat-shock protein 360 2e-98	HTS29/	gi 20973653 go AAO64147.1 putative Trk-tepeat protein	302 410	00-01
HTS320 gi   7441310   pir   104316 heat-shock protein MTS1r precusor 207 36-32   HTS337 gi   3341464   emb   CAA12387.1   Hsp20.1 protein 268 1e-70   HTS135 gi   39579116   gb   AAR28754.1   Bax inhibitor 385 e-106   HTS377 gi   19813   emb   CAA42660.1   luminal binding protein (BiP) 276 3e-91   HTS400 gi   15219028   ref   NP_175665.1   26.5 kDa class   sHSP 172 8e-42   HTS345 gi   7447302   pir     T06239 probable glutathione transferase 328 1e-88   HTS460 gi   37904866   gb   AAP57477.1   small heat-shock protein 360 2e-98   HTS477 gi   37905913   ab   AAO38853 1   debudrin like protein 360 2e-98		gi z441210 piel 104216 host shock protoin MTSHD productor	415	20 52
H15357 gi [3541484]emb[CAA12367.1] Hsp20.1 protein 266 16-70   HTS135 gi [39579116]gb[AAR28754.1] Bax inhibitor 385 e-106   HTS377 gi [19813]emb[CAA42660.1] luminal binding protein (BiP) 276 3e-91   HTS400 gi [15219028]ref[NP_175665.1] 26.5 kDa class I sHSP 172 8e-42   HTS345 gi [7447302]pir][T06239 probable glutathione transferase 328 1e-88   HTS460 gi [10697184]dbj[BAB16318.1] chaperonin-60 alpha subunit 359 5e-98   HTS470 gi [37904866]gb[AAP57477.1] small heat-shock protein 360 2e-98   HTS487 gi [37005913]alb]AAO38853 11 dobudrin like protein 182 5n 45	HT5320	gi / 441510 pir   104516 heat-shock protein M15r r precursor	207	10.70
HTS155 gi [39379116]gb [AAR20734.1] bax limitation 363 64106   HTS377 gi [19813]emb [CAA42660.1] luminal binding protein (BiP) 276 3e-91   HTS400 gi [15219028]ref [NP_175665.1] 26.5 kDa class I sHSP 172 8e-42   HTS345 gi [7447302]pir [106239 probable glutathione transferase 328 1e-88   HTS460 gi [10697184]dbj [BAB16318.1] chaperonin-60 alpha subunit 359 5e-98   HTS470 gi [37904866]gb [AAP57477.1] small heat-shock protein 360 2e-98   HTS487 gi [37005913]alb [AAO38853 1] dobudrin like protein 360 2e-98	HI3337	gi 20570116 John A P29754 1 L Pay inhibitor	200	0.106
HTS377 gi [19813]emb[CAA42660.1] tuminar binding protein (bir) 276 36-91   HTS400 gi [15219028]ref]NP_175665.1] 26.5 kDa class I sHSP 172 8e-42   HTS345 gi [7447302]pir][T06239 probable glutathione transferase 328 1e-88   HTS460 gi [10697184]dbj]BAB16318.1] chaperonin-60 alpha subunit 359 5e-98   HTS470 gi [37904866]gb]AAP57477.1] small heat-shock protein 360 2e-98   HTS487 gi [37005913]alb]AAO38853 11 dobudrin like protein 182 5m 45	H15133	gi   1997/91 10   gD   AAK207 54.1   Ddx III 10 10 1 gi   19912   amb   CAA42660 1   Juminal hinding protain (PiD)	202	20.01
HTS460 gi   7247302   pir     T06239 probable glutathione transferase 328 1e-88   HTS460 gi   10697184   dbj   BAB16318.1   chaperonin-60 alpha subunit 359 5e-98   HTS470 gi   37904866   gb   AAP57477.1   small heat-shock protein 360 2e-98   HTS487 gi   37005913   gb   AAO38853 1   dobudrin like protein 360 2e-98	HT\$400	$g_{1}$ $g_{2}$ $g_{1}$ $g_{2}$ $g_{2$	∠/0 170	30-71 80-43
HTS450 gi   10697184   dbj   BAB16318.1   chaperonin-60 alpha subunit 359 5e-98   HTS470 gi   37904866   gb   AAP57477.1   small heat-shock protein 360 2e-98   HTS487 gi   37005913   ab   AAO38853 1   dob/drin like protein 360 2e-98	HT\$3/5	gi 13213020 [ref] 17.0003.1 20.3 La Class Estist gi 17447302 [nir] 1706239 probable dutathione transferase	17∠ 328	100-42 10-88
HTS480 gi   37904866   gb   AAP57477.1   small heat-shock protein 360 2e-98   HTS487 gi   37905913   gb   AAO38853 1   dobydrin like protein 182 59.45	нтулал Нтулал	gi 10697184 dhi BAB16318 1 chaperonin-60 alpha subunit	359	5e-00
$HTS487 = ai   27005012   ab   \Delta \Delta \Omega 38852   1   dobudrin like protain = 192 = 5.45$	HTS470	gi 37904866 ah AAP57477 1 small heat-shock protein	360	26-90 26-98
$10.3 \qquad 10.2 \qquad $	HTS487	gi 37905913 gb AAO38853.11 dehvdrin-like protein	183	20-50 5e-45

