Evolutionary features of the central nervous system revealed by the comparative approach of the gene expression profiles

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ABSTRACT

The understanding of the evolutionary process of the central nervous system (CNS), in particular a brain, is one of the challenging tasks in modern biology. It is easily imaginable that biological complexity of the CNS is mainly due to not only structural complexity but also complicated and elaborated network of function. There is no doubt that functional network must be maintained by a network of multiple gene interaction that are intriguingly maintained by gene expression control. The extreme difficulty of studying the CNS might be due to a lack of definite approach to understand multiple interaction of gene expression. However, it is fortunate that the recent advancement of genome projects and cDNA projects provided us with the molecular biological methods for identifying gene sets and the degree of gene expression in a particular organ of a given species. When we define a gene expression profile as an occurrence frequency of the expressed gene species in a given organ, I thought that comparative studies of gene expression profiles in the CNS among various organisms might give profound insight into the understanding of evolutionary processes of the CNS. Here in my thesis, I proposed a novel approach for the evolutionary study of CNS, focusing on the gene expression profiles. Since an expression profile results from the transcriptional activities of all genes involved in the networks, the expression profile should reflect the outcome of transcriptional regulations of all genes expressed in a given organ. Thus, the purpose of my thesis is to answer the question whether the evolutionary

process of CNSs can be understood from the gene expression profiles.

To attain the purpose, I examined the gene expression profiles at the following levels; (1) a conservation pattern of the nervous system-related genes, (2) the divergence of the gene expression profiles at the cell level, and (3) the divergence of the gene expression profiles at the level of the organs such as a brain. In particular, I examined if the correspondence is good between the species tree conventionally obtained and the tree of gene expression profile invented in my study.

This thesis is composed of five chapters. In **chapter 1**, I described the outline of the present thesis, placing particular emphasis on the motivation and purpose of my study. I also noted that the evolutionary study of the CNS, in particular a brain, is of biological significance. In **chapter 2**, taking the planarian CNS as an example, I, first, examined the evolutionary divergence of the genes that were related to the nervous system, because the planarian is known to possess one of the most primitive brains. To elucidate the evolutionary process of CNS, I then conducted the comparative genomics studies of gene expression profiles in the CNS among different organisms. We sequenced 5,433 5'-ESTs from the cDNA library that was derived from the head portions of planarians (*Dugesia japonica*), obtaining a total of 3,101 non-redundant EST clones.

To deal with the large amount of EST data, I have developed a computer software package, FinEST, in which an information analysis of EST sequence data including homology search can be done automatically. Conducting the homology search in my software package, I found that 44% of the 3,101 clones had significant similarity of amino acid sequences of gene products whose functions were known. Among these genes, at least 116 genes were found to be homologous to the CNS-related genes. I compared these 116 planarian gene sequences with all ORFs of the complete genome sequences of human, fruit fry and nematode. I then found that 110 genes were evolutionarily shared among all the bilateral animals examined, although only the remaining 6 genes were shared among a limited number of species. This feature of gene conservation can be considered as strong reflection of the selective constraints against CNS-related genes, suggesting that these shared genes are a part of the basic gene set of CNS which might have existed in the common ancestral CNS of bilateral animals. Based on these findings, I proposed a model of the evolutionary process of the CNS.

In **chapter 3**, with the aim of studying the diversity of the genes expressed in different cell types, we took a comparative approach using the gene expression profiles of single cells of ascidians (*Ciona intestinalis*). The swimming larval stage of ascidian has two different sensory organs, called "ocellus" and "otolith". These organs exist in a cerebral vesicle, which is often called as a brain. It has been reported that there are only two pigment cells in a total of about 2,600 cells that form the swimming larva. One pigment cell is found in the ocellus and the other is otolith. Thus, in this study, these pigment cells were called as ocellus cell and otolith cell. To attain our purpose, we examined the expression profiles of the ocellus cell and the otolith cell, and compared the expression profiles between these two different types of cells. First, we sequenced 964 and 774 ESTs from the cDNA libraries of the pigment cells of ocellus and otolith, respectively. As a result, we obtained 485 and 505 non-redundant clones from the ocellus and otolith cells, respectively. The composition of the highly expressed clones illustrated clear difference from that of planarian head ESTs, showing that one of characteristic features of the gene expression profiles in these single cells is less amount of the cytoskeltal genes expressed. Comparing the gene expression profiles between ocellus and otolith cells, we found that 60 clones were commonly expressed between two pigment cells. The relative frequencies of these 60 clones showed obviously distinct patterns between these two cells. This is the first report about the gene expression profiles of the single cells that compose an organ, showing clear characteristic features of the expression profiles at the single cell level.

In **chapter 4**, I made an attempt to understand the evolutionary process of a brain from the viewpoint of gene expression profiles. To attain the purpose, I raised a question of whether the degree of the differences in the gene expression profiles of a particular organ between different species corresponds proportionally to the degree of the evolutionary divergence between the species. In practice, we sequenced EST clones from the cDNA libraries of brains of chickens (*Gallus gallus*) and lampreys (*Lampetra japonica*), the head of planarians (see above), and the whole body of the jellyfish (*Aureria aurita*), obtaining over 2,000 clones from each library. If difference of the gene expression profiles corresponds to the evolutionary divergence of species, a topology of the tree based on the difference in the gene expression profiles (designated as a gene expression tree) might correspond to a topology of the species tree. To examine this statement, I quantified the differences in the gene expression profiles between different species by the Euclidean distance, and then constructed a gene expression tree. As a result, the topology of the gene expression tree showed clear correspondence to that of the species tree, though the current number of clones sequenced was still relatively small. Thus, I concluded that the gene expression profiles of brains might reflect the evolutionary process of the brain.

Finally, in **chapter 5,** I described the summary and conclusion of the present study. I also discussed the future perspectives of the present study. In conclusion, this is the first attempt to conduct an evolutionary study by use of the gene expression profiles, successfully showing that the evolutionary process of the CNS can be traceable by use of the gene expression profiles.

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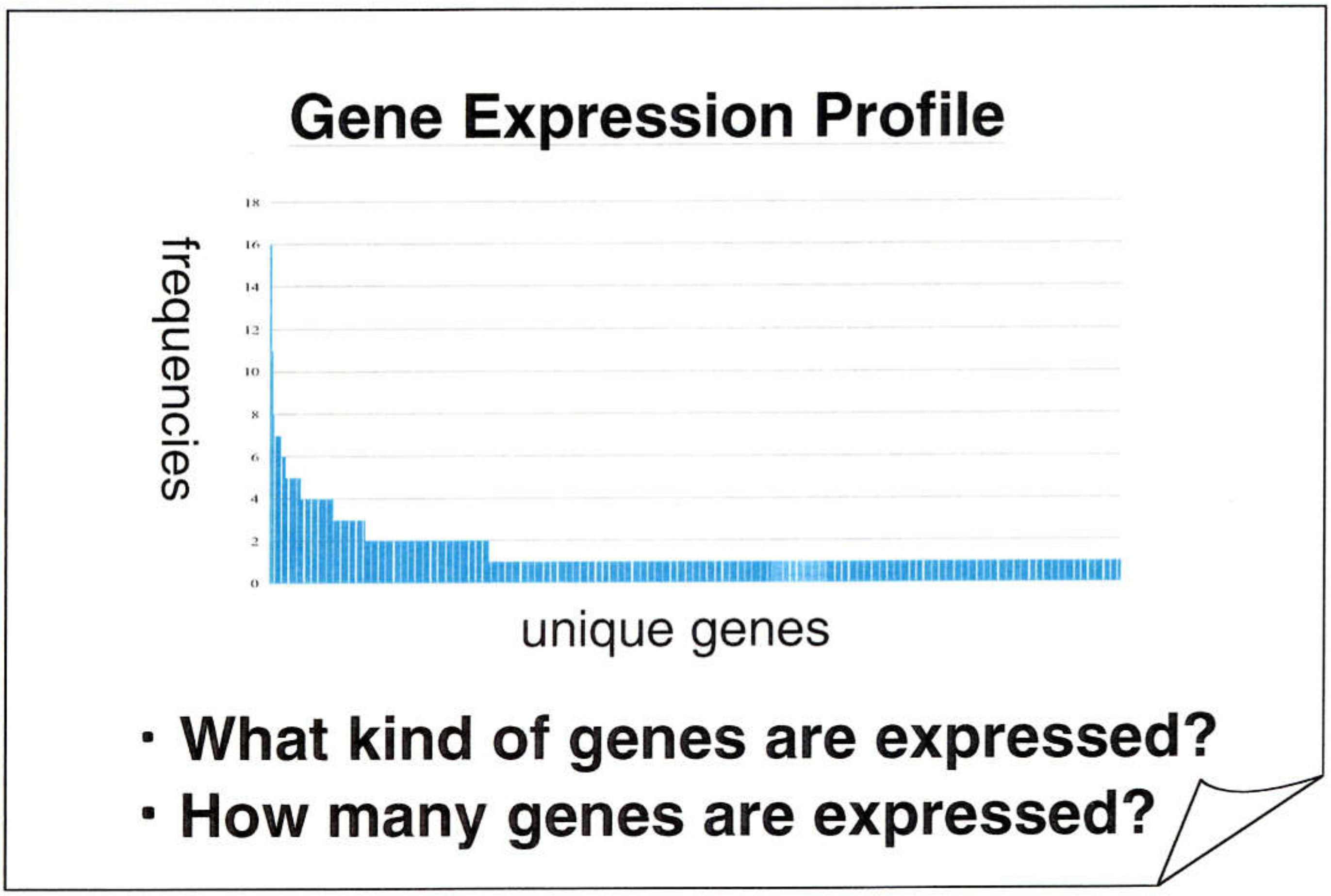
Chapter 1

Introduction

The understanding of the evolutionary process of the central nervous system (CNS), in particular a brain, is one of the challenging tasks in the modern biology. It is easily imaginable that biological complexity of the CNS is mainly due to not only structural complexity but also complicated and elaborated network of function. There is no doubt that functional network must be maintained by a network of multiple gene interactions that are intriguingly maintained by gene expression control. The extreme difficulty of studying the CNS might be due to a lack of definite approach to understand multiple interactions of gene expression. However, it is fortunate that the recent advancement of genome projects (cf. International human genome sequencing consortium 2001) and cDNA projects (reviewed by Bortoluzzi *et al.* 1999) provided us with the molecular biological methods for identifying gene sets and the degree of gene expression in a particular organ of a given species. When we define a gene expression profile as an occurrence frequency of the mRNA or the species of the expressed genes in a given organ (Figure 1.1), I thought that a comparative studies of gene expression profiles in the CNS among various organisms may give profound insight into the understanding of evolutionary processes of the CNS.

Here in my thesis, I proposed a novel approach for the evolutionary study of CNS, focusing on the gene expression profiles. Since an expression profile results



Gene Expression Profile

- **What kind of genes are expressed?**
- **How many genes are expressed?**

Figure 1.1: What is the "Gene expression profiles"? In this thesis, I defined the gene expression profile as an occurance frequency of mRNA and gene species of the genes expressed.

from the transcriptional activities of all genes involved in the networks, the expression profile should reflect the outcome of transcriptional regulations of all genes expressed in a given organ. Thus, the purpose of my thesis is to answer the question whether the evolutionary process of CNSs can be understood from the gene expression profiles.

To attain the purpose, I examined the gene expression profiles at the following levels; (1) a conservation pattern of the nervous system-related genes, (2) the divergence of the gene expression profiles at the cell level, and (3) the divergence of the gene expression profiles at the level of the organ such as a brain. In particular, I examined if the correspondence is good between the species tree conventionally obtained and the tree of gene expression profiles invented in my study.

In the bilateral animals, the centralized nervous system is found in both clades of deuterostome and protostome (Neilsen 2001; Gerhart & Kirschner 1997; and Figure 1.2). It is thought that CNSs were derived from the common ancestor between deuterostome and protostome (Arendt & Nubler-Jung 1997). To understand the evolutionary process of the CNS, it is an essential question to know what kinds of genes had existed in the CNS of the common ancestor. In chapter 2, to answer this question, I took a comparative approach using different species, focusing on one of the lower bilateral animals, planarian (Platyhelminthes, Tricladida) which is known to possess the CNS. Planarians CNS has a simple and primitive morphology (Baguna 1998; Riger *et al.* 1991), which is composed of the cephalic ganglions and a pair of ventral nerve cords. The cephalic ganglions form an inverted U-shaped structure with nine branches

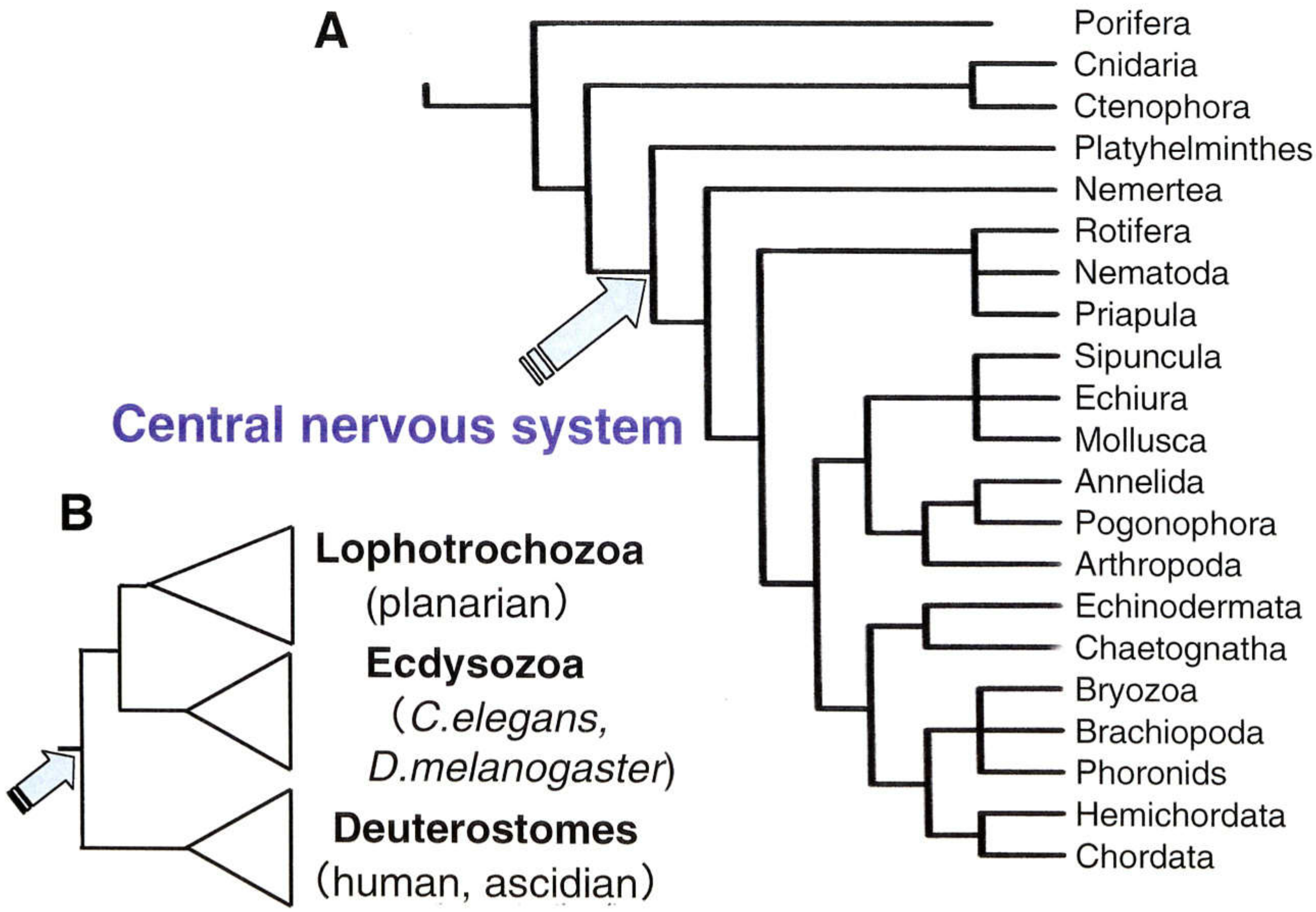


Figure 1.2: Phylogenetic tree of the metazoan and the emergence of the CNS. Blue arrow shows the emergence of the CNS. (A) The phylogenetic tree based on the morphological evidences (modified from Gerhart & Kirschner 1997). (B) The one of the phylogenetic trees based on the 18S rRNA (modified from Aguinaldo *et al.* 1998).

connecting to the sensory organs on each side (Tazaki *et al.* 1999; Agata *et al.* 1998).

Planarian cephalic ganglion exhibits many morphological features similar to the vertebrate CNSs such as the multi-polarized neurons (Sarat & Netsky 1985). Moreover, planarian homologs of the *otx* (or *orthodenticle*) were expressed specifically in the region of cephalic ganglions (Umesono *et al.* 1999). Therefore, the planarian cephalic ganglion can be considered as a primitive brain. Though a phylogenetic position of Platyhelminthes is still under discussion, it is possible to state that the planarian is one of early protostomes (Neilsen 2001; Hyman 1951; Aguinaldo *et al.* 1997; Adoutte *et al.* 2000). The comparative study of the CNS based on the planarian gene set might reveal the common gene set which had emerged at the common ancestral CNS.

As I have already mentioned earlier, the purpose of the present study is to examine the difference of the gene expression profiles in order to answer the question whether the gene expression profile can trace the evolutionary process of the CNS, in particular a brain. However, because a brain is the most complicated organ that is composed of various types of cells, it is of particular interest to know an expression profile of a single cell type. In chapter 3, I will examine the gene expression profiles of the single cell to understand the divergence of the gene expression profiles at the level of single cells. If the fate of the cells used in the analysis is well-documented, differences in the gene expression between different types of single cells can be understood taking into account possible cell-to-cell interaction during the developmental process. From these reasons, I have chosen the ascidians as a material of the study in this chapter. Ascidians belong to the subphylum Urochordata, which is phylogenetically positioned at the base of Chordate. Thus, its phylogenetic position might provide us with a hint to understand the evolution of the brain such as a highly complicated human brain. The swimming larva stage of ascidian is composed of about 2,600 cells that form several distinct types of tissues (Satoh 1994). It is known that there are only two melanin-containing pigment cells among these 2,600 cells. The head portion of the swimming larva contains a cerebral vesicle, which is often called as a brain, with two sensory organs, ocellus and otolith. (reviewed by Satoh and Jeffery 1995). The ocellus is an organ for the photoreception, consisting of 17 cells. It is reported that only one in 17 ocellus cells is the pigment cell (Satoh 1994). The otolith, which is composed of only one pigment cell, is considered to be an organ for the gravity-reception (Satoh 1994). In the present study, I used the otolith cell and the pigment cell of ocellus to examine the divergence of the gene expression profiles at the single cell level.

In chapter 4, I raised a question of whether the degree of differences in the gene expression profiles among various species corresponds proportionally to the degree of evolutionary differences in the species examined. To answer the question, I obtained the gene expression profiles for brains of chickens (*Gallus gallus*) and lampreys (*Lampetra japonica*), the head of planarians (see above), and the whole body of the jellyfish (*Aureria aurita*). If differences of the gene expression profiles correspond to the evolutionary divergence of species, a topology of the tree based on the differences in the gene expression profiles must correspond to a topology of the species tree. Thus, I examined the above-mentioned statement on this chapter.

Finally, I would emphasize that this is the first attempt to conduct an evolutionary study by use of the gene expression profiles. In particular, I would conclude that the evolutionary process of CNS, at least in part, might be understood from the viewpoint of gene expression profiles.

CHAPTER 2

The well-organized CNS was revealed by the comparative approach of planarian EST analysis

Summary

In the bilateral animals, the centralized nervous system was found in both clades of deuterostome and protostome (Neilsen 2001). It is thought that central nervous systems (CNSs) were derived from a common ancestor between deuterostome and protostome (Arendt & Nubler-Jung 1997). It is an essential question what kinds of genes had existed in the CNS of the common ancestor. To answer this question, I took a comparative approach using different species, focusing on one of the lower bilateral animals, planarian (Platyhelminthes, Tricladida) which is known to possess the CNS. We determined the nucleotide sequence of expressed sequence tags (ESTs) from planarians, obtaining 3,101 non-redundant EST clones. As a result of homology search, I found that 116 clones had significant similarity to the genes related to the nervous system. Here, I conducted a comparative analysis using these planarian 116 EST clones with all ORFs of the complete genome sequences of human, *D.*

melanogaster and *C. elegans*, showing 100%, 97% and 95% of the evolutionary conservation of these nervous system-related genes, respectively. Moreover, I found that about 30% of planarian neural-related genes had homologous sequences in *A. thaliana* and *S. cerevisiae*, implying that the origin of neural-related genes was possibly much older than the emergence of the nervous system. My results provide the first evidence of an extreme extent of the conservation of the CNS at the molecular level during a long-term evolution.

Introduction

Planarians possess the CNS that has a simple and primitive morphology (Baguna 1998; Riger *et al.* 1991). The planarian CNS is composed of the cephalic ganglions and a pair of ventral nerve cords. The cephalic ganglions form an inverted U-shaped structure with nine branches connecting to the sensory organs on each side (Tazaki *et al.* 1999; Agata *et al.* 1998). Planarian cephalic ganglion exhibits many morphological features similar to the vertebrate CNSs such as the multi-polarized neurons (Sarat & Netsky 1985). Moreover, planarian homologs of the *otx* (or *orthodenticle*) were expressed specifically in the region of cephalic ganglions (Umesono *et al.* 1999). Therefore, the planarian cephalic ganglion can be considered as a primitive brain.

Planarians belong to the phylum, Platyhelminthes. Though a phylogenetic position of Platyhelminthes is still under discussion, Platyhelminthes is positioned at or near the root of bilateral animals from the viewpoint of its morphology and developmental biology (Neilsen 2001; Hyman 1951). Recently, Aguinaldo *et al.* (1997) proposed a new taxonomy based on the molecular analysis of the 18S rRNA sequences, showing that bilateral animals were classified into three groups; deuterostomia, ecdysozoa and lophotrochozoa. The traditional protozoan group was separated into ecdysozoa and lophotrochozoa. The former has a moulting process whereas the latter does not. In their phylogenetic tree, Platyhelminthes was positioned near the root of the lophotrochozoa. Though there is contradiction between molecular and morphological evidences (Adoutte *et al.* 2000), it is no doubt that the planarian is one of the descendants of early bilateral animals (Figure 2.1). From these reasons, planarian is an animal suitable for studying the evolutionary process of the CNS, in particular, that of the brain.

The CNS has the most important role in the organisms. To understand the evolutionary divergence of the CNS, the comparative study will give us a valuable clue to elucidation of the evolutionary mechanism of the CNS. However, the vertebrate CNS is known to be complex in the structures and functions, whereas invertebrate CNS, in general, less complicated (Breidbach & Kutsch 1995). Planarian is one of the useful invertebrates to study the evolutionary process of the CNS by the above reasons. Thus, the purpose of the present study is to identify CNS-related genes of planarian in order to elucidate evolutionary process of the CNS.

In this study, I found 116 neural-related genes in planarian and compared these genes with those of other species. We also found the extreme extent of evolutionary conservation of neural-related genes between planarian and human.

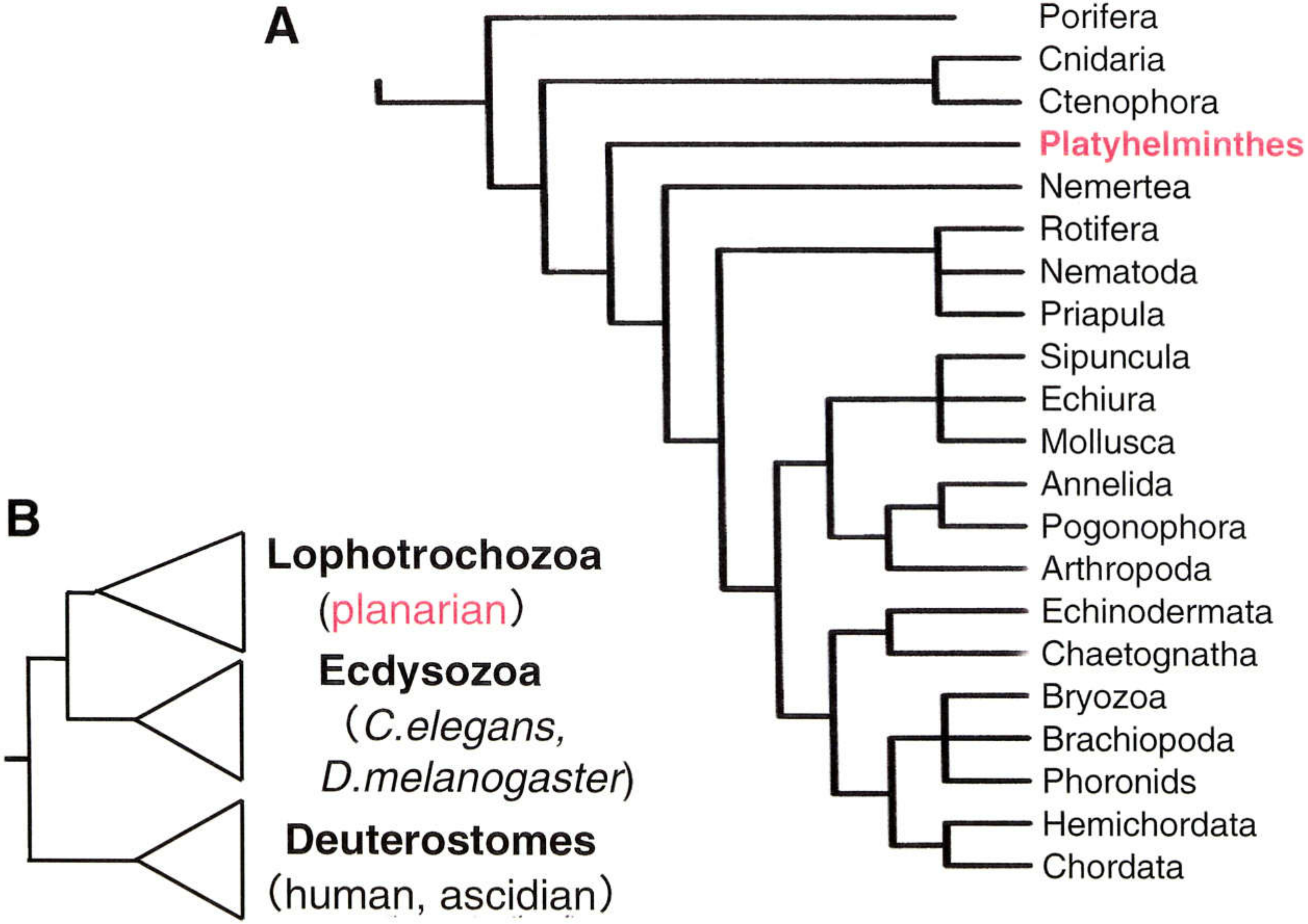


Figure 2.1: Phylogenetic position of planarians (Platyhelminthes) (A) The phylogenetic tree based on the morphological evidences (modified from Gerhart & Kirschner 1997). (B) The one of the phylogenetic trees based on the 18S rRNA (modified from Aguinaldo *et al.* 1998).

Materials and Methods

Animals

I used a clonal strain of planarian, *Dugesia japonica*, which was established by Dr. K. Watanabe (Himeji Tech. Inst.) in the following studies. Intact worms were cultured in autoclaved tap water at 22 °C.

Construction of a cDNA library

Planarians of 5-7 mm starved for 7-10 days were used. Over 500 of planarians were cut at the pre-pharyngeal region under the phase contrast microscope, and their head portions were collected. The cDNA library was constructed in lambda ZAP II (Stratagene, USA) using oligo d (T) primers. Then, positive clones were excised to generate subclones in pBluescript SK (Stratagene, USA) for the sequencing. In this protocol, we did not amplify the cDNA by PCR method, so that this library was expected to reflect the mRNA frequency *in vivo.*

Sequence analyses of the cDNA clones

Purified plasmid DNA was sequenced by a 377, 310 or 3700 ABI sequencer using the Big-Dye terminator sequencing kit following the manufacturer's instructions (Applied Biosystem, USA). Those products were edited as follows, using the in-house EST analyzing system, the FinEST (Mineta *et al.*, submitted; See also Appendix A). The sequence was cut into 500 bp long and less than 100 bp clones were removed. The quality of sequence was adjusted to less than 5 % of N (non-determined) sites.

The redundancy of sequences was checked by BLASTN program (Altschul *et al.* 1990; 1997) under the criteria of $\geq$ 90% identity among $\geq$ 100bp overlapped region, and then I obtained non-redundant data set with their frequency. Then these non-redundant sequences were searched against the available DNA and protein databases of DDBJ/EMBL/GenBank using BLASTN and BLASTX programs, respectively. Here, I chose a criterion of less than 10^{-4} in E-value for identifying homologous sequences based on these alignments in the preliminary study.

Identification of neural-related clones

Clones homologous to the neural-related protein were identified. The neural-related clones were defined as those homologous to genes in the following categories: (A) neurotransmission, (B) neural network, (C) brain morphogenesis / neural differentiation (D) sensory system, and (E) others. In particular, category (E) included clones which have a similarity to the genes that are functionally unknown but known to be specifically expressed or the most abundantly expressed in the brain or nervous system such as an "adult brain protein 239" in the other species.

Whole-mount in situ hybridization

Digoxigenin-labeled RNA probes were prepared according to the manufacturer's instruction (Boehringer, USA), using the clone ID 04307_HH, 00517_HH, 01242_HH, 01791_HH and 02467_HH cDNA as templates. We chose these clones from the five categories described above. Whole-mount *in situ* hybridization was performed as described by Umesono *et al.* (1999). This experiment was performed by F. Cebria (CDB, RIKEN), one of the collaborators.

Comparison of ESTs against other species

Among planarian neural-related clones, the comparison was performed against all translated ORFs in the complete genome sequences of *Homo sapiens* (International Human Genome Sequencing Consortium 2001), *Drosophila melanogaster* (Adams 2000), *Caenorhabditis elegans* (The *C. elegans* Sequencing Consortium 1998), *Arabidopsis thaliana* (The Arabidopsis Genome Initiative 2000) and *Saccharomyces cerevisiae* (Mewes *et al.* 1997), obtained from EMBL proteome database (http://www.ebi.ac.uk/proteome/), using BLASTX. In particular, I also conducted extensive searches against *H. sapiens*, *D. melanogaster* and *C. elegans*. This search was designated as a "boomerang search" and done in the following two processes: (1) a planarian EST was used as a query, and searched against public database with E-value $\leq 10^{-4}$. Then, (2) the highest match sequence was used as a query, and search against each genomic database setting the thereshold E-value $\leq 10^{-4}$. After this procedure with a manual modification, we confirmed the existence of the similar sequences in the inferred bilateral animals.

Phylogenetic analysis

Homologous sequences in other species were obtained by homology search using BLASTX program. The multiple alignment was performed using the clustalX program (Thompson *et al.* 1997) with a manual modification. Distance calculation was made using the only overlapped region with EST clones. The neighbor-joining method (Saitou & Nei 1986) was used for the tree reconstruction.

Results and Discussions

The gene expression profile and ESTs

We obtained 5,433 of 5'-ESTs from a planarian head library after removal of clones similar to the ribosomal RNAs and clones of no inserts. Counting the occurrence frequencies of different clones in these 5'-ESTs, I obtained 3,101 non-redundant clones (Table 2.1). Using non-redundant clones, the occurrence of each clone was analyzed. The gene expression profile defined as the frequency distribution of non-redundant clones is shown in Figure 2.2. It should be noted, however, that one might obtain clones that represent different parts of single mRNA. Nevertheless, most clones, particularly highly expressed clones, should reflect, at large, the expression pattern *in vivo*, because we picked clones randomly.

The most highly expressed clones from planarian heads ranked in the following order; beta-actin, alpha-actin, beta-tubulin and alpha-tubulin (See the legend of Figure 2.2), whereas the highly expressed clones of human brain (cortex) were in the following order; myelin basic protein, hng/RC3, apolipoprotein J and aldolase C (Kawamoto *et al.* 2000). In planarian, cytoskelatal genes seem to be highly expressed. In human, on the other hand, myelin basic protein was expressed with the highest frequency. It is consistent with an observation of the cellular structure that the axon of a human neuron has a myelin but the planarian's does not. Thus, the gene expression profiles distinctively indicate the difference between planarian and human, revealing the characteristic of each species. It is of my particular interest to see if these differences of the gene expression profiles can be spread to different species (See chapter 3 and 4).

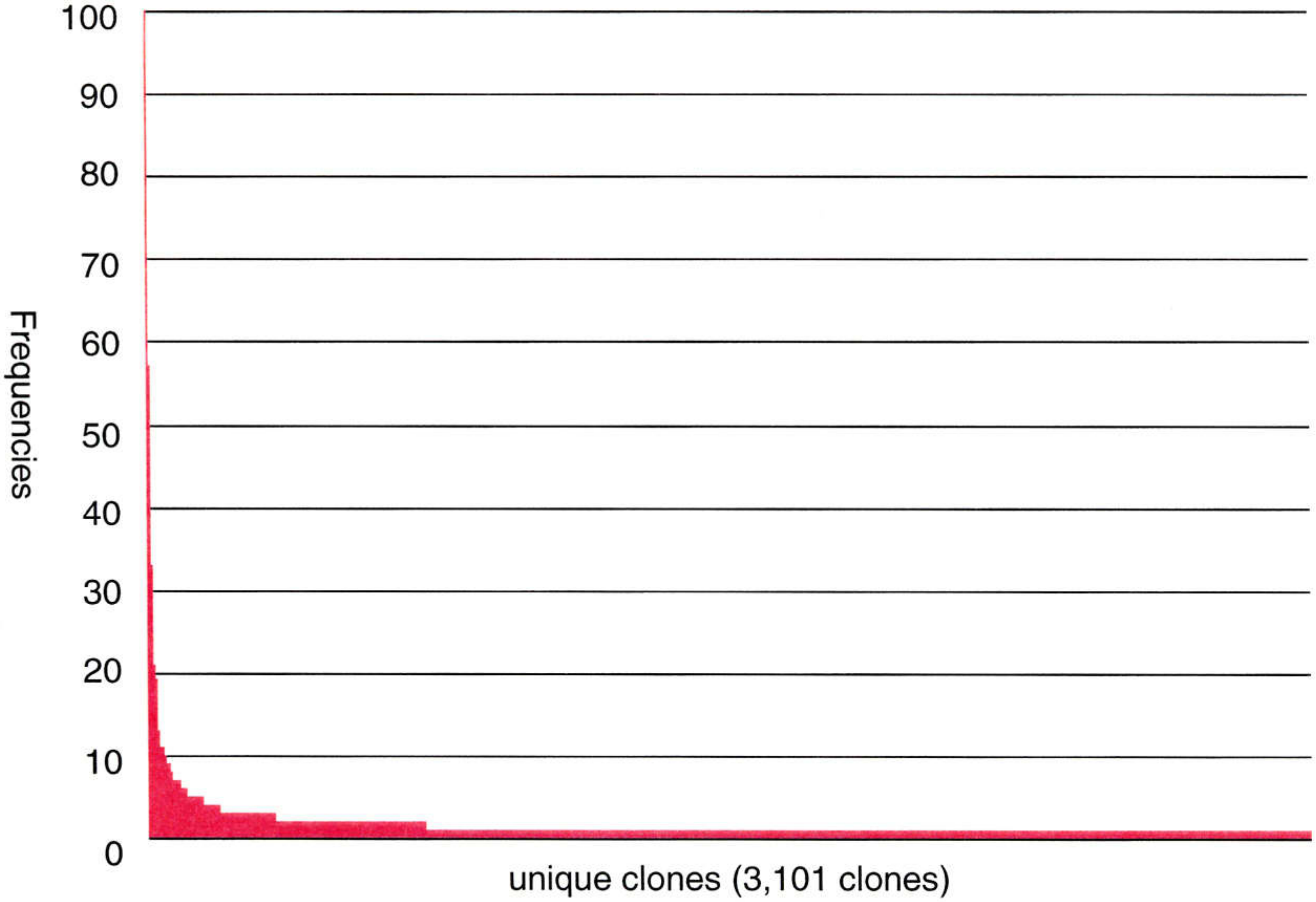


Figure 2.2: The gene expression profile of planarian head. For each non-redundant clone, the frequency was plotted. Highly expressed clones are homologous to beta actin (100 times), alpha actin (77 times), alpha tubulin (70 times), beta tubulin (57 times) and elongation factor-1 alpha (46 times). Majority (77%) of the clones is expressed as a singleton.