### Table 1. (continued).

EST ID	Description of best data match plus database accession number for homologous gene	Score	E-value
	Transcription		
HTS9	gi 15224062 ref NP_179958.1  zinc finger(C3HC4-type RING)	238	1e-61
HTS187	gi 30690620 ref NP_850470.1  myb family transcription factor	197	1e-49
HTS397	gi 6862918 gb AAF30307.1  putative RING zinc finger protein	146	7e-34
HTS14	gi   42561972   gb   AAS20427.1   ethylene-responsive factor-like	397	e-115
HTS185	gi 42563295 ref NP_177903.4  PHD finger family protein	257	2e-67
HTS245	gi 55297001 dbj BAD68476.1 bromodomain-containing protein	274	3e-72
and the state of t	Transport facilitation		
HTS350	dbj BAB40141.1 (AB035272) plasmamembrane intrinsic protein	130	2e-11
HTS387	gi 12006187 gb AAG44776.1  biotin carboxyl carrier protein	65	1e-11
HTS265	gi 50254435 gb EAL17184.1  hypothetical protein CNBN0130	133	2e-33
HTS425	gi 6996562 emb CAB75430.1 putative 16kDa membrane protein	250	3e-65
	Cellular communication and signal transduction		
HTS157	gi 30679085 ref NP_195722.2  protein kinase family protein	190	4e-47
HTS13	gi 29376496 ref NP_815650.1  GTP pyrophosphokinase	35	3.3
HTS445	gi 15235152 ref NP_195118.1 protein phosphatase 2C family	234	9e-61
HTS480	gi 17104725 gb AAL34251.1 putative ADP ribosylation factor	238	2e-65
· · · · · · · · · · · · · · · · · · ·	Cellular organization		
HTS43	gi 5327263 emb CAB46351.1  aquaporin	432	e-120
HTS210	gi 3163946 emb CAA06619.1 alpha-tubulin 1 [Eleusine indica]	390	e-124
HTS340	gi 8928432 sp Q9ZRR5 TBA3_HORVU tubulin alpha-3 chain	426	e-131
HTS285	sp P30175  actin-depolymerization (ADF)	210	2e-61
HTS325	sp Po9469  vacuolar ATP synthase catalytic subunit A	183	6e-4
HTS227	gb AAK96884.1 (AY009094) beta tubulin	146	7e-34
HTS450	gi 8928432 sp Q9ZRR5 TBA3_HORVU tubulin alpha-3 chain	426	e-131
	Transposable elements; viral and plasmid proteins		
HTS355	gi 47825015 gb AAT38786.1  putative gag-pol polyprotein	92	1e-32
HTS290	gi   7269781   emb   CAB77781.1   polyprotein of LTR transposon	173	6e-49
HTS6	gi 53689713 gb AAU89728.1  retroelement pol polyprotein	156	3e-62
	Cell cycle and DNA processing		
HTS81	gi 22326839 ref NP_197131.2  Rad21/Rec8-like family protein	174	4e-42
HTS260	gi 42408051 dbj BAD09193.1  putative PrMC3 [Oryza sativa]	182	8e-45
	Classification not yet clear-cut (unknown)		
HTS22	gi 11994706 dbj BAB02944.1  unnamed protein product	203	3e-84
HTS23	gi 30683790 ref NP_567512.2  exostosin family protein	162	3e-08
HTS24	gi 18415962 ref NP_568211.1  expressed protein	228	2e-58
HTS26	gi 21536807 gb AAM61139.1  unknown	174	2e-12
HTS28	gi 8919877 emb CAB96200.1  hypothetical protein	185	2e-15
HTS31	gi 32352168 dbj BAC78577.1  hypothetical protein	161	2e-38
HTS330	gi 25513587 pir  E86289 T16N11.7 protein [A. thaliana]	136	3e-41
HTS34	gi 18402380 ref NP_565700.1  expressed protein	133	3e-56
HTS59	gi 42570879 ref NP_973513.1  expressed protein	189	2e-16
HTS64	gi 18405124 ref NP_565909.1  radical SAM domain-containing	135	1e-30
HTS71	gi 18396280 ref NP_564274.1  expressed protein	109	1e-22
HTS79	gi 15220924 ref NP_176682.1  expressed protein [A. thaliana]	269	6e-71
HTS80	gi 27808548 gb AAO24554.1  At1g61150 [A. thaliana]	342	6e-93
HTS84	gi 15234433 ref NP_195371.1 hydrolase, alpha/beta fold protein	286	5e-76