A well-organized planarian CNS inferred from the neural-related genes

To identify the CNS-related genes in planarian clones, I searched for the neural-related genes among all the functionally known 1,385 clones (groups A and B in Table 2.1). I successfully identified 116 clones that exhibited significant similarity to neural-related genes previously characterized in other organisms (Table 2.2). These 116 clones were categorized into the following 5 functional groups: (A) 42 clones related to neurotransmission including neurotransmitter, receptor/channel, synaptic vesicle and its transport, (B) 33 clones for neural network including the Ig-CAM family, the cadherin family and the axon guidance, (C) 21 clones with homology to the genes for brain morphogenesis/neural differentiation such as the BMP cascade, the Wnt cascade, the FGF cascade and the notch cascade, (D) 11 clones for sensory system including the photosensory, chemosensory and mechanosensory system, and (E) 9 clones for others such as brain protein AB239. These genes in all functional groups were known to be important for the CNS (Table 2.3). In particular, the clones in category (C) of brain morphogenesis/neural differentiation are known to be essential for the CNS development in higher organisms. The expression pattern of a representative clone in each category was analyzed by the whole-mount *in situ* hybridization and shown in Figure 2.3. These genes having significant similarities to the neural-related proteins were expressed specifically in the CNS. Moreover, the expression patterns of these clones showed that the CNS of planarian consists of wide-variety of subtypes of the neuronal cells. The clones can serve as very valuable tools for the further

Table 2.2: list of the neural-related genes appeared in the planarian ESTs

CLONE ID	FREQ.	ACC. NO.	PROTEIN WITH THE BEST E-VALUE	E-VALUE
NEUROTRANSMISSION				
03162 HH	1	AAB86606.1	acetylcholinesterase catalytic subunit precursor [Electrophorus electricus]	9.00E-40
04307 HH	1	AAD32697.1	putative nicotinic acetylcholine receptor alpha 7-1 subunit [Heliothis virescens]	9.00E-19
04808 HH	1	P30532	neuronal acetylcholine receptor protein, alpha-5 chain precursor [Homo sapiens]	9.00E-28
06703 HH	1	P18845	neuronal acetylcholine receptor protein, alpha-3 chain precursor (GF-alpha-3) [Carassius auratus]	2.00E-14
01517 HH	1	BAA90484.1	high-affinity choline transporter CHT1 [Rattus norvegicus]	3.00E-40
03855 HH	1	AAB86609.1	vesicular acetylcholine transporter [Drosophila melanogaster]	2.00E-50
04854 HH	3	NP_009209.1	GABA(A) receptor-associated protein [Homo sapiens]	3.00E-46
00130 HH	7	JC4027	glutamine synthetase [Paracentrotus lividus]	2.00E-75
01406 HH	3	NP_055434.1	glutamate receptor, ionotropic, kainate 4 [Homo sapiens]	3.00E-39
04073 HH	1	T13603	probable N-methyl-D-aspartate receptor [Drosophila melanogaster]	3.00E-42
00172 HH	1	CAB65182.1	AMPA-selective receptor subunit [Loligo opalescens]	2.00E-41
00471 HN	5	AAC24752.1	transglutaminase precursor [Dirofilaria immitis]	1.00E-43
03604 HH	1	P43006	excitatory amino acid transporter EEAT2 / glutamate transporter MGLT1 [Mus musculus]	2.00E-28
04149 HH	1	AAA36018.1	serine hydroxymethyltransferase [Homo sapiens]	2.00E-60
00546_HN	1	NP_064356.1	sortilin 1 [Mus musculus]	5.00E-35
06173 HH	1	Q18179	putative neuropeptide Y receptor (NPY-R) [Caenorhabditis elegans]	2.00E-19
06727 HH	1	NP_062129.1	P2X purinoceptor 7 (ATP receptor) (P2X7) (purinergic receptor) (P2Z receptor) [Rattus norvegicus]	5.00E-21
02930 HH	1	NP_004183.1	acetylserotonin O-methyltransferase-like [Homo sapiens]	4.00E-24
06862 HH	1	BAA22403.1	serotonin receptor-like planarian receptor 4 [Dugesia japonica]	5.00E-88
01367 HH	2	AAC27663.1	tryptophan oxygenase [Anopheles gambiae]	3.00E-40
03804_HH	1	S27270	prohormone convertase LPC2 [Lymnaea stagnalis]	2.00E-18
01290 HH	2	P49951	clathrin heavy chain [Bos taurus]	1.00E-82
06596 HH	1	CAA28542.1	clathrin LCa [Bos taurus]	6.00E-16
02476 HH	2	T33569	strong similarity to C. elegans UNC-101 clathrin coat assembly protein AP50 [Caenorhabditis elegans]	5.00E-64
04002 HH	1	NP_001119.1	gamma-adaptin (golgi adaptor HA1/AP1 adaptin gamma subunit) (clathrin assembly protein complex 1 gamma large chain) [Homo sapiens]	7.00E-29
05948 HH	1	CAA06918.1	clathrin-associated adaptor complex AP-1 medium chain [Drosophila melanogaster]	2.00E-66
06460 HH	1	AAD37366.1	AP180-like adaptor protein [Caenorhabditis elegans]	3.00E-54
06785 HH	3	P49020	cop-coated vesicle membrane protein p24 precursor [Cricetulus griseus]	5.00E-47
00325 HH	1	AAF81653.1	RIM2-5B [Rattus norvegicus]	3.00E-07
00951 HH	1	T42213	m-tomosyn [Rattus norvegicus]	9.00E-13
00805 HH	2	AAF75839.1	putative gap junction protein pannexin [Clione limacina]	4.00E-18
02763 HH	1	NP_000715.1	voltage-dependent calcium channel beta-2c subunit [Homo sapiens]	3.00E-36
00391 HN	2	T13799	neurexin IV [Drosophila melanogaster]	2.00E-26
01239 HH	3	Q12959	presynaptic protein SAP97 (synapse-associated protein 97) (discs, large homolog 1) [Homo sapiens]	4.00E-06
04800 HH	1	Q92796	presynaptic protein SAP102 (synapse-associated protein 102) (neuroendocrine-dlg) (ne-dlg) [Homo sapiens]	6.00E-09
00700 HH	1	AAC47499.1	SNAP-25 homolog [Hirudo medicinalis]	2.00E-61
00382 HN	1	NP_036651.1	calcium/calmodulin-dependent protein kinase type II delta chain (CaM-kinase II delta chain) (CaMK-II, delta subunit) [Rattus norvegicus]	1.00E-73
06065 HH	1	NP_004701.1	synaptogyrin 2 (cellugyrin) [Homo sapiens]	1.00E-31
05093_HH	1	P20488	synaptophysin (major synaptic vesicle protein p38) [Bos taurus]	9.00E-11
02814 HH	1	AAC24823.1	synapsin s-syn-long [Loligo pealei]	2.00E-56
00126 HH	5	BAA85622.1	Djsyt protein [Dugesia japonica]	3.00E-84
03491_HH	2	NP_061271.1	synaptotagmin VII [Mus musculus]	4.00E-06
NEURAL NETWORK				
05189 HH	1	AAC83376.1	netrin precursor [Hirudo medicinalis]	2.00E-48
06563_HH	1	NP_061241.1	semaF cytoplasmic domain associated protein 1 [Mus musculus]	7.00E-23
06717 HH	1	AAF71926.1	Dscam [Drosophila melanogaster]	8.00E-05
07105 HH	1	AAC17967.1	Down syndrome cell adhesion molecule [Homo sapiens]	7.00E-06
00944 HH	1	P16170	neural cell adhesion molecule precursor [Xenopus laevis]	4.00E-05
04747 HH	1	AAC52262.1	neural cell adhesion protein BIG-2 precursor [Rattus norvegicus]	2.00E-09
00517 HH	1	O02695	protein-tyrosine phosphatase x precursor (R-PTP-X) (m1851) [macaca nemestrina]	2.00E-11
01438 HH	1	AAC16552.1	putative prenylated protein tyrosine phosphatase PRL-1 [Drosophila melanogaster]	4.00E-07
01773_HH	1	T16894	Similar to protein-tyrosine phosphotase [Caenorhabditis elegans]	1.00E-24
01805 HH	1	JW0049	protein tyrosine phosphatase [Gallus gallus]	3.00E-12
06241 HH	1	AAF67472.1	protein tyrosine phosphatase [Homo sapiens]	2.00E-16
02298 HH	2	NP_032774.1	neuronal tyrosine/threonine phosphatase 1 [Mus musculus]	1.00E-13
03518 HH	1	AAB96620.1	protein tyrosine phosphatase and tensin homolog/mutated in multiple advanced cancers protein [Rattus norvegicus]	3.00E-42
03797_HH	1	AAD43782.1	protocadherin gamma B6 short form protein [Homo sapiens]	2.00E-11
04532 HH	1	NP_059074.1	protocadherin 14 [Mus musculus]	2.00E-16
05685 HH	1	AAD43761.1	protocadherin beta 7 [Homo sapiens]	7.00E-08
01301 HH	4	T31737	calmodulin [Caenorhabditis elegans]	9.00E-81
02721 HH	1	CAA86994.1	Calpain, without calmodulin-like domain [Drosophila melanogaster]	1.00E-43

01418 HH	1	AAC47111.1	axonemal dynein light chain p33 [Strongylocentrotus purpuratus]	9.00E-55
01557 HH	2	Q39575	gamma heavy chain subunit of outer-arm dynein [Chlamydomonas reinhardtii]	3.00E-37
01900 HH	1	Q16960	dynein intermediate chain 3 [Anthocidaris crassispina]	4.00E-74
02529 HH	1	AAC70939.1	cytoplasmic dynein intermediate chain isoform DIC3a [Drosophila melanogaster]	2.00E-16
03394 HH	1	Q16959	dynein intermediate chain 2 [Anthocidaris crassispina]	7.00E-59
05659 HH	3	O02414	outer arm dynein LC6 [Anthocidaris crassispina]	1.00E-40
06238 HH	1	BAA97048.1	cytoplasmic dynein heavy chain [Rattus norvegicus]	3.00E-35
00067 HH	5	AAD29248.1	intermediate filament gliarin [Hirudo medicinalis]	7.00E-31
01978 HH	2	CAB38185.1	cytoplasmic intermediate filament protein [Stylochus sp.]	1.00E-35
03571 HH	1	S54123	neurofilament protein NF70 [Helix aspersa]	1.00E-32
05174 HH	2	CAA68255.1	intermediate filament protein [Lineus sanguineus]	3.00E-07
06802 HH	1	A46194	neurofilament protein NF-220, high-molecular-weight splice form [Loligo pealei]	8.00E-19
00645 HN	7	AAF23826.1	tetraspanin [Drosophila melanogaster]	3.00E-12
04734 HH	1	AAF90137.1	tetraspanin 29Fa [Drosophila melanogaster]	3.00E-06
05952 HH	1	AAF19031.1	neuronal tetraspanin [Gallus gallus]	4.00E-22
BRAIN MORPHOGENESIS / NEURAL DIFFERENTIATION				
02702 HH	2	T31069	tolloid-BMP-1 like protein 1 [Aplysia californica]	1.00E-17
05855 HH	1	BAA22437.1	BMP receptor [Xenopus laevis]	7.00E-32
03592_HH	1	AAD43133.1	Noggin 2 [Danio rerio]	3.00E-14
02975_HH	1	AAF76201.1	aFGF intracellular binding protein [Mus musculus]	2.00E-18
00868 HN	1	AAB39211.1	mutant cysteine-rich FGF receptor [Gallus gallus]	1.00E-15
00448 HN	2	I50719	C-Delta-1 [Gallus gallus]	1.00E-08
05726 HH	1	CAA68369.1	delta protein [Drosophila melanogaster]	5.00E-07
00600 HN	1	NP_005069.1	transducin-like enhancer of split 3, homolog of Drosophila E(sp1) [Homo sapiens]	2.00E-38
00409 HN	1	NP_004662.1	protein inhibitor of activated STAT protein PIASx-beta [Homo sapiens]	9.00E-21
00896 HH	3	NP_031922.1	APC-binding protein EB1 homolog [Mus musculus]	2.00E-52
01443 HH	1	BAA92185.1	beta-catenin [Ciona intestinalis]	7.00E-08
01362 HH	1	AAF21645.1	frizzled homolog [Danio rerio]	7.00E-06
01166 HH	1	NP_003003.2	secreted frizzled-related protein [Homo sapiens]	2.00E-26
03133 HH	1	AAD45010.1	HMG protein Tcf/Lef [Strongylocentrotus purpuratus]	1.00E-23
01242 HH	2	NP_004515.1	Human giant larvae homologue [Homo sapiens]	9.00E-06
03104 HH	11	T09457	numb-binding protein LNXp80 [Mus musculus]	1.00E-06
06588 HH	1	P31370	POU domain protein 1 (DjPOU1) [Dugesia japonica]	2.00E-91
05133 HH	1	AAB19602.2	retinoic acid receptor alpha; RAR alpha [Homo sapiens]	1.00E-25
07031_HH	1	BAA95482.1	glia maturation factor beta [Cyprinus carpio]	6.00E-33
02957 HH	1	BAA95215.1	neuronal differentiation-related gene [Rattus norvegicus]	3.00E-45
03408_HH	1	1BWR	Brain Platelet-Activating Factor Acetylhydrolase [Bos taurus]	5.00E-41
SENSORY SYSTEM				
00251 HH	1	NP_004032.1	beta-arrestin 1A [Homo sapiens]	2.00E-32
00287 HN	2	Q01062	cGMP-dependent 3',5'-cyclic phosphodiesterase (cyclic GMP stimulated phosphodiesterase) (CGS-PDE) [Rattus norvegicus]	4.00E-47
01116 HH	1	A47300	cell adhesion protein retina cognin [Gallus gallus]	2.00E-42
01781 HH	1	NP_033056.1	retinoblastoma-binding protein [Mus musculus]	4.00E-81
02585 HH	1	NP_004930.1	DEAD box protein 1 (DEAD box protein-retinoblastoma) (DBP-RB) [Homo sapiens]	2.00E-28
03132 HH	2	P49193	retinal-binding protein [Todarodes pacificus]	4.00E-25
06472 HH	1	P24603	rhodopsin [Loligo forbesi]	6.00E-08
01791 HH	1	AAC67569.1	cone transducin alpha subunit [Ambystoma tigrinum]	6.00E-34
01997 HH	1	NP_038559.1	guanine nucleotide-binding protein beta subunit 4 (transducin beta chain 4) [Mus musculus]	8.00E-31
02211_HH	1	Q27433	mechanosensory protein 2 [Caenorhabditis elegans]	1.00E-33
05976_HH	1	JC5638	pH-sensing regulatory factor of peptide transporter [Homo sapiens]	2.00E-24
OTHERS				
02467 HH	1	O15442	adult brain protein 239 (239AB) [homo sapiens]	4.00E-39
01279_HH	1	JE0209	brain-specific angiogenesis inhibitor-associated protein 1 [Homo sapiens]	1.00E-21
01704_HH	7	JC5759	brain-specific serine proteinase [Mus musculus]	7.00E-19
05816_HH	1	S70554	calcineurin A homolog CnnA14D splice form I [Drosophila melanogaster]	8.00E-38
00929 HH	1	NP_009167.1	calcium-binding protein p22 (calcium-binding protein CHP) (calcineurin B homologous protein) [homo sapiens]	3.00E-31
01237_HH	1	CAC00661.1	Glycogen Phosphorylase, brain form [Homo sapiens]	2.00E-64
05177_HH	1	AAF14284.1	neural polypyrimidine tract binding protein [Homo sapiens]	9.00E-17
05723_HH	1	BAA35092.1	neural specific sr protein NSSR 1 [Mus musculus]	2.00E-15
00720_HN	1	NP_063920.1	neuronal guanine nucleotide exchange factor [Mus musculus]	1.00E-16

*The clones with the red letters mean the clones shared among *C. elegans*, *D.melanogaster*, *H. sapiens* and *D. japonica*.

Table 2.3: Types of the neural-related genes expressed in the planarian head ESTs

Category	representative functional groups	Number of clones
Neurotransmittion		47
	neurotransmitter (syntesis/degradation)	
	receptor / channel	
	synaptic vesicle (transport, junction)	
Neural network		30
	Ig-CAM family	
	cadherin family	
	axon guidance	
Brain morphogenesis/neural differentiation		18
	BMP cascade	
	Wnt cascade	
	FGF cascade	
	notch cascade	
Sensory system		11
	photoreception	
	chemical reception	
	mechanical reception	
Others		10
	total	116

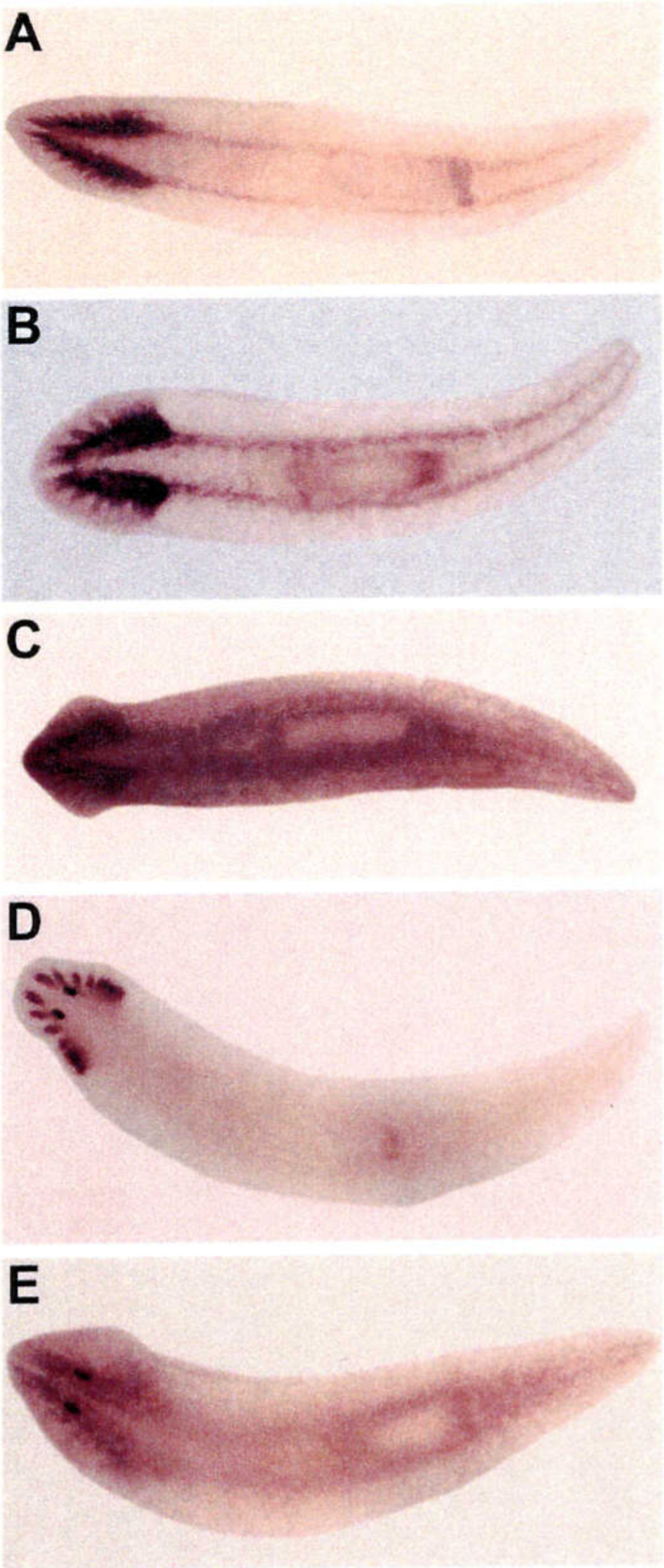


Figure 2.3: Whole-mount *in situ* hybridization of the neural-related clones in intact planarians. (A) clone ID: 04307_HH (homologous to the nicotinic acetylcholine receptor alpha 7-1 subunit), (B) clone ID: 00517_HH (homologous to the protein tyrosine phosphatase X receptor), (C) clone ID: 01242_HH, (D) clone ID: 01791_HH (homologous to the cone transducin alpha subunit) and (E) clone ID: 02467_HH (homologous to the adult brain protein AB239).

neuroanatomical research as molecular markers. Our recent study using microarray of cDNA clones has also uncovered important genes involved in the CNS in planarian (Nakazawa & Cebria *et al.*, submitted). A complex cytoarchitecture of planarian CNS was clearly shown by the expression pattern of 30 clones examined by *in situ* hybridization. Since the planarian clones contain a variety of neural-related genes that showed complex expression patterns, the planarian CNS is also well organized at the molecular level.

The extreme conservation of the neural-related genes between planarian and human

As the available number of complete genome sequences has increased, it is possible to discuss whether the inferred genes in each species exist or not. To study the evolutionary emergence of the gene set in a common ancestral CNS, I took an approach of the comparative genomics. The homologous sequences of the above 116 neural-related clones were searched against all ORFs in the complete genome sequences of human, *D. melanogaster, C. elegans, A. thaliana* and *S. cerevisiae* (Figure 2.4).

Interestingly, all the 116 clones examined were completely shared between human and planarian. The phylogenetic position of planarian is still under discussion, as I mentioned earlier, but it is generally accepted that planarian belongs to the protostome. However, Sarat and Netskey (1985) have presented a morphological evidence that the planarian brain, cephalic ganglions, has many morphological features similar to those of a vertebrate brain, such as the presence of multipolar nerve cells and

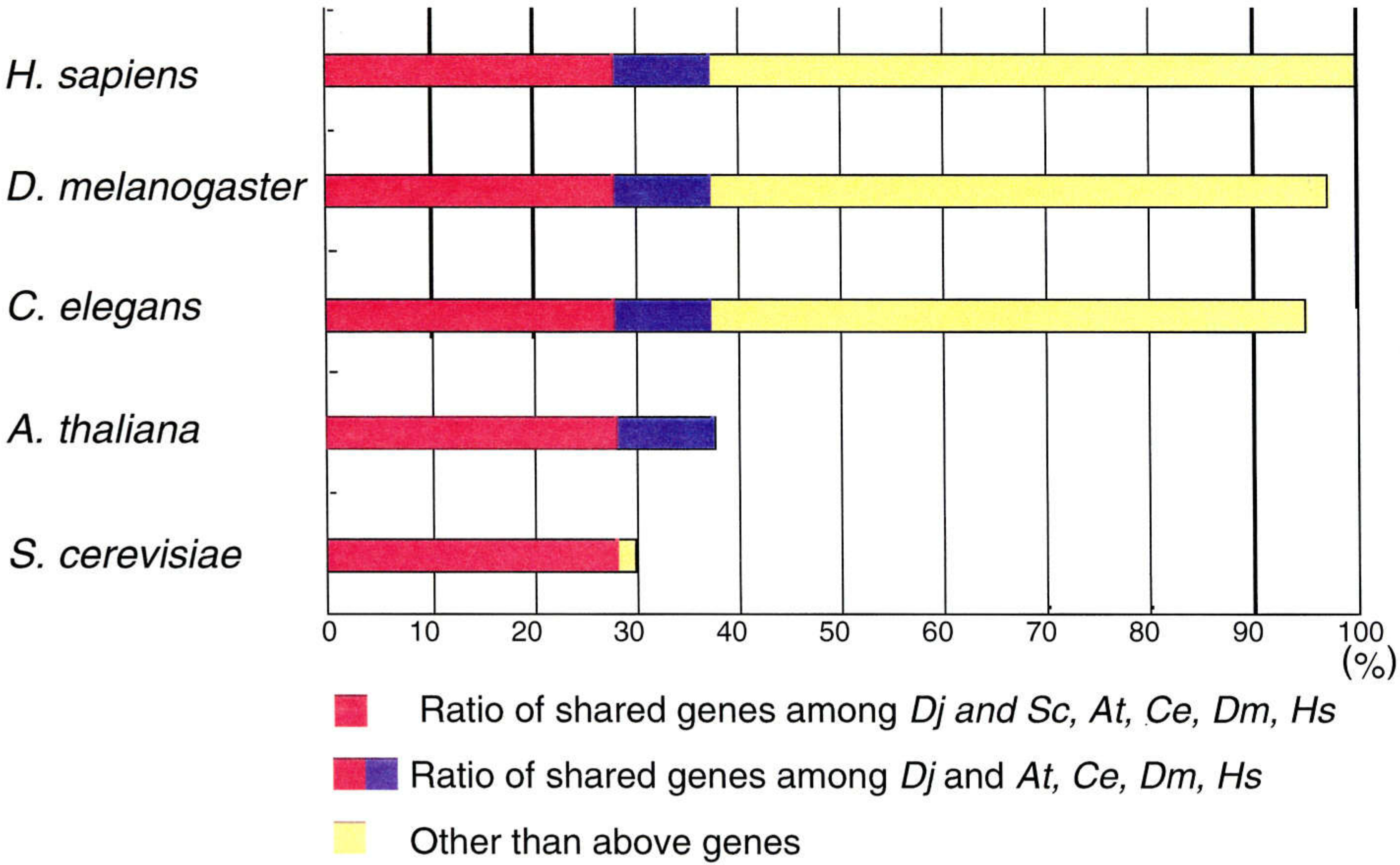


Figure 2.4: The comparisons among the all ORFs in the complete genomes of *S. cerevisiae, A. thaliana, C. elegans, D. melanogaster, H. sapiens* and neural-related clones of planarian. The horizontal axis showed the match ratio of all ORFs in the genomes examined against the planarian neural-related clones. Analyses of Ce, Dm and Hs were performed by boomerang search (see Method).

dendrite spine-like structures. My results showed that the similarity of the neural-related genes existed between planarian and human. The morphological evidences support our findings obtained from the sequence comparison. My result is the first evidence of the evolutionary conservation of the CNS-related gene set at the molecular level between planarian and human. Even if planarian and human have independently evolved in each lineage after divergence of the common ancestral CNS, it was of interest to note that the gene set had a similarity between human and planarian in spite of their distinct phylogenetic position. Therefore, the study of the planarian CNS should give us an excellent cue to understand the complicated human brain from the viewpoint of the evolution.

I found that 110 clones of a total of 116 clones were commonly shared among the bilateral animals examined, *C. elegans, D. melanogaster* and human, showing that more than 95% of clones were evolutionarily conserved among these species (clones in red letters in Table 2.2,). The species examined belong to the three different groups of bilateral animals (Deuterostomia, Ecdysozoa and Lophotrochozoa) and they all possessed the CNS (Neilsen 2001). Thus, these neural-related genes can be considered as a part of basic gene set of the ancestral CNS that appeared on the base of the bilateral animals. The basic gene set is thought to be essential for the CNS and have remained unchanged from the ancestral CNS to a highly ordered human brain. It is reported that the evolutionary rates of the neural-related genes are very slow, in general, showing a high degree of conservation at the sequence level of neural-related genes (Kuma *et al.* 1995). Thus, our finding of strong conservation (95%) of the gene set related to the nervous system strongly suggests that genes related to the CNS might have functional constraints not only against the nature of sequences but also against the gene composition during evolution.

I conducted phylogenetic analyses for each member of the basic gene set, though some clones could not be used to construct a tree because their sequences were partial. The phylogenetic analysis showed that most of the neural-related genes examined were highly duplicated after the divergence of vertebrates. I show a phylogenetic tree of synaptogyrin as an example (Figure 2.5). Thus, the well-organized brain of vertebrates may have evolved along with the genes that have highly duplicated from the basic gene set of the ancestral CNS in order to archive the diversity of the CNSs.

I also discovered that 30% of a total of 116 clones were shared between *S. cerevisiae* and planarian, and 37% were shared between *A. thaliana* and planarian (Figure 2.4). Since *A. thaliana* and *S. cerevisiae* do not possess a nervous system, these results showed that the origin of neural-related genes was much older than the emergence of nervous system. Making classification of these clones into 5 categories, I found that the category having the largest number of clones was (A) neurotransmission in table 2.2, which includes 17 clones homologous to the ORFs of *S. cerevisiae* and 24 clones homologous to the ORFs of *A. thaliana*. The gene set related to the neurotransmission contained functional categories of transmitter synthesis, receptors and synaptic vesicle transports. There is the functional similarity between the Golgi transport system in eukaryotic cells and the synaptic vesicle transport system in the

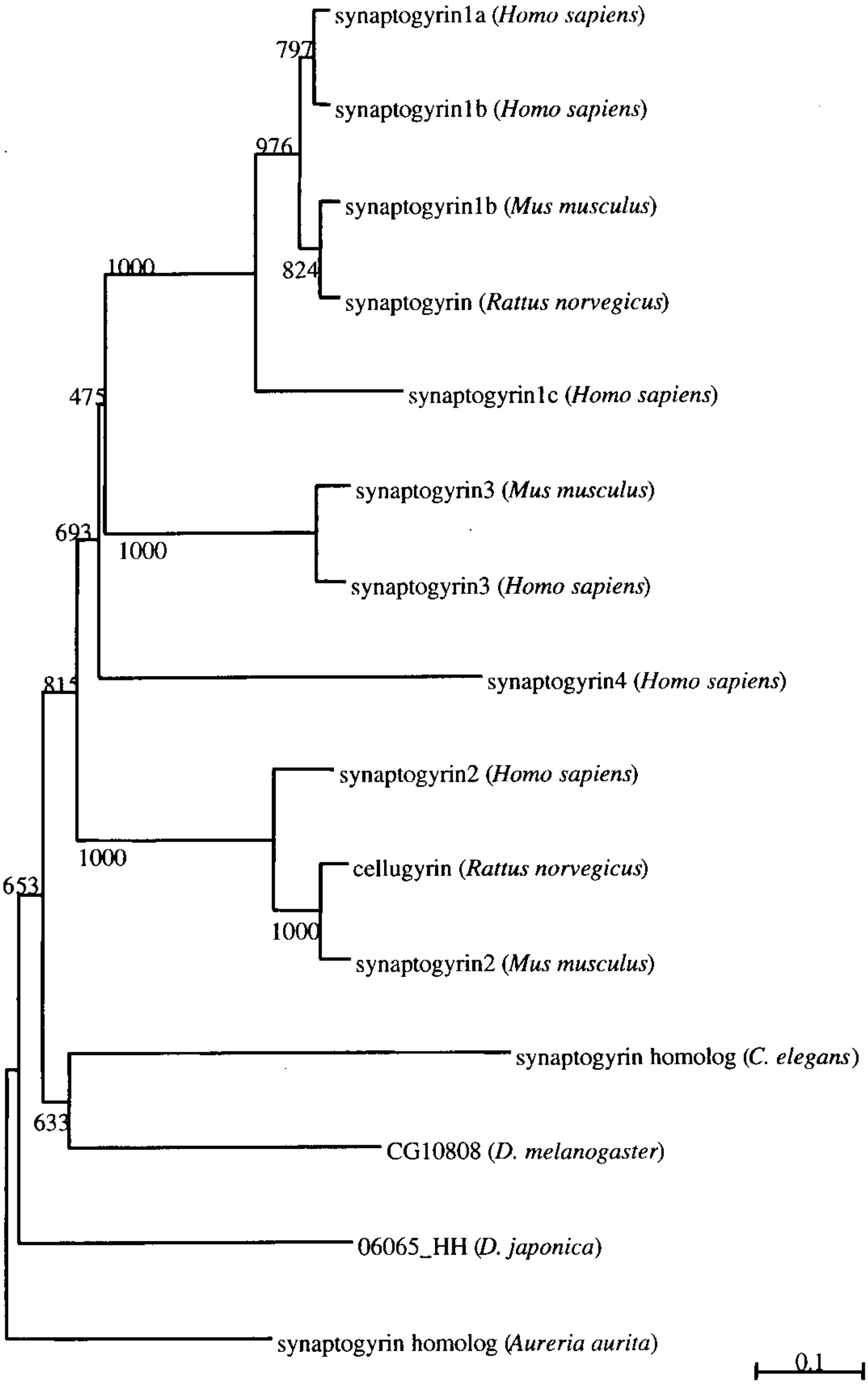


Figure 2.5: The phylogenetic tree of the clone 06065_HH (homologous to the synaptogyrin). The tree was re-constructed by the neighbor-joining method. The homologous sequences used were obtained from DDBJ/EMBL/GenBank database. Bootstrap confidence levels were reported at the node of each branch.

nervous system (Kandel *et al.* 2000). Thus, the genes which is functioned on a CNS may be recruited from the genes used in the unicellular systems during the evolution of nervous system.

Possible events of gene loss during the evolution of the CNS

I found that a total of 116 planarian neural-related clones were completely shared between planarian and human. However, when these clones were searched in the complete genomes of *C. elegans* and *D. melanogaster*, six clones were not always found in the two species (Table 2.4). Because the six genes were shared between planarian and human, these neural-related genes must have been lost or highly diverged in an evolutionary lineage toward *C. elegans* or *D. melanogaster.* For example, the glia maturation factor beta was not found in the *C. elegans*, but its homolog was found in the *Brugia malayi* that belongs to the same Nematoda family (Liu *et al.* 1997). This suggests that glia maturation factor beta might be lost or highly diverged in the lineage of *C. elegans* after the divergence of *C. elegans* and *B. malayi.* This result is consistent with my idea that some genes might be lost or highly diverged during the evolutionary process of the CNS. Another example is a noggin gene. A noggin is an inducer of neural tissue from the dorsal ectoderm in chordate, blocking the BMP signaling pathway (Smith *et al.* 1993). In *Drosophila* and *C. elegans*, we failed to identify any noggin homolog by the extensive search using PSI-BLAST. However, I found that planarian has a similar sequence of noggin by the homology search (see Method). Because planarian has also BMP and its receptor homologs (Table 2.2, and Orii *et al.* 1998), the cascade of noggin may exist in planarian, implying that the system

Table 2.4: List of planarian neural-related clones which did not have similar sequence in the specific organisms

***D.japonica* clone ID**	homologous protein	E-value in nr database	***C.elegans***	***D.melanogaster***	***H.sapiens***
00546_HN	sortilin 1 [Mus musculus]	5.00E-35	-	-	○
05093_HH	synaptophysin [Bos taurus]	9.00E-11	○	-	○
03592_HH	Noggin 2 [Danio rerio]	3.00E-14	-	-	○
02975_HH	aFGF intracellular binding protein [Mus musculus]	2.00E-18	-	○	○
07031_HH	glia maturation factor beta [Cyprinus carpio]	6.00E-33	-	○	○
03408_HH	Brain Platelet-Activating Factor Acetylhydrolase	5.00E-41	-	○	○

*Circle represents an existence of similar sequence with significant E-value, and bar represents that no similar sequence identified under the same criteria.

**Note that the clone 00805 HH (homologous to gap junction protein pannexin [Clione limacine], E-value: 4.0x10-18) did not show significant similarity with a human protein (E-value: 1.0x10-3) by our search. However, there was a report about the human pannexin (Accession number: BC016931 and others), so that 00805 HH existed in all of the species examined. Therefore, we excluded the clone of 00805 HH from the table 3. This misidentification may be caused by the long evolutionary distance between Clione and human (see Method).

of neural induction is more similar to that in chordates than in protostomes. Moreover, the transgenic experiment has shown that the *Xenopus* noggin had induced neural tissue differentiation in *D. melanogaster* (Holley *et al.* 1995), though noggin in *D. melanogaster* has never been found so far. It suggests that the potential function of noggin can be manifested in *D. melanogaster.* This result shows the flexibility of the gene set used in the organisms. Thus, This gene loss event and the flexibility of the gene set used is one of the possible forces in order to sophisticate the CNS functions specific to the species.

Conclusion

In this study, I discovered the 116 clones homologous to the neural-related genes in planarians (Table 2.2). Of the 116 neural-related clones, I found 95 % (110 clones / 116 clones) showed the strong conservation of the gene set among the bilateral animals examined (Table 2.2 and 2.3; Figure 2.4), suggesting that these 116 genes are a part of basic gene set that appeared in the common ancestral CNS.

In particular, planarian and human showed the 100% conservation of a total of 116 planarian neural-related genes. Even if planarian and human have independently evolved in each lineage after divergence of the common ancestral CNS, it was of interest to note that the gene set showed a similarity between human and planarian. On the other hand, the expression profiles of planarian head and human brain were different at the order of the frequent expressed genes. Since an expression profile is obtained from the transcriptional activities of all genes involved in a function, the expression profile should reflect the outcome of the transcriptional regulations. Thus, the difference between the strong conservation of gene set and the difference of gene composition in the gene expression profiles implies that there might occur the change of the transcriptional regulatory system during the evolutionary process of the CNS (See also Chapter 4). In Figure 2.6, I summarized the model of the CNS evolution from the results of this study.

In planarian, the experimental methods have been developed such as single cell PCR method (Gaudieri et al, in preparation), RNA interference method (Alvarado & Newmark 1999) and DNA microarray method (Nakazawa & Cebria *et al.*, submitted).

Moreover, we have obtained over 3,000 genes of planarians (shown in this study). As I mentioned above, the neural-related genes were highly shared between planarian and human. Further comparative studies using planarians will effectively bring us an insight on evolutionary mechanisms how the highly ordered brain such as a human brain was realizedS.

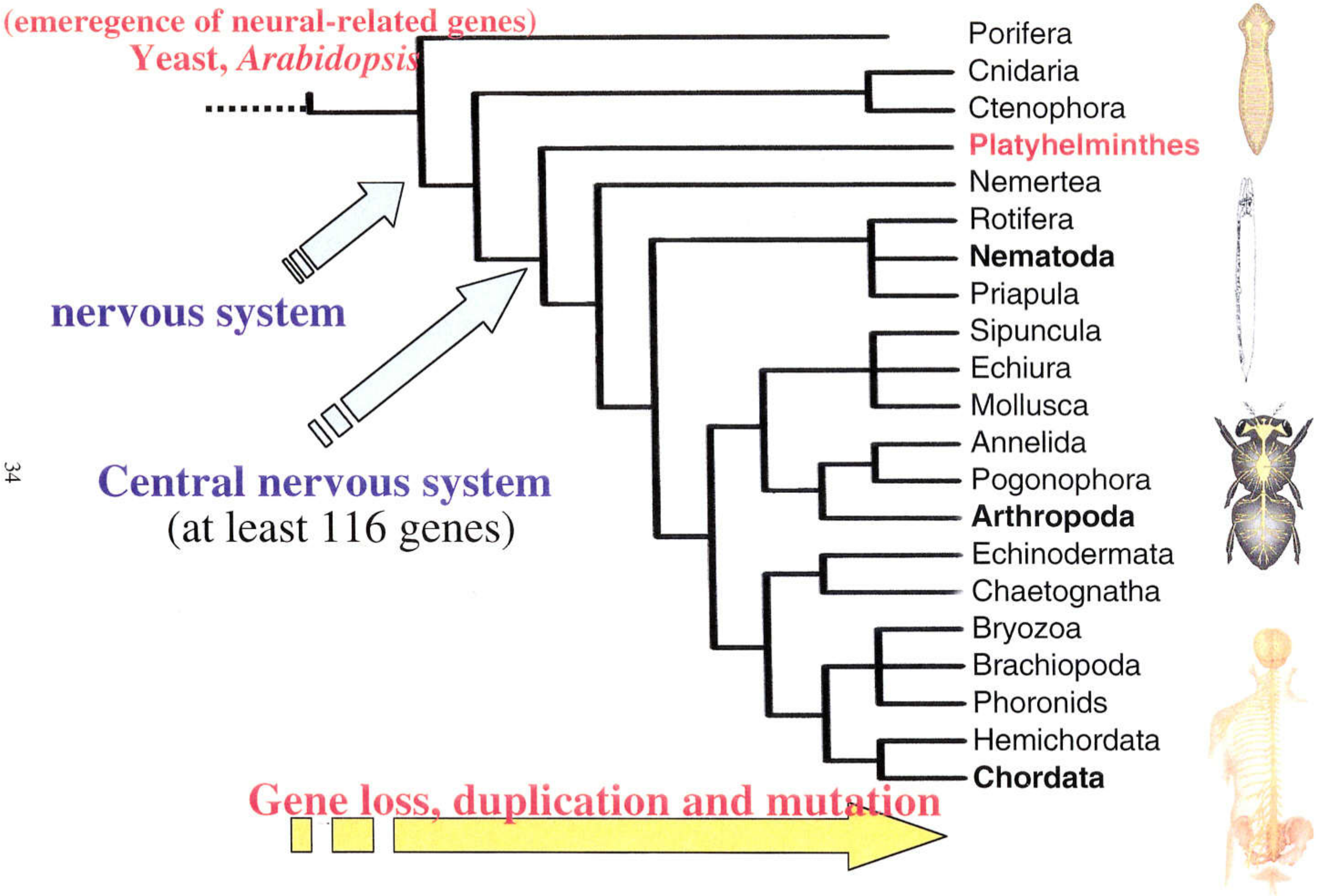


Figure 2.6: Summary of the evolutionary process of the CNS.

Chapter 3

Comparison of the gene expression profiles between two neural pigment cells, ocellus and otolith cells

Summary

With the aim of studying the diversity of the genes expressed in different cell types, we took a comparative approach using the gene expression profiles of single cells of ascidians (*Ciona intestinalis*). The swimming larval stage of ascidian has two different sensory organs, called "ocellus" and "otolith". These organs exist in the cerebral vesicle, which is often called as a brain. It has been reported that there are only two pigment cells in a total of 2,600 cells that form the swimming larva. One pigment cell is found in ocellus and the other is otolith. In this study, these pigment cells were respectively called as ocellus cell and otolith cell. To attain our purpose, we examined and compared the expression profiles of the ocellus cell and the otolith cell. First, we sequenced 964 and 774 ESTs from the cDNA libraries of the ocellus cells and the otolith cells, respectively. As a result, we obtained 485 non-redundant clones from the ocellus and 505 from the otolith cells. The composition of the highly expressed

clones in the pigment cells illustrated the clear difference from that of planarian head ESTs. One of the characteristic features of the gene expression profiles in the pigment cells is smaller amount of the cytoskeltal genes expressed in these single cells. Comparing the gene expression profiles between the ocellus cells and the otolith cells, we found that 60 clones were commonly expressed in two pigment cells. The relative frequencies of these 60 clones showed obviously distinct patterns between these two cells. This is the first report about the gene expression profiles of the single cells that is composed of an organ, showing the clear characteristic features of the expression profiles at the single cell level.

Introduction

To understand the evolutionary diversification of brains in various organisms, I focus on genes expressed in a brain. However, a brain is composed of various types of the cells. For example, an adult human body is consisted of 256 different types of the cells (Kauffman 1995), and each organ is composed of a subset of these cells at the various compositions. Thus, it is of particular interest to know an expression profile of a single cell. However, there is little information about the gene expression profile of a single cell, because it is extremely difficult to make a cDNA library by isolating single cells from an organ of interest. Although the studies of the gene expression profiles in single cells have been conducted for the cultured cells (Okubo *et al.* 1992) and fertilized eggs (Makabe *et al.* 2001), no study was conducted for the single cells that compose an organ. Thus, I focused on the gene expression profiles of the single cells from the ocellus and otolith of an ascidian (*Ciona intestinalis*) larvae.

It will be effective if the lineage of the cells used in the analysis of gene expression profiles is well-documented, because difference in the gene expression can be interpreted taking into account possible cell-to-cell interaction during the developmental process. For these reasons, I have chosen ascidians as the material of our study. Ascidians belong to the subphylum Urochordata, which is phylogenetically positioned on the base of Chordata. Adult ascidians are sessile and specialized for filter feeding, but during the developmental process, ascidians have a stage of swimming larva. The swimming larva of ascidian is composed of about 2,600 cells that form several distinct types of tissues (Satoh 1994). It is known that there are only two melanin-containing pigment cells among these 2,600 cells (Dilly 1962; 1964). The head portion of the swimming larva contains a cerebral vesicle with two sensory organs, ocellus and otolith. (reviewed by Satoh & Jeffery 1995). The ocellus is an organ for the photoreception, consisting of 17 cells. It is reported that only one in 17 ocellus cells is the pigment cell. The otolith, which is composed of only one pigment cell, is considered to be an organ for the gravity-reception. We used the otolith cell and the pigment cell of ocellus in the present study.

Previous studies using the tyrosinase gene, a key enzyme of the melanin synthetic pathway, have shown that those two pigment cells are derived from the same parental cell (the a10.98 cell). (Sato *et al.* 1997; 1999; Nishida & Satoh 1989; Nicol & Meinertzhagen 1991). These pigment cells are parts of sensory organs in the larval brain as I mentioned. Therefore, I will be able to make inference about the function of the brains of this organism in analyzing the gene expression profiles of single cells from the ocellus and the otolith.

By using a comparative approach of the gene expression profiles, I found that a large fraction (89%) of non-redundant genes were different in the expression profiles between the ocellus cells and the otolith cells leaving about 11% as commonly expressed.

Materials and Methods

Biological materials and Construction of the cDNA libraries

Ascidians (*Ciona intestinalis*) were obtained at the Education and Research Center of Marine Bio-resources of Tohoku University, Miyagi, Japan. The pigment cells of ocellus and otolith were obtained surgically from the swimming larva stage (Figure 3.1). After washing larva, the mRNA was extracted from 16 pigment cells. The cDNA libraries were constructed by using a SMART cDNA library construction kit (CLONTECH, USA), following the manufacturer's instruction. This process was performed by Ms. H. Munakata and Dr. H. Yamamoto at Tohoku university in collaboration with my study.

EST Sequencing.

Clones were picked up from the plates, and the presence of cDNA inserts were confirmed by the agarose gel electrophoresis. The purified plasmid DNA was sequenced using a ABI3700 auto-sequencer by the Big-Dye terminator sequencing kit, following the manufacturer's instructions (ABI, Perkin Elmer US). The sequencing was performed from the both sides of the multi-cloning sites.

Sequence editing, clustering and homology search

The products were edited as follows using the in-house EST analyzing system, FinEST (Mineta *et al.*, submitted; Appendix A). A sequence was cut into 500 bp long, and clones of less than 100 bp were excluded from the analysis. The quality of

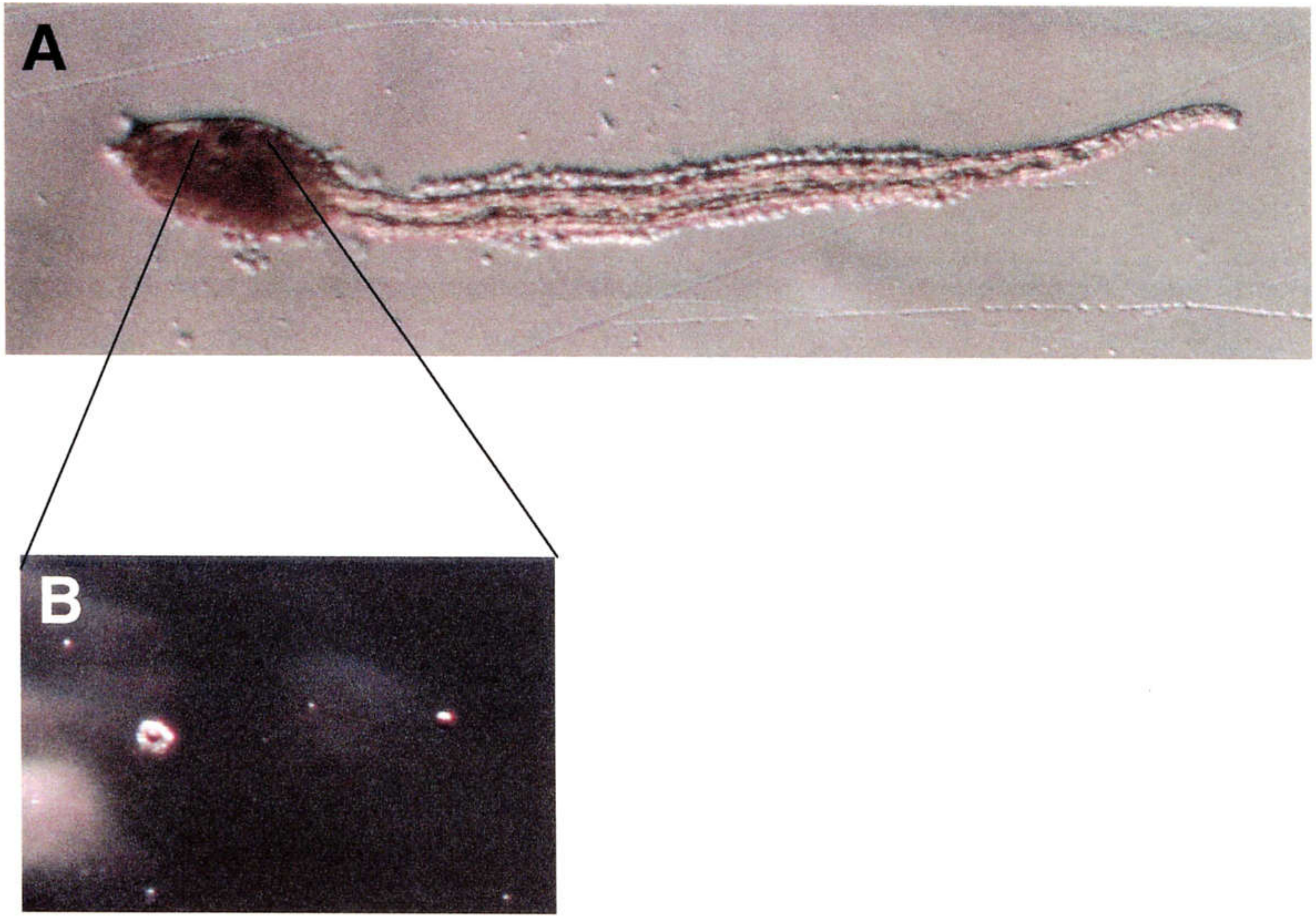


Figure 3.1: The ocellus cell and the otolith cell used in this study. (A) The swimming larva stage of the asicidian. (B) The ocellus pigment cell and the otolith cell. (These pictures are kindly provided by Dr. H. Yamamoto and Ms. H. Munakata (Tohoku univ.))

sequence was adjusted to be less than 5 % of unidentified sites. The redundancy of sequences was checked out by BLASTN program (Altschul *et al.* 1990) under the criteria of $\geq$ 90% identity among $\geq$ 100bp overlapped region of the 3' ESTs. Then, we constructed non-redundant data set including the frequency. These non-redundant sequences were searched against the available DNA databases of DDBJ/EMBL/GenBank using BLASTX (Altschul *et al.* 1990). Here, I have chosen a criterion of less than 10^{-4} in E-value for identifying the possible homologous sequences.

Comparison of the gene expression profiles derived from EST data of the Ocellus and Otolith cells

For the comparative study, we identified the clones that are commonly expressed both in ocellus and otolith cells by the homology search in which is based upon the same algorism using the EST clustering. Then, we combined both frequency data and annotation data of ocellus and otolith cells into a table. The clones were listed by the rank of the average of the relative frequency between two expression profiles of ocellus and otolith cells.

Results and discussion

Overview of gene expression profile and ESTs

We determined nucleotide sequences of both 5'- and 3'-ends of a total of 964 and 772 cDNA clones that are derived from ascidian ocellus and otolith cells, respectively (Table 3.1). The 3'-end sequences were used to examine the redundancy of the clones expressed. As a result, we obtained 485 and 505 non-redundant clones of ocellus and otolith cells, respectively (Table 3.1). From the distribution pattern of the occurrence frequency of the expressed clones, I found that over 80% of the clones are expressed only once, which are called as singletons (Figure 3.2 and Figure 3.3). This result clearly shows that most of clones were rarely expressed in both single cell libraries.

EST identification by matching with public database

Using 5'-ESTs and 3'-ESTs, I conducted a homology search by blastx against nr (non-redundant protein) database of NCBI, which is one of the representative data sets from DDBJ/EMBL/GenBank databases. I found that 164 (in ocellus) and 142 (in otolith) clones were homologous to the nucleotide sequences in the database (Table 3.2). On the other hand, nearly 60% of the clones in both libraries were unknown in function. If the EST does not contain a well-conserved region, it is difficult to detect the homologous sequences. It is also possible that a sequence has diverged through long evolutionary processes of ascidians and other animals such as human or mouse. However, these unknown clones included the novel genes not found so far in the other

Table 3.1: Summary of the ESTs from ocellus and otolith cell cDNA libraries of ascidians

	Ocellus		Otolith	
	5'EST	3'EST	5'EST	3'EST
Number of sequenced clones	964	964	772	772
Number of clones after editing*	405	860	663	678
Number of non-redundant clones**	-	485	-	505

*This process contains (1) vector removal, (2) length check (more than 100bp), and (3) quality check (less than 5% of undetermined sites).

**To construct non-redundant clusters, we defined the criteria of the clones derived from the same mRNA as clones which have more than 90% identitiy among more than 100 bp overlapped region.

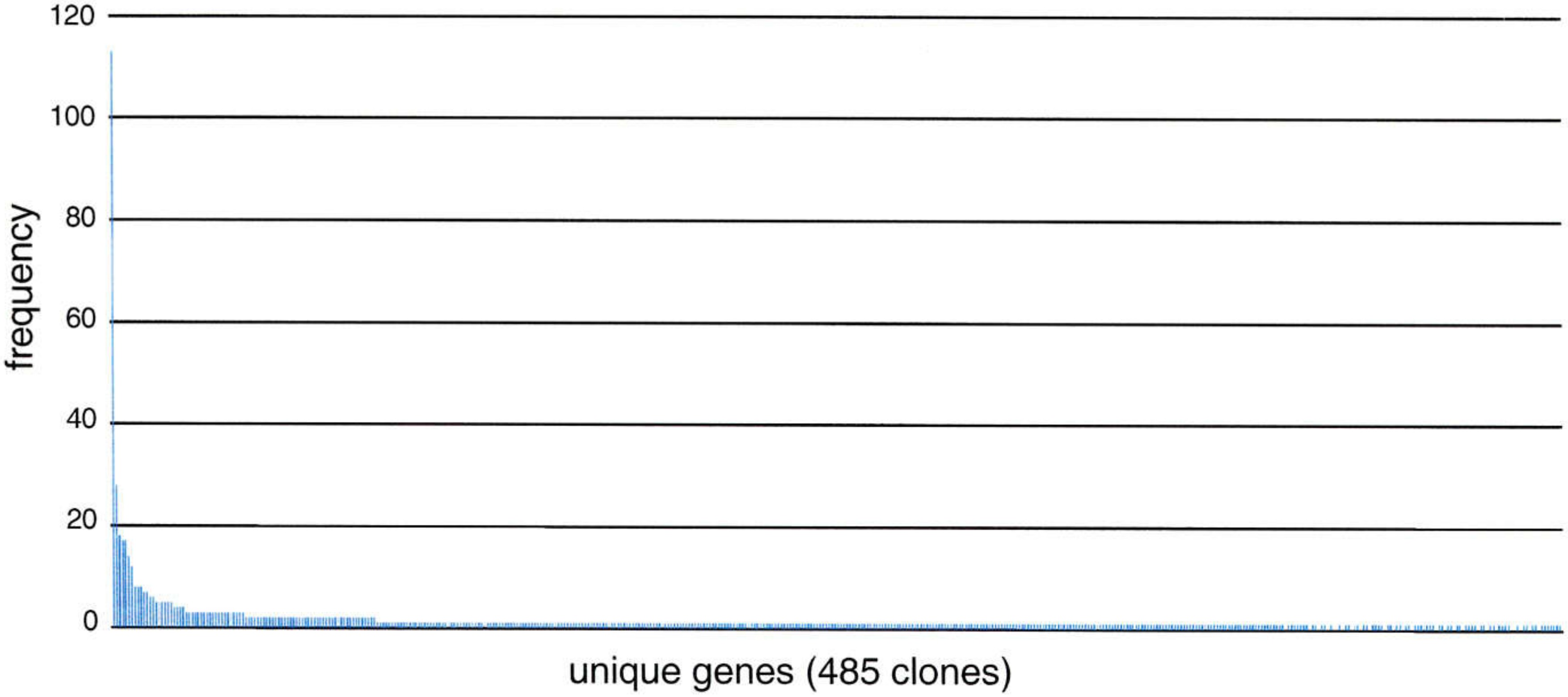


Figure 3.2: The gene expression profile of ocellus cells.

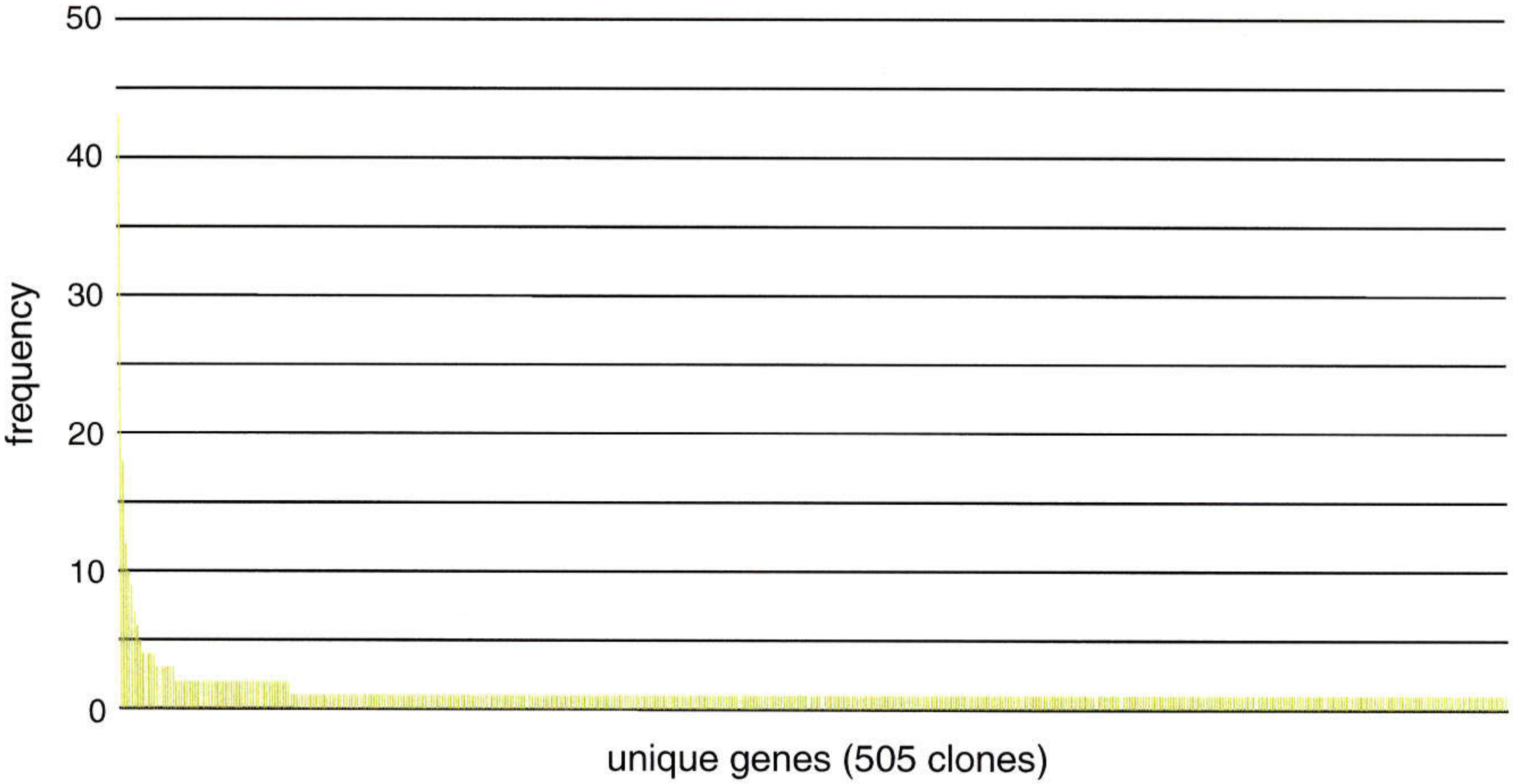


Figure 3.3: The gene expression profile of otolith cells.

Table 3.2: The number of identified clones by the homology search

	Ocellus	Otolith
Number of total non-redundant clones	485	505
Clones which have significant E-value (only 3' EST)	157	95
Clones which have significant E-value (both 3' and 5' EST	164	142

*The homology search was prformed against NCBI nr database. We defined the significant E-value as less than 1.0e-4 using BLASTX program.

species.

In the case of the expression profile of the planarian head cDNA library (chapter 2 in this thesis; Mineta *et al.*, submitted), the highly expressed clones were found in the following order: beta-actin, alpha-actin, beta-tubulin and alpha-tubulin. These highly expressed clones in planarian heads were all related to the cytoskeltal functions. In the case of the gene expression profiles of the ascidian pigment cells, however, there are no clones related to the cytoskeltal function among the highly expressed top 20 clones of both ocellus and otolith cells (Table 3.3 and Table 3.4). The planarian head portion contained neural cells, muscle cells, epithelial cells, mesanchymal cells and others (Baguna 1998), while the gene expression profiles of ascidian were derived from the single pigment cells. Thus, I thought that these differences among the gene expression profiles of the planarian head and ascidian cells clearly demonstrated the characteristics of the gene expression profiles of the single cells, for example less amount of expression of the cytoskeltal genes.

Diverged expression profiles in the ocellus cells and the otolith cells

In the comparison between the gene expression profiles of ocellus and otolith cells, I found that the 60 clones were commonly expressed (Figure 3.4), which represent ca. 11% of a total non-redundant clones of both libraries. The relative frequencies of these 60 clones showed obviously distinct patterns between these two cells (Figure 3.5). The contents of these 60 clones were shown in table 3.5. Among these 60 clones, 28 clones did not show the significant similarity among known databases. 22 clones were

Table 3.3: List of the highly expressed clones in ascidian ocellus cell (top20)

clone ID	frequency	homologous sequence which showed the highest E-value	E-value	sequenced side used for the search
00002_Ci_oc	113	No Match		3
00531_Ci_oc	28	No Match		5
00237_Ci_oc	18	No Match		5
00074_Ci_oc	17	No Match		5
00421_Ci_oc	17	No Match		5
00570_Ci_oc	14	No Match		5
00260_Ci_oc	12	No Match		5
00507_Ci_oc	8	No Match		5
00905_Ci_oc	8	No Match		5
00428_Ci_oc	8	No Match		5
00021_Ci_oc	7	CG9091 gene product [Drosophila melanogaster]	8.00E-22	5
00140_Ci_oc	7	ribosomal protein S22 [Xenopus laevis]	2.00E-51	5
00524_Ci_oc	6	No Match		3
00184_Ci_oc	6	calmodulin [Ciona intestinalis]	9.00E-30	3
00058_Ci_oc	5	acidic ribosomal phophoprotein P0 [Danio rerio]	3.00E-29	3
00553_Ci_oc	5	No Match		5
00162_Ci_oc	5	No Match		5
00173_Ci_oc	5	ribosomal protein S1a [Xenopus laevis]	3.00E-49	5
00397_Ci_oc	5	No Match		5
00720_Ci_oc	5	No Match		5

Table 3.4: List of the highly expressed clones in ascidian otolith cell (top20)

clone ID	frequency	homologous sequence which showed the highest E-value	E-value	sequenced side used for the search
00009_Ci_ot	43	No Match		5
00305_Ci_ot	18	No Match		5
00412_Ci_ot	12	No Match		5
00132_Ci_ot	10	No Match		5
00676_Ci_ot	9	No Match		5
00748_Ci_ot	7	No Match		5
00699_Ci_ot	6	No Match		5
00005_Ci_ot	5	No Match		5
00604_Ci_ot	4	No Match		3
00238_Ci_ot	4	ribosomal protein L18 [Oreochromis niloticus]	2.00E-63	5
00289_Ci_ot	4	cytoskeletal actin 1 [Molgula oculata]	6.00E-78	5
00680_Ci_ot	4	U6 snRNA-associated Sm-like protein [Homo sapiens]	1.00E-41	5
00441_Ci_ot	4	retinaldehyde-binding protein 1 [Mus musculus]	2.00E-20	5
00108_Ci_ot	3	No Match		5
00117_Ci_ot	3	No Match		5
00127_Ci_ot	3	No Match		5
00176_Ci_ot	3	ribosomal protein L23 [Homo sapiens]	1.00E-55	5
00236_Ci_ot	3	No Match		5
00281_Ci_ot	3	No Match		5
00327_Ci_ot	3	ribosomal protein S23 [Homo sapiens]	2.00E-70	5

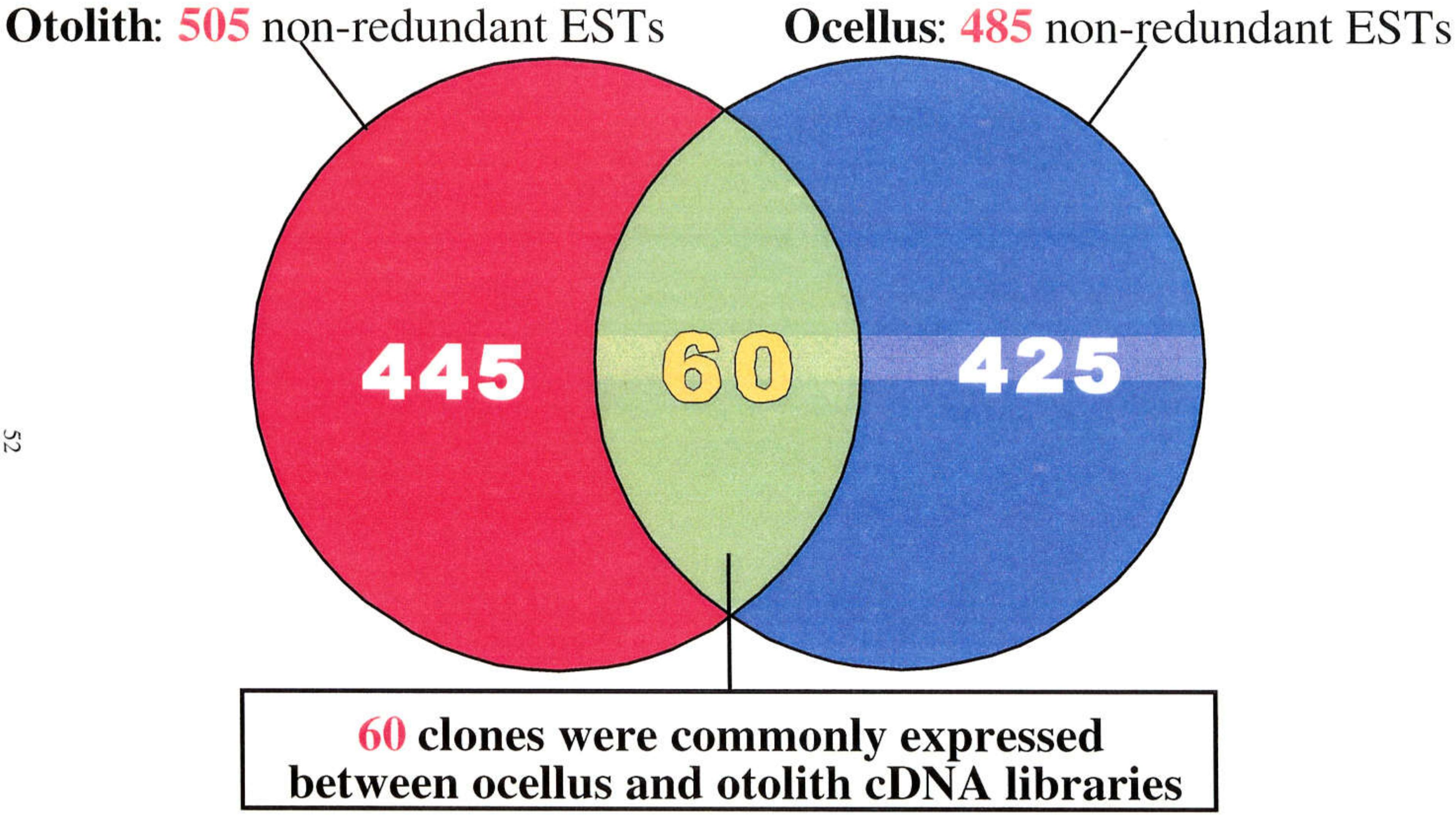


Figure 3.4: The ratio of clones commonly expressed between ocellus and otolith cells.

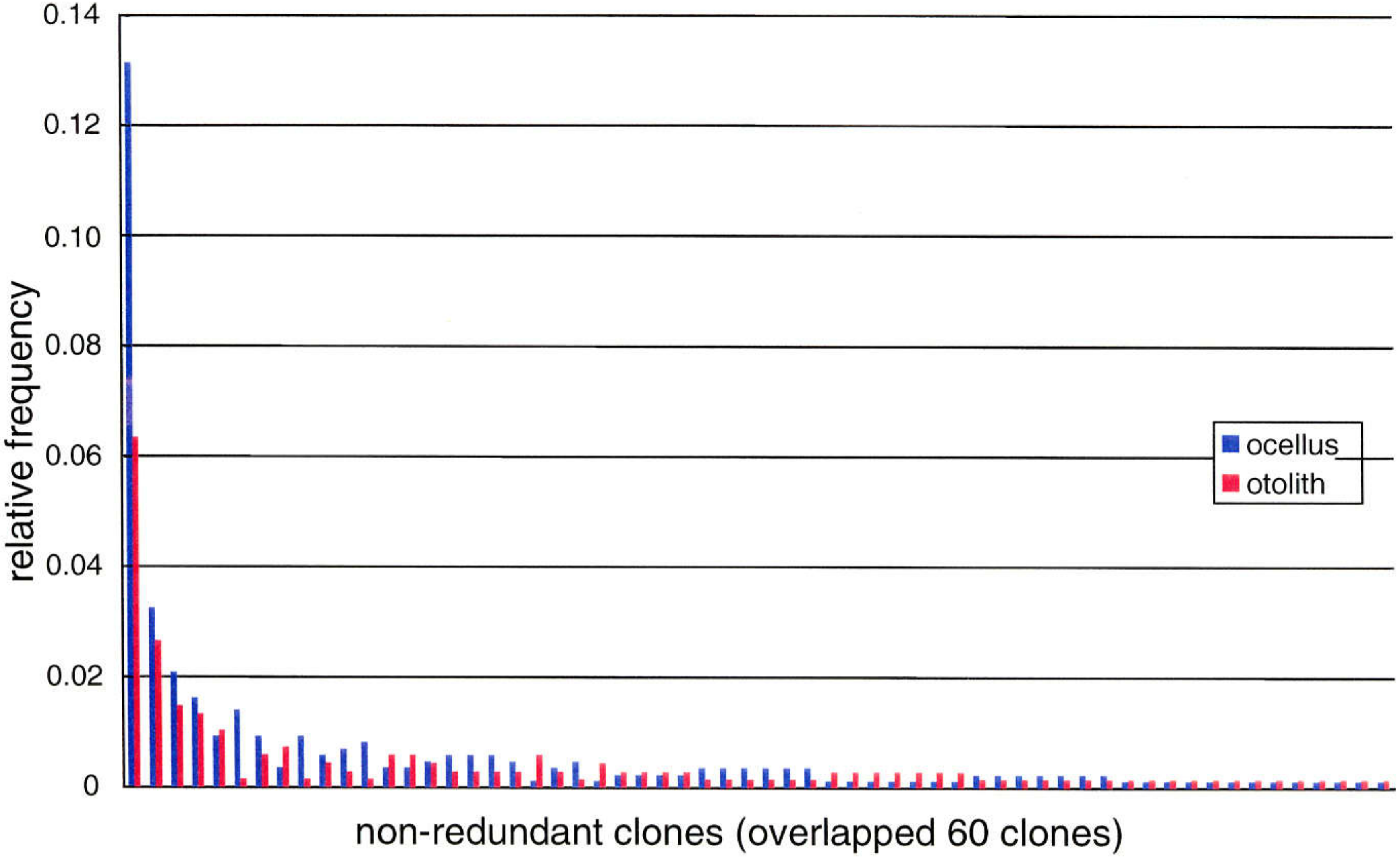


Figure 3.5: The comparison of gene expression profiles of clones commonly expressed between ocellus and otolith cells shows distinct expression frequencies of the clones.

related to house keeping functions such as ribosomal proteins and actin. Six clones were matched with unknown or hypothetical proteins. Remaining four clones were retinal aldehyde-binding protein, G protein beta subunit-like / receptor of activated protein kinase C, SEC61 gamma subunit and *mago mashi* gene product (Figure 3.6).

As we expected, the most abundant category was house-keeping function. However, the top 6 highly expressed clones were all unknown clones in my search (See method). Though the functional importance and the higher frequency do not directly correspond, these highly expressed 6 clones were the most active in both pigment cells. Of course, I have to be careful about these clones commonly expressed, because we have not yet checked the expression patterns in the other cells. Even if these unknown clones were commonly expressed in other cells, it may be possible to state that these clones were specific to the ascidians, because these unknown clones did not show any significant similarity against the all known sequences including the complete genomes of the species such as human or *D. melanogaster.*

The other clones that were not shared by both ocellus and otolith cells may contain clones specific to each cell. As opsin genes are expressed only in the ocellus cell, these clones specific to the each cell might reflect the characteristics of the cell types.

Table 3.5: List of commonly expressed clones between ocellus and otolith library

		ocellus			otolith				
rank	average relative frequency	clone ID	raw frequency	relative frequency	clone ID	raw frequency	relative frequency	annotation	category
1	0.097409	00002_Ci_oc	113	0.131395	00009_Ci_ot	43	0.063422		unknown
2	0.029553	00531_Ci_oc	28	0.032558	00305_Ci_ot	18	0.026549		unknown
3	0.017840	00237_Ci_oc	18	0.020930	00132_Ci_ot	10	0.014749		unknown
4	0.014777	00570_Ci_oc	14	0.016279	00676_Ci_ot	9	0.013274		unknown
5	0.009813	00507_Ci_oc	8	0.009302	00748_Ci_ot	7	0.010324		unknown
6	0.007714	00260_Ci_oc	12	0.013953	00072_Ci_ot	1	0.001475		unknown
7	0.007601	00428_Ci_oc	8	0.009302	00680_Ci_ot	4	0.005900	U6 snRNA-associated Sm-like protein [Homo sapiens]	house-keeping
8	0.005432	00180_Ci_oc	3	0.003488	00005_Ci_ot	5	0.007375		unknown
9	0.005389	00905_Ci_oc	8	0.009302	00133_Ci_ot	1	0.001475		unknown
10	0.005119	00162_Ci_oc	5	0.005814	00117_Ci_ot	3	0.004425		unknown
11	0.004963	00524_Ci_oc	6	0.006977	00634_Ci_ot	2	0.002950		unknown
12	0.004807	00140_Ci_oc	7	0.008140	00122_Ci_ot	1	0.001475	RIBOSOMAL PROTEIN S20 (S22)	house-keeping
13	0.004694	00054_Ci_oc	3	0.003488	00289_Ci_ot	4	0.005900	cytoplasmic actin / cytoskeletal actin 1 [Molgula oculata]	house-keeping
13	0.004694	00270_Ci_oc	3	0.003488	00441_Ci_ot	4	0.005900	retinaldehyde-binding protein	sensory system
15	0.004538	00543_Ci_oc	4	0.004651	00176_Ci_ot	3	0.004425	ribosomal protein L23	house-keeping
16	0.004382	00058_Ci_oc	5	0.005814	00447_Ci_ot	2	0.002950	acidic ribosomal phophoprotein P0	house-keeping
16	0.004382	00553_Ci_oc	5	0.005814	00278_Ci_ot	2	0.002950		unknown
16	0.004382	00720_Ci_oc	5	0.005814	00262_Ci_ot	2	0.002950		unknown
19	0.003801	00262_Ci_oc	4	0.004651	00366_Ci_ot	2	0.002950	hypothetical protein [Plasmodium falciparum]	unknown
20	0.003531	00962_Ci_oc	1	0.001163	00238_Ci_ot	4	0.005900	ribosomal protein L18	house-keeping
21	0.003219	00686_Ci_oc	3	0.003488	00472_Ci_ot	2	0.002950		unknown
22	0.003063	00305_Ci_oc	4	0.004651	00675_Ci_ot	1	0.001475	ribosomal protein L29	house-keeping
23	0.002794	00815_Ci_oc	1	0.001163	00108_Ci_ot	3	0.004425	RIBOSOMAL PROTEIN L44 (L41)	house-keeping
24	0.002638	00053_Ci_oc	2	0.002326	00093_Ci_ot	2	0.002950	ribosomal protein S15A	house-keeping
24	0.002638	00281_Ci_oc	2	0.002326	00328_Ci_ot	2	0.002950		unknown
24	0.002638	00335_Ci_oc	2	0.002326	00126_Ci_ot	2	0.002950		unknown
24	0.002638	00718_Ci_oc	2	0.002326	00051_Ci_ot	2	0.002950	G protein beta subuit like [Mus musculus] / RECEPTOR OF ACTIVATED PROTEIN KINASE C (RACK) [Oreochromis niloticus]	signal transduction
28	0.002482	00112_Ci_oc	3	0.003488	00152_Ci_ot	1	0.001475	ribosomal protein L11	house-keeping
28	0.002482	00125_Ci_oc	3	0.003488	00671_Ci_ot	1	0.001475	ribosomal protein S29	house-keeping
28	0.002482	00476_Ci_oc	3	0.003488	00706_Ci_ot	1	0.001475	hypothetical protein XP_016419 [Homo sapiens]	unknown
28	0.002482	00567_Ci_oc	3	0.003488	00240_Ci_ot	1	0.001475	ribosomal protein S7	house-keeping
28	0.002482	00810_Ci_oc	3	0.003488	00653_Ci_ot	1	0.001475		unknown
28	0.002482	00854_Ci_oc	3	0.003488	00747_Ci_ot	1	0.001475	ribosomal protein S7 / protein translocation complex beta; protein transport protein SEC61 beta subunit [Homo sapiens]	house-keeping
34	0.002056	00037_Ci_oc	1	0.001163	00106_Ci_ot	2	0.002950		unknown
34	0.002056	00155_Ci_oc	1	0.001163	00217_Ci_ot	2	0.002950	ribosomal protein L23a	house-keeping

34	0.002056	00232_Ci_oc	1	0.001163	00091_Ci_ot	2	0.002950	ribosomal protein S19	house-keeping
34	0.002056	00234_Ci_oc	1	0.001163	00751_Ci_ot	2	0.002950		unknown
34	0.002056	00337_Ci_oc	1	0.001163	00189_Ci_ot	2	0.002950		unknown
34	0.002056	00411_Ci_oc	1	0.001163	00339_Ci_ot	2	0.002950	ribosomal protein S12	house-keeping
34	0.002056	00802_Ci_oc	1	0.001163	00235_Ci_ot	2	0.002950	(Wnt inhibitory factor 1 [Mus musculus] E=0.075)	unknown (1)
41	0.001900	00094_Ci_oc	2	0.002326	00754_Ci_ot	1	0.001475	ribosomal protein S2	house-keeping
41	0.001900	00100_Ci_oc	2	0.002326	00349_Ci_ot	1	0.001475		unknown
41	0.001900	00147_Ci_oc	2	0.002326	00163_Ci_ot	1	0.001475		unknown
41	0.001900	00401_Ci_oc	2	0.002326	00124_Ci_ot	1	0.001475	ribosomal protein L24	house-keeping
41	0.001900	00455_Ci_oc	2	0.002326	00717_Ci_ot	1	0.001475		unknown
41	0.001900	00459_Ci_oc	2	0.002326	00042_Ci_ot	1	0.001475	CG3195 [Drosophila melanogaster] / ribosomal protein L12	house-keeping
41	0.001900	00493_Ci_oc	2	0.002326	00396_Ci_ot	1	0.001475	hypothetical protein R08B4.3 [Caenorhabditis elegans]	unknown
48	0.001319	00061_Ci_oc	1	0.001163	00760_Ci_ot	1	0.001475		unknown
48	0.001319	00128_Ci_oc	1	0.001163	00478_Ci_ot	1	0.001475	ribosomal protein L36	house-keeping
48	0.001319	00129_Ci_oc	1	0.001163	00433_Ci_ot	1	0.001475	ribosomal protein L8	house-keeping
48	0.001319	00141_Ci_oc	1	0.001163	00480_Ci_ot	1	0.001475	protein transport protein SEC61 gamma subunit [Homo sapiens] / CG8860 [Drosophila melanogaster]	protein transport
48	0.001319	00220_Ci_oc	1	0.001163	00186_Ci_ot	1	0.001475		unknown
48	0.001319	00333_Ci_oc	1	0.001163	00750_Ci_ot	1	0.001475		unknown
48	0.001319	00340_Ci_oc	1	0.001163	00006_Ci_ot	1	0.001475		unknown
48	0.001319	00394_Ci_oc	1	0.001163	00147_Ci_ot	1	0.001475	hypothetical protein [Macaca fascicularis]	unknown
48	0.001319	00472_Ci_oc	1	0.001163	00391_Ci_ot	1	0.001475	CG10753 [Drosophila melanogaster]	unknown
48	0.001319	00520_Ci_oc	1	0.001163	00213_Ci_ot	1	0.001475	hypothetical protein FLJ10292 [Homo sapiens] / mago nashi [Drosophila melanogaster]	development of cell polarity
48	0.001319	00628_Ci_oc	1	0.001163	00211_Ci_ot	1	0.001475	ribosomal protein L7	house-keeping
48	0.001319	00826_Ci_oc	1	0.001163	00092_Ci_ot	1	0.001475		unknown
48	0.001319	00119_Ci_oc	1	0.001163	00342_Ci_ot	1	0.001475	unnamed protein product [Homo sapiens]	unknown

*This list was constructed as follows (See also Method):

(1) Identification of the clone pairs between ocelus and otolith library was based on the same criteria as removal of the redundancy.

(2) The relative frequencies means "raw frequency / total clone number (OC: 860, OT: 678)".

(3) The annotation was based on the homology search result of both 3' and 5' ESTs. When the E-value of clone at the highest score was less than 1.0E-4 among four results (OC 3', 5' and OT 3', 5'), that clone was regarded as a putative homologous clone.

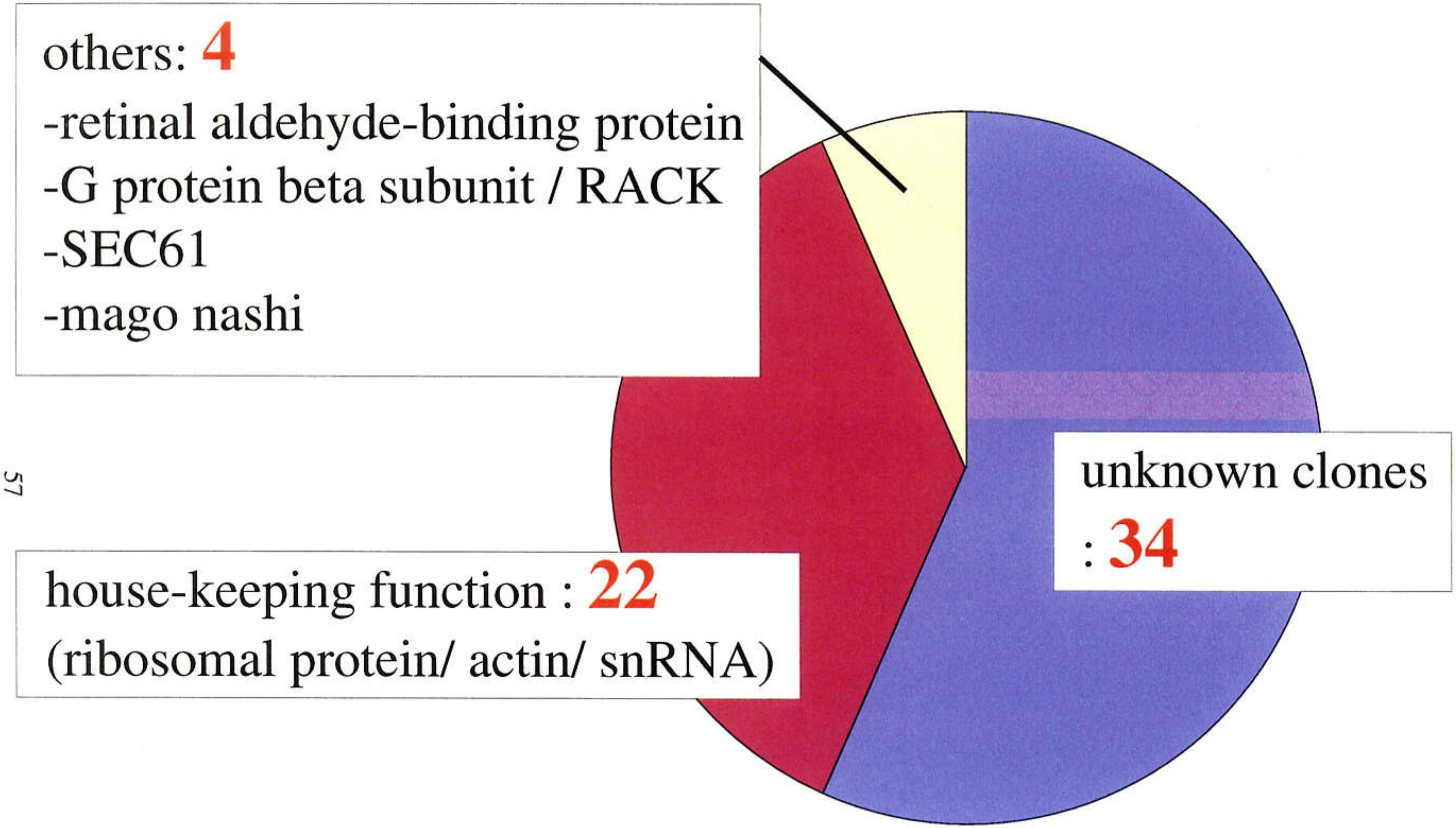


Figure 3.6: Functional categories of 60 shared clones between ocellus and otolith cells.

Conclusion

This is the first report about the gene expression profiles of the single cells that is composed of an organ. My comparative study showed the clear difference in the gene expression profiles between the ascidian sensory cells and planarian head, showing that contents of the genes expressed in each library are biased. I thought that these differences among the gene expression profiles of the planarian head and ascidian cells clearly demonstrated the characteristics of the gene expression profiles of the single cells, for example less amount of expression of the cytoskeltal genes.