Table	e 1.	(continued	).
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EST ID	Description of best data match plus database accession number for homologous gene	Score	E-value
HTS115	gi 584825 sp P37707 B2_DAUCA B2 PROTEIN	120	8e-27
HTS117	gi 17065046 gb AAL32677.1  unknown protein [A. thaliana]	360	2e-98
HTS127	gi 28874734 emb CAC80137.1  progesterone 5-beta-reductase	259	4e <b>-</b> 76
HTS207	gi 21593353 gb AAM65302.1  unknown (A. thaliana)	300	3e-82
HTS237	gi 38344078 emb CAE01738.2  OSJNBb0056F09.1	85	2e-15
HTS257	gi 15239148 ref NP_196729.1  expressed protein [A. thaliana]	329	6e-89
HTS240	gi 6322674 ref NP_012747.1  Ykl174cp	135	6e-23
HTS417	gi 9294516 dbj BAB02778.1  unnamed protein product	325	1e-87
HTS455	gi 18396859 ref NP_566224.1  expressed protein [A. thaliana]	232	1e-59
HTS477	gi 18398123 ref NP_565388.1  expressed protein [A. thaliana]	195	7e-57
HTS485	gi 26452567 dbj BAC43368.1  unknown protein (A. <i>thaliana</i> )	382	e-105
HTS365	gi 40736997 gb AAR89010.1  expressed protein [ <i>O. sativa</i> ]	221	3e-59
HTS95	gi 21554147 gb AAM63227.1  unknown [A. thaliana]	311	3e-96
HTS120	gi 18419954 ref NP_568013.1  expressed protein [A. thaliana]	246	4e-64
HTS130	gi 15218701 ref NP_171806.1  expressed protein [A. thaliana ]	323	2e-87
	Unclassified protein and no hit		
HTS2	No significant similarity found.		
HTS100	gi 38603804 gb AAR24647.1  At2g23330 (A. thaliana)	155	3e-61
HTS17	gi 15224172 ref NP_179434.1  expressed protein	135	5e-53
HTS30	gi 34849885 gb AAQ82839.1  At4g04790	133	4e-47
HTS37	gi 50080326 gb AAT69660.1  unknown protein	146	2e-32
HTS40	gi 46911551 emb CAG27615.1  putative leucine-rich repeat	141	1e-04
HTS41	gi 34902002 ref NP_912347.1 ser/arg rich ribonucleoprotein	50	2e-10
HTS44	gi 18394220 ref NP_563969.1  expressed protein	165	2e-09
HTS49	gi 31209269 ref XP_313601.1  ENSANGP00000013268	142	2e-15
HTS52	No significant similarity found.		
HTS72	gi 6322674 ref NP_012747.1  hypothetical ORF; Ykl174cp	135	2e-54
HTS73	gi 28373837 pdb 1N0R A designed Ankyrin repeat protein	179	2e-13
HTS197	gi 47497554 dbj BAD19626.1  hypothetical protein	133	1e-65
HTS200	gi 15239148 ref NP_196729.1  expressed protein [A. thaliana]	329	6e-89
HTS215	gi 30694498 ref NP_175343.2  expressed protein [A. thaliana]	172	9e-42
HTS247	No significant similarity found		
HTS280	gi[15642295 ref NP_231928.1  conserved hypothetical protein	135	1e-77
HTS287	gi 5596352 dbj BAA82607.1  sALK-7 [Ephydatia fluviatilis]	133	1e-08
HTS295	gi 42568382 ref NP_199594.2  expressed protein [A. thaliana]	147	1e-04
HTS310	gi 46092516 dbj BAD14378.1  hypothetical protein	131	2e-29
HTS315	gi   15233196   ref   NP_191076.1   expressed protein [A. thaliana]	129	1e-28
HTS347	gi 21428994 gb AAM50216.1  GM13228p	136	1e-54
HTS440	gi 31211851 ref XP_314910.1  ENSANGP00000012448	134	2e-77
HTS465	No significant similarity found		
HTS60	gi 50290053 ref XP_447458.1  unnamed protein product	133	3e-28
HTS490	No significant similarity found		
HTS69	gi 25518436 pir  C86390 hypothetical protein T1K7.26	138	2e-31
HTS75	gi 50290053 ref XP_447458.1  unnamed protein product	133	2e-24
HTS77	gi 50302195 ref XP_451031.1  unnamed protein product	139	1e-77
HTS90	gi 42567155 ref NP_194332.2  expressed protein [A. thaliana]	122	1e-26
HTS125	gi 18394407 ref NP_564007.1  expressed protein [A. thaliana ]	180	6e-14
HTS145	gi 25345695 pir  E86367 protein F26F24.22 [imported]	150	2e-09
HTS155	gi 9294484 dbj BAB02703.1  unnamed protein product	201	4e-74