The analysis of the gene expression profiles of the cell will lead to profound understanding of the gene expression profiles of the organs or tissues in the further comparative analyses in order to study the developmental and the evolutionary diversification from the cell level.

Chapter 4

Evolution of a brain from the viewpoint of gene expression profiles

Summary

In the present study, I made an attempt to understand the evolutionary process of a brain from the viewpoint of gene expression profiles. To attain the purpose, I raised a question of whether the degree of the differences in the gene expression profiles smong various species correspond proportionally to the degree of the evolutionary divergence of the species examined. As materials, we sequenced EST clones from the cDNA libraries of brains of chickens (*Gallus gallus*) and lampreys (*Lampetra japonicum*), the head of planarians (see above), and the whole body of the jellyfish (*Aureria aurita*), obtaining over 2,000 clones from each library. Based on these EST clones, I produced the gene expression profiles of brains. The assumption I used here was that, if differences of the gene expression profiles correspond to the evolutionary divergence of species, a topology of the tree based on the differences in the gene expression profiles (designated as a gene expression tree) might correspond to a topology of the species tree. To examine this assumption, first, I quantified the

differences among the gene expression profiles by the Euclidean distance, and then constructed a gene expression tree. As a result, the topology of the gene expression tree showed the clear correspondence to that of the species tree, though the current sequenced number was relatively small. Thus, I conclude that the gene expression profiles of brains, at least in part, might trace the evolutionary process of the brain.

Introduction

To understand the evolutionary diversification of brains in various organisms, I focus on genes expressed in a brain. Recently, the expression data is becoming available in various organs or tissues (reviewed by Bortoluzzi *et al* 1999). These data include the occurrence frequencies of expressed mRNA species in a given organs. In this thesis, I defined such data as a gene expression profile. In studies of the gene expression profile, most of the researchers have focused on functional identification of genes expressed specifically in particular organs. Here, I propose that an expression profile is also useful for the evolutionary studies of organs. Since an expression profile results from the transcriptional activities of all genes involved in a system, the expression profile should reflect the outcome of transcriptional regulations of all genes expressed in a given organ. Given that there have been virtually no means to study evolutionary mechanisms of gene regulation except in a few cases focusing on particular genes, the comparison based on the gene expression profile might open the door to a new approach in the evolutionary study.

My interest is specifically on the evolutionary diversification of the brain. The brain, which is a representative organ of the CNS, characterizes the organisms, because the brain plays important role such as the control of the behavior or the intelligence (Breidbach & Kutsch, 1995). Generally, the following main reasons are given for the divergence of the species; (1) the mutation (Kimura 1968), (2) the gene duplication (Ohno 1970), (3) the gene loss (Chapter 2 in this thesis; The Arabidopsis Genome Initiative 2000) and (4) the change of genetic network (Chapter 2 and 3 in this thesis; Gehring & Ikeo 1999; Force *et al.* 1999). As I showed in chapter 2 in this thesis, the gene set used in the common ancestor of CNS was shared to a high degree among bilateral animals. Because the evolution of the brain corresponds to the evolution of the organisms, in this study, we focused on the change of the genetic networks during the evolutionary process of brains. To understand the change of genetic networks in a brain, the approach based on the gene expression profiles was taken. This is the first attempt to see the evolutionary divergence of brains among different animals from the viewpoint of the gene expression profiles. The basic question I has was whether the divergence of gene expression profiles corresponds to the divergence of species. To answer this question, we determined the gene expression profiles of different chordate brains and compared them. In the end, I will discuss the effectiveness of studying the evolutionary divergence of brains among different animals from the viewpoint of the gene expression profiles.

Materials and Methods

Samples

The brains of lamprey (*Lampetra japonicum*) and chicken (*Gallus gallus*) were isolated surgically at the end of the medulla oblongata and collected. The whole planulae of jellyfish (*Aureria aurita*) and the head portion of planarian (See Chapter 2) are used for the experiments.

Construction of a cDNA library.

The all cDNA libraries used were constructed in lambda ZAP II (Stratagene USA) using oligo d (T) primers. The phages containing inserts were excised *in vivo* to generate subclones in pBluescript SK (Stratagene USA) for DNA sequencing. In this protocol, we did not amplify the cDNA by PCR method, so that these libraries were expected to reflect the mRNA frequency *in vivo.*

Sequence and analyses of the cDNA clones.

Purified plasmid DNA was sequenced using a 3700 ABI sequencer using the Big-Dye terminator sequencing kit following the manufacturer's instructions (ABI, Perkin Elmer US). The products were edited as follows using in-house EST analyzing system (Mineta *et al.*, submitted; See also Appendix A in this thesis). The sequence was cut into 500 bp long and less than 100 bp clones were removed. Only the sequences with less than 5 % of non-determined sites were used for the subsequent analysis. The redundancy of sequences was checked by BLASTN program (Altschul *et al.* 1990) under the criteria of $\geq 90\%$ identity among $\geq$ 100bp overlapped region, and then we constructed non-redundant data set with their frequency. Then these non-redundant sequences were searched against the available DNA and protein databases of DDBJ/EMBL/GenBank using BLASTX programs. Here, I set a criterion of less than 10^{-4} in E-value for identifying homologous sequences.

Comparison of the gene expression profiles among different species of brains

For comparison, I used top 20 clones in their frequency of occurrence in order to avoid the saturation problem in our EST database (See "Result and Discussion"). The possible orthologous clone pairs were determined, based on its annotation. In order to measure the difference in the gene expression profiles of a brain between different organisms, first, the frequency of ESTs was normalized so that the sum of all frequencies is one. Then, the Euclidean distance, d_{jk}, between species j and k was calculated as below,

$$d_{jk} = \frac{1}{n}\sqrt{\sum_{i=1}^{n}(X_{ij} - X_{ik})^2},$$

where X_{ij} is the normalized frequency of mRNA i in species j, and n is the total number of mRNA species examined. We also calculated the Euclidean distance based on the TF-IDF score w_{ij} in order to examine the effect of the house-keeping genes (See "Result and Discussion"). In that case, each frequency of the clone was calculated as the following equation,

$$w_{ij} = X_{ij} \cdot (1 + \log \frac{N}{m})$$

,where N is the total number of the species examined, and m is the number of species that the mRNA i expressed. The "gene expression tree" was constructed by the neighbor-joining method (Saitou & Nei 1987) from the distance matrix based on the differences of gene expression profiles.

Results and Discussion

Summary of EST clones

As shown in Table 4.1, we sequenced over 2,000 EST clones from the cDNA libraries of each species. As a result, we obtained more than 1,200 non-redundant clones in each species. The overall distribution patterns in all 4 species (Figure 4.1, 4.2, 4.3, 4.4 and summarized in Figure 4.5) showed that most of the clones (ca. 70 to 90%) were rarely expressed, suggesting that this distribution pattern is a common feature of the gene expression profiles among the organisms. This common feature of the overall distribution patterns implied the fundamental biological mechanism commonly used in the system of the transcriptional regulation.

I show the top 20 highly expressed clones of each library in Tables 4.2, 4.3, 4.4 and 4.5, and we also showed the list combined with all lists of top20 clones (Table 4.6). Though the overall pattern of the gene expression profiles had a common feature among different species, the genes expressed in each library were obviously different (Figure 4.6). For example, in the case of chicken brain, 8 nervous system-related genes were expressed, but in the case of jellyfish, there were no nervous system related genes in that list. Another example was the myelin basic protein. This gene was highly expressed in the chicken brain, but not in others. It is consistent with an observation of the cellular structure that an axon of a chicken neuron has a myelin stele but neurons of others do not (Kandel *et al.* 2000).

On the other hand, we also found a similar tendency of the expressed clones. The genes of cytochrome c oxidase subunit 1 were the most highly expressed

Table 4.1: Number of sequenced clones

species name	part/stage	number of total sequenced clones	number of non-redudant clones
jellyfish (*Aureria auria*)	whole body/planula	3,356	1,255
planarian (*Dugesia japonica*)	head/adult	5,433	3,101
lamprey (*Lampetra japonica*)	brain/adult	2,863	1,491
chicken(*Gallus gallus*)	brain/adult	2,106	1,469

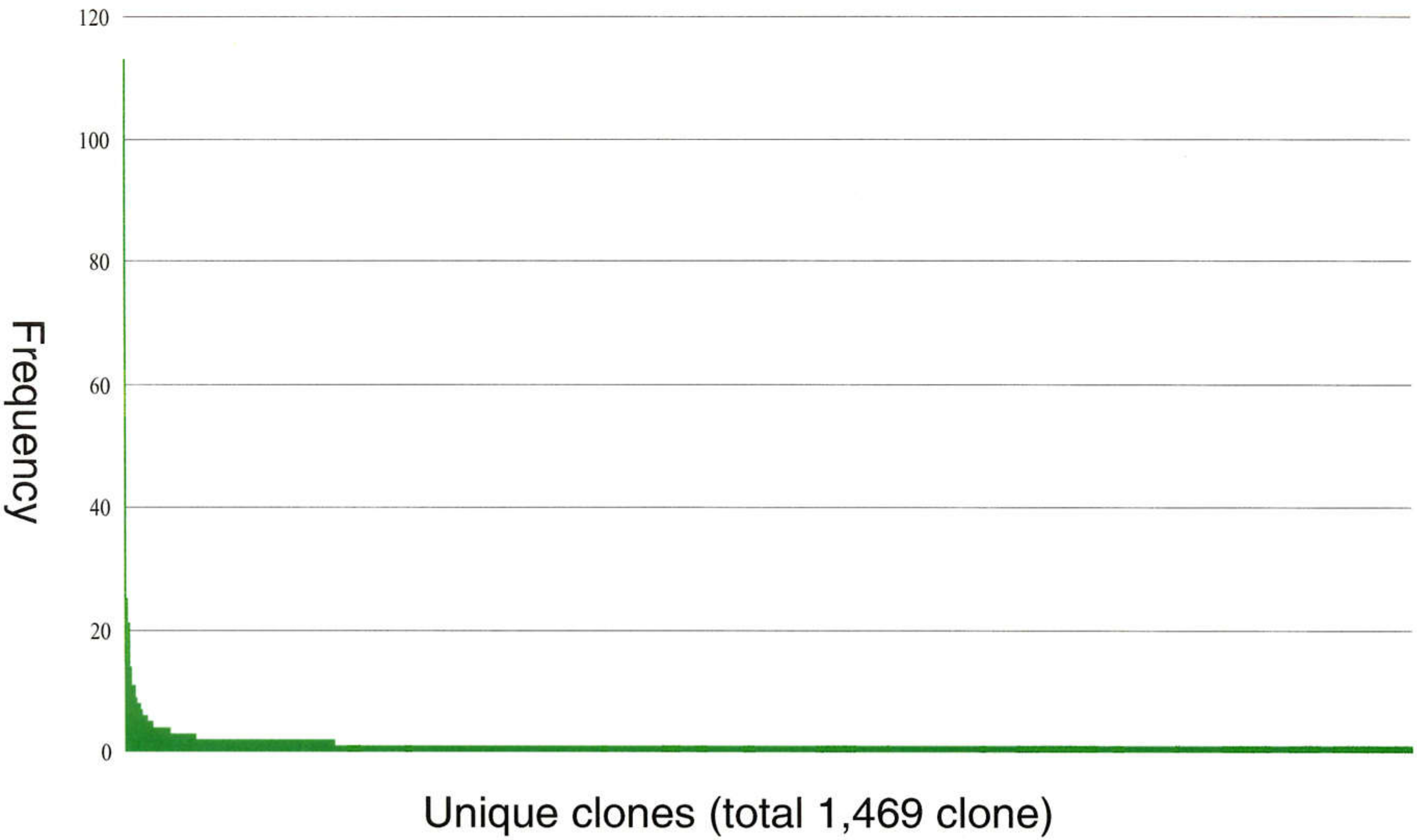


Figure 4.1: The gene expression profile of chicken brain.

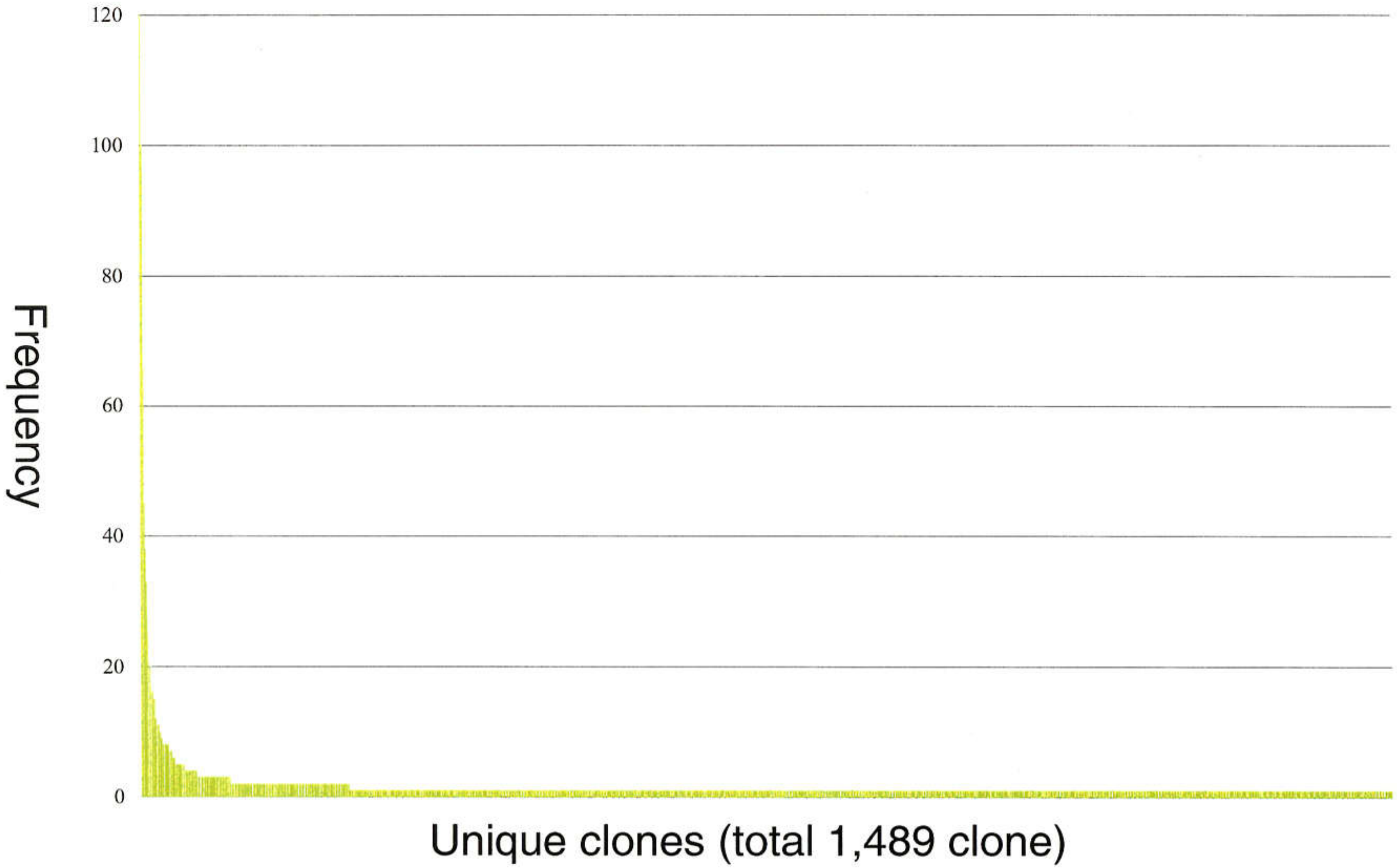


Figure 4.2: The gene expression profile of lamprey brain.

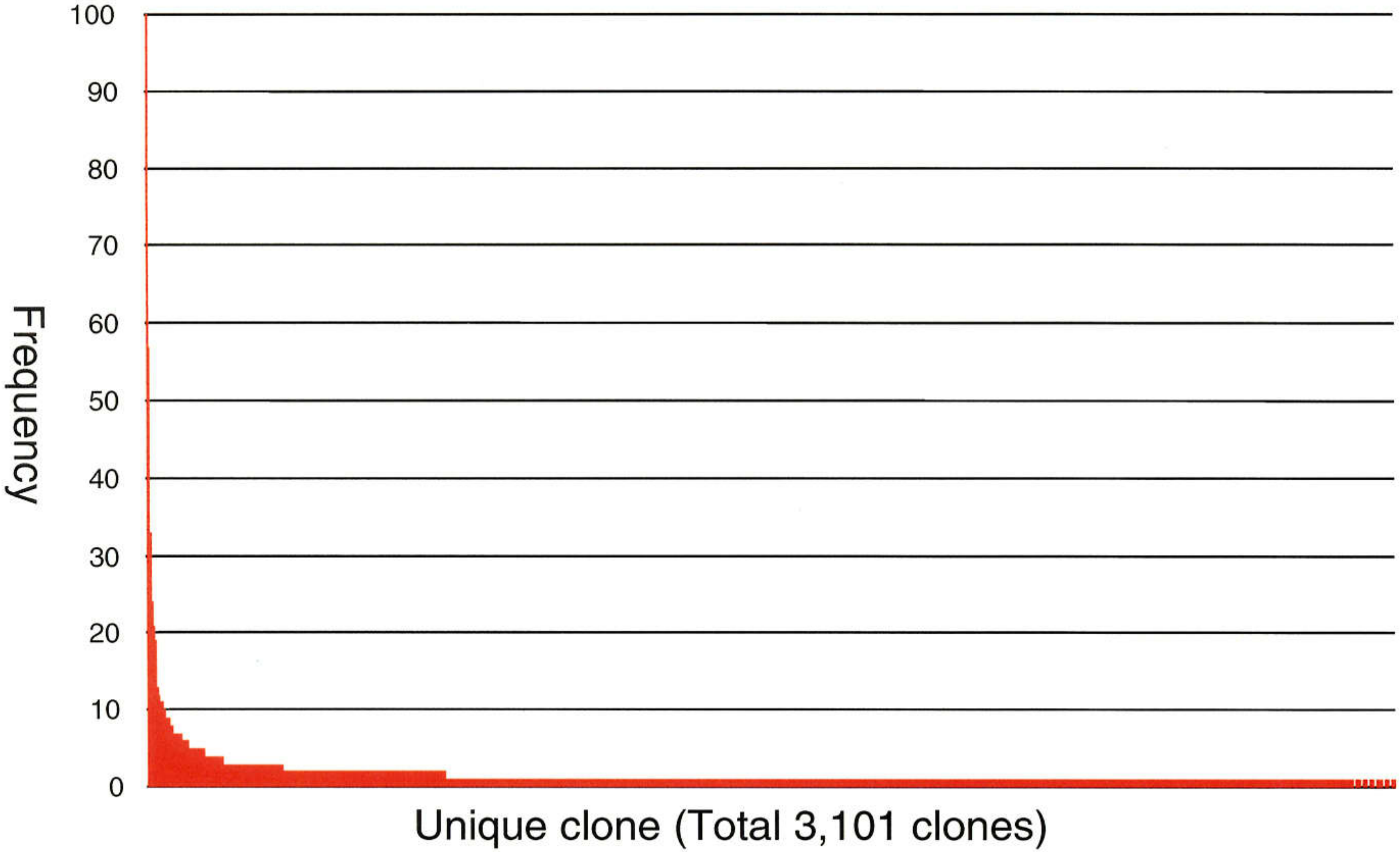


Figure 4.3: The gene expression profile of planarian head.

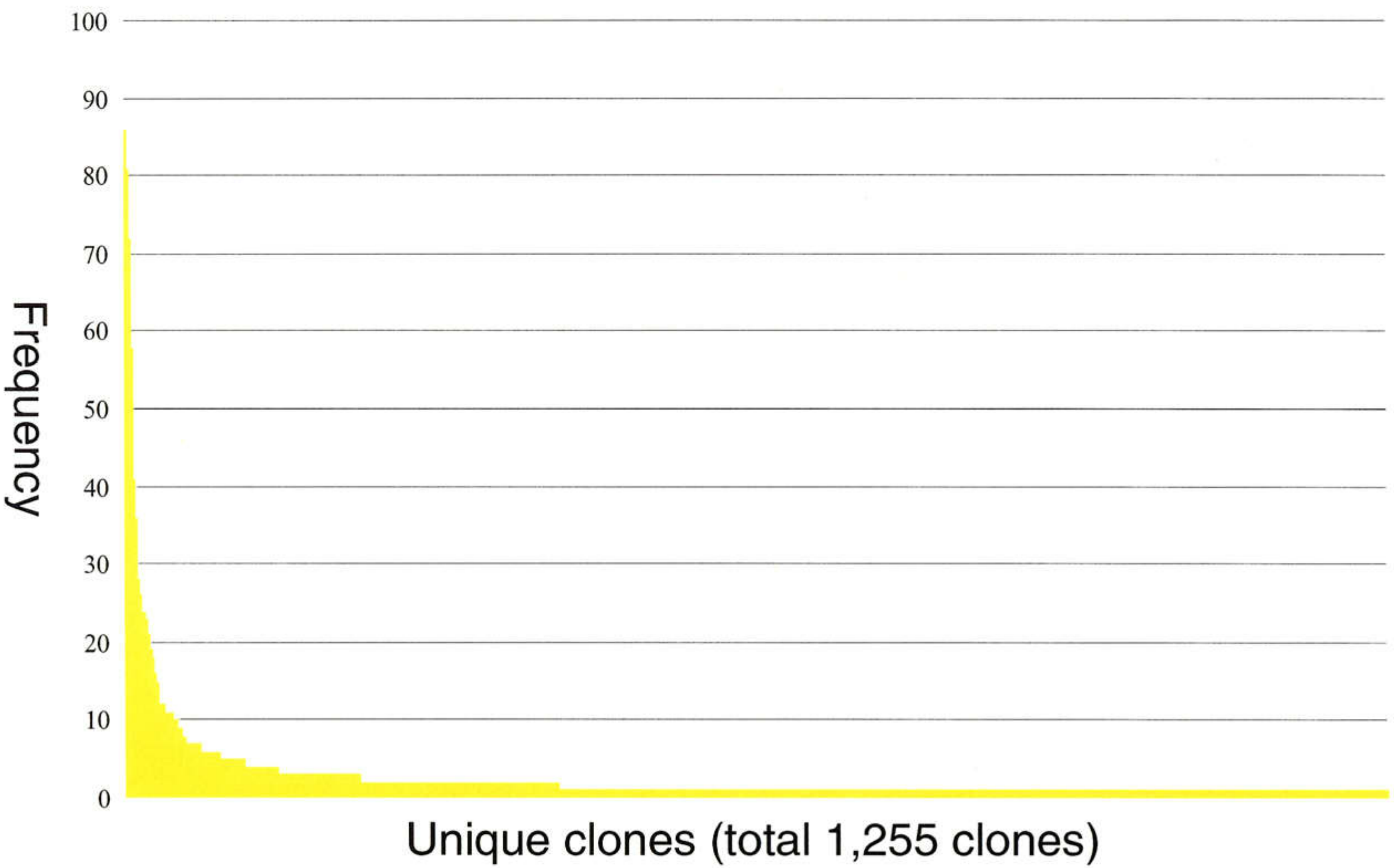


Figure 4.4: The gene expression profile of whole bofy of jellyfish at the planula stage.

Figure 4.5: Common feature of thepattern of frequency distribution in the gene expression profiles

Table 4.2: List of top20 of the highly expressed clones of the chicken brain

frequency	protein with the lowest E-value in nr database	E-value
113	cytochrome c oxidase subunit 1 [Gallus gallus]	1.00E-103
25	cytochrome c oxidase subunit 3 [Aythya americana]	5.00E-97
21	ATP synthase F0 subunit 6 [Gallus gallus]	3.00E-56
21	myelin basic protein [Gallus gallus]	3.00E-90
15	tubulin alpha chain, neuron-specific isoform - marbled electric ray	1.00E-119
14	glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Gallus gallus]	8.00E-93
14	polyubiquitin [Cricetulus griseus]	1.00E-126
11	synaptosomal-associated protein (25kD), SNAP25 [Homo sapiens]	7.00E-97
11	hypothetical 18K protein - goldfish mitochondrion	9.00E-10
11	lifeguard, KIAA0950 protein [Homo sapiens]	3.00E-60
9	cytochrome b [Gallus gallus]	1.00E-106
9	Hsc70 (72)-ps1 [Rattus norvegicus]	3.00E-91
8	NADH dehydrogenase subunit 1 [Gallus gallus]	1.00E-70
8	no match	-
8	calcium/calmodulin-dependent protein kinase II isoform D [Caenorhabditis elegans]	1.00E-97
8	pyruvate kinase [Gallus gallus]	1.00E-119
7	(Na+,K+)-ATPase-beta-2 (3) subunit [Gallus gallus]	6.00E-50
7	similar to calmodulin 2 (phosphorylase kinase, delta, H. sapiens) [Homo sapiens]	2.00E-75
6	beta-actin [Cricetulus griseus]	1.00E-126
6	gamma enolase (neural enolase) [Gallus gallus]	1.00E-103
6	glial fibrillary acidic protein delta [Rattus norvegicus]	9.00E-43
6	beta tubulin [Stylonychia mytilus]	1.00E-112
6	translation initiation factor eIF-4A II - mouse	1.00E-127
6	14-3-3 epsilon [Homo sapiens]	1.00E-125

Table 4.3: List of top20 of the highly expressed clones of the lamprey brain

frequency	proteins with the lowest E-value in nr database	E-value
228	cytochrome c oxidase subunit I [Lampetra fluviatilis]	1.00E-71
123	cytochrome c oxidase subunit III [Petromyzon marinus]	3.00E-62
100	ATP synthase F0 subunit 6 [Lampetra fluviatilis]	1.00E-24
96	cytochrome c oxidase subunit II [Lampetra fluviatilis]	2.00E-65
66	cytochrome b [Lampetra fluviatilis]	7.00E-68
45	NADH dehydrogenase subunit 1 [Lampetra fluviatilis]	9.00E-49
38	hypothetical 18K protein [goldfish]	9.00E-05
33	ferritin heavy chain [Xenopus laevis]	1.00E-27
28	lactate dehydrogenase [Petromyzon marinus]	2.00E-56
25	elongation factor 1-alpha [Homo sapiens]	1.00E-86
21	NADH dehydrogenase subunit 4 [Lampetra fluviatilis]	2.00E-51
20	NADH dehydrogenase subunit 2 [Lampetra fluviatilis]	7.00E-15
17	no match	-
16	no match	-
16	adenine nucleotide translocase [Xenopus laevis]	1.00E-45
15	glyceraldehyde 3-phosphate dehydrogenase (GAPDH) [Xenopus laevis]	1.00E-52
15	NADH dehydrogenase subunit 5 [Petromyzon marinus]	6.00E-65
12	no match	-
12	alpha-tubulin [Mus musculus]	8.00E-93
11	calmodulin [Bos taurus]	2.00E-69
11	no match	-
11	no match	-

Table 4.4: List of top20 of the highly expressed clones of the planrian head

frequency	protein with the lowest E-value in nr database	E-value
100	beta actin [Pleuronectes americanus]	8.00E-60
77	actin [Girardia tigrina]	1.00E-91
70	alpha tubulin [Schistosoma mansoni]	5.00E-81
57	TUBULIN BETA-2 CHAIN [Homo sapiens]	4.00E-77
46	elongation factor-1alpha [Dugesia japonica]	5.00E-89
45	CG10527 gene product [Drosophila melanogaster]	2.00E-22
34	DnaJ-like protein [Mus musculus]	8.00E-43
33	cathepsin L [Danio rerio]	4.00E-40
32	ADP/ATP carrier [Trypanosoma brucei brucei]	2.00E-51
28	myosin heavy chain [Dugesia japonica]	4.00E-66
27	glyceraldehyde-3-phosphate dehydrogenase [Schistosoma japonicum]	9.00E-66
24	glutathione S-transferase [Schistosoma japonicum]	2.00E-29
23	Y-box protein [Dugesia japonica]	3.00E-69
22	heat shock protein 82 [Anopheles albimanus]	3.00E-63
22	rasputin [Drosophila melanogaster]	4.00E-25
21	polyubiquitin [Bombyx mori]	9.00E-80
21	14-3-3 PROTEIN EPSILON (SUPPRESSOR OF RAS1 3-9) [Drosophila melanogaster]	2.00E-57
19	no match	-
19	CATHEPSIN B PRECURSOR - bovine	1.00E-64
19	no match	-

Table 4.5: List of top20 of the highly expressed clones of jellyfish at the planula stage

frequency	protein with the lowest E-value in nr database	E-value
86	alpha-tubulin isotype 2 [Paracentrotus lividus]	2.00E-46
84	elongation factor 1-alpha [Mytilus edulis]	1.00E-115
81	actin - Phaffia rhodozyma	1.00E-114
74	no match	-
72	polyA binding protein [Xenopus laevis]	3.00E-82
67	beta-tubulin [Halocynthia roretzi]	1.00E-128
58	40S RIBOSOMAL PROTEIN SA (P40) (33 KD LAMININ BINDING PROTEIN) - Chlorohydra viridissima	1.00E-71
44	calmodulin 2 (phosphorylase kinase, delta) [Homo sapiens]	3.00E-40
41	no match	-
37	ribosomal protein S6 [Branchiostoma floridae]	6.00E-77
36	ribosomal protein L4, cytosolic - rat	1.00E-97
34	ribosomal protein L3 [Drosophila melanogaster]	2.00E-83
28	ribosomal protein L5 [Styela clava]	1.00E-81
27	no match	-
26	polyubiquitin [Cricetulus sp.]	1.00E-130
24	ELONGATION FACTOR 1-GAMMA (EEF-1B GAMMA) [Mus musculus]	9.00E-66
24	60S ACIDIC RIBOSOMAL PROTEIN P0 - Caenorhabditis elegans	3.00E-51
24	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (RECEPTOR OF ACTIVATED PROTEIN KINASE C) (RACK) [Danio rerio]	1.00E-114
24	membrane glycoprotein [Equine herpesvirus 1]	3.00E-07
23	ATP synthase beta-subunit [Cyprinus carpio]	1.00E-133
23	heat shock 70 protein [Parastrongyloides trichosuri]	2.00E-96
22	PROBABLE 60S RIBOSOMAL PROTEIN L7 (L30P) [Caenorhabditis elegans]	2.00E-70

Table 4.6: List of top 20 clones showing the different freuqencies (relative frequecy)

Genes	jellyfish	planaria	lamprey	chicken	RANK
cytochrome c oxidase subunit I	0	0	0.079636745	0.05365622	0.033323241
cytochrome c oxidase subunit III	0	0	0.042961928	0.011870845	0.013708193
alpha-tubulin	0.025625745	0.012884226	0.004191408	0.007122507	0.012455972
ATP synthase F0 subunit 6	0	0	0.034928397	0.00997151	0.011224977
elongation factor 1-alpha	0.025029797	0.008466777	0.008732099	0	0.010557168
actin	0.024135876	0.014172649	0	0	0.009577131
cytochrome c oxidase subunit II	0	0	0.033531261	0	0.008382815
beta-tubulin	0.019964243	0.010491441	0	0.002849003	0.008326172
cytochrome b	0	0	0.023052742	0.004273504	0.006831562
no match / unknown	0.02205006	0	0	0	0.005512515
polyA binding protein	0.021454112	0	0	0	0.005363528
beta actin	0	0.018406037	0	0.002849003	0.00531376
NADH dehydrogenase subunit 1	0	0	0.015717779	0.00379867	0.004879112
hypothetical 18K protein	0	0	0.013272791	0.005223172	0.004623991
polyubiquitin	0.007747318	0.003865268	0	0.006647673	0.004565065
RIBOSOMAL PROTEIN SA (P40)	0.017282479	0	0	0	0.00432062
GAPDH	0	0.00496963	0.00523926	0.006647673	0.004214141
calmodulin 2 (phosphorylase kinase, delta)	0.013110846	0	0	0.003323837	0.004108671
no match / unknown	0.012216925	0	0	0	0.003054231
ferritin heavy chain	0	0	0.011526371	0	0.002881593
ribosomal protein S6	0.01102503	0	0	0	0.002756258
ribosomal protein L4	0.010727056	0	0	0	0.002681764
ribosomal protein L3	0.010131108	0	0	0	0.002532777
myelin basic protein	0	0	0	0.00997151	0.002492878
L-lactate dehydrogenase	0	0	0.009779951	0	0.002444988
ribosomal protein L5	0.008343266	0	0	0	0.002085817
no match / unknown	0	0.008282717	0	0	0.002070679
no match / unknown	0.008045292	0	0	0	0.002011323
NADH dehydrogenase subunit 4	0	0	0.007334963	0	0.001833741
RIBOSOMAL PROTEIN P0	0.007151371	0	0	0	0.001787843
membrane glycoprotein	0.007151371	0	0	0	0.001787843
G-protein beta-subunit (RACK)	0.007151371	0	0	0	0.001787843
ELONGATION FACTOR 1-GAMMA	0.007151371	0	0	0	0.001787843
NADH dehydrogenase subunit 2	0	0	0.006985679	0	0.00174642
heat shock 70	0.006853397	0	0	0	0.001713349
ATP synthase beta-subunit	0.006853397	0	0	0	0.001713349
14-3-3 PROTEIN EPSILON (SUPPRESSOR OF RAS1 3-9)	0	0.003865268	0	0.002849003	0.001678568
RIBOSOMAL PROTEIN L7 (or L30P)	0.006555423	0	0	0	0.001638856
DnaJ-like protein	0	0.006258053	0	0	0.001564513
cathepsin L	0	0.006073992	0	0	0.001518498
no match / unknown	0	0	0.005937827	0	0.001484457
ADP/ATP carrier	0	0.005889932	0	0	0.001472483
no match / unknown	0	0	0.005588543	0	0.001397136
adenine nucleotide translocase	0	0	0.005588543	0	0.001397136
NADH dehydrogenase subunit 5	0	0	0.00523926	0	0.001309815
SNAP25	0	0	0	0.005223172	0.001305793
lifeguard, KIAA0950 protein	0	0	0	0.005223172	0.001305793
myosin heavy chain	0	0.00515369	0	0	0.001288423
glutathione S-transferase	0	0.004417449	0	0	0.001104362
Hsc70 (72)-ps1	0	0	0	0.004273504	0.001068376
Y-box protein	0	0.004233389	0	0	0.001058347
no match / unknown	0	0	0.004191408	0	0.001047852

rasputin	0	0.004049328	0	0	0.001012332
heat shock protein 82	0	0.004049328	0	0	0.001012332
no match / unknown	0	0	0.003842124	0	0.000960531
no match / unknown	0	0	0.003842124	0	0.000960531
calmodulin	0	0	0.003842124	0	0.000960531
pyruvate kinase	0	0	0	0.00379867	0.000949668
no match / unknown	0	0	0	0.00379867	0.000949668
CaMK II isoform D	0	0	0	0.00379867	0.000949668
no match / unknown	0	0.003497147	0	0	0.000874287
no match / unknown	0	0.003497147	0	0	0.000874287
CATHEPSIN B PRECURSOR	0	0.003497147	0	0	0.000874287
(Na+,K+)-ATPase-beta-2 (3) subunit	0	0	0	0.003323837	0.000830959
translation initiation factor eIF-4A II	0	0	0	0.002849003	0.000712251
glial fibrillary acidic protein delta	0	0	0	0.002849003	0.000712251
gamma enolase (neural enolase)	0	0	0	0.002849003	0.000712251

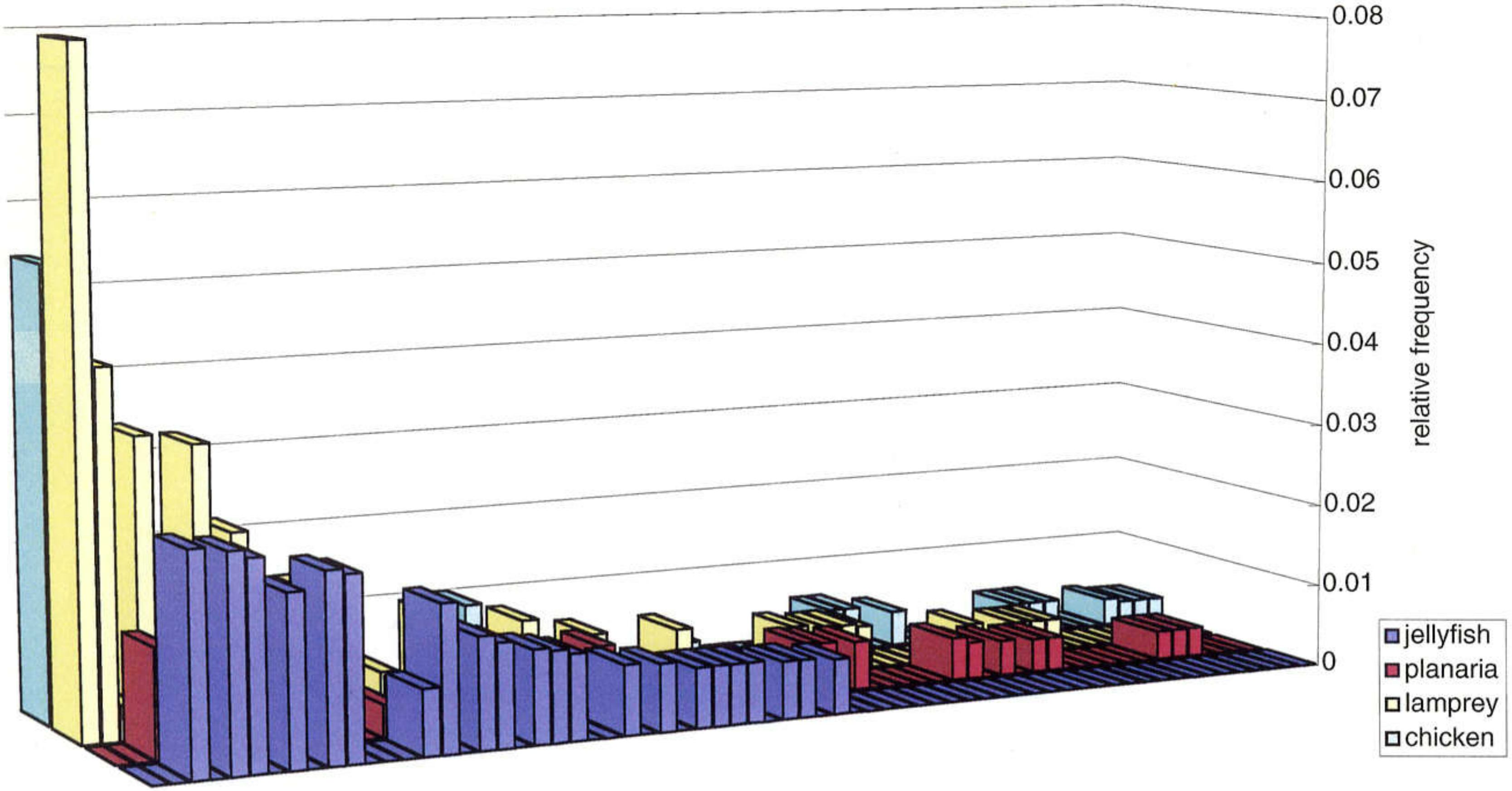


Figure 4.6: The difference among the gene expression profiles (unweighted frequency).

commonly among the chicken and lamprey brain, whereas beta-actin was the most highly expressed in the planarian and beta-tubulin was the most highly expressed in the jellyfish. The cytochrome c oxidase subunit 1 forms the functional core of the enzyme complex that is the component of the respiratory chain catalyzing the reduction of oxygen to water (Alberts *et al.* 1994). Generally, the brain is the one of the organs that consumes the energy so much. The respiratory system produces the energy, so that our finding from the viewpoint of the gene expression profiles is consistent with the previous knowledge. As I mentioned above, from the viewpoint of gene expression profiles, these differences and similarities represent the characteristics of each species. It is of particular interest to see if these differences of the gene expression profiles among different species correspond to the difference of the species.

Correspondence between the gene expression tree and the species tree

Do the differences in the gene expression profiles correspond to the difference in the species? To answer this question, first, we quantified the differences among the gene expression profiles. There are various approaches exploiting the multivariate analysis that determine the difference among the different numerical data sets. In my analysis, I chose an Euclidean distance for the calculation of the difference among the gene expression profiles. Because this is the first attempt to quantify the difference among the gene expression profiles of the distinct organisms from the viewpoint of evolution, the simplicity of the Euclidean distance is suitable for this analysis. Based on the distance matrix obtained, we constructed a phylogenetic tree-like figure (designated as a “gene expression tree”).

We analyzed four different gene expression profiles for the tree construction, thus there are three possible topologies of the gene expression tree; (1) ((jellyfish, planarian), (lamprey, chicken)), (2) ((jellyfish, lamprey), (planarian, chicken)), and (3) ((jellyfish, chicken), (planarian, lamprey)). My assumption was that the topology of the gene expression tree and the species tree should correspond, if the differences of the gene expression profiles correspond to the evolutionary difference of species. Since the topology of the species tree is (1) (Figure 4.7), I expected, the gene expression tree to have a topology of (1). The result obtained was that the topology of the resultant gene expression tree is (1) (Figure 4.8), showing the clear correspondence to the species tree. Thus, the differences in the gene expression profiles among different species correspond to the divergence of the species. Previously, I found the extreme conservation of CNS-related genes among the bilateral animals shown in chapter 2. Since the gene expression profile reflects the outcome of transcriptional regulations of all genes expressed in a given organ, these results suggest that the mechanism of transcriptional regulations changed according to the evolutionary divergence of the species. Generally, the sequence divergence corresponds to the divergence of the species (Zuckerkandl & Pauling 1965). Here, I found that the divergence of the expression profiles, that is, output of the transcriptional regulations, corresponds to the divergence of the species. Thus, it is possible to state that the comparative study of the gene expression profiles of brains among various organisms can be traced for the evolutionary process of the brain.

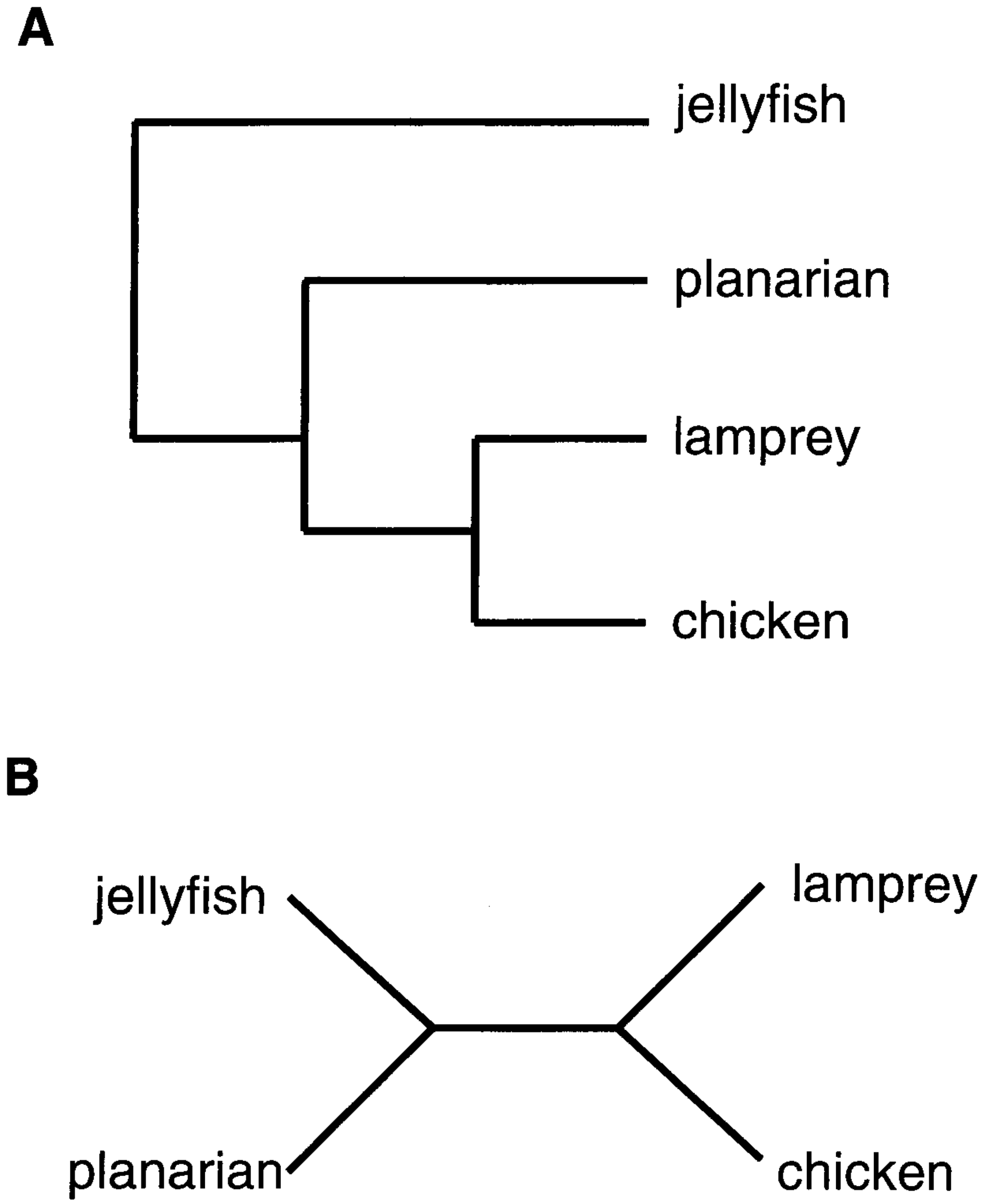


Figure 4.7: Species tree of jellyfish, planarian, lamprey and chicken. (A) rooted tree, (B) unrooted tree. (Modified from Nielsen 2001)

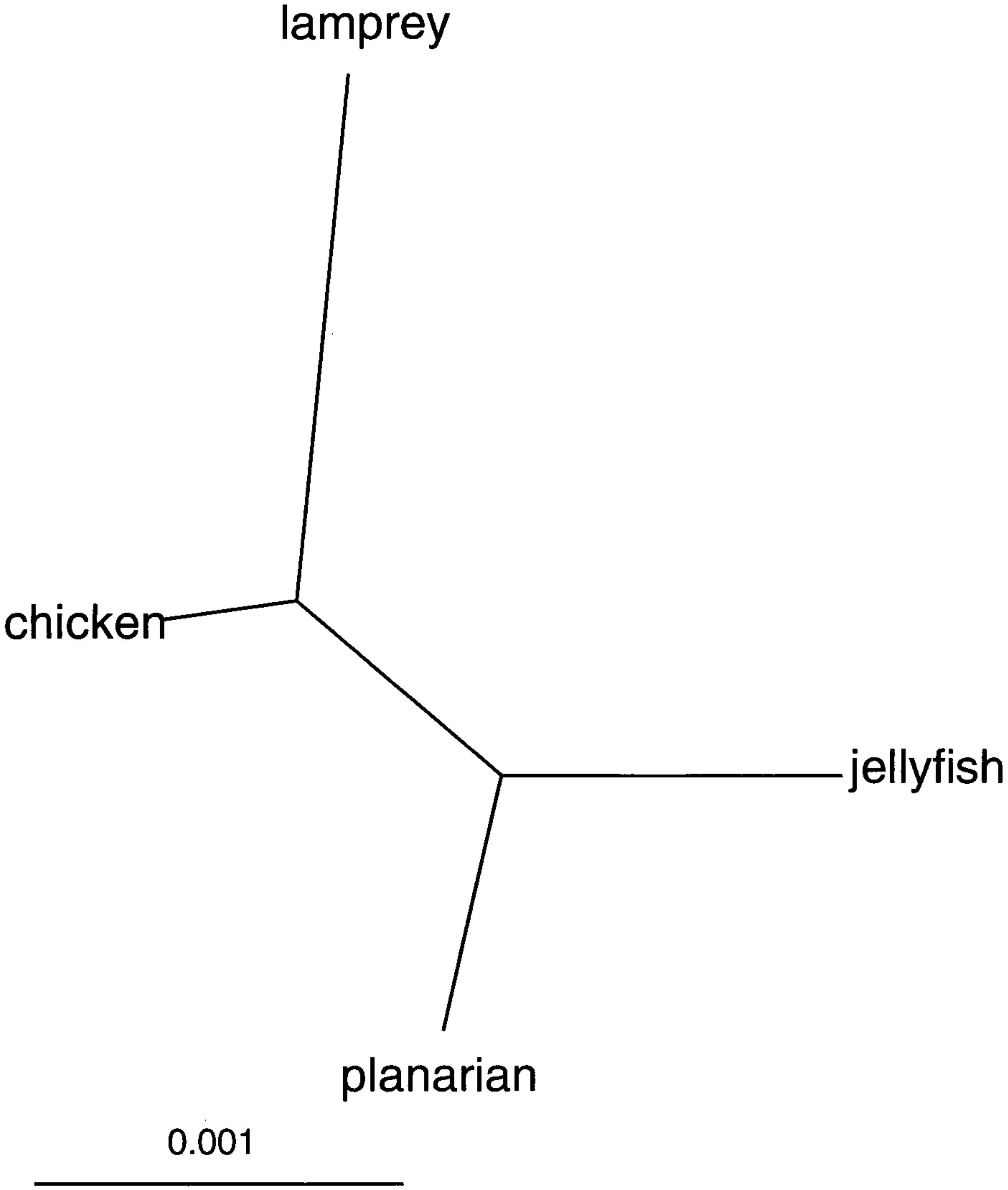


Figure 4.8: GENE EXPRESSION TREE using top20 of highly expressed clones based on the unweighted frequency.

Effect of the house-keeping genes for the topology

Because the majority of the highly expressed clones represented house-keeping functions, a possible explanation for the consistence between the species tree and the gene expression tree may be the effects of house-keeping genes. To examine the effect of the house-keeping genes on my analysis, I first define the house-keeping gene as a gene commonly expressed among the organisms. Then, under this definition, I adopted the weight system of the mRNA frequency for the calculation, utilizing the method of the "Term Frequency-Inversed Document Frequency" (TF-IDF) scoring (See Materials and Methods in this chapter). In this method, less weight is given to the house-keeping genes. By using the TF-IDF scoring, I reconstructed the gene expression tree (Table 4.7, and Figure 4.9). The resultant tree shows the same topology with the gene expression tree of the normal frequency such as ((jellyfish, planarian), (lamprey, chicken)) (Figure 4.10). Therefore, the effect of the house-keeping genes was not a major reason for the consistence between the gene expression tree and the species tree. Even if the house-keeping genes have significant effects, I still thought that the differences of the gene expression profiles are representative outcome of all the transcriptional activities. This is because the genes high in hierarchy of the genetic network which are specific to a particular organ could regulate down stream house-keeping genes. For example, Pax6 is known as the master control gene of the eye development (Gehring 1998). This gene is expected on the top of the hierarchical genetic network of eye development. Though the Pax6 regulates its direct

Table 4.7: List of top 20 clones showing the different freuqencies (TF-IDF)

Genes	jellyfish	planaria	lamprey	chicken	RANK
cytochrome c oxidase subunit I	0	0	0.103609794	0.069808352	0.043354536
cytochrome c oxidase subunit III	0	0	0.055894757	0.015444326	0.017834771
ATP synthase F0 subunit 6	0	0	0.045442892	0.012973234	0.014604031
cytochrome c oxidase subunit II	0	0	0.053719092	0	0.013429773
actin	0.031401499	0.018439041	0	0	0.012460135
alpha-tubulin	0.025625745	0.012884226	0.004191408	0.007122507	0.012455971
elongation factor 1-alpha	0.028156989	0.009524606	0.009823077	0	0.011876168
beta-tubulin	0.02245855	0.011802229	0	0.003204954	0.009366433
cytochrome b	0	0	0.029992309	0.005559957	0.008888066
no match / unknown	0.035325518	0	0	0	0.00883138
polyA binding protein	0.034370775	0	0	0	0.008592694
NADH dehydrogenase subunit 1	0	0	0.025180824	0.006085698	0.007816631
hypothetical 18K protein	0	0	0.021263807	0.008367835	0.00740791
RIBOSOMAL PROTEIN SA (P40)	0.027687568	0	0	0	0.006921892
beta actin	0	0.023946806	0	0.003706638	0.006913361
calmodulin 2 (phosphorylase kinase, delta)	0.017057604	0	0	0.004324411	0.005345504
polyubiquitin	0.008715258	0.004348189	0	0.007478225	0.005135418
no match / unknown	0.019572247	0	0	0	0.004893062
GAPDH	0	0.005590529	0.005893846	0.007478225	0.00474065
ferritin heavy chain	0	0	0.018465938	0	0.004616484
ribosomal protein S6	0.017662759	0	0	0	0.00441569
ribosomal protein L4	0.017185387	0	0	0	0.004296347
ribosomal protein L3	0.016230644	0	0	0	0.004057661
myelin basic protein	0	0	0	0.015974957	0.003993739
L-lactate dehydrogenase	0	0	0.015668068	0	0.003917017
ribosomal protein L5	0.013366412	0	0	0	0.003341603
no match / unknown	0	0.013269409	0	0	0.003317352
no match / unknown	0.01288904	0	0	0	0.00322226
NADH dehydrogenase subunit 4	0	0	0.011751051	0	0.002937763
ELONGATION FACTOR 1-GAMMA	0.011456925	0	0	0	0.002864231
G-protein beta-subunit (RACK)	0.011456925	0	0	0	0.002864231
membrane glycoprotein	0.011456925	0	0	0	0.002864231
RIBOSOMAL PROTEIN P0	0.011456925	0	0	0	0.002864231
NADH dehydrogenase subunit 2	0	0	0.011191477	0	0.002797869
ATP synthase beta-subunit	0.010979553	0	0	0	0.002744888
heat shock 70	0.010979553	0	0	0	0.002744888
RIBOSOMAL PROTEIN L7 (or L30P)	0.010502181	0	0	0	0.002625545
DnaJ-like protein	0	0.010025776	0	0	0.002506444
cathepsin L	0	0.0097309	0	0	0.002432725
no match / unknown	0	0	0.009512756	0	0.002378189
ADP/ATP carrier	0	0.009436024	0	0	0.002359006
adenine nucleotide translocase	0	0	0.008953182	0	0.002238295
no match / unknown	0	0	0.008953182	0	0.002238295
14-3-3 PROTEIN EPSILON (SUPPRESSOR OF RAS1 3-9)	0	0.005028829	0	0.003706638	0.002183867
NADH dehydrogenase subunit 5	0	0	0.008393608	0	0.002098402
lifeguard, KIAA0950 protein	0	0	0	0.008367835	0.002091959
SNAP25	0	0	0	0.008367835	0.002091959
myosin heavy chain	0	0.008256521	0	0	0.00206413
glutathione S-transferase	0	0.007077018	0	0	0.001769255
Hsc70 (72)-ps1	0	0	0	0.00684641	0.001711603
Y-box protein	0	0.006782142	0	0	0.001695536
no match / unknown	0	0	0.006714886	0	0.001678722
heat shock protein 82	0	0.006487267	0	0	0.001621817
rasputin	0	0.006487267	0	0	0.001621817
calmodulin	0	0	0.006155313	0	0.001538828
no match / unknown	0	0	0.006155313	0	0.001538828
no match / unknown	0	0	0.006155313	0	0.001538828
CaMK II isoform D	0	0	0	0.006085698	0.001521424

no match / unknown	0	0	0	0.006085698	0.001521424
pyruvate kinase	0	0	0	0.006085698	0.001521424
CATHEPSIN B PRECURSOR	0	0.005602639	0	0	0.00140066
no match / unknown	0	0.005602639	0	0	0.00140066
no match / unknown	0	0.005602639	0	0	0.00140066
(Na+,K+)-ATPase-beta-2 (3) subunit	0	0	0	0.005324986	0.001331246
translation initiation factor eIF-4A II	0	0	0	0.004564273	0.001141068
gamma enolase (neural enolase)	0	0	0	0.004564273	0.001141068
glial fibrillary acidic protein delta	0	0	0	0.004564273	0.001141068

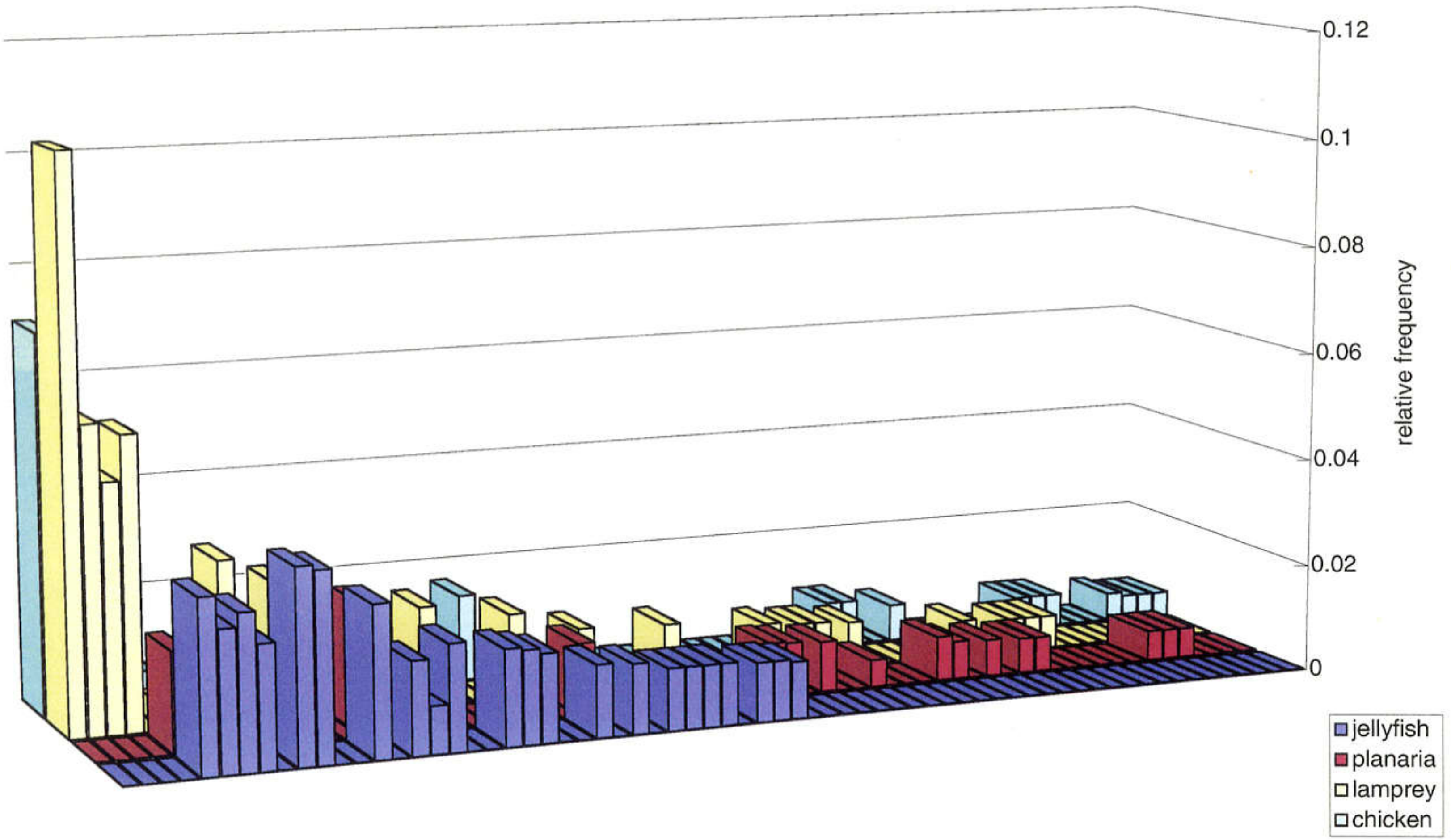


Figure 4.9: The difference among the gene expression profiles (weighted frequency by TF-IDF method).

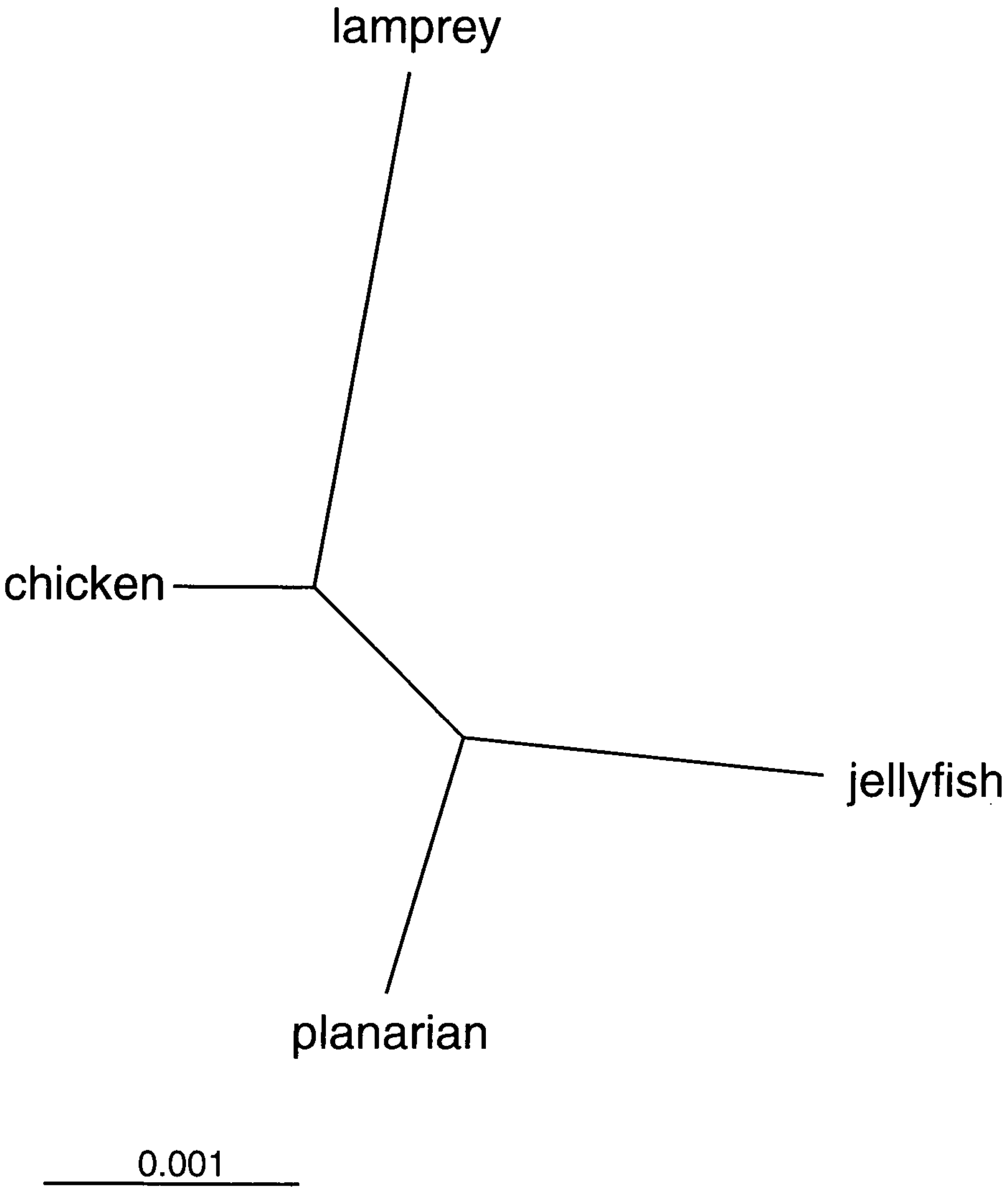


Figure 4.10: GENE EXPRESSION TREE using top20 of highly expressed clones based on the weighted frequency (TF-IDF method).

down stream genes, the signal of the Pax6 linked to the lower parts of that hierarchical network. Some of the lower part of the network might be house-keeping genes such as cytoskeltal genes because it is necessary for the construction of the eye formation.

Problems in the comparative studies of ESTs

When we took an approach of the EST sequencing to compare the different libraries, there is a question whether these ESTs includes all the transcripts *in vivo* or not. The number of ESTs used in this study appears not to be saturated at the current status (data not shown). When we compare the expression profiles of different libraries, this incompleteness may cause some problems (Audic & Claverie, 1997). For example, in the case of genes which did not turn up, we cannot tell whether they are not expressed or simply not detected. Further complication could arise if we obtain different parts of a particular single cDNA. Our ESTs were sequenced from the 5' end of the multi-cloning site and some clones were derived from the same cDNA even if these were clustered into different clones. However, most clones, particularly highly expressed clones, should reflect, at large, the expression pattern *in vivo*, because we took a random sampling method of clone picking. Thus, in the present analysis, we used only top 20 highly expressed clones in order to avoid such problems. As I showed earlier, the comparative analysis of the composition of top 20 clones exhibited the characteristics of each species such as the expression frequency of the gene of cytochrome c oxidase subunit 1 (Table 4.6). This result justified my approach of focusing on the top 20 clones for the comparative study.

At the present, there is a limitation in undertaking a comparative approach of the gene expression profiles. That is, very restricted number of EST data are available that contain the occurrence frequency of each clone, for example, a BODYMAP (Okubo *et al.* 1992). On the other hands, the large-scale expression data by the cDNA microarray method have been produced rapidly, because the method is much more convenient compared to the EST sequencing. Therefore, I would like to combine both gene expression data derived from the cDNA microarray and EST sequencing in the future studies.

Conclusion

In the present study, I found that the divergence of the expression profiles corresponds to the divergence of the species. The highly expressed clones in the expression profiles clearly showed the distinct patterns corresponding to the morphological differences that might be acquired during the evolutionary process of the brain. Although the numbers of the sequenced clone and species are restricted, the results showed the correspondence between the species tree and gene expression tree in the present study. Thus, it is possible to state that the comparative study of the gene expression profiles of brains among various organisms, in part, can trace the evolutionary process of the brain, and thus we have obtained a new measure for the analysis of the evolution other than the degree of the sequence divergence called as a molecular clock.

Finally, before this study, it was difficult to study the evolutionary divergence at the level of the organs, tissues and cells, except for the analysis based on a single gene such as homeobox genes. We believe that the study of gene expression profile might open the door for a new insight in the evolutionary study.

CHAPTER 5

CONCLUSION

In this thesis, I examined the gene expression profiles of the jellyfish, planarian, ascidian, lamprey, and chicken in order to understand the evolutionary process of the brains from the viewpoint of the gene expression profiles. My research of the gene expression profiles was performed at the following levels; (1) genes, (2) cells, and (3) organs. In these studies, I found that (1) CNS-related gene set is extremely conserved from the common ancestor of CNS, (2) 89% of the genes expressed in the ascidian otolith and ocellus cells were not shared by them, and (3) divergences in the gene expression profiles of brain among distinct animals correspond to the diversification of the species. Thus, I conclude that the gene expression profile can understand the evolutionary process of CNS, in particular a brain.

Based on the above findings, I assume that the CNS, in particular brain, might evolve as following process; first, there is no specific genes functioned on the CNS such as the genes in *S. cerevisiae* and *A. thaliana*. Second, the genes were recruited into the system used by the CNS, possibly accompanied by the change of the gene usage such as the change of the transcriptional regulations. Moreover, the differentiation of the cell types used in the CNS had occurred. As a consequence, the gene set related to the CNS functions had emerged in the common ancestral CNS, which is on the root of the bilateral animals. Third, utilizing those gene set, species-dependent gene duplication or gene loss might occur to sophisticate the CNS functions specific to the species. The genes used in the system of CNS must have flexibility such as the noggin genes or chordin genes in the neural tissue induction system. In particular, the change of the system of the transcriptional regulation used in the brain might occur gradually such as the evolutionary divergence of sequences. Thus, the differences in the gene expression profiles of brains well correspond to the evolutionary divergences of the species.

Finally, until this study, it is difficult to study the evolutionary divergence at the level of the organs, tissues and cells, except for the analysis based on a single gene (s) such as homeobox genes. I believe that the comparison based on the gene expression profile might open the door for a new insight in the evolutionary study.

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Appendix A

Computer analysis and Its Useful Tools, FinEST, for the Comparative Studies in In-House EST projects

Summary

As the capacity of the nucleotide sequence determination increases, the EST analysis becomes increasingly important. The EST contains two important information; the tag of each gene and the data of the expression of genes. From the viewpoint of the study for gene expression profile, I have developed a novel EST analyzing tool, designated as FinEST. The FinEST is an EST analyzing software package that includes a sequence editing, a removal of redundancy, an annotation based on the homology search, and a comparison among different EST data. Thus, FinEST can easily manage the whole repertoire of EST analyses. Moreover, FinEST is able to perform the comparison not only within the same species but also between the different species, which may provide a new insight from the viewpoint of the gene expression profile. Our approach using FinEST gives a new aspect to analyze EST data and gene expression profiles for the post genomic studies.

Introduction

The expressed sequence tags (ESTs) provide us the status of active genes and seeds of identification of genes. Thus, for the study of variations, structures and localizations of molecules that consist of a cell and a tissue, the approach of the EST sequencing is very useful. Recently, because of the improvement of the sequencing capacity, EST sequencing is performed at many places, even if in small laboratories. It is often true that there exists a difficulty of data management when the mass amount of data is produced in a small laboratory without any computational assistance. Therefore, I developed an integrated EST data analyzing system, designated as **FinEST** (Full-automatic in-house EST analyzing software), by which one can easily manage the ESTs during the whole processes of EST sequencing.

Biologically, genes expressed in tissues or cells can be roughly divided into two categories: (1) the genes having housekeeping function and (2) the genes having specific function in each cell or tissue. From the housekeeping genes, we expect to get the common feature of living cell or tissue, while, from the specific genes, we can obtain the insights about the cell or tissue-specific structure and function. As previous studies reported, particular genes were studied and discussed on their functions in the cell or tissue. However a whole set of genes is expressed in a particular tissue rather than particular genes. Thus to analyze the properties of a tissue or a cell, it would be better to consider all genes expressed in a particular tissue or cell, rather than to focus on a single gene. The EST data contained the gene species expressed in a particular tissue or cell and the occurrence frequency of the mRNAs. The gene expression profile is defined as both aspects of EST data. Thus, we should study the gene expression profile from a viewpoint of whole expressed genes. The FinEST provides an easy way to perform comparative analyses of EST data. Namely, the FinEST has two major features: (1) integrated tools for the EST analysis and (2) assistance for the comparison of the gene expression profiles.

Systems

An Integrated system: FinEST

I developed a tool designated as FinEST for the assistance of the EST analysis. FinEST runs under the system of java (JDK 1.1 or higher), which allows it to run on multi-platforms with CORBA (Common Object Request Broker Architecture; Siegel 2000) based server-client system. Managing from the output of sequencer to the construction of database (Figure A.1), the FinEST integrated external programs such as blast (Altschul *et al.* 1997), fasta (Pearson & Lipman 1988), phred (Ewing *et al.* 1998; Ewing & Green 1998). All these programs were integrated into one interface (Figure A.2), so the programs are used seamlessly for the automatic EST analysis and also separately focusing on a certain specific function. In particular, the algorism for the removal of redundancy from EST data is one of the difficult tasks (Bouck *et al.* 1999). In the case of FinEST, EST clusters derived from the same mRNA are constructed by use of the results of simple homology searches.

Another feature of the FinEST is a comparative analysis of EST data. In this part, we integrated two tools, one is for the search of similar (or orthologous) sequence pairs by the reciprocal matching method (Watanabe *et al.* 1997), and the other is for the combination between different expression data based on the similar sequence pairs. Using these features, we can manage and compare the EST data not only within the same species but also between the different species. Finally, I also integrated additional functions to assist and enhance the submission of ESTs to public databases. Using this function, analyzed EST data produced by FinEST is easily converted into the DDBJ mass-submission form following the description of DDBJ (http://www.ddbj.nig.ac.jp/).

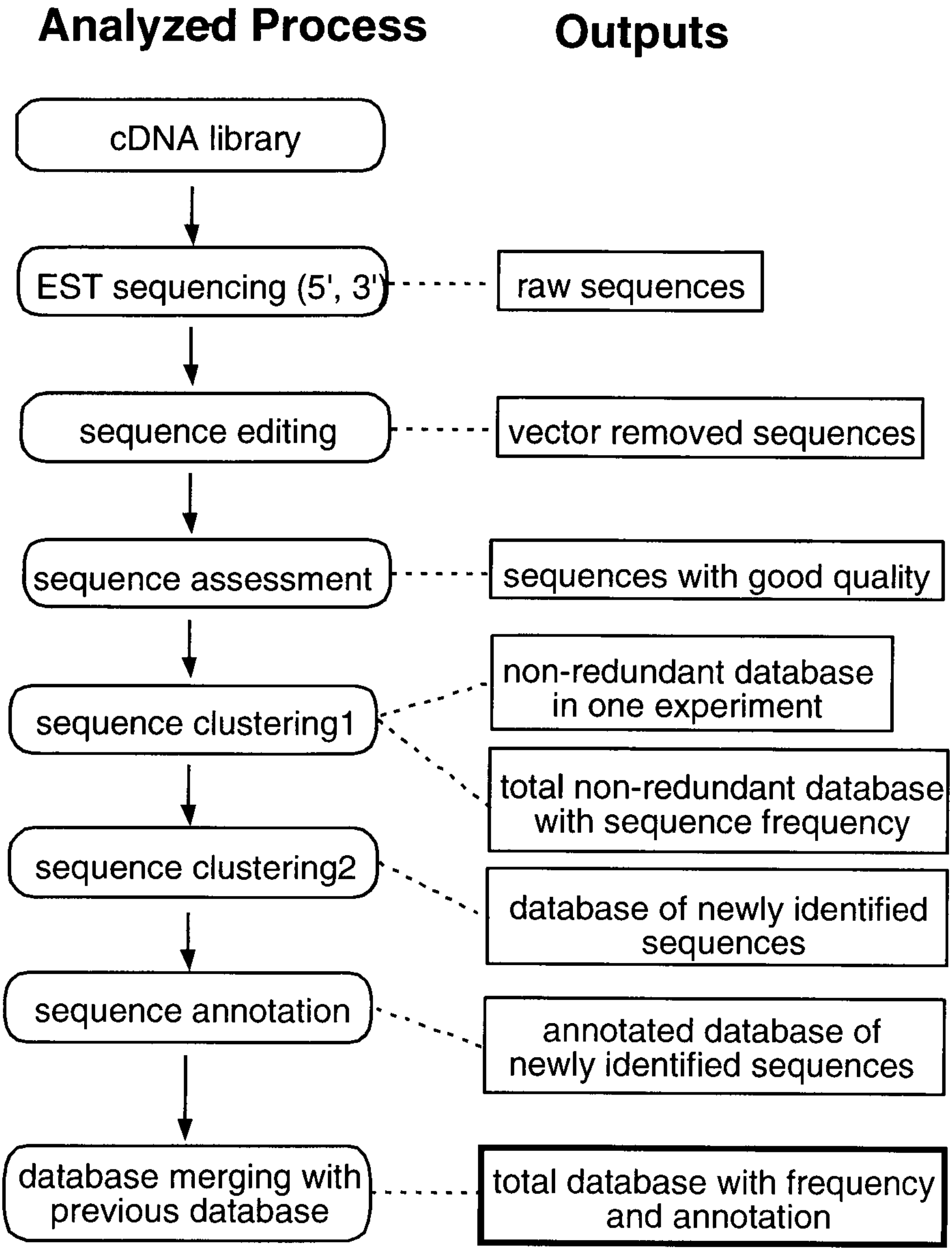

Figure A.1: The schematic flow of the EST analysis integrated into the FinEST. The daily updated data is analyzed through this scheme. Especially, the clustering of EST data is oriented for the daily updating.

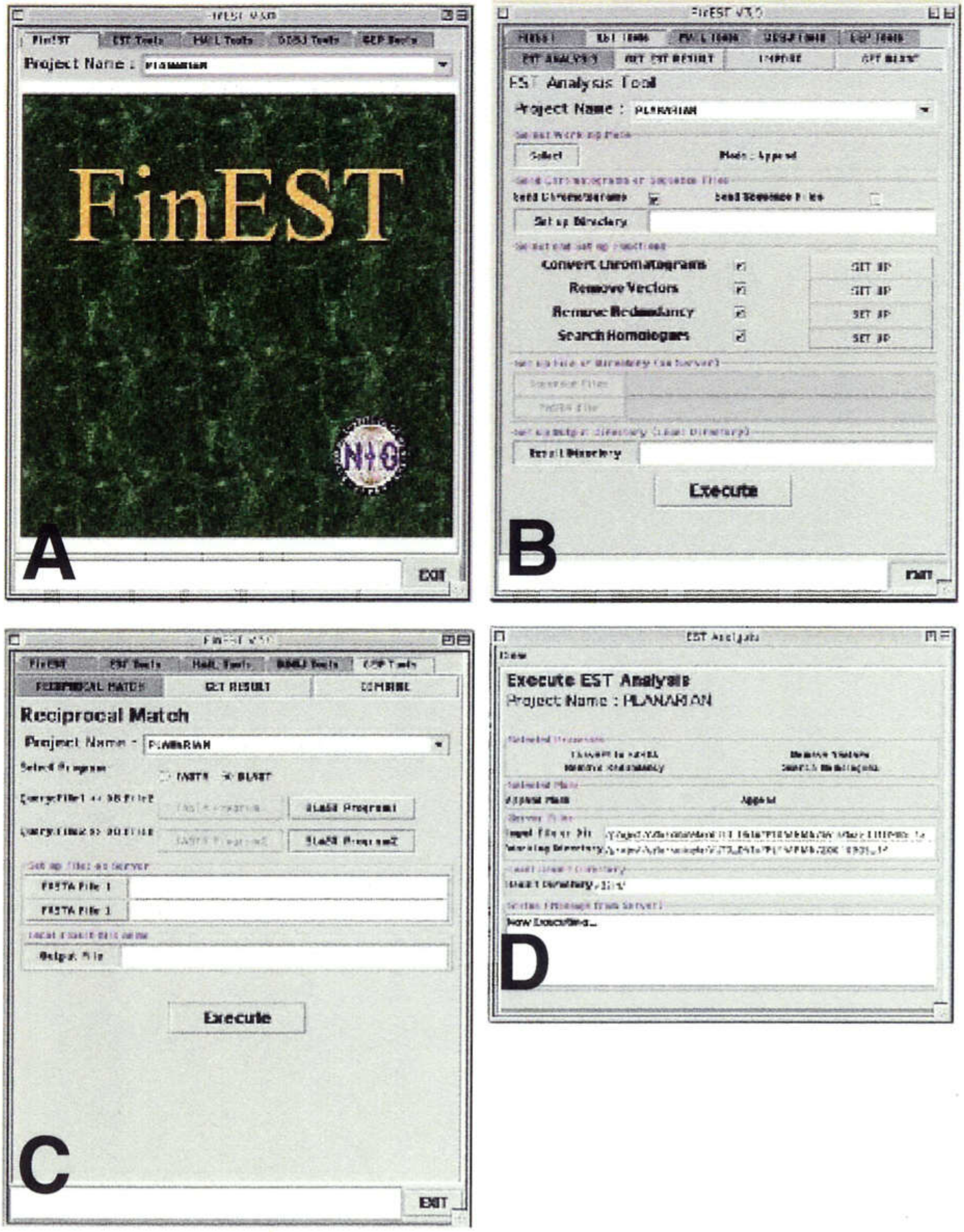

Figure A.2: The representative windows of the FinEST. (**A**) The initial window of the FinEST. From the top of the window, we can select a project to be analyzed. The tablature at the top of main window corresponds to each tools integrated. (**B**) The one of the windows of comparative tools. We select two fasta-formatted file from the server-side, and then the similar (orthologous) sequence pairs were outputted. (**C**) The main window of FinEST showing a systematic EST analysis section. Integrated main functions are selected by the check box at the right side of the each name of functions. Once click the execute button at the bottom of the window, analyses will be done sequentially from top to bottom of the selected functions. (**D**) The window of analyzing status. When we are analyzing a data, the status of the analysis can be seen through this window.

Because most of projects analyzed their EST by their own method such as the threshold of sequence qualities or the editing of obtained raw sequences, it is difficult to use in the comparative study of ESTs. For the further analysis, it is better to use the same protocols among the analyses of ESTs. FinEST may be one of the possible candidates to standardize the EST analysis.

Conclusion

I reported the new EST analyzing tool, FinEST. By use of the FinEST, one can not only collect and create any kinds of EST data, but also perform the comparison among them. Especially, the comparison of EST data (gene expression profiles) is one of the next targets in post genomic studies (as shown in this thesis). Thus, I am convinced that the FinEST would provide a chance to all scientists to study and analyzes EST data, and obtain novel biological findings.

APPENDIX B

List of EST clones derived from head portions of planarians

Summary

As I showed in the Chapter 2, we sequenced EST clones from planarian head cDNA library. Here, I attached the whole list of the sequenced clones that was used in this thesis (Table B.1). The list contains 3,101 of a total of non-redundant clones with their frequency and annotation. The methods and results were described on chapter 2.

Table B.1: List of ESTs derived from the planarian head

clone ID	frequency	accession No.	homologous sequence which showed the highest E-value	Score	Identity(%)	E-value
00001_HN	27	AAB52408.1	(U75511) glyceraldehyde-3-phosphate dehydrogenase [Schistosoma japonicum]	250	72	9.00E-66
00002_HN	32	AAC23561.1	(AF049130) ADP/ATP carrier [Trypanosoma brucei brucei]	202	64	2.00E-51
00004_HH	2	NP_036232.1	aspartyl aminopeptidase gb|AAD01211.2| (AF005050) aspartyl aminopeptidase [Homo sapiens]	101	53	4.00E-38
00005_HN	1	NP_062616.1	ribophorin dbj|BAA06525.1| (D31717) ribophorin [Mus musculus]	94	35	9.00E-19
00007_HN	19	AAB49628.1	(U65312) RNA-dependent RNA polymerase [Avian pneumovirus]	32.5	35	3.1
00008_HH	3	AAD32867.1	AC005489_5 (AC005489) F14N23.5 [Arabidopsis thaliana]	73	38	1.00E-26
00008_HN	100	AAC32808.1	(AF043384) beta actin [Pleuronectes americanus]	215	96	8.00E-60
00011_HN	1	D64385	aspartate transaminase (EC 2.6.1.1) - Methanococcus jannaschii	37.9	23	0.07
00013_HN	7	AAC62254.1	(AF006678) lysophospholipase homolog [Schistosoma mansoni]	170	55	7.00E-42
00014_HN	1	AC007391.3	AC007391 Homo sapiens clone RP11-429J10, complete sequence	42.1	100	0.22
00018_HN	12	AAF23824.1	AF220040_1 (AF220040) cathepsin D precursor [Drosophila melanogaster] gb|AAF59186.1| (AE003839) CG1548 gene product [Drosophila melanogaster]	205	61	3.00E-52
00021_HN	1	AAG01299.1	(AF274609) maturase K [Choristylis rhamnoides]	33.6	24	1.4
00022_HN	1	AAF49430.1	(AE003526) CG3971 gene product [Drosophila melanogaster]	73.4	39	1.00E-12
00024_HN	2	BAA91354.1	(AK000741) unnamed protein product [Homo sapiens]	69.9	33	2.00E-11
00027_HN	1	P41239	CSK_CHICK TYROSINE-PROTEIN KINASE CSK (C-SRC KINASE) pir||A41973 protein-tyrosine kinase (EC 2.7.1.112) CSK - chicken (fragment) gb|AAA51436.1| (M85039) src kinase [Gallus gallus]	127	39	8.00E-29
00028_HH	9	T32546	hypothetical protein ZC416.6 - Caenorhabditis elegans gb|AAB88369.1| (AF036701) similar to the peptidase family M1 (zinc metalloproteases) [Caenorhabditis elegans]	74.1	52	4.00E-39
00029_HN	10	T23759	hypothetical protein M117.2 - Caenorhabditis elegans emb|CAA98138.1| (Z73910) predicted using Genefinder~Identity to C.elegans 14-3-3-like protein (SW:1433_CAEEL)~cDNA EST EMBL:T00100 comes from this gene; cDNA EST EMBL:T01097 comes from this gene~cDNA EST yk61d1.3 comes from this gene; cDNA EST yk67f7.3 comes from this>	186	65	1.00E-46
00030_HN	8	AAD55420.1	AF181634_1 (AF181634) BcDNA.GH06451 [Drosophila melanogaster] gb|AAF53768.1| (AE003661) BcDNA:GH06451 gene product [Drosophila melanogaster]	104	38	5.00E-22
00031_HH	3	NP_005207.1	dolichyl-diphosphooligosaccharide-protein glycosyltransferase dbj|BAA23670.1| (D89060) oligosaccharyltransferase [Homo sapiens]	205	61	3.00E-52
00033_HN	1	CAB95845.1	(AJ297352) leucine zipper transcription factor-like 1 [Mus musculus]	157	52	7.00E-38
00034_HN	1	AAC60216.1	(U77351) smooth muscle protein phosphatase type 1-binding subunit [Gallus gallus]	43.4	31	0.002
00037_HH	2	NP_009215.1	protein tyrosine kinase 9-like (A6-related protein) emb|CAB38055.1| (Y17169) A6 related protein [Homo sapiens] emb|CAB66707.1| (AL136773) hypothetical protein [Homo sapiens]	109	43	4.00E-25
00038_HH	2	P19889	RLA0_DROME 60S ACIDIC RIBOSOMAL PROTEIN P0 (DEOXYRIBONUCLEASE (APURINIC OR APYRIMIDINIC)) (APURINIC-APYRIMIDINIC ENDONUCLEASE) pir||R5FFP0 acidic ribosomal protein P0 - fruit fly (Drosophila melanogaster) gb|AAA53372.1| (M25772) DNA repair protein [Drosophila melanogaster] gb|AAF51807.1| (AE003596) RpP0 gene product [Drosophila melanogaster]	124	49	4.00E-39
00038_HN	1	NP_055248.1	rhabdoid tumor deletion region protein 1 gb|AAF02484.1|AF133587_1 (AF133587) rhabdoid tumor deletion region protein 1 [Homo sapiens]	97.1	40	1.00E-19
00039_HH	45	AAF46666.1	(AE003452) CG10527 gene product [Drosophila melanogaster]	106	39	2.00E-22
00039_HN	1	CAB44334.1	(Y17462) cysteine conjugate beta-lyase [Fugu rubripes]	155	49	2.00E-37
00041_HN	1	AAF46292.1	(AE003442) CG1514 gene product [Drosophila melanogaster]	33.6	38	1.4
00042_HN	3	AAF48863.1	(AE003509) CG15040 gene product [Drosophila melanogaster]	40.6	22	0.011
00043_HH	1	O61305	DB80_DROME DEAD-BOX HELICASE DBP80 gb|AAC23709.1| (AF005239) DEAD-box helicase [Drosophila melanogaster]	143	44	9.00E-34
00046_HH	1	NP_055683.1	ring finger protein 10 dbj|BAA13392.1| (D87451) Contains C3HC4 type zinc finger signature [Homo sapiens]	41.4	27	0.006
00046_HN	1	NP_005871.1	HIRA interacting protein 4 (dnaJ-like) emb|CAA04669.1| (AJ001309) DnaJ protein [Homo sapiens]	167	53	6.00E-41
00049_HN	1	AAA51410.1	(M81742) branched chain alpha-keto acid dehydrogenase E1-beta subunit [Bos taurus]	168	57	4.00E-41
00050_HH	21	BAA76676.1	(AB021974) polyubiquitin [Bombyx mori]	169	97	9.00E-80
00051_HH	3	NP_057117.1	CGI-90 protein gb|AAD34085.1|AF151848_1 (AF151848) CGI-90 protein [Homo sapiens]	75.3	38	3.00E-18
00053_HN	70	A48433	tubulin alpha chain - fluke (Schistosoma mansoni) gb|AAA29918.1| (M80214) alpha tubulin [Schistosoma mansoni]	300	90	5.00E-81
00059_HH	7	AAD52675.1	AF178958_1 (AF178958) Rho family GTPase RhoA [Mus musculus] gb|AAD52676.1|AF178959_1 (AF178959) Rho family GTPase RhoA [Mus musculus] gb|AAD52677.1|AF178960_1 (AF178960) Rho family GTPase RhoA [Mus musculus] gb|AAD52678.1|AF178961_1 (AF178961) Rho family GTPase RhoA [Mus musculus]	198	96	2.00E-73
00059_HN	1	AAG09720.1	AF225418_1 (AF225418) lipase [Homo sapiens]	44.5	28	7.00E-04
00061_HH	1	AAF46710.1	(AE003453) CG10074 gene product [Drosophila melanogaster]	33.6	42	1.4
00063_HN	1	CAB54244.1	(Z30215) cDNA EST yk528c6.5 comes from this gene~cDNA EST yk549e8.5 comes from this gene~cDNA EST yk598f7.5 comes from this gene [Caenorhabditis elegans]	36.7	27	0.16
00064_HH	1	AAA19672.1	(L21838) tektin B1 [Strongylocentrotus purpuratus]	75.3	42	3.00E-31
00067_HH	5	AAD29248.1	AF101065_1 (AF101065) intermediate filament gliarin [Hirudo medicinalis]	125	49	7.00E-31
00067_HN	2	CAA21832.1	(AL033125) 1-evidence=predicted by content~1-method=genefinder;084~1-method_score=36.92~1- evidence_end~2-evidence=predicted by match~2-match_accession=SWISS-PROT:P26351~2- match_description=THYMOSIN BETA-11.~2-match_species=ONCORHYNCHUS MYKISS (RAINBOW > gb|AAF45919.1| (AE003430) EG:EG0007.11 gene product [alt 1] [Drosophila melanogaster] gb|AAF45920.1| (AE003430) EG:EG0007.11 gene product [alt 2] [Drosophila melanogaster]	62.5	50	2.00E-09
00068_HH	2	AAF43627.1	AF199022_1 (AF199022) tetratricopeptide repeat protein 2 [Drosophila melanogaster] gb|AAF53540.1| (AE003651) CG4599 gene product [Drosophila melanogaster]	49.6	33	2.00E-05
00068_HN	77	AAD11530.1	(U52519) actin [Girardia tigrina]	336	99	1.00E-91
00069_HN	3	BAA05648.1	(D26601) protein kinase [Nicotiana tabacum]	125	43	3.00E-28
00070_HH	1	C71129	probable reverse gyrase - Pyrococcus horikoshii dbj|BAA29893.1| (AP000003) 1624aa long hypothetical reverse gyrase [Pyrococcus horikoshii]	34.8	27	0.61

00070_HN	2	AAF60546.1	(AC006757) contains similarity to Plasmodium falciparum guanidine nucleotide exchange factor (GB:AF048836) [Caenorhabditis elegans]	79.2	39	3.00E-14
00071_HN	3	P12001	RL18_RAT 60S RIBOSOMAL PROTEIN L18 pir||R5RT81 ribosomal protein L18 - rat gb|AAA42070.1| (M20156) ribosomal protein L18 [Rattus norvegicus]	152	60	3.00E-42
00073_HH	1	B26696	hypothetical protein 1 (CYb-COII intergenic region) - Leishmania tarentolae mitochondrion (fragment) gb|AAA96601.1| (M10126) NH2 terminus uncertain [Leishmania tarentolae]	41	30	0.008
00074_HH	1	AAF46505.1	(AE003447) CG2996 gene product [Drosophila melanogaster]	41	48	0.008
00075_HH	1	AAD56725.1	(AF124727) acinusS [Homo sapiens]	73.4	26	1.00E-12
00077_HH	3	AAF58910.1	(AE003832) Uba1 gene product [Drosophila melanogaster]	154	44	5.00E-37
00078_HN	2	P47321	Y075_MYCGE HYPOTHETICAL PROTEIN MG075 pir||C64208 hypothetical protein MG075 - Mycoplasma genitalium gb|AAC71293.1| (U39688) 116 kDa surface antigen [Mycoplasma genitalium]	33.2	24	1.8
00079_HN	1	NP_034292.1	exostoses (multiple) 1 emb|CAA65443.1| (X96639) responsible for hereditary multiple exotosis [Mus musculus]	50	38	2.00E-05
00081_HH	1	NP_005868.1	splicing factor 3a, subunit 1, 120kD sp|Q15459|S114_HUMAN SPLICEOSOME ASSOCIATED PROTEIN 114 (SAP 114) (SF3A120) pir||S60735 splicing factor SF3a 120K chain - human emb|CAA59494.1| (X85237) human splicing factor [Homo sapiens] gb|AAC23435.1| (AC004997) spliceosome associated protein 114 (SF3a) [Homo sapiens]	88.9	76	3.00E-17
00081_HN	1	AAF50022.1	(AE003544) CG7319 gene product [Drosophila melanogaster]	37.5	31	0.034
00082_HH	1	NP_064637.1	P38 gb|AAG01277.1|AF246223_2 (AF246223) P38 [Mycoplasma virus P1]	31.7	28	5.3
00084_HH	18	S37144	tubulin beta chain - winter flounder emb|CAA52604.1| (X74492) B-tubulin [Pleuronectes americanus]	342	98	1.00E-93
00086_HH	9	P42649	1432_ENTHI 14-3-3 PROTEIN 2 (14-3-3-2) gb|AAA80186.1| (U13419) 14-3-3-2 protein [Entamoeba histolytica]	200	59	6.00E-51
00086_HN	1	NP_005122.1	nuclear matrix protein p84 pir||A53545 protein p84 - human gb|AAA53571.1| (L36529) protein p84 [Homo sapiens]	116	35	2.00E-25
00087_HN	1	NP_036518.1	p95 paxillin-kinase linker gb|AAD38496.1|AF112366_1 (AF112366) p95 paxillin-kinase linker [Homo sapiens]	104	37	8.00E-22
00088_HH	1	NP_036313.1	FK506-binding protein 8 (38kD) sp|Q14318|FK38_HUMAN 38 KDA FK-506 BINDING PROTEIN HOMOLOG (FKBPR38) gb|AAB00102.1| (L37033) FK-506 binding protein homologue [Homo sapiens] gb|AAC28753.1| (AC005387) FK-506 binding protein homologue [Homo sapiens]	64.8	38	5.00E-10
00088_HN	3	T27227	hypothetical protein Y57G11C.15 - Caenorhabditis elegans emb|CAB16516.1| (Z99281) similar to protein transport protein SEC61 alpha subunit~cDNA EST yk42b1.3 comes from this gene~cDNA EST yk112e4.3 comes from this gene~cDNA EST yk42b1.5 comes from this gene~cDNA EST yk98e9.3 comes from this gene~cDNA EST yk111h12.3 comes fro>	281	83	4.00E-75
00089_HH	1	E71622	probable membrane associated protein PFB0125c - malaria parasite (Plasmodium falciparum) gb|AAC71815.1| (AE001374) predicted membrane associated protein [Plasmodium falciparum]	32.8	22	2.3
00090_HN	1	NP_037417.1	nucleolar GTPase sp|Q13823|NGP1_HUMAN AUTOANTIGEN NGP-1 gb|AAC37588.1| (L05425) nucleolar GTPase [Homo sapiens]	139	49	2.00E-32
00091_HH	2	NP_036565.1	splicing factor 3b, subunit 1, 155kD gb|AAC97189.1| (AF054284) spliceosomal protein SAP 155 [Homo sapiens]	273	77	6.00E-73
00091_HN	12	7ODC	A Chain A, Crystal Structure Ornithine Decarboxylase From Mouse, Truncated 37 Residues From The C-Terminus, To 1.6 Angstrom Resolution	150	46	7.00E-36
00092_HH	3	NP_035249.1	proliferation-associated protein 1 sp|P50580|PLS1_MOUSE PROLIFERATION-ASSOCIATED PROTEIN 1 (PROTEIN P38-2G4) gb|AAB60513.1| (U43918) proliferation-associated protein 1 [Mus musculus]	129	44	1.00E-29
00092_HN	1	CAB84423.1	(AL162755) putative outer-membrane receptor protein [Neisseria meningitidis]	30.9	26	9.1
00093_HH	3	NP_015512.1	Transcription factor IIIA (TFIIIA) with putative Zn-fingers; Pzf1p sp|P39933|TF3A_YEAST TRANSCRIPTION FACTOR IIIA (TFIIIA) pir||S20050 transcription factor IIIA - yeast (Saccharomyces cerevisiae) gb|AAB08014.1| (M80611) transcription factor IIIA [Saccharomyces cerevisiae] gb|AAB64615.1| (U25841) Transcription factor TFIIIA (PIR accession number S20050) [Saccharomyces cerevisiae]	35.6	26	0.35
00094_HH	9	D78307.1	D78307 Chlorella virus DNA for DNA binding protein, complete cds	46.1	96	0.014
00094_HN	2	NP_034429.1	GM2 ganglioside activator protein sp|Q60648|SAP3_MOUSE GANGLIOSIDE GM2 ACTIVATOR PRECURSOR (CEREBROSIDE SULFATE ACTIVATOR PROTEIN) (SHINGOLIPID ACTIVATOR PROTEIN 3) (SAP-3) gb|AAA61929.1| (L19526) GM2 activator protein [Mus musculus] gb|AAB06275.1| (U34359) GM2 activator protein [Mus musculus]	75.7	30	3.00E-13
00095_HH	8	AAA74394.1	(U30456) heat shock cognate protein [Urechis caupo]	305	86	1.00E-82
00096_HH	1	Q27778	K6PF_SCHMA 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) gb|AAA29911.1| (L31531) phosphofructokinase [Schistosoma mansoni]	199	59	2.00E-50
00096_HN	1	AAF47924.1	(AE003482) Rpd3 gene product [Drosophila melanogaster]	259	73	1.00E-68
00097_HN	1	BAA34527.1	(AB018350) KIAA0807 protein [Homo sapiens]	62.1	39	4.00E-09
00098_HH	1	NP_003745.1	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) sp|O00303|IF35_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 5 (EIF-3 EPSILON) (EIF3 P47) gb|AAD03467.1| (U94855) translation initiation factor 3 47 kDa subunit [Homo sapiens]	152	46	2.00E-36
00099_HH	1	AAF50079.1	(AE003545) CG6199 gene product [Drosophila melanogaster]	73.4	29	1.00E-12
00100_HH	1	S37775	filamin, muscle - human (fragment) emb|CAA49689.1| (X70084) filamin [Homo sapiens]	210	60	8.00E-54
00101_HH	3	T16428	hypothetical protein F52E4.1 - Caenorhabditis elegans gb|AAB54030.1| (U56964) Similar to propionyl-CoA carboxylase beta; coded for by C. elegans cDNA yk74f9.5; coded for by C. elegans cDNA yk51d4.5; coded for by C. elegans cDNA yk90b1.5; coded for by C. elegans cDNA yk104d12.5; coded for by C. elegans cDNA yk82f4.5; cod>	154	69	6.00E-37
00102_HH	1	NP_048219.1	ORF MSV148 putative DNA helicase (vaccinia A18R), similar to SW:P20534 gb|AAC97786.1| (AF063866) ORF MSV148 putative DNA helicase (vaccinia A18R), similar to SW:P20534 [Melanoplus sanguinipes entomopoxvirus]	35.6	27	0.35
00103_HH	19	P07688	CATB_BOVIN CATHEPSIN B PRECURSOR	246	63	1.00E-64
00104_HH	2	AAF58126.1	(AE003810) CG8186 gene product [Drosophila melanogaster]	216	71	9.00E-56
00104_HN	1	T28670	hypothetical protein - Salmonella choleraesuis emb|CAA68056.1| (X99719) orf2; similarity to adenine methylase; putative [Salmonella enterica]	36	32	0.27

00105_HN	18	P29520	EF1A_BOMMO ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) pir||S35513 translation elongation factor eEF-1 alpha chain - silkworm dbj|BAA02601.1| (D13338) elongation factor 1 alpha [Bombyx mori]	312	94	2.00E-84
00107_HH	9	BAA89018.1	(AB028237) TAA stop codon is completed by the addition of 3' A residues to the mRNA [Pupa strigosa] gnl|NCBI_MITO|ND1_15272 NADH dehydrogenase subunit 1	150	48	1.00E-35
00108_HN	6	AAD41942.1	AF160864_30 (AF160864) orf1386 [Tetrahymena pyriformis]	33.2	41	1.8
00110_HH	2	CAB56698.1	(AJ249754) sec61beta protein [Drosophila melanogaster] gb|AAF58229.1| (AE003814) CG10130 gene product [Drosophila melanogaster]	117	60	5.00E-26
00110_HN	1	NP_000056.1	Complement component 6 precursor sp|P13671|CO6_HUMAN COMPLEMENT COMPONENT C6 PRECURSOR gb|AAA59668.1| (J05024) completement component C6 [Homo sapiens] emb|CAA50994.1| (X72177) complement component C6 [Homo sapiens]	64.4	31	7.00E-10
00112_HH	21	P92177	143E_DROME 14-3-3 PROTEIN EPSILON (SUPPRESSOR OF RAS1 3-9) gb|AAC47519.1| (U84897) 14-3-3 epsilon isoform [Drosophila melanogaster] gb|AAC47520.1| (U84898) 14-3-3 epsilon isoform [Drosophila melanogaster] gb|AAF55519.1| (AE003721) 14-3-3epsilon gene product [alt 3] [Drosophila melanogaster]	222	65	2.00E-57
00113_HH	2	T23125	hypothetical protein H27A22.1 - Caenorhabditis elegans emb|CAB08740.1| (Z95392) similar to guanylate cyclase~cDNA EST yk115b9.5 comes from this gene~cDNA EST yk115b9.3 comes from this gene~cDNA EST yk479b11.3 comes from this gene~cDNA EST yk479b11.5 comes from this gene [Caenorhabditis elegans] emb|CAA19471.1| (AL023829) similar to guanylate cyclase~cDNA EST yk115b9.5 comes from this gene~cDNA EST yk115b9.3 comes from this gene~cDNA EST yk479b11.3 comes from this gene~cDNA EST yk479b11.5 comes from this gene [Caenorhabditis elegans]	136	46	2.00E-31
00114_HH	1	AE000596.1	AE000596 Helicobacter pylori 26695 section 74 of 134 of the complete genome	42.1	100	0.22
00114_HN	1	NP_013432.1	Ylr328wp pir||S53405 probable membrane protein YLR328w - yeast (Saccharomyces cerevisiae) gb|AAB64524.1| (U20618) Ylr328wp [Saccharomyces cerevisiae]	38.7	27	0.04
00115_HN	2	NP_003748.1	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD) sp|Q13347|IF32_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 2 (EIF-3 BETA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) pir||S60335 TGF-beta receptor interacting protein 1 - human gb|AAC50224.1| (U36764) TGF-beta receptor interacting protein 1 [Homo sapiens] gb|AAC97144.1| (U39067) translation initiation factor eIF3 p36 subunit [Homo sapiens]	155	42	3.00E-37
00116_HH	1	AAF15298.1	AF204882_1 (AF204882) AcORF17 homolog [Amsacta albistriga nucleopolyhedrovirus]	32.1	32	4
00116_HN	5	AAG09404.1	AF179481_1 (AF179481) very long-chain acyl-CoA synthetase [Homo sapiens]	181	50	4.00E-45
00117_HH	2	P28497	CAZ2_CHICK F-ACTIN CAPPING PROTEIN ALPHA-2 SUBUNIT (CAPZ 36/32) (BETA-ACTININ SUBUNIT I) pir||S36093 actin-capping protein alpha-2 chain - chicken gb|AAA48656.1| (M80589) capping protein alpha 2 isoform [Gallus gallus]	144	47	7.00E-34
00118_HN	6	CAB46839.1	(AJ388538) F1-ATPase beta-subunit [Canis familiaris]	153	62	8.00E-37
00119_HH	4	P41759	PGK_SCHMA PHOSPHOGLYCERATE KINASE gb|AAA93516.1| (L36833) phosphoglycerate kinase [Schistosoma mansoni]	234	76	5.00E-61
00120_HN	3	D71612	hypothetical protein PFB0540w - malaria parasite (Plasmodium falciparum) gb|AAC71897.1| (AE001401) hypothetical protein [Plasmodium falciparum]	46.1	25	2.00E-04
00121_HH	1	T18418	hypothetical protein C0120w - Plasmodium falciparum emb|CAB10572.2| (Z97348) PFC0120w (MAL3P1.5), Cytoadherence linked asexual protein (3D7-clag3.1), len: 1418 aa, possible signal sequence, predicted using hexExon [Plasmodium falciparum]	31.7	32	5.2
00122_HH	2	E71611	hypothetical protein PFB0580w - malaria parasite (Plasmodium falciparum) gb|AAC71905.1| (AE001404) hypothetical protein [Plasmodium falciparum]	30.9	42	9.1
00124_HH	1	S35220	hypothetical protein - Pseudomonas syringae pv. tomato gb|AAA25728.1| (L20425) avirulence protein [Pseudomonas syringae] prf||1916396A avrPro gene [Pseudomonas syringae pv. tomato]	32.1	33	4
00125_HH	3	Q29099	PTB_PIG POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) pir||S68857 polypyrimidine tract-binding protein - pig emb|CAA63597.1| (X93009) polypyrimidine tract-binding protein [Sus scrofa]	72.6	43	3.00E-12
00126_HH	5	BAA85622.1	(AB027148) Djsyt protein [Dugesia japonica]	311	89	3.00E-84
00126_HN	1	S47596	HMG1-like protein - fruit fly (Drosophila melanogaster)	171	52	6.00E-42
00128_HH	1	AAC33458.2	(AF067140) exopolysaccharide export protein PssN [Rhizobium leguminosarum bv. trifolii]	31.3	39	1.9
00129_HH	1	T26806	hypothetical protein Y41C4A.13 - Caenorhabditis elegans emb|CAA21550.1| (AL032627) predicted using Genefinder [Caenorhabditis elegans]	31.3	31	2.7
00129_HN	5	AAF44064.1	AF217286_1 (AF217286) calponin-like protein Chd64 [Drosophila melanogaster]	61.3	29	6.00E-09
00130_HH	7	JC4027	glutamate--ammonia ligase (EC 6.3.1.2) - sea urchin (Paracentrotus lividus) gb|AAC41562.1| (L32699) glutamine synthetase [Paracentrotus lividus]	282	72	2.00E-75
00131_HH	1	T25467	hypothetical protein B0507.4 - Caenorhabditis elegans gb|AAB04816.1| (U64833) B0507.4 gene product [Caenorhabditis elegans]	33.2	37	0.83
00132_HH	3	AAF57560.1	(AE003796) RpL11 gene product [Drosophila melanogaster]	222	73	2.00E-57
00132_HN	2	CAB60906.1	(AL132896) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans]	30.5	48	2.2
00133_HH	2	CAB81934.1	(AJ276428) adhesive serine protease [Anopheles gambiae]	102	40	2.00E-21
00133_HN	3	P46023	GPCR_LYMST G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR pir||S40241 G protein-coupled receptor - great pond snail emb|CAA80651.1| (Z23104) G protein-coupled receptor [Lymnaea stagnalis]	64.8	30	6.00E-10
00135_HH	12	JH0795	calreticulin precursor - California sea hare gb|AAB24569.1| (S51239) calreticulin [Aplysia californica=marine snails, Peptide, 405 aa]	199	62	2.00E-50
00137_HH	9	S71821	probable interleukin 1 signal-transducing protein TRAF6 - human	58.9	28	3.00E-08
00139_HN	1	CAA61857.1	(X89713) death associated protein 5 [Homo sapiens]	94.4	36	7.00E-19
00140_HH	1	Q27883	DCAM_ONCVO S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) emb|CAA65017.1| (X95713) S-adenosylmethionine decarboxylase [Onchocerca volvulus] emb|CAA65018.1| (X95714) S-adenosylmethionine decarboxylase [Onchocerca volvulus]	132	50	2.00E-30
00143_HH	1	NP_046584.1	putative transglycosylase pir||T12796 probable transglycosylase - Bacillus subtilis phage SPBc2 emb|CAB14053.1| (Z99115) yomI [Bacillus subtilis] gb|AAC13005.1| (AF020713) putative transglycosylase [Bacteriophage SPBc2]	40.2	24	0.014
00144_HN	2	AAF46146.1	(AE003437) Rpt4 gene product [Drosophila melanogaster]	304	90	3.00E-82
00145_HN	1	Q9Z1M8	RED_MOUSE RED PROTEIN (RER PROTEIN) emb|CAA06880.1| (AJ006130) rer [Mus musculus]	36.4	31	0.002

00148_HH	6	P19120	HS7C_BOVIN HEAT SHOCK COGNATE 71 KDA PROTEIN pir||S11456 dnaK-type molecular chaperone hsc70 - bovine emb|CAA37823.1| (X53827) 79KDa heat shock cognate protein [Bos taurus] emb|CAA37422.1| (X53335) heat shock protein (AA 1-650) [Bos taurus]	259	79	9.00E-69
00151_HH	2	O51246	Y228_BORBU HYPOTHETICAL PROTEIN BB0228 pir||D70128 conserved hypothetical protein BB0228 - Lyme disease spirochete gb|AAC66621.1| (AE001133) conserved hypothetical protein [Borrelia burgdorferi]	39.5	23	0.022
00152_HH	4	T32855	hypothetical protein Y8G1A.2 - Caenorhabditis elegans gb|AAB95049.1| (AF040656) similar to C. elegans UNC-7 (SW:Q03412) and drosophilia passover gene (GB:U17330) [Caenorhabditis elegans]	108	39	3.00E-23
00153_HH	1	BAA75633.1	(D88434) protein abundantly expressed during apple fruit development [Malus x	223	62	8.00E-58
00154_HN	2	CAB51908.1	(AJ000992) GDT1 protein [Dictyostelium discoideum]	35.2	22	0.46
00155_HH	3	A71001	hypothetical protein PH1305 - Pyrococcus horikoshii dbj|BAA30409.1| (AP000006) 252aa long hypothetical protein [Pyrococcus horikoshii]	46.5	30	2.00E-04
00156_HH	3	AAF50159.1	(AE003548) CG12362 gene product [Drosophila melanogaster]	57.4	25	1.00E-07
00156_HN	1	AAC99998.1	(U39402) ORF; Method: conceptual translation supplied by author. [Homo sapiens]	240	68	6.00E-63
00159_HH	5	BAA86216.1	(AB034209) cytoplasmic actin [Oikopleura longicauda]	324	98	3.00E-88
00160_HH	1	NP_015185.1	protein kinase; Mkk2p sp|P32491|MKK2_YEAST PROTEIN KINASE MKK2/SSP33 pir||S69045 protein kinase MKK2 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) gb|AAB68220.1| (U43703) Mkk2p [Saccharomyces cerevisiae]	74.5	37	7.00E-13
00162_HH	1	AAF52471.1	(AE003615) snRNP70K gene product [Drosophila melanogaster]	210	57	1.00E-53
00163_HH	2	AAF52705.1	(AE003622) CG9321 gene product [Drosophila melanogaster]	77.3	72	1.00E-13
00163_HN	1	AAF48961.1	(AE003512) CG14199 gene product [Drosophila melanogaster]	52.7	51	3.00E-10
00164_HH	5	I52603	MPS1 protein - mouse (fragment) gb|AAA73957.1| (L20315) MPS1 protein [Mus	103	36	1.00E-21
00164_HN	1	AAF56205.1	(AE003745) Pros26.4 gene product [Drosophila melanogaster]	320	96	5.00E-87
00166_HH	1	CAB38975.1	(AL034556) hypothetical protein, PFC0625w [Plasmodium falciparum]	35.2	39	0.46
00168_HH	1	AAF23952.1	AF200357_1 (AF200357) pantothenate kinase 1 beta [Mus musculus]	67.9	28	7.00E-11
00168_HN	1	P00349	6PGD_SHEEP 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING pir||DESHGC phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - sheep emb|CAA42751.1| (X60195) 6-phosphogluconate dehydrogenase (decarboxylating) [Ovis aries]	194	59	5.00E-49
00169_HH	2	NP_004584.1	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10 ref|NP_033212.1| silica-induced gene 41 pir||S68798 RNA-binding protein SIG41 - mouse dbj|BAA08556.1| (D49708) RNA binding protein (transformer-2-like) [Rattus norvegicus] emb|CAA56518.1| (X80232) SIG41 [Mus musculus] gb|AAC28242.1| (U61267) htra2-beta [Homo sapiens] gb|AAB08701.1| (U68063) transformer-2 beta [Homo sapiens] gb|AAD19277.1| (AF057159) transformer-2-beta isoform 1 [Homo sapiens]	113	54	1.00E-24
00171_HN	11	NP_062415.1	N-acetylglucosamine kinase emb|CAB61849.1| (AJ242909) N-Acetylglucosamine kinase [Mus musculus]	109	36	1.00E-23
00172_HH	1	CAB65182.1	(AJ242600) AMPA-selective receptor subunit [Loligo opalescens]	169	50	2.00E-41
00173_HH	5	NP_033450.1	Tnf receptor-associated factor 6 dbj|BAA12705.1| (D84655) TRAF6 [Mus musculus]	69.1	33	3.00E-11
00174_HH	1	AAA91648.1	(U26588) Method: conceptual translation supplied by author.; purine salvage pathway enzyme [Cricetulus griseus]	155	49	4.00E-37
00176_HH	1	AAF80245.1	AF146692_1 (AF146692) filamin 2 [Homo sapiens]	89.3	53	2.00E-17
00177_HH	57	NP_006079.1	tubulin, beta, 2 sp|P05217|TBB2_HUMAN TUBULIN BETA-2 CHAIN pir||C25437 tubulin beta-3 chain - mouse pir||I38370 beta-tubulin - human emb|CAA26203.1| (X02344) beta-tubulin [Homo sapiens] prf||1304282B tubulin Mbeta 3 [Mus musculus]	287	85	4.00E-77
00178_HH	6	NP_005138.1	tumorous imaginal discs (Drosophila) homolog gb|AAC29066.1| (AF061749) tumorous imaginal discs protein Tid56 homolog [Homo sapiens]	129	44	1.00E-29
00179_HN	1	T26067	hypothetical protein W01G7.5 - Caenorhabditis elegans emb|CAA21599.1| (AL032634) W01G7.5 [Caenorhabditis elegans] emb|CAB03457.1| (Z81135) W01G7.5 [Caenorhabditis elegans]	39.9	36	0.018
00180_HN	5	P13272	UCRI_BOVIN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) [CONTAINS: UBIQUINOL-CYTOCHROME C REDUCTASE 8 KD PROTEIN (COMPLEX III SUBUNIT IX)] pir||A34660 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - bovine gb|AAB26197.1| (S58789) Rieske iron-sulfur [Bos taurus]	76.9	34	1.00E-13
00181_HH	1	AAF55957.1	(AE003737) CG5740 gene product [Drosophila melanogaster]	33.6	27	1.3
00182_HN	1	AAF30911.1	AE002148_3 (AE002148) unique hypothetical [Ureaplasma urealyticum]	31.7	28	5.3
00183_HN	22	AAB05638.1	(L47285) heat shock protein 82 [Anopheles albimanus] gb|AAB05639.1| (L47285) heat shock protein 82 [Anopheles albimanus]	220	86	3.00E-63
00184_HH	2	NP_033402.1	transgene insert site 737, insertional mutation, polycystic kidney disease pir||I49564 polycystic kidney disease-related protein - mouse gb|AAB59705.1| (L31959) [Mus musculus (strain C3HF/RL) ORF mRNA, complete cds.], gene product	228	68	4.00E-59
00185_HN	1	AC010879.2	AC010879 Homo sapiens clone RP11-235I1, complete sequence	42.1	100	0.22
00189_HN	28	BAA34955.1	(AB015485) myosin heavy chain [Dugesia japonica]	251	80	4.00E-66
00193_HH	4	NP_000160.1	galactosidase, alpha sp|P06280|AGAL_HUMAN ALPHA-GALACTOSIDASE A PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) (ALPHA-D-GALACTOSIDASE A) pir||GBHUA alpha-galactosidase (EC 3.2.1.22) A precursor - human emb|CAA32617.1| (X14448) alpha-D-galactosidase A [Homo sapiens] emb|CAA29232.1| (X05790) alpha-galactosidase [Homo sapiens] gb|AAB64203.1| (U78027) alpha-D-galactosidase A [Homo sapiens] emb|CAB55878.1| (AL035422) dJ164F3.2 (galactosidase, alpha) [Homo sapiens] prf||1612342A alpha galactosidase [Homo sapiens]	161	55	5.00E-40
00193_HN	1	O50565	EFG_THICU ELONGATION FACTOR G (EF-G) gb|AAB87733.1| (U78300) elongation factor G [Thiomonas cuprina]	31.3	30	6.9
00194_HN	1	BAA87831.1	(AP000815) Similar to Arabidopsis thaliana chromosome II BAC T27A16 sequence; hypothetical protein. (AC005496) [Oryza sativa]	64.4	28	7.00E-10
00195_HN	1	NP_060561.1	hypothetical protein FLJ10422 dbj|BAA91600.1| (AK001284) unnamed protein product [Homo sapiens]	267	87	1.00E-75
00197_HN	1	AAC79681.1	(AF059251) lipoxygenase [Mus musculus]	34.8	27	0.61
00199_HN	2	NP_035614.1	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1 pir||JC4917 signal transducing adaptor - mouse gb|AAC52840.1| (U43900) STAM [Mus musculus]	105	47	3.00E-22
00200_HN	15	BAA88477.1	(AB025324) aldolase-1 [Eptatretus burgeri]	220	79	1.00E-63

00201_HH	1	NP_032724.1	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans) emb|CAA04634.1| (AJ001260) NIPSNAP1 protein [Mus musculus]	192	51	3.00E-48
00202_HH	1	AAF50591.1	(AE003559) CG8609 gene product [Drosophila melanogaster]	116	36	1.00E-25
00204_HH	1	BAB03308.1	(AB046443) potassium channel interacting protein 1 [Rattus norvegicus]	146	47	1.00E-34
00205_HH	1	AAF56334.1	(AE003749) CG6879 gene product [Drosophila melanogaster]	38.3	27	0.053
00205_HN	2	NP_001009.1	ribosomal protein S15 ref|NP_033117.1| ribosomal protein S15 ref|NP_058847.1| ribosomal protein S15 sp|P11174|RS15_HUMAN 40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN) pir||R3HU15 ribosomal protein S15, cytosolic - human pir||R3RT15 ribosomal protein S15, cytosolic - rat pir||R3HY15 ribosomal protein S15 - golden hamster pir||B34823 ribosomal protein S15 - chicken pir||A34823 ribosomal protein S15 - mouse gb|AAA40055.1| (M33330) insulinoma protein (rig) [Mus musculus] gb|AAA42044.1| (M19393) DNA-binding protein (putative); putative [Rattus norvegicus] gb|AAA49057.1| (M33331) insulinoma protein (rig) [Gallus gallus] dbj|BAA01984.1| (D11388) ribosomal protein S15 [Rattus norvegicus] dbj|BAA01036.1| (D10167) ribosomal protein S15 [Gallus gallus] gb|AAA37094.1| (J02983) Rig DNA-binding protein (putative); putative [Mesocricetus auratus] gb|AAA36036.1| (J02984) rig-analog protein (putative); putative [Homo sapiens] gb|AAA36568.1| (M32405) human homologue of rat insulinoma gene (rig); putative [Homo sapiens] dbj|BAA21510.1| (AB005624) rig-analog DNA-binding protein [Sus scrofa]	183	63	7.00E-46
00206_HH	1	AAF64151.1	AF232691_1 (AF232691) tyrosine kinase 5 [Schistosoma mansoni]	149	47	2.00E-35
00208_HN	3	NP_004720.1	Ac-like transposable element dbj|BAA34505.1| (AB018328) KIAA0785 protein [Homo sapiens] emb|CAA76545.1| (Y16947) putative transposase Ac-like [Homo sapiens] emb|CAA76660.1| (Y17156) putative transposase [Homo sapiens]	54.3	38	8.00E-07
00209_HH	1	P32225	VC07_SPVKA HYPOTHETICAL PROTEIN C7 gb|AAC37864.1| (L22013) ORF C7L [Swinepox virus]	33.6	43	1.4
00211_HH	1	CAA74583.1	(Y14196) heterogeneous nuclear ribonucleoprotein H [Mus musculus]	61.7	22	5.00E-09
00213_HN	1	NP_003720.1	RNA 3'-terminal phosphate cyclase sp|O00442|RTC1_HUMAN RNA 3'-TERMINAL PHOSPHATE CYCLASE 1 (RNA-3'-PHOSPHATE CYCLASE 1) (RNA CYCLASE 1) emb|CAA72364.1| (Y11651) phosphate cyclase [Homo sapiens]	129	49	2.00E-29
00214_HH	1	AAC32284.1	(AF081585) developmental protein DG1110 [Dictyostelium discoideum]	35.6	22	0.35
00216_HH	1	NP_034371.1	fused toes pir||S33513 gene Fif protein - mouse emb|CAA50800.1| (X71978) Fif [Mus musculus] emb|CAA91902.1| (Z67963) FT1 protein [Mus musculus]	121	45	6.00E-27
00217_HN	9	AAF58858.1	(AE003831) CG18445 gene product [Drosophila melanogaster]	97.9	37	6.00E-20
00218_HN	2	AAF57842.1	(AE003803) CG4878 gene product [Drosophila melanogaster]	50.8	22	9.00E-06
00219_HH	13	T25138	hypothetical protein T22H2.6b - Caenorhabditis elegans emb|CAB54305.1| (Z81595) T22H2.6b [Caenorhabditis elegans]	104	37	5.00E-22
00219_HN	1	P54677	PI4K_DICDI PHOSPHATIDYLINOSITOL 4-KINASE (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA) pir||T18275 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 4 - slime mold (Dictyostelium discoideum) gb|AAA85725.1| (U23479) phosphatidylinositol 4-kinase [Dictyostelium discoideum]	38.3	37	0.054
00220_HH	3	NP_006083.1	caspase recruitment domain 4 gb|AAD28350.1|AF113925_1 (AF113925) Nod1 [Homo sapiens] gb|AAD29125.1|AF126484_1 (AF126484) CARD4 [Homo sapiens] gb|AAD43922.1| (AF149774) NOD1 protein [Homo sapiens]	51.5	30	6.00E-06
00220_HN	8	T11091	cytochrome-c oxidase (EC 1.9.3.1) chain II - Dinodon semicarinatus mitochondrion (fragment) dbj|BAA33025.1| (AB008539) cytochrome oxidase subunit II [Dinodon semicarinatus] gnl|NCBI_MITO|COX2_13972 cytochrome c oxidase subunit II	64	32	1.00E-09
00221_HH	1	AC002076.1	AC002076 Human BAC clone GS1-345D13 from 7q31-q32, complete sequence [Homo sapiens]	38.2	100	3.5
00222_HH	1	AAF54372.1	(AE003682) CG8135 gene product [Drosophila melanogaster]	107	39	7.00E-23
00225_HH	1	NP_057490.1	hypothetical protein gb|AAF29119.1|AF161504_1 (AF161504) HSPC155 [Homo sapiens]	281	77	3.00E-75
00226_HH	3	S51791	Drosophila translocation protein 1 - fruit fly (Drosophila melanogaster) emb|CAA86222.1| (Z38100) Drosophila translocation protein 1 [Drosophila melanogaster]	61.7	36	5.00E-09
00226_HN	3	P11141	HS7F_CAEEL HEAT SHOCK 70 KD PROTEIN F, MITOCHONDRIAL PRECURSOR pir||T25613 hypothetical protein C37H5.8 - Caenorhabditis elegans gb|AAB42371.1| (U88315) Similar to heat shock 70 protein; coded for by C. elegans cDNA yk28a1.5; coded for by C. elegans cDNA yk25c1.5; coded for by C. elegans cDNA yk18h12.5; coded for by C. elegans cDNA yk25c1.3; coded for by C. elegans cDNA yk28a1.3; coded for by >	252	82	2.00E-66
00227_HH	5	NP_001003.1	ribosomal protein S8 ref|NP_033124.1| ribosomal protein S8 sp|P09058|RS8_HUMAN 40S RIBOSOMAL PROTEIN S8 pir||R3RT8 ribosomal protein S8 - rat pir||S25022 ribosomal protein S8, cytosolic - human pir||S42110 ribosomal protein S8 - mouse emb|CAA47670.1| (X67247) ribosomal protein S8 [Homo sapiens] emb|CAA29732.1| (X06423) ribosomal protein S8 (AA 1-208) [Rattus norvegicus] emb|CAA52050.1| (X73829) ribosomal protein S8 [Mus musculus]	196	59	1.00E-49
00227_HN	1	NP_012942.1	YKR017cp sp|P36113|YKZ7_YEAST HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION pir||S38086 hypothetical protein YKR017c - yeast (Saccharomyces cerevisiae) emb|CAA82089.1| (Z28242) ORF YKR017c [Saccharomyces cerevisiae]	34.8	36	0.61
00228_HH	2	Q19673	YTQJ_CAEEL HYPOTHETICAL TYROSINE-LIKE PROTEIN F21C3.2 IN CHROMOSOME I pir||T21192 hypothetical protein F21C3.2 - Caenorhabditis elegans emb|CAA95805.1| (Z71261) Similarity to Streptomyces tyrosinase (SW:TYRO_STRAT)~cDNA EST yk126c1.5 comes from this gene~cDNA EST yk180b5.3 comes from this gene~cDNA EST yk194b1.3 comes from this gene~cDNA EST yk194b1.5 comes from this gene~cDNA EST yk180b5.5 comes from>	112	33	3.00E-24
00229_HH	1	AAC69101.1	(U41552) Contains similarity to Pfam domain: PF01268 (FTHFS), Score=1277.4, E-value=0, N=1 [Caenorhabditis elegans]	201	58	4.00E-51
00229_HN	13	P13060	EF2_DROME ELONGATION FACTOR 2 (EF-2) pir||S05988 translation elongation factor eEF-2 - fruit fly (Drosophila melanogaster) emb|CAA33804.1| (X15805) translation elongation factor 2 (AA 1-844) [Drosophila melanogaster]	211	69	5.00E-54
00230_HH	19	CAA96581.1	(Z72500) cytochrome oxidase, subunit I [Pilayella littoralis]	34.4	92	0.8
00230_HN	1	AAF19122.1	AF143464_1 (AF143464) BdrB2 [Borrelia hermsii]	36.4	29	0.21
00234_HH	4	P23232	GBB_LOLFO GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT pir||RGOOBE GTP-binding regulatory protein beta chain - northern European squid emb|CAA40077.1| (X56757) GTP-binding protein beta subunit [Loligo forbesi] prf||1705183A GTP binding protein [Loligo forbesi]	234	91	4.00E-61
00234_HN	2	T40627	probable ribonucleoprotein SPBC660.15 - fission yeast (Schizosaccharomyces pombe) emb|CAA22535.1| (AL034563) RNA-binding protein [Schizosaccharomyces pombe]	143	41	1.00E-33

00236_HH	1	AAF30800.1	AE002136_7 (AE002136) unique hypothetical [Ureaplasma urealyticum]	37.1	26	0.12
00237_HH	1	AAF51237.1	(AE003582) CG9881 gene product [Drosophila melanogaster]	108	38	3.00E-23
00237_HN	34	NP_032324.1	heat shock protein, DNAJ-like 2 sp|P54102|HS44_MOUSE HEAT SHOCK 40 KDA PROTEIN 4 (DNAJ PROTEIN HOMOLOG 2) (HSJ-2) gb|AAA98855.1| (U53922) DnaJ-like protein [Rattus norvegicus] gb|AAC78597.1| (AF055664) DnaJ-like protein [Mus musculus]	173	53	8.00E-43
00238_HN	1	AAF48984.1	(AE003512) CG12788 gene product [Drosophila melanogaster]	64	32	1.00E-09
00239_HN	1	H71611	probable secreted protein PFB0565w - malaria parasite (Plasmodium falciparum) gb|AAC71902.1| (AE001403) predicted secreted protein [Plasmodium falciparum]	30.9	25	8
00240_HH	1	NP_033541.1	Wiskott-Aldrich syndrome protein sp|P70315|WASP_MOUSE WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP) gb|AAC52556.1| (U54788) Wiskott-Aldrich Syndrome Protein [Mus musculus] gb|AAC99855.1| (U29673) Wiskott-Aldrich syndrome protein (WASP) [Mus musculus] prf||2122283A Wiskott-Aldrich syndrome protein [Mus musculus]	64.8	32	6.00E-10
00241_HH	1	BAA84766.1	(AB022691) TAF-Ibeta1 [Xenopus laevis]	183	61	7.00E-46
00241_HN	2	prf|1803425C	myosin:SUBUNIT=regulatory light chain [Mercenaria mercenaria]	153	64	2.00E-51
00242_HH	1	Q15046	SYK_HUMAN LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) (KIAA0070)	139	43	2.00E-32
00243_HN	1	T18682	3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) precursor - Caenorhabditis elegans emb|CAB03798.1| (Z81453) similar to 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) (FRAGMENT)~cDNA EST yk309f8.5 comes from this gene~cDNA EST yk137g10.5 comes from this gene~cDNA EST yk232a12.3 comes from this gene~cDNA EST yk232a12.5 comes from > emb|CAA21003.1| (AL031630) similar to 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) (FRAGMENT)~cDNA EST yk309f8.5 comes from this gene~cDNA EST yk137g10.5 comes from this gene~cDNA EST yk232a12.3 comes from this gene~cDNA EST yk232a12.5 comes fro>	65.2	38	4.00E-10
00244_HH	1	AAF58476.1	(AE003821) CG8632 gene product [Drosophila melanogaster]	159	45	2.00E-38
00245_HN	7	PC4158	ribosomal protein S3a - cat (fragment) gb|AAB01669.1| (U22231) ribosomal protein S3a [Felis catus]	191	56	3.00E-48
00246_HH	1	AAA37292.1	(M75122) acid beta-galactosidase [Mus musculus]	142	47	2.00E-33
00247_HN	1	NP_014910.1	Yor267cp pir||S67164 probable membrane protein YOR267c - yeast (Saccharomyces cerevisiae) emb|CAA99490.1| (Z75175) ORF YOR267c [Saccharomyces cerevisiae]	35.6	29	0.33
00248_HH	1	AE003518.1	AE003518 Drosophila melanogaster genomic scaffold 142000013386050 section 5 of 54, complete sequence	46.1	100	0.014
00249_HH	1	AAD26911.1	AC006429_1 (AC006429) unknown protein [Arabidopsis thaliana]	99.1	35	3.00E-20
00250_HN	1	AC009039.6	AC009039 Homo sapiens chromosome 16 clone RP11-152O14, complete sequence	42.1	96	0.22
00251_HH	1	NP_004032.1	arrestin, beta 1 gb|AAC33295.1| (AF084040) beta-arrestin 1A [Homo sapiens]	139	40	2.00E-32
00252_HH	1	AAF46282.1	(AE003442) CG10932 gene product [Drosophila melanogaster]	170	52	1.00E-41
00253_HH	1	O62619	KPYK_DROME PYRUVATE KINASE (PK) gb|AAC15808.1| (AF061507) pyruvate kinase [Drosophila melanogaster] gb|AAC16244.1| (AF062478) pyruvate kinase [Drosophila melanogaster]	159	55	1.00E-38
00254_HH	2	CAA06555.1	(AJ005458) protein Phosphatase 2C beta [Bos taurus]	185	56	3.00E-46
00256_HN	5	Q36428	NU5M_LOCMI NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5	71.8	26	4.00E-12
00258_HN	3	AAF94385.1	(AE004202) thiopurine methyltransferase [Vibrio cholerae]	104	35	5.00E-22
00261_HN	6	AAC48632.1	(U53421) betaine-homocysteine methyltransferase [Sus scrofa]	236	70	1.00E-61
00263_HN	8	AAF64527.1	AF254148_1 (AF254148) PUR-alpha-like protein [Schistosoma mansoni]	174	62	5.00E-43
00266_HH	1	AAF82310.1	(AF277804) p21-activated protein kinase-like protein [Dictyostelium discoideum]	32.8	36	2.3
00266_HN	1	NP_001130.1	arachidonate 12-lipoxygenase, 12R type gb|AAC39770.1| (AF038461) 12R-lipoxygenase [Homo sapiens] gb|AAC79680.1| (AF059250) lipoxygenase [Homo sapiens]	94.8	34	5.00E-19
00267_HN	1	CAA74350.1	(Y14023) EciB protein [Staphylococcus epidermidis]	36.7	20	0.16
00269_HH	1	T08058	aspartic proteinase inhibitor - winter squash (fragment) gb|AAC39473.1| (AF038166) aspartic proteinase inhibitor [Cucurbita maxima]	30.9	33	9.1
00269_HN	1	NP_059277.1	ORF129 gb|AAF05243.1|AF162221_129 (AF162221) ORF129 [Xestia c-nigrum granulovirus]	30.9	46	9.1
00271_HH	3	P49900	ARGI_RANCA ARGINASE, HEPATIC gb|AAA68073.1| (U26351) arginase [Rana catesbeiana]	146	40	1.00E-34
00271_HN	1	CAB73732.1	(AL139078) hypothetical protein Cj1305c (617 family) [Campylobacter jejuni]	35.6	29	0.35
00272_HN	1	P08397	HEM3_HUMAN PORPHOBILINOGEN DEAMINASE (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) (PBG-D)	59.3	32	2.00E-08
00273_HH	2	JE0171	ribonuclease T2 (EC 3.1.27.1) - Japanese flying squid	105	37	3.00E-22
00274_HH	2	NP_036029.1	signal recognition particle 54 kDa sp|P14576|SR54_MOUSE SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN (SRP54) emb|CAA34386.1| (X16319) SRP 54K subunit (AA 1-504) [Mus musculus]	205	68	3.00E-52
00275_HN	1	BAA86533.1	(AB033045) KIAA1219 protein [Homo sapiens]	38.7	28	0.039
00276_HH	1	T20392	hypothetical protein DY3.4 - Caenorhabditis elegans emb|CAB09413.1| (Z96047) similar to Reverse transcriptase (RNA-dependent DNA polymerase)~cDNA EST yk241a9.3 comes from this gene~cDNA EST yk241a9.5 comes from this gene~cDNA EST yk579g12.3 comes from this gene~cDNA EST yk579g12.5 comes from this gene [Caenorhabditis e>	35.6	28	0.35
00276_HN	2	AAF53873.1	(AE003665) CG10747 gene product [Drosophila melanogaster]	83.1	40	2.00E-15
00277_HN	3	AAF16704.1	AF117582_1 (AF117582) calcyphosine-like protein [Manduca sexta]	155	49	3.00E-37
00278_HH	10	AAD05030.1	(AC006144) glutamate dehydrogenase 2 precursor [Homo sapiens]	194	60	5.00E-49
00278_HN	2	BAA88078.1	(AB035447) argonaute protein [Drosophila melanogaster] gb|AAF58315.1| (AE003816) AGO1 gene product [alt 1] [Drosophila melanogaster]	291	85	3.00E-78
00279_HN	2	NP_006833.1	splicing factor 3b, subunit 2, 145kD sp|Q13435|S145_HUMAN SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) gb|AAA97461.1| (U41371) spliceosome associated protein [Homo sapiens]	234	81	6.00E-61
00281_HN	2	CAB71108.1	(AL132959) putative protein [Arabidopsis thaliana]	33.2	27	1.8
00282_HN	1	P47496	DNLJ_MYCGE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [NAD+]) pir||A64228 DNA ligase (NAD+) (EC 6.5.1.2) - Mycoplasma genitalium gb|AAC71474.1| (U39704) DNA ligase [Mycoplasma genitalium]	31.7	43	5.3
00283_HN	2	I49069	A+U-rich RNA-binding protein - mouse (fragment) gb|AAA64653.1| (U11273) A+U-rich RNA-binding protein [Mus musculus]	136	53	1.00E-31
00286_HH	1	T22384	hypothetical protein F48F5.4 - Caenorhabditis elegans emb|CAB04413.1| (Z81541) predicted using Genefinder [Caenorhabditis elegans]	31.3	32	6.9

00287_HH	2	Q61554	FBN1_MOUSE FIBRILLIN 1 PRECURSOR pir||A55624 fibrillin-1 precursor - mouse gb|AAA56840.1| (L29454) fibrillin [Mus musculus]	113	37	2.00E-24
00287_HN	2	Q01062	CN2A_RAT CGMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE (CYCLIC GMP STIMULATED PHOSPHODIESTERASE) (CGS-PDE) pir||JC2486 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - rat gb|AAA63683.1| (U21101) cyclic GMP stimulated phosphodiesterase [Rattus norvegicus]	188	55	4.00E-47
00288_HH	5	P31009	RS2_DROME 40S RIBOSOMAL PROTEIN S2 (STRINGS OF PEARLS PROTEIN) pir||S50325 ribosomal protein S2 - fruit fly (Drosophila melanogaster) gb|AAC34198.1| (U01334) ribosomal protein S2 [Drosophila melanogaster] gb|AAA87053.1| (U01335) ribosomal protein S2 [Drosophila melanogaster] gb|AAF52822.1| (AE003626) sop gene product [Drosophila melanogaster]	280	81	8.00E-75
00289_HN	2	JC4751	FK506-binding protein p50 - fluke (Schistosoma mansoni) gb|AAB05213.1| (L42969) immunophilin [Schistosoma mansoni]	160	56	8.00E-39
00290_HH	1	T31102	filamentous hemagglutinin 1 - Haemophilus ducreyi gb|AAC79757.1| (AF057695) large supernatant protein 1 [Haemophilus ducreyi]	36	23	0.27
00291_HH	11	AAC32040.1	(U77932) preprocathepsin C [Schistosoma japonicum]	117	37	8.00E-26
00291_HN	5	NP_003338.1	ubiquitin-conjugating enzyme E2L 3 ref|NP_033482.1| ubiquitin-conjugating enzyme 7 sp|P51966|UBC7_HUMAN UBIQUITIN-CONJUGATING ENZYME E2-18 KDA UBCH7 (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) pir||JC6163 ubiquitin-conjugating enzyme - mouse pdb|1C4Z|D Chain D, Structure Of E6ap: Insights Into Ubiquitination Pathway emb|CAA63538.1| (X92962) ubiquitin-conjugating enzyme UbcH7 [Homo sapiens] emb|CAA65755.1| (X97042) UbcM4 protein [Mus musculus] gb|AAB36017.1| (S81003) L-UBC=ubiquitin conjugating enzyme [human, odontogenic keratocysts, Peptide, 154 aa] [Homo sapiens] emb|CAA04156.1| (AJ000519) ubiquitin-conjugating enzyme UbcH7 [Homo sapiens] emb|CAA10265.1| (AJ130961) ubiquitin-conjugating enzyme [Mus musculus]	136	44	2.00E-31
00292_HN	1	AL023279.1	HS326L12 Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1-27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence	50.1	100	0.001
00293_HH	1	AAA30655.1	(L22092) manganous superoxide dismutase [Bos taurus]	208	65	4.00E-53
00293_HN	5	O67687	ALR_AQUAE ALANINE RACEMASE pir||E70457 alanine racemase - Aquifex aeolicus gb|AAC07650.1| (AE000758) alanine racemase [Aquifex aeolicus]	36.7	36	0.16
00295_HH	1	M85302.1	SCMSMOXIV Schistosoma mansoni homeodomain protein (smox-4) gene, 3' end	46.1	100	0.011
00296_HN	1	CAA83608.1	(Z32681) cDNA EST EMBL:Z14649 comes from this gene~cDNA EST EMBL:T00953 comes from this gene~cDNA EST EMBL:T01003 comes from this gene~cDNA EST CEMSE82F comes from this gene~cDNA EST EMBL:T00455 comes from this gene~cDNA EST EMBL:T00456 comes from this>	42.6	26	0.003
00297_HH	8	CAA75383.1	(Y15109) heat shock protein 70 [Sycon raphanus]	210	74	8.00E-54
00298_HN	1	Q94523	DHSA_DROME SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT, MITOCHONDRIAL PRECURSOR (FP) (FLAVOPROTEIN SUBUNIT OF COMPLEX II) emb|CAA70285.1| (Y09064) succinate dehydrogenase flavoprotein subunit [Drosophila melanogaster]	280	82	8.00E-75
00299_HH	1	BAA88769.1	(AB015798) DnaJ homolog [Homo sapiens]	110	51	1.00E-23
00299_HN	2	AAC34395.1	(AF056116) unknown [Takifugu rubripes]	157	46	7.00E-38
00301_HN	1	T32861	hypothetical protein T20H9.6 - Caenorhabditis elegans gb|AAB95054.1| (AF040657) T20H9.6 gene product [Caenorhabditis elegans]	42.2	27	0.004
00302_HN	2	AAF50582.1	(AE003559) CG8602 gene product [Drosophila melanogaster]	129	48	1.00E-29
00303_HH	1	P25824	KAD_SCHMA ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) (AK) gb|AAA29907.1| (M80542) nucleoside monophosphate kinase [Schistosoma mansoni]	164	58	7.00E-40
00303_HN	3	BAA83539.1	(AB031286) NADH dehydrogenase subunit 2 [Taenia hydatigena]	44.9	33	5.00E-04
00306_HN	3	AL122023.3	CNS01DSX Human chromosome 14 DNA sequence IN PROGRESS BAC R-120E11 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence	44.1	100	0.057
00307_HH	1	S77340	hypothetical protein sll1722 - Synechocystis sp. (strain PCC 6803) dbj|BAA17443.1| (D90906) hypothetical protein [Synechocystis sp.]	35.6	35	0.34
00308_HH	2	AAF08387.1	AF145306_1 (AF145306) 26S proteasome regulatory complex subunit p48A [Drosophila melanogaster] gb|AAF48001.1| (AE003485) Rpt3 gene product [Drosophila melanogaster]	242	78	1.00E-63
00311_HH	46	BAA08663.1	(D49924) elongation factor-1alpha [Dugesia japonica]	327	95	5.00E-89
00311_HN	1	AAF49551.1	(AE003529) CG5841 gene product [Drosophila melanogaster]	94.4	39	7.00E-19
00312_HH	11	T26427	hypothetical protein Y106G6H.2 - Caenorhabditis elegans emb|CAA21572.1| (AL032631) predicted using Genefinder~similar to RNA recognition motif. (aka RRM, RBD, or RNP domain) ; Poly-adenylate binding protein, unique domain.~cDNA EST yk433d3.5 comes from this gene; cDNA EST EMBL:T00720 comes from this gene; cDNA EST yk46e7.3>	215	63	2.00E-55
00312_HN	1	Q9Y2G3	AT1R_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IR dbj|BAA76800.1| (AB023173) KIAA0956 protein [Homo sapiens]	124	42	5.00E-28
00314_HH	1	AAC28864.1	(AF080568) CTP:phosphoethanolamine cytidylyltransferase [Rattus norvegicus]	87	47	1.00E-16
00314_HN	4	AAF47998.1	(AE003485) Hsp60 gene product [alt 1] [Drosophila melanogaster] gb|AAF47999.1| (AE003485) Hsp60 gene product [alt 2] [Drosophila melanogaster]	235	75	2.00E-61
00315_HH	2	AAC46898.1	(U30263) similar to human carbonyl reductase (NADPH), PIR Accession Number A61271; Method: conceptual translation supplied by author [Schistosoma mansoni]	141	46	3.00E-33
00315_HN	7	AAF44676.1	AF239265_1 (AF239265) cathepsin L [Fasciola gigantica]	125	46	2.00E-28
00316_HH	5	NP_033419.1	troponin C, cardiac/slow skeletal sp|P19123|TPCC_MOUSE TROPONIN C, SLOW SKELETAL AND CARDIAC MUSCLES (TN-C) pir||A32620 troponin C, cardiac muscle - mouse gb|AAA37493.1| (M29793) slow/cardiac troponin C [Mus musculus] gb|AAA37492.1| (J04971) slow/cardiac troponin C [Mus musculus]	47.6	31	8.00E-05
00318_HH	1	1CTE	B Chain B, Molecule: Cathepsin B; Ec: 3.4.22.1; Mutation: Ser115ala; Engineered; Heterogen: Pyridyl Sulfide Blocking Group At Active-Site Cys 29 pdb|1CTE|A Chain A, Molecule: Cathepsin B; Ec: 3.4.22.1; Mutation: Ser115ala; Engineered; Heterogen: Pyridyl Sulfide Blocking Group At Active-Site Cys 29	176	60	1.00E-43
00320_HN	1	AAF55164.1	(AE003708) Tm1 gene product [alt 1] [Drosophila melanogaster]	69.5	28	2.00E-11

00321_HN	3	NP_002711.1	protein phosphatase 4 (formerly X), catalytic subunit ref|NP_062648.1| protein phosphatase X sp|P33172|PPP4_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE 4 (PP4) (PROTEIN PHOSPHATASE X) (PP-X) gb|AAC96297.1| (AF088911) protein phosphatase X [Mus musculus] gb|AAC96318.1| (AF097996) protein phosphatase X [Homo sapiens] emb|CAA49753.1| (X70218) protein phosphatase X [Homo sapiens]	303	85	6.00E-82
00322_HH	1	AAF49748.1	(AE003535) CG7924 gene product [Drosophila melanogaster]	42.2	35	0.004
00323_HN	3	Q29458	LIPG_BOVIN TRIACYLGLYCEROL LIPASE, PREGASTRIC PRECURSOR (PREGASTRIC LIPASE) (GL) (PREGASTRIC ESTERASE) (PGE) pir||JC4017 triacylglycerol lipase (EC 3.1.1.3) PGE precursor - bovine gb|AAA57037.1| (L26319) pregastric esterase [Bos taurus]	121	55	7.00E-34
00324_HN	1	AAC09069.1	(AF001947) U4/U6-associated RNA splicing factor [Homo sapiens]	81.9	32	4.00E-15
00325_HH	1	AAF81653.1	AF199331_1 (AF199331) RIM2-5B [Rattus norvegicus]	55.8	28	3.00E-07
00325_HN	1	AAF52279.1	(AE003611) CG7236 gene product [Drosophila melanogaster]	205	65	2.00E-57
00326_HN	1	AAD39927.1	AF126285_3 (AF126285) DNA polymerase [Pleurotus ostreatus]	31.7	25	5.3
00327_HN	1	AAF39218.1	(AE002303) phospholipase D family protein [Chlamydia muridarum]	35.2	28	0.46
00330_HH	1	AAD39150.1	AF139518_1 (AF139518) A-kinase anchor protein [Rattus norvegicus]	35.2	26	0.41
00330_HN	3	O77622	TCPZ_RABIT T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) gb|AAC19379.1| (AF068483) chaperonin Cct6 [Oryctolagus cuniculus]	146	74	1.00E-36
00331_HN	1	NP_005403.1	serine hydroxymethyltransferase 2 (mitochondrial) gb|AAA64572.1| (U23143) mitochondrial serine hydroxymethyltransferase [Homo sapiens]	218	71	3.00E-56
00332_HN	2	NP_005909.1	malate dehydrogenase 2, NAD (mitochondrial) sp|P40926|MDHM_HUMAN MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR gb|AAC03787.1| (AF047470) malate dehydrogenase precursor [Homo sapiens]	239	73	2.00E-62
00333_HN	1	prf||2208397A	dynactin:SUBUNIT=50kD [Bos taurus]	73.4	25	1.00E-12
00336_HN	1	AAF46469.1	(AE003446) CG12121 gene product [Drosophila melanogaster]	53.9	27	1.00E-06
00337_HN	2	CAB93422.3	(AL133324) dJ1161H23.1 (similar to acetyl-coenzyme A synthetase) [Homo sapiens]	280	73	6.00E-75
00339_HH	8	AB022690.1	AB022690 Solanum tuberosum gene for 3-hydroxy-3-methylglutaryl coenzyme A reductase, complete cds	42.1	100	0.22
00340_HN	1	AAB52621.2	(U47144) weak similarity over a short region to Plasmodium vivax merozoite surface antigen 1 (GB:M94420) [Caenorhabditis elegans]	97.5	34	8.00E-20
00342_HH	1	CAB91803.1	(AL356192) probable ubiquitin--protein ligase [Neurospora crassa]	53.9	50	1.00E-06
00342_HN	1	AAF46011.1	(AE003433) Akap550 gene product [Drosophila melanogaster]	75.7	49	3.00E-13
00343_HN	1	AAF89988.1	AF210630_1 (AF210630) unknown [Rhizobium leguminosarum]	55	27	5.00E-07
00344_HH	1	AAF57834.1	(AE003802) CG6501 gene product [Drosophila melanogaster]	35.6	43	0.35
00344_HN	2	P70711	UB5D_RAT UBIQUITIN-CONJUGATING ENZYME E2-17 KD 4 (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 4) gb|AAC52942.1| (U56407) Ubiquitin conjugating enzyme [Rattus norvegicus]	196	61	1.00E-49
00345_HN	1	Q25011	FANA_HELAS FMRFAMIDE-ACTIVATED AMILORIDE-SENSITIVE SODIUM CHANNEL (FANACH) pir||S68434 FMRFamide-activated sodium channel protein, amiloride-sensitive - brown garden snail emb|CAA63084.1| (X92113) FMRFamide-activated amiloride-sensitive sodium channel [Helix aspersa] prf||2202327A FMRFamide-gated Na channel [Helix aspersa]	43.8	24	0.001
00346_HH	1	T24871	hypothetical protein T12G3.5 - Caenorhabditis elegans emb|CAA92984.1| (Z68752) T12G3.5 [Caenorhabditis elegans]	51.9	43	4.00E-06
00347_HN	1	AC007738.2	AC007738 Homo sapiens clone NH0032P22, complete sequence	42.1	100	0.22
00348_HH	1	T40225	hypothetical protein SPBC32F12.01c - fission yeast (Schizosaccharomyces pombe) (fragment) emb|CAA19362.1| (AL023796) putative lipid metabolism protein [Schizosaccharomyces pombe]	64.8	40	6.00E-10
00349_HH	4	NP_033859.1	ATPase-like vacuolar proton channel sp|P23967|VATL_MOUSE VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT pir||JN0063 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain - mouse pir||JX0226 H+-transporting ATPase (EC 3.6.1.35) 16K chain, vacuolar - rat gb|AAA39775.1| (M64298) vacuolar H(+)-ATPase [Mus musculus] gb|AAC52413.1| (U13842) vacuolar adenosine triphosphatase subunit c [Mus musculus] dbj|BAA01643.1| (D10874) H(+)-transporting ATPase [Rattus norvegicus]	189	75	2.00E-47
00351_HH	5	O01802	RL7_CAEEL PROBABLE 60S RIBOSOMAL PROTEIN L7 pir||T29034 hypothetical protein F53G12.10 - Caenorhabditis elegans gb|AAB54165.1| (AF003139) strong similarity to the L30P family of ribosomal proteins [Caenorhabditis elegans]	155	61	4.00E-37
00351_HN	2	P13983	EXTN_TOBAC EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) pir||S06733 hydroxyproline-rich glycoprotein precursor - common tobacco emb|CAA32090.1| (X13885) extensin (AA 1-620) [Nicotiana tabacum]	40.2	35	0.014
00352_HN	3	NP_058022.1	cell division cycle 37 homolog (S. cerevisiae) gb|AAB18761.1| (U43076) cdc37 homolog [Mus musculus]	122	42	2.00E-27
00353_HN	2	NP_058809.1	granulin sp|P23785|GRN_RAT GRANULINS PRECURSOR (ACROGRANIN) [CONTAINS: GRANULIN 1 (GRANULIN G); GRANULIN 2 (GRANULIN F); GRANULIN 3 (GRANULIN B) (EPITHELIN 2); GRANULIN 4 (GRANULIN A) (EPITHELIN 1); GRANULIN 5 (GRANULIN C); GRANULIN 6 (GRANULIN D); GRANULIN 7 (GRANULIN E)] gb|AAA16903.1| (M97750) granulin [Rattus norvegicus]	132	42	3.00E-30
00354_HN	1	NP_031865.1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15 (RNA helicase A) sp|O35286|DD15_MOUSE PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 15) gb|AAC36129.1| (AF017153) putative RNA helicase and RNA dependent ATPase [Mus musculus]	307	88	5.00E-83
00356_HN	2	AAA96714.1	(L40328) ATPase [Schistosoma mansoni]	295	89	2.00E-79
00357_HN	1	AAB80628.1	(AC002376) EST gb|T04104 comes from this gene. [Arabidopsis thaliana]	34.4	25	0.8
00359_HN	1	AAF17610.1	AF206715_1 (AF206715) transcription factor GT-3a [Arabidopsis thaliana] emb|CAB81921.1| (AL161746) transcription factor GT-3a [Arabidopsis thaliana]	36.7	30	0.16
00361_HN	4	Q08200	RL10_CHICK 60S RIBOSOMAL PROTEIN L10 (JUN-BINDING PROTEIN JIF-1) pir||A48226 ribosomal protein L10, cytosolic - chicken (fragment) gb|AAA48928.1| (L13234) Jun-binding protein [Gallus gallus]	281	81	3.00E-75
00363_HN	1	AAF50647.1	(AE003561) CG10115 gene product [Drosophila melanogaster]	41.4	24	0.006
00370_HN	2	T15494	hypothetical protein C14F11.1 - Caenorhabditis elegans gb|AAA80361.1| (U39645) similar to aspartate aminotransferase [Caenorhabditis elegans]	218	61	3.00E-56
00371_HN	2	NP_003785.1	sorting nexin 4 gb|AAC83149.1| (AF065485) sorting nexin 4 [Homo sapiens]	52.7	31	2.00E-06
00372_HN	1	P21894	SYA_BOMMO ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) pir||SYMTAT alanine--tRNA ligase (EC 6.1.1.7) - silkworm gb|AAA27821.1| (M55993) transfer RNA-Ala synthetase [Bombyx mori]	148	45	5.00E-35

00377_HN	7	AAD11976.1	(AF040386) calponin homolog [Schistosoma japonicum]	241	75	4.00E-63
00380_HN	2	T21956	hypothetical protein F38B7.3 - Caenorhabditis elegans emb|CAA98477.1| (Z74033) similar to PH (pleckstrin homology) domain~cDNA EST yk117e9.3 comes from this gene~cDNA EST yk117e9.5 comes from this gene~cDNA EST yk500e4.3 comes from this gene~cDNA EST yk444h8.3 comes from this gene~cDNA EST yk444h8.5 comes from this gene>	66	31	3.00E-10
00382_HN	1	NP_036651.1	Ca++/calmodulin-dependent protein kinase II, delta subunit sp|P15791|KCCD_RAT CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM-KINASE II DELTA CHAIN) (CAMK-II, DELTA SUBUNIT) pir||A34366 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II delta chain - rat gb|AAA40866.1| (J05072) calmodulin-dependent protein kinase II-delta (EC 2.7.1.37) [Rattus norvegicus]	240	81	1.00E-73
00383_HN	2	T00631	hypothetical protein T27I1.14 - Arabidopsis thaliana gb|AAC34337.1| (AC004122) Hypothetical protein [Arabidopsis thaliana]	36.4	39	0.21
00384_HH	2	AAA81125.1	(U40029) exon 5 contains a tRNA-Leu [Caenorhabditis elegans]	68.3	24	5.00E-11
00385_HH	3	AAD51625.1	AF169022_1 (AF169022) seed maturation protein PM37 [Glycine max]	104	46	6.00E-22
00388_HH	1	T42228	P-glycoprotein sister - rat gb|AAC24753.1| (AF010597) P-glycoprotein sister [Rattus norvegicus]	102	35	2.00E-21
00391_HN	2	T13799	neurexin IV - fruit fly (Drosophila melanogaster) emb|CAA60383.1| (X86685) neurexin IV [Drosophila melanogaster]	119	40	2.00E-26
00393_HN	1	NP_014999.1	Yor354cp pir||S67266 hypothetical protein YOR354c - yeast (Saccharomyces cerevisiae) emb|CAA99683.1| (Z75262) ORF YOR354c [Saccharomyces cerevisiae]	32.1	23	3.9
00394_HH	1	AAB80763.1	(AF022391) immediate early protein; ICP0 [Feline herpesvirus 1]	57.8	40	7.00E-08
00394_HN	2	CAA73041.1	(Y12431) 5S ribosomal protein [Mus musculus]	225	68	3.00E-58
00395_HH	3	P48605	TCPG_DROME T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA) (CCT-GAMMA) gb|AAF55350.1| (AE003714) Cctgamma gene product [Drosophila melanogaster]	229	65	1.00E-59
00396_HH	1	AAF56431.1	(AE003751) CG11857 gene product [Drosophila melanogaster]	164	57	5.00E-40
00398_HN	1	P29053	TF2B_RAT TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) (RNA POLYMERASE II ALPHA INITIATION FACTOR) pir||S26299 transcription initiation factor IIB - rat emb|CAA46766.1| (X65948) alpha initiation factor [Rattus norvegicus]	151	51	5.00E-36
00399_HH	1	NP_006357.1	adenylyl cyclase-associated protein 2 sp|P40123|CAP2_HUMAN ADENYLYL CYCLASE-ASSOCIATED PROTEIN 2 (CAP 2) pir||I38409 CAP2 - human gb|AAA20587.1| (U02390) CAP2 [Homo sapiens]	103	38	1.00E-21
00400_HH	8	AAB07727.1	(U67675) alpha-1 tubulin [Hirudo medicinalis] gb|AAB07890.1| (U67677) alpha-1 tubulin [Hirudo medicinalis]	310	89	8.00E-84
00400_HN	1	AAF08879.1	AF194848_1 (AF194848) NADH dehydrogenase [Montia diffusa]	32.5	28	3.1
00402_HN	1	NP_045257.1	39 sp|P24430|VGLH_HSVE4 GLYCOPROTEIN H PRECURSOR pir||VGBE41 glycoprotein H precursor - equine herpesvirus 4 (strain 1942) dbj|BAA03379.1| (D14486) ORF3; (gH) [Equine herpesvirus 4] gb|AAC59556.1| (AF030027) 39 [Equine herpesvirus 4]	31.3	29	6.9
00403_HH	22	AAF68949.1	AF231031_1 (AF231031) rasputin [Drosophila melanogaster]	115	42	4.00E-25
00403_HN	1	F72254	hypothetical protein TM1433 - Thermotoga maritima (strain MSB8) gb|AAD36503.1|AE001795_6 (AE001795) oxidoreductase, putative [Thermotoga maritima]	35.6	29	0.33
00405_HH	2	B44511	fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli gb|AAC77083.1| (AE000485) fumarase B= fumarate hydratase Class I; anaerobic isozyme [Escherichia coli]	149	54	2.00E-35
00406_HN	1	AAF56217.1	(AE003745) CG13604 gene product [Drosophila melanogaster]	68.3	52	5.00E-11
00407_HN	1	AAB86566.1	(AF030965) unknown [Schistosoma mansoni]	252	76	2.00E-66
00409_HN	1	NP_004662.1	Protein inhibitor of activated STAT X gb|AAC36705.1| (AF077954) protein inhibitor of activated STAT protein PIASx-beta [Homo sapiens]	100	52	9.00E-21
00410_HN	1	AL138775.6	AL138775 Human DNA sequence from clone RP5-933E2 on chromosome 10 Contains STSs and GSSs, complete sequence [Homo sapiens]	48.1	93	0.004
00412_HN	4	P31483	TIA1_HUMAN NUCLEOLYSIN TIA-1 (RNA-BINDING PROTEIN TIA-1) (P40-TIA-1) [CONTAINS: P15-TIA-1]	79.2	30	3.00E-14
00413_HH	5	A45935	dnaK-type molecular chaperone hsc70 - mouse gb|AAA37869.1| (M19141) heat shock protein 70 cognate [Mus musculus] gb|AAB18391.1| (U73744) heat shock 70 protein [Mus musculus]	300	87	5.00E-81
00416_HH	1	NP_003550.1	phosphatidylinositol-4-phosphate 5-kinase, type II, beta pdb|1BO1|A Chain A, Phosphatidylinositol Phosphate Kinase Type Ii Beta pdb|1BO1|B Chain B, Phosphatidylinositol Phosphate Kinase Type Ii Beta gb|AAB48596.1| (U85245) phosphatidylinositol-4-phosphate 5-kinase type II beta [Homo sapiens]	120	48	7.00E-27
00417_HH	2	Q27268	HE47_DROME PROBABLE ATP-DEPENDENT RNA HELICASE WM6 pir||S51601 DEAD-box RNA helicase WM6 - fruit fly (Drosophila melanogaster) gb|AAB65835.1| (L06018) DECD family putative RNA helicase [Drosophila melanogaster] emb|CAA56197.1| (X79802) WM6 [Drosophila melanogaster] gb|AAF52261.1| (AE003610) Hel25E gene product [Drosophila melanogaster]	204	87	6.00E-52
00417_HN	3	NP_033067.1	radixin emb|CAA43087.1| (X60672) radixin [Mus musculus]	208	58	3.00E-53
00419_HH	33	CAA69623.1	(Y08321) cathepsin L [Danio rerio]	164	51	4.00E-40
00419_HN	2	NP_005004.1	nucleobindin 2 sp|P80303|NEFA_HUMAN DNA-BINDING PROTEIN NEFA PRECURSOR pir||S55272 DNA-binding protein NEFA precursor - human emb|CAA54148.1| (X76732) NEFA protein [Homo sapiens] gb|AAC06300.1| (AF052642) DNA binding protein NEFA precursor [Homo sapiens] gb|AAC06301.1| (AF052643) DNA binding protein NEFA precursor [Homo sapiens] gb|AAC06302.1| (AF052644) DNA binding protein NEFA precursor [Homo sapiens]	149	42	2.00E-35
00420_HN	2	P11884	DHAM_RAT ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (ALDH CLASS 2) (ALDH1) (ALDH-E2) pir||S03564 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 2 precursor, mitochondrial - rat emb|CAA33101.1| (X14977) aldehyde dehydrogenase preprotein [Rattus norvegicus]	262	75	2.00E-69
00422_HH	2	P81656	VA5_POLDO VENOM ALLERGEN 5 (ANTIGEN 5) (AG5) (ALLERGEN POL D 5)	52.7	35	2.00E-06
00423_HN	1	AAF34697.1	(AF223578) secretion calcium-dependent activator protein [Drosophila melanogaster]	168	53	4.00E-41
00425_HH	1	U15038.1	SFU15038 Spodoptera frugiperda immunophilin FKBP46 mRNA, complete cds	48.1	100	0.004
00426_HH	3	AAF57871.1	(AE003803) CG4798 gene product [alt 1] [Drosophila melanogaster] gb|AAF57872.1| (AE003803) CG4798 gene product [alt 3] [Drosophila melanogaster]	180	64	1.00E-44
00427_HH	3	AAF49127.1	(AE003516) CG8782 gene product [Drosophila melanogaster]	254	69	6.00E-67
00428_HH	1	AAF19251.1	AC007130_1 (AC007130) similar to 3-hydroxyisobutyrate dehydrogenase [Rattus norvegicus]; similar to P29266 (PID:g416873) [Homo sapiens]	205	61	3.00E-52

00430_HN	1	T13160	protein CNK - fruit fly (Drosophila melanogaster) gb|AAC80557.1| (AF100152) connector enhancer of KSR protein CNK [Drosophila melanogaster] gb|AAF57874.1| (AE003803) cnk gene product [Drosophila melanogaster]	52.3	47	3.00E-06
00435_HN	1	O81395	DRTS_MAIZE BIFUNCTIONAL DIHYDROFOLATE REDUCTASE-THYMIDYLATE SYNTHASE (DHFR-TS) [INCLUDES: DIHYDROFOLATE REDUCTASE ; THYMIDYLATE SYNTHASE] pir||T01684 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - maize gb|AAC26003.1| (AF073488) bifunctional dihydrofolate reductase-thymidylate synthase [Zea mays]	220	60	9.00E-57
00438_HH	2	BAA34448.1	(AB018271) KIAA0728 protein [Homo sapiens]	88.5	32	4.00E-17
00439_HH	1	AAD41141.1	U87145_10 (U87145) ribosomal protein S5 [Toxoplasma gondii]	31.3	33	6.9
00439_HN	9	CAA75483.1	(Y15184) cytochrome oxidase III [Myxine glutinosa]	60.5	28	1.00E-08
00440_HH	1	AAC32602.1	(AF083029) caspase-3 [Gallus gallus]	115	42	2.00E-25
00441_HH	1	P53582	AMP1_HUMAN PUTATIVE METHIONINE AMINOPEPTIDASE 1 (METAP 1) (PEPTIDASE M 1) (KIAA0094) dbj|BAA07679.1| (D42084) KIAA0094 gene product is related to S.cerevisiae methionine aminopeptidase. [Homo sapiens]	152	45	2.00E-36
00445_HH	1	NP_001616.1	adenylate kinase 2 isoform a sp|P54819|KAD2_HUMAN ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL (ATP-AMP TRANSPHOSPHORYLASE) pir||G02248 adenylate kinase (EC 2.7.4.3) 2 - human gb|AAC52061.1| (U39945) adenylate kinase 2 [Homo sapiens] gb|AAB41790.1| (U84371) adenylate kinase 2A [Homo sapiens]	180	63	9.00E-45
00446_HH	3	NP_005713.1	ARP2 (actin-related protein 2, yeast) homolog sp|O15142|ARP2_HUMAN ACTIN-LIKE PROTEIN 2 gb|AAB64187.1| (AF006082) Arp2 [Homo sapiens]	297	82	6.00E-80
00446_HN	1	CAB38989.1	(AL034558) predicted using hexExon; MAL3P2.2 (PFC0165w), Hypothetical protein, len: 1676 aa [Plasmodium falciparum]	43	24	0.002
00448_HN	2	I50719	C-Delta-1 - chicken gb|AAC59689.1| (U26590) C-Delta-1 [Gallus gallus]	60.5	35	1.00E-08
00449_HH	1	NP_038785.1	granuphilin dbj|BAA84656.1| (AB025258) granuphilin-a [Mus musculus]	55.4	22	4.00E-07
00449_HN	1	1DGF	A Chain A, Human Erythrocyte Catalase pdb|1DGF|B Chain B, Human Erythrocyte Catalase pdb|1DGF|C Chain C, Human Erythrocyte Catalase pdb|1DGF|D Chain D, Human Erythrocyte Catalase pdb|1DGG|A Chain A, Human Erythrocyte Catalse Cyanide Complex pdb|1DGG|B Chain B, Human Erythrocyte Catalse Cyanide Complex pdb|1DGG|C Chain C, Human Erythrocyte Catalse Cyanide Complex pdb|1DGG|D Chain D, Human Erythrocyte Catalse Cyanide Complex	226	79	1.00E-58
00450_HH	1	AAF50903.1	(AE003571) CG15456 gene product [Drosophila melanogaster]	40.2	31	0.014
00450_HN	2	AAF56404.1	(AE003750) CG11844 gene product [Drosophila melanogaster]	78.4	36	4.00E-14
00452_HH	1	CAB55356.1	(Y17775) carnitine/acylcarnitine translocase [Homo sapiens]	194	59	7.00E-49
00453_HN	1	BAA81874.1	(AB022156) chaperonin containing TCP-1 beta subunit [Mus musculus]	263	77	7.00E-70
00454_HH	2	AAF68970.1	AF251145_1 (AF251145) Ran binding protein 7 [Drosophila melanogaster]	140	37	8.00E-33
00455_HH	2	NC_001993.1	Melanoplus sanguinipes entomopoxvirus, complete genome	46.1	100	0.014
00456_HN	1	CAB08591.1	(Z95327) Cleavage Stimulation Factor (CF-1, Polyadenylation Factor) 64 kD subunit [Homo sapiens]	113	56	1.00E-24
00457_HH	5	R3RT3	ribosomal protein S3 - rat	240	73	6.00E-63
00462_HN	2	P09806	RF4_KLULA RF4 PROTEIN pir||S07916 RF4 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 emb|CAA30138.1| (X07127) RF4 gene product (AA 1 - 428) [Kluyveromyces lactis] emb|CAA25335.1| (X00762) ORF3 [Kluyveromyces lactis] emb|CAA25570.1| (X01095) URFP4 (aa 1-428);(immunity determinant) [Kluyveromyces lactis]	34.4	36	0.8
00464_HN	1	CAB39045.1	(AL034559) hypothetical protein, PFC1015c [Plasmodium falciparum]	31.3	34	6.9
00465_HN	10	S64710	cysteine proteinase (EC 3.4.22.-) CPP32 - Chinese hamster	68.3	30	5.00E-11
00466_HH	2	JE0307	membrane protein - rat	87.4	34	9.00E-17
00467_HN	1	AAF17484.1	AF189776_1 (AF189776) NLI-interacting factor isoform R5; NLI/Ldb1/CLIM interacting factor [Gallus gallus]	201	63	3.00E-51
00468_HN	1	AC024861.1	AC024861 Caenorhabditis elegans clone Y71H2B, complete sequence	40.1	90	0.22
00469_HH	1	AAB94928.1	(AF038654) apolipophorin II [Aedes aegypti]	34.4	32	0.8
00469_HN	1	AAD49249.1	(AF159405) cytochrome b [Meriones unguiculatus]	33.6	33	1.4
00470_HH	2	AAB84398.1	(AF026507) mitochondrial processing protease beta precursor [Drosophila silvestris]	116	45	2.00E-25
00470_HN	2	AE002140.1	AE002140 Ureaplasma urealyticum section 41 of 59 of the complete genome	46.1	100	0.014
00471_HH	3	BAA32798.1	(AB012391) Na+/K+-ATPase alpha-subunit [Dugesia japonica]	237	77	5.00E-62
00471_HN	5	AAC24752.1	(AF008300) transglutaminase precursor [Dirofilaria immitis]	176	49	1.00E-43
00472_HN	2	D71614	hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum) gb|AAC71881.1| (AE001396) hypothetical protein [Plasmodium falciparum]	33.2	24	1.8
00473_HH	1	P19891	ASNS_CRIGR ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) pir||AJHYNC asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) - Chinese hamster gb|AAA36977.1| (M27838) asparagine synthetase [Cricetulus longicaudatus]	161	53	4.00E-39
00474_HH	2	AAC47308.1	(U63744) p21-activated kinase CePAK [Caenorhabditis elegans]	67.9	26	7.00E-11
00474_HN	1	T28793	diacylglycerol kinase - Caenorhabditis elegans gb|AAC48134.1| (U49946) diacylglycerol kinase [Caenorhabditis elegans]	178	57	3.00E-44
00478_HN	2	AAD34860.1	AF139987_3 (AF139987) Wbscr1 alternative spliced product [Mus musculus]	112	55	2.00E-24
00479_HH	4	T18501	hypothetical protein C0760c - Plasmodium falciparum emb|CAB11140.1| (Z98551) hypothetical protein, PFC0760c [Plasmodium falciparum]	48.8	26	4.00E-05
00479_HN	11	NP_005902.1	methionine adenosyltransferase II, alpha sp|P31153|METK_HUMAN S-ADENOSYLMETHIONINE SYNTHETASE GAMMA FORM (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) (MAT-II) pir||S27257 methionine adenosyltransferase (EC 2.5.1.6) 2 alpha chain - human emb|CAA48726.1| (X68836) S-adenosylmethionine synthetase [Homo sapiens] prf||2121386A Met adenosyltransferase:SUBUNIT=alpha [Homo sapiens]	240	69	7.00E-63
00480_HN	3	P19483	ATP0_BOVIN ATP SYNTHASE ALPHA CHAIN HEART ISOFORM, MITOCHONDRIAL PRECURSOR pir||PWBOA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain precursor, cardiac - bovine emb|CAA45865.1| (X64565) H(+)-transporting ATP synthase [Bos taurus] gb|AAB59266.1| (M22465) alpha subunit ATP synthase isoform precursor (EC 3.6.1.34) [Bos taurus]	206	64	1.00E-52
00481_HH	1	CAB08110.1	(Z94160) dJ63G5.3 (putative Leucine rich protein) [Homo sapiens]	49.6	32	2.00E-05

<table>
<tr><td>00481_HN</td><td>1</td><td>O14359</td><td>YB4E_SCHPO HYPOTHETICAL 27.4 KD PROTEIN C30D10.14 IN CHROMOSOME II pir||T40182 conserved hypothetical protein SPBC30D10.14 - fission yeast (Schizosaccharomyces pombe) emb|CAB10809.1| (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]</td><td>55.8</td><td>28</td><td>3.00E-07</td></tr>
<tr><td>00482_HH</td><td>1</td><td>NP_061943.1</td><td>hypothetical protein dbj|BAA91606.1| (AK001294) unnamed protein product [Homo sapiens]</td><td>144</td><td>49</td><td>5.00E-34</td></tr>
<tr><td>00483_HH</td><td>1</td><td>AAF51167.1</td><td>(AE003581) CG3558 gene product [Drosophila melanogaster]</td><td>46.1</td><td>48</td><td>2.00E-04</td></tr>
<tr><td>00484_HN</td><td>1</td><td>AAC28261.1</td><td>(AF035566) transposase [Drosophila teissieri]</td><td>70.6</td><td>34</td><td>1.00E-11</td></tr>
<tr><td>00485_HN</td><td>1</td><td>BAA91881.1</td><td>(AK001750) unnamed protein product [Homo sapiens]</td><td>32.8</td><td>26</td><td>2.3</td></tr>
<tr><td>00486_HN</td><td>1</td><td>AAC60207.1</td><td>(U65893) carbamoyl-phosphate synthetase III [Oncorhynchus mykiss]</td><td>220</td><td>62</td><td>5.00E-57</td></tr>
<tr><td>00487_HH</td><td>2</td><td>AAF89953.1</td><td>AF175265_1 (AF175265) vacuolar sorting protein 35 [Homo sapiens]</td><td>125</td><td>38</td><td>4.00E-28</td></tr>
<tr><td>00487_HN</td><td>1</td><td>Q60301</td><td>YY02_METJA HYPOTHETICAL PROTEIN MJECS02 pir||B64516 hypothetical protein MJECS02 - Methanococcus jannaschii plasmid pURB801 gb|AAC37060.1| (L77119) M. jannaschii predicted coding region MJECS02 [Methanococcus jannaschii]</td><td>36.7</td><td>28</td><td>0.16</td></tr>
<tr><td>00488_HH</td><td>1</td><td>AAF49462.1</td><td>(AE003527) CG4561 gene product [Drosophila melanogaster]</td><td>85.8</td><td>34</td><td>3.00E-16</td></tr>
<tr><td>00490_HH</td><td>1</td><td>T21992</td><td>hypothetical protein F39B2.11 - Caenorhabditis elegans emb|CAB07391.1| (Z92834) cDNA EST yk364c2.3 comes from this gene~cDNA EST yk368f11.3 comes from this gene~cDNA EST yk368f11.5 comes from this gene~cDNA EST yk364d2.3 comes from this gene~cDNA EST yk364d2.5 comes from this gene~cDNA EST yk364c2.5 comes from this gene~c></td><td>67.9</td><td>25</td><td>7.00E-11</td></tr>
<tr><td>00490_HN</td><td>1</td><td>AL135787.13</td><td>AL135787 Human DNA sequence from clone RP11-16L21 on chromosome 9, complete sequence [Homo sapiens]</td><td>54</td><td>100</td><td>6.00E-05</td></tr>
<tr><td>00492_HH</td><td>1</td><td>AAD54016.1</td><td>AF090435_1 (AF090435) cytochrome P450 2N2 [Fundulus heteroclitus]</td><td>72.6</td><td>29</td><td>3.00E-12</td></tr>
<tr><td>00493_HH</td><td>1</td><td>NP_048273.1</td><td>ORF MSV202 hypothetical protein gb|AAC97758.1| (AF063866) ORF MSV202 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]</td><td>34.4</td><td>29</td><td>0.8</td></tr>
<tr><td>00496_HN</td><td>2</td><td>NP_036617.1</td><td>hyaluronan-mediated motility receptor (RHAMM)</td><td>42.2</td><td>24</td><td>0.003</td></tr>
<tr><td>00498_HN</td><td>9</td><td>AAF00500.1</td><td>AF182946_1 (AF182946) BRCA1-associated RING domain protein 1 [Rattus norvegicus]</td><td>64.4</td><td>36</td><td>7.00E-10</td></tr>
<tr><td>00499_HN</td><td>1</td><td>JQ1161</td><td>Gag protein - Maedi/Visna virus (strain EV1)</td><td>39.5</td><td>53</td><td>0.024</td></tr>
<tr><td>00501_HH</td><td>1</td><td>AAF56946.1</td><td>(AE003771) CG18112 gene product [Drosophila melanogaster]</td><td>32.5</td><td>26</td><td>3.1</td></tr>
<tr><td>00502_HN</td><td>1</td><td>CAB87808.1</td><td>(AJ269539) TEP2 protein [Drosophila melanogaster]</td><td>74.9</td><td>33</td><td>5.00E-13</td></tr>
<tr><td>00503_HH</td><td>1</td><td>AAC97497.1</td><td>(AF095927) protein phosphatase 2C [Rattus norvegicus]</td><td>45.3</td><td>40</td><td>4.00E-04</td></tr>
<tr><td>00503_HN</td><td>1</td><td>Z84487.2</td><td>HS346O6 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 346O6, complete sequence [Homo sapiens]</td><td>44.1</td><td>100</td><td>0.018</td></tr>
<tr><td>00504_HH</td><td>6</td><td>CAA76577.1</td><td>(Y17003) polyubiquitin [Suberites domuncula]</td><td>322</td><td>99</td><td>1.00E-87</td></tr>
<tr><td>00505_HN</td><td>3</td><td>AAC39086.1</td><td>(AF017096) region with similarity to Homo sapiens TAFII55 encoded by Genbank Accession Number U18062 and C. elegans unknown protein encoded by Genbank Accession Number Z67755 [Drosophila melanogaster]</td><td>122</td><td>39</td><td>3.00E-27</td></tr>
<tr><td>00508_HN</td><td>1</td><td>NP_055490.1</td><td>KIAA0445 gene product dbj|BAA32290.1| (AB007914) KIAA0445 protein [Homo sapiens] emb|CAB96825.1| (AL049569) dJ37C10.5 (KIAA0445) [Homo sapiens]</td><td>113</td><td>34</td><td>1.00E-24</td></tr>
<tr><td>00512_HH</td><td>1</td><td>U17336.1</td><td>IBU17336 Ipomoea batatas clone PGEM-TIC sporamin mRNA, partial cds</td><td>44.1</td><td>100</td><td>0.057</td></tr>
<tr><td>00514_HN</td><td>1</td><td>T21044</td><td>hypothetical protein F17A2.9 - Caenorhabditis elegans emb|CAA92160.1| (Z68114) F17A2.9 [Caenorhabditis elegans]</td><td>33.6</td><td>22</td><td>1.4</td></tr>
<tr><td>00515_HH</td><td>2</td><td>B71614</td><td>probable multiple transmembrane domain protein PFB0485c - malaria parasite (Plasmodium falciparum) gb|AAC71886.1| (AE001397) predicted multiple transmembrane domain protein [Plasmodium falciparum]</td><td>37.9</td><td>28</td><td>0.07</td></tr>
<tr><td>00515_HN</td><td>2</td><td>P35558</td><td>PPCC_HUMAN PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC [GTP] (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK-C)</td><td>246</td><td>67</td><td>1.00E-64</td></tr>
<tr><td>00516_HH</td><td>2</td><td>P35418</td><td>MYSP_TAESO PARAMYOSIN (PMY) (ANTIGEN B) gb|AAA16278.1| (L13723) paramyosin [Taenia solium]</td><td>192</td><td>64</td><td>3.00E-48</td></tr>
<tr><td>00517_HH</td><td>1</td><td>O02695</td><td>PTPX_MACNE PROTEIN-TYROSINE PHOSPHATASE X PRECURSOR (R-PTP-X) (M1851) gb|AAC51186.1| (U91574) M1851 [Macaca nemestrina]</td><td>69.5</td><td>53</td><td>2.00E-11</td></tr>
<tr><td>00517_HN</td><td>1</td><td>AAB86570.1</td><td>(AF030969) unknown [Schistosoma mansoni]</td><td>150</td><td>50</td><td>9.00E-36</td></tr>
<tr><td>00518_HN</td><td>1</td><td>T22736</td><td>hypothetical protein F55F3.3 - Caenorhabditis elegans emb|CAB04477.1| (Z81550) predicted using Genefinder~similar to Sodium and potassium ATPases~cDNA EST yk192h3.5 comes from this gene~cDNA EST yk578d8.5 comes from this gene [Caenorhabditis elegans]</td><td>80.4</td><td>33</td><td>1.00E-14</td></tr>
<tr><td>00519_HN</td><td>1</td><td>AAF25689.1</td><td>AF222717_1 (AF222717) myosin PfM-C [Plasmodium falciparum]</td><td>36.4</td><td>25</td><td>0.2</td></tr>
<tr><td>00523_HH</td><td>1</td><td>AAD30963.2</td><td>(AF118151) SNF1/AMP-activated kinase [Dictyostelium discoideum]</td><td>36.7</td><td>35</td><td>0.16</td></tr>
<tr><td>00523_HN</td><td>1</td><td>P35669</td><td>GSHB_SCHPO GLUTATHIONE SYNTHETASE LARGE CHAIN (GLUTATHIONE SYNTHASE LARGE CHAIN) (GSH SYNTHETASE LARGE CHAIN) (GSH-S) (PHYTOCHELATIN SYNTHETASE) pir||T38705 glutathione synthetase large chain - fission yeast (Schizosaccharomyces pombe) emb|CAA93302.1| (Z69369) glutathione synthetase large chain [Schizosaccharomyces pombe] emb|CAA69691.1| (Y08414) phytochelatin-synthetase [Schizosaccharomyces pombe]</td><td>34.8</td><td>38</td><td>0.61</td></tr>
<tr><td>00524_HN</td><td>1</td><td>BAB11811.1</td><td>(AB030901) MKK4 [Danio rerio]</td><td>161</td><td>58</td><td>4.00E-39</td></tr>
<tr><td>00525_HN</td><td>1</td><td>NP_035536.1</td><td>solute carrier family 8 (sodium/calcium exchanger), member 1 gb|AAB69167.1| (AF004666) sodium-calcium exchanger [Mus musculus]</td><td>178</td><td>55</td><td>4.00E-44</td></tr>
<tr><td>00526_HH</td><td>1</td><td>CAB92314.1</td><td>(AJ278120) putative ankyrin-repeat containing protein [Homo sapiens]</td><td>58.6</td><td>38</td><td>4.00E-08</td></tr>
<tr><td>00527_HN</td><td>1</td><td>AAF55812.1</td><td>(AE003732) CG15694 gene product [Drosophila melanogaster]</td><td>133</td><td>38</td><td>9.00E-31</td></tr>
<tr><td>00529_HN</td><td>1</td><td>CAB71312.1</td><td>(AJ130879) proline racemase [Clostridium sticklandii]</td><td>109</td><td>39</td><td>1.00E-23</td></tr>
<tr><td>00530_HN</td><td>1</td><td>NP_000982.1</td><td>ribosomal protein L28 sp|P46779|RL28_HUMAN 60S RIBOSOMAL PROTEIN L28 pir||S55915 ribosomal protein L28 - human gb|AAA85657.1| (U14969) ribosomal protein L28 [Homo sapiens] prf||2113200D ribosomal protein L28 [Homo sapiens]</td><td>76.5</td><td>34</td><td>1.00E-13</td></tr>
<tr><td>00533_HH</td><td>11</td><td>AAD31042.1</td><td>AF144646_1 (AF144646) heat shock protein 70 [Crassostrea gigas]</td><td>240</td><td>71</td><td>1.00E-62</td></tr>
<tr><td>00535_HN</td><td>1</td><td>B75441</td><td>conserved hypothetical protein - Deinococcus radiodurans (strain R1) gb|AAF10633.1|AE001957_1 (AE001957) conserved hypothetical protein [Deinococcus radiodurans]</td><td>71</td><td>45</td><td>8.00E-12</td></tr>
<tr><td>00538_HN</td><td>1</td><td>AAC26868.1</td><td>(AF074334) cyclin H homolog [Drosophila melanogaster] gb|AAF51784.1| (AE003595) CycH gene product [Drosophila melanogaster]</td><td>97.1</td><td>32</td><td>1.00E-19</td></tr>
<tr><td>00540_HH</td><td>1</td><td>AAF53988.1</td><td>(AE003670) CG18362 gene product [alt 1] [Drosophila melanogaster] gb|AAF53989.1| (AE003670) CG18362 gene product [alt 2] [Drosophila melanogaster]</td><td>125</td><td>54</td><td>2.00E-28</td></tr>
<tr><td>00540_HN</td><td>1</td><td>AAB53983.1</td><td>(AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]</td><td>53.1</td><td>26</td><td>2.00E-06</td></tr>
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00542_HH	2	AAF56580.1	(AE003755) Ald gene product [alt 1] [Drosophila melanogaster]	217	65	8.00E-56
00542_HN	1	AAD48063.1	AF172605_1 (AF172605) major vault protein [Mytilus edulis]	215	58	3.00E-55
00543_HH	1	AAC64633.1	(AF077541) contains similarity to class-I aminoacyl-tRNA synthetases [Caenorhabditis elegans]	51.9	29	4.00E-06
00546_HN	1	NP_064356.1	sortilin 1 gb|AAF22639.1|AF175279_1 (AF175279) neurotensin receptor 3 [Mus musculus]	148	44	5.00E-35
00547_HN	1	CAB55498.1	(AJ249388) vacuolar ATPase subunit C [Manduca sexta]	198	57	4.00E-50
00549_HH	1	BAA06124.2	(D29641) KIAA0052 protein [Homo sapiens]	31.3	31	6.9
00551_HH	3	AAF51103.1	(AE003579) CG8844 gene product [Drosophila melanogaster]	110	44	1.00E-23
00554_HH	1	P31921	YCX2_EUGGR HYPOTHETICAL 59.8 KD PROTEIN IN PSBD INTRON 8 (ORF506) pir||S34497 hypothetical protein 506 (psbD 3' region) - Euglena gracilis chloroplast emb|CAA50078.1| (X70810) orf506 orf in PSII D2-polypeptide (psbD) [Euglena gracilis]	40.2	30	0.014
00559_HN	2	S23692	erythrocyte membrane-associated antigen (clone pPf K16) - Plasmodium falciparum (fragment)	43.8	30	0.001
00562_HH	1	T42440	phospholipase C homolog - Caenorhabditis elegans gb|AAC38963.1| (AF044576) phospholipase C PLC210 [Caenorhabditis elegans]	57	30	1.00E-07
00564_HN	6	Q92122	KPYK_XENLA PYRUVATE KINASE, MUSCLE ISOZYME (CYTOSOLIC THYROID HORMONE BINDING PROTEIN) (CTHBP) pir||S51374 pyruvate kinase (EC 2.7.1.40), muscle - clawed frog gb|AAA63581.1| (U03878) cytosolic thyroid hormone binding protein/pyruvate kinase type M2 [Xenopus laevis]	142	45	2.00E-34
00565_HH	1	CAA70018.1	(Y08765) SF1-HI1 isoform [Homo sapiens]	74.9	40	5.00E-13
00565_HN	2	S49423	hypothetical protein - Lactobacillus helveticus emb|CAA57503.1| (X81980) orf [Lactobacillus helveticus]	34	38	1
00566_HN	1	AAC31815.1	(AF076183) cytosolic sorting protein PACS-1a [Rattus norvegicus]	35.6	26	0.35
00567_HN	7	P21187	PABP_DROME POLYADENYLATE-BINDING PROTEIN (POLY(A) BINDING PROTEIN) (PABP) gb|AAA70421.1| (L05109) poly(A)-binding protein [Drosophila melanogaster]	83.5	42	1.00E-15
00568_HH	1	NP_001448.1	filamin 1 (actin-binding protein-280)-like gb|AAC39842.1| (AF042166) beta-filamin [Homo sapiens] gb|AAF72339.1| (AF191633) filamin [Homo sapiens]	176	50	1.00E-43
00569_HN	1	T21925	hypothetical protein F37H8.2 - Caenorhabditis elegans emb|CAB04348.2| (Z81534) F37H8.2 [Caenorhabditis elegans] emb|CAA87377.2| (Z47074) F37H8.2 [Caenorhabditis elegans]	33.2	23	1.8
00570_HH	2	NP_033037.1	RAD23b homolog (S. cerevisiae) sp|P54728|R23B_MOUSE UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B (MHR23B) (XP-C REPAIR COMPLEMENTING COMPLEX 58 KDA PROTEIN) (P58) emb|CAA63146.1| (X92411) MHR23B [Mus musculus] prf||2206377B MHR23B gene [Mus musculus]	116	37	2.00E-25
00570_HN	1	NP_032155.1	glutamate cysteine ligase (gamma-glutamylcysteine synthetase), regulatory gb|AAB96893.1| (U95053) glutamate-cysteine ligase regulatory subunit [Mus musculus]	81.5	38	5.00E-15
00571_HN	1	NC_001718.1	Porcine parvovirus strain NADL-2	40.1	95	0.88
00572_HN	1	CAB96536.1	(AJ278608) myosin VI [Gallus gallus]	103	71	8.00E-45
00573_HH	1	AAA40873.1	(M31602) carboxypeptidase E (EC 3.4.17.10) [Rattus norvegicus]	145	47	2.00E-34
00574_HH	2	S50114	DNA helicase Q1 - human dbj|BAA07200.1| (D37984) DNA helicase Q1 [Homo sapiens]	105	43	3.00E-22
00574_HN	7	T08810	probable ABC-type transport protein DKFZp586K1823.1 - human emb|CAB43392.1| (AL050291) hypothetical protein [Homo sapiens]	115	54	2.00E-25
00575_HN	1	D75002	chemotaxis histidine kinase (chea) PAB1332 - Pyrococcus abyssi (strain Orsay) emb|CAB50458.1| (AJ248288) chemotaxis histidine kinase (cheA) [Pyrococcus abyssi]	30.9	26	9.1
00578_HH	4	P32429	RL7A_CHICK 60S RIBOSOMAL PROTEIN L7A pir||S18159 ribosomal protein L7a, cytosolic - chicken emb|CAA44506.1| (X62640) ribosomal protein L7a [Gallus gallus] dbj|BAA03395.1| (D14522) ribosomal protein L7a [Gallus gallus]	176	63	1.00E-43
00580_HH	1	AAB48410.1	(U75538) putative 2b protein [tobacco streak virus]	36	29	0.27
00581_HH	24	AAC00518.1	(AF044411) glutathione S-transferase [Schistosoma japonicum]	129	41	2.00E-29
00582_HH	9	AAF31683.1	AF178680_1 (AF178680) NADH dehydrogenase subunit 1 [Helobdella robusta]	32.8	26	2.3
00582_HN	1	NP_032016.1	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived) pir||I48346 ribosomal protein fau - mouse emb|CAA46715.1| (X65922) fau [Mus musculus] gb|AAA91564.1| (L33715) Fau gene product [Mus musculus] dbj|BAA05655.1| (D26610) monoclonal nonspecific suppressor factor beta [Mus musculus] gb|AAF80246.1|AF147745_1 (AF147745) monoclonal non-specific suppressor factor beta [Mus musculus]	122	48	2.00E-27
00583_HH	2	AAD16120.1	(AF094508) dentin phosphoryn [Homo sapiens]	37.9	43	0.07
00583_HN	6	AAC50892.1	(U69126) FUSE binding protein 2 [Homo sapiens]	86.6	35	2.00E-16
00584_HH	4	O02350	CBPA_ANOGA ZINC CARBOXYPEPTIDASE A PRECURSOR gb|AAB96576.1| (AF000953) carboxypeptidase A [Anopheles gambiae].	70.2	26	1.00E-11
00586_HH	4	Q04820	MDHC_ECHGR MALATE DEHYDROGENASE, CYTOPLASMIC pir||T09228 malate dehydrogenase (EC 1.1.1.37), cytosolic - tapeworm (Echinococcus granulosus) gb|AAC28239.1| (L08894) malate dehydrogenase [Echinococcus granulosus]	226	70	9.00E-59
00586_HN	1	BAA13219.1	(D86983) similar to D.melanogaster peroxidasin(U11052) [Homo sapiens] gb|AAF06354.1|AF200348_1 (AF200348) melanoma-associated antigen MG50 [Homo sapiens]	43.8	28	0.001
00587_HH	1	O01258	YLNO_CAEEL HYPOTHETICAL 37.4 KD PROTEIN T20D3.7 IN CHROMOSOME IV pir||T25029 hypothetical protein T20D3.7 - Caenorhabditis elegans emb|CAA92489.1| (Z68220) Similarity to Mouse H(beta)58 protein (SW:HB58_MOUSE) [Caenorhabditis elegans]	149	46	2.00E-35
00588_HH	3	AAB36702.1	(U68754) putative transcription factor [Dictyostelium discoideum]	33.2	30	1.8
00590_HH	1	AAF53049.1	(AE003630) RpL9 gene product [alt 1] [Drosophila melanogaster]	161	56	5.00E-39
00593_HN	1	AAF54883.1	(AE003698) CG7472 gene product [Drosophila melanogaster]	38.7	29	0.041
00595_HN	1	AAC56774.1	(U69463) envelope glycoprotein [Human immunodeficiency virus type 1]	34	43	1
00596_HN	1	P31319	KAPR_APLCA CAMP-DEPENDENT PROTEIN KINASE REGULATORY CHAIN (N4 SUBUNIT OF PROTEIN KINASE A) pir||OKGAR1 protein kinase (EC 2.7.1.37), cAMP-dependent, type I regulatory chain - California sea hare emb|CAA44246.1| (X62382) type N4 regulatory subunit of protein kinase A [Aplysia californica]	271	77	4.00E-72
00597_HH	1	AAF15366.1	AF206632_1 (AF206632) ring-infested erythrocyte surface antigen [Plasmodium falciparum]	44.5	26	7.00E-04

00597_HN	1	NP_001753.1	chaperonin containing T-complex subunit 6 sp|P40227|TCPZ_HUMAN T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (CCT-ZETA-1) (TCP20) (HTR3) pir||S48087 t-complex-type molecular chaperone CCT6 - human gb|AAA61061.1| (L27706) chaperonin-like protein [Homo sapiens]	239	75	1.00E-62
00598_HH	2	AAF51675.1	(AE003593) CG10577 gene product [Drosophila melanogaster]	146	44	1.00E-34
00599_HN	2	Q26619	KAPR_STRPU CAMP-DEPENDENT PROTEIN KINASE TYPE II REGULATORY CHAIN gb|AAA61966.1| (U19887) cyclic AMP-dependent protein kinase type II regulatory subunit [Strongylocentrotus purpuratus]	124	44	7.00E-28
00600_HN	1	NP_005069.1	transducin-like enhancer of split 3, homolog of Drosophila E(sp1) sp|Q04726|TLE3_HUMAN TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3) pir||D56695 transducin-like enhancer-of-split homolog TLE-3 - human gb|AAA61194.1| (M99438) transducin-like enhancer protein [Homo sapiens]	159	69	2.00E-38
00602_HH	1	T18739	hypothetical protein B0393.5 - Caenorhabditis elegans emb|CAA86058.1| (Z37983) contains five copies of the EGF-like aspartic acid and asparagine hydroxylation site (Prosite accession number PS00010)~cDNA EST yk3d6.3 comes from this gene~cDNA EST yk3d6.5 comes from this gene~cDNA EST yk200c10.3 comes from this gene~cDNA	128	43	4.00E-29
00604_HH	1	T32989	hypothetical protein C05D2.8 - Caenorhabditis elegans gb|AAC02725.1| (AF047651) C05D2.8 gene product [Caenorhabditis elegans]	53.5	33	1.00E-06
00604_HN	1	CAB48885.1	(AL031431) dJ462O23.2 (novel protein) [Homo sapiens]	66	32	3.00E-10
00607_HH	1	AAB59321.1	(L35564) ORF [Saccharomyces cerevisiae]	37.5	36	0.092
00608_HN	1	NP_002764.1	protease, serine, 8 (prostasin) sp|Q16651|PSS8_HUMAN PROSTASIN PRECURSOR pir||A57014 prostasin (EC 3.4.21.-) precursor - human gb|AAC41759.1| (L41351) prostasin [Homo sapiens] gb|AAB19071.1| (U33446) prostasin [Homo sapiens] prf||2208326A prostasin [Homo sapiens]	69.9	29	2.00E-11
00611_HH	5	P42638	TPM2_SCHMA TROPOMYOSIN 2 (TMII) gb|AAA29942.1| (M97555) tropomyosin [Schistosoma mansoni]	153	54	1.00E-36
00612_HN	7	T34092	hypothetical protein C07A12.4 - Caenorhabditis elegans gb|AAC69237.1| (U41542) Similar to protein disulfide isomerase; coded for by C. elegans cDNA CEESB65F; coded for by C. elegans cDNA CEESH23FB; coded for by C. elegans cDNA CEESH23FC; coded for by C. elegans cDNA CEESN70F; coded for by C. elegans cDNA CEESO88F; coded ~	201	60	3.00E-51
00613_HH	1	NP_036096.1	proteasome (prosome, macropain) subunit, alpha type 4 sp|Q9R1P0|PRC9_MOUSE PROTEASOME COMPONENT C9 (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9) gb|AAD50538.1|AF060093_1 (AF060093) proteasome subunit C9 [Mus musculus]	268	71	4.00E-71
00615_HH	2	BAB08808.1	(AB007649) gene_id:MLE2.6~pir||T01257~similar to unknown protein [Arabidopsis thaliana]	32.5	27	3.1
00617_HH	1	AAF55372.1	(AE003715) CG16941 gene product [Drosophila melanogaster]	99.8	46	2.00E-20
00617_HN	1	P75361	P115_MYCPN P115 PROTEIN HOMOLOG pir||S73741 P115 protein homolog A05_orf982 - Mycoplasma pneumoniae (strain ATCC 29342) gb|AAB96063.1| (AE000040) Mycoplasma pneumoniae, P115 protein homolog; similar to GenBank Accession Number JQ0894, from M. hyorhinis	39.1	26	0.031
00618_HH	2	B70356	chromosome assembly protein homolog - Aquifex aeolicus gb|AAC06839.1| (AE000699) chromosome assembly protein homolog [Aquifex aeolicus]	51.9	30	4.00E-06
00621_HN	1	AAA87180.1	(U20788) ORF-3 [Porcine reproductive and respiratory syndrome virus]	30.9	32	5
00622_HN	1	P22011	CYPH_CANAL PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) (CPH) pir||CSCK peptidylprolyl isomerase (EC 5.2.1.8) - yeast (Candida albicans) gb|AAA34336.1| (M60628) peptidyl-prolyl cis-trans isomerase [Candida albicans]	235	70	2.00E-61
00625_HN	1	AAC72233.1	(AF092090) cp151 [Rattus norvegicus]	37.1	26	0.12
00626_HN	1	AAB68893.1	(U10556) Nmd2p: Protein involved in decay of mRNA containing nonsense codons [Saccharomyces cerevisiae] gb|AAA74948.1| (U28158) Ifs1p [Saccharomyces cerevisiae]	32.5	36	3.1
00629_HH	1	P19226	CH60_MOUSE 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR (HSP60) (60 KDA CHAPERONIN) (CPN60) (HEAT SHOCK PROTEIN 60) (HSP-60) (MITOCHONDRIAL MATRIX PROTEIN P1) (HSP-65)	190	58	7.00E-48
00629_HN	3	CAB56566.1	(AL035701) dJ8B1.3 (similar to PLASMA-CELL MEMBRANE GLYCOPROTEIN PC-1) [Homo sapiens]	112	41	3.00E-24
00630_HN	1	AAD33905.2	AF143408_1 (AF143408) outer capsid protein VP4 [Human rotavirus MP409]	32.5	46	3.1
00631_HH	1	NP_004394.1	deafness, autosomal dominant 5; nonsyndromic hearing impairment protein gb|AAC69324.1| (AF073308) nonsyndromic hearing impairment protein [Homo sapiens]	44.5	19	7.00E-04
00632_HH	5	AAB41442.1	(U83906) putative cytosol aminopeptidase [Schistosoma mansoni]	147	49	6.00E-35
00632_HN	12	CAB42097.1	(AJ011646) N protein [Topografov hantavirus]	30.9	29	9.1
00633_HN	2	S72291	ribosomal protein S3 - Plasmodium falciparum plastid emb|CAA64581.1| (X95276) rps3 [Plasmodium falciparum]	32.1	30	4
00634_HH	8	CAA91440.1	(Z66536) C-type lectin-like protein [Girardia tigrina]	84.7	32	6.00E-16
00635_HH	3	NP_035897.1	zinc finger RNA binding protein pir||T14343 zinc finger RNA binding protein, chromosome-associated - mouse gb|AAC25762.1| (AF071059) zinc finger RNA binding protein [Mus musculus]	56.2	22	2.00E-07
00636_HN	1	T13413	probable alpha-actinin isoform 1 - fruit fly (Drosophila melanogaster) emb|CAA21121.1| (AL031765) alternatively spliced form [Drosophila melanogaster] emb|CAA15689.1| (AL009192) alternatively spliced form [Drosophila melanogaster]	161	48	4.00E-39
00637_HN	1	AL049780.3	CNS00007 Human chromosome 14 DNA sequence IN PROGRESS BAC R-950C14 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete	52	96	2.00E-04
00638_HN	1	CAA32663.1	(X14519) spectrin alpha-chain (AA 28 - 2479) (1 is 2nd base in codon) [Gallus gallus]	31.3	25	6.9
00640_HN	2	CAB62893.1	(AL035475) hypothetical protein, MAL4P2.52 [Plasmodium falciparum]	38.3	23	0.05
00641_HN	5	4JDW	A Chain A, Crystal Structure And Mechanism Of L-Arginine: Glycine Amidinotransferase: A Mitochondrial Enzyme Involved In Creatine Biosynthesis	73.4	34	2.00E-12
00642_HH	1	AAF49825.1	(AE003538) CG10191 gene product [Drosophila melanogaster]	153	42	1.00E-36
00642_HN	1	NP_037349.1	afadin pir||T41751 l-afadin - rat gb|AAC53390.1| (U83230) l-Afadin [Rattus norvegicus]	38.3	28	0.054
00643_HN	7	CAB71335.1	(AJ271729) glucose-regulated protein [Homo sapiens] gb|AAF42836.1|AF216292_1 (AF216292) endoplasmic reticulum lumenal Ca2+ binding protein grp78; BiP [Homo sapiens]	269	80	1.00E-71
00644_HH	1	AAF56679.1	(AE003759) CG6001 gene product [Drosophila melanogaster]	57.8	47	7.00E-08
00644_HN	1	I38346	elastic titin - human (fragment) emb|CAA62189.1| (X90569) elastic titin [Homo sapiens]	46.1	27	2.00E-04

00645_HH	1	AC016943.7	AC016943 Homo sapiens 3 BAC RP11-380G10 (Roswell Park Cancer Institute Human BAC Library) complete sequence	40.1	100	0.31
00645_HN	7	AAF23826.1	AF220042_1 (AF220042) tetraspanin [Drosophila melanogaster]	72.6	32	3.00E-12
00646_HH	1	AAF55181.1	(AE003708) CG5044 gene product [Drosophila melanogaster]	132	41	3.00E-30
00646_HN	1	AL031431.8	HS462O23 Human DNA sequence from clone 462O23 on chromosome 1p35.1-36.12. Contains genes for two novel proteins, ESTs, STSs, GSSs and putative CpG island, complete sequence [Homo sapiens]	42.1	100	0.22
00647_HH	3	AAF23186.1	U42847_4 (U42847) Hypothetical protein F39H12.4 [Caenorhabditis elegans]	41.4	24	0.006
00647_HN	1	NP_032942.1	putative phosphatase gb|AAC60757.1| (U96726) putative phosphoinositide 5-phosphatase type II; C62 [Mus musculus] gb|AAC53265.1| (U96724) putative phosphoinositide 5-phosphatase type II [Mus musculus]	62.8	25	2.00E-09
00649_HH	1	AAB58300.1	(AF001042) RNA editase [Homo sapiens]	71.4	37	6.00E-12
00650_HN	2	Q29024	HE47_PIG PROBABLE ATP-DEPENDENT RNA HELICASE P47 pir||I47126 nuclear RNA helicase (DEAD family) BAT1 - pig emb|CAA84355.1| (Z34846) BAT1 [Sus scrofa]	240	73	6.00E-63
00651_HN	1	AAD46412.1	AF096262_1 (AF096262) ER6 protein [Lycopersicon esculentum]	54.3	26	8.00E-07
00652_HN	1	AC004866.1	AC