EST ID	Description of best data match plus database accession number for homologous gene	Score	E-value
HTS165	gi 15237534 ref NP_196003.1 expressed protein [A. thaliana ]	130	1e-12
HTS167	gi 209078 gb AAA72893.1  alpha-peptide >gi 3603281 gb A	70	4e-11
HTS62	gi   42567155   ref   NP_194332.2   expressed protein	122	2e-26
HTS225	gi 13172242 gb AAK14060.1  major latex-like protein	135	1e-30
HTS305	gi 37532246 ref NP_920425.1 hydroxyproline-rich glycoprotein	276	4e-73
HTS8	gi 30682618   ref   NP_187941.2   expressed protein	268	1e-70
HTS105	gi 20453247 gb AAM19862.1  AT4g03420/F9H3_4(A. thaliana)	267	2e-70
HTS110	gi 42568382 ref NP_199594.2 expressed protein [A. thaliana]	159	1e-37
HTS160	gi 30694478 ref NP_191218.2  hydroxyproline-rich glycoprotein	156	6e-37
HTS56	gi 12005328 gb AAG44394.1  unknown [Hevea brasiliensis]	186	1e-15
HTS175	gi 34903328 ref NP_913011.1  unnamed protein product	299	e-106
HTS360	gi 26452567 dbj BAC43368.1  unknown protein (A. <i>thaliana</i> )	344	1e-93
HTS497	gi 21553932 gb AAM63013.1  unknown [A. thaliana]	146	4e-47
HTS180	gi 23198154 gb AAN15604.1 putative protein [A. thaliana]	374	e-102
HTS420	gi 34902002 ref NP_912347.1 unnamed protein	150	2e-10
HTS32	gi 37202090 gb AAQ89660.1  At1g70760 (A. thaliana)	183	6e-45
HTS267	gi 53850511 gb AAU95432.1  At1g04635 (A. thaliana)	127	2e-28
HTS380	gi 25402836 pir  H86313 protein F2H15.10 [imported]	276	1e-73
HTS395	gi 12642910 gb AAK00397.1  unknown protein (A. thaliana)	107	4e-22
HTS405	gi 20465579 gb AAM20272.1  unknown protein (A. thaliana)	237	3e-61
HTS220	gi 30793919 gb AAP40412.1  unknown protein [A. thaliana ]	244	2e-63

Table 1. (continued).

Seki et al., 2002). These genes include homologues of glutathione S-transferase, S-adenosylmethionine synthetase, receptor-like protein kinase, protein kinase, and protein phosphatase 2C-like proteins. Similarly, a comparison with gene expression profiles from *Arabidopsis* under drought and cold stresses has also revealed a number of common genes, such as those for ascorbate peroxidase, a glycine-rich protein, and an ethylene-responsive element binding protein (Seki et al., 2001).

Large-scale EST projects are often accompanied by high redundancy; thus, an increased input of effort for novel gene discovery is required. The limited data from 200 ESTs of our cDNA library showed 6 ESTs of putative transcription factors and 4 ESTs of putative signal transduction pathway component genes, numbers that are even higher than previously reported for normalized rice cDNA. Reddy et al. (2002) used a large-scale EST approach to isolate drought-responsive genes from a normalized cDNA library, but could locate only 1% of the ESTs in the categories of transcription factor genes and signal transduction pathway component genes. Thus, our modified differential screening "double negative screening" approach, though using only a relatively small number of analyzed ESTs, seemed to enable us to detect low-abundance transcripts with high similarity to expressed proteins, unknown protein products, and novel sequences.

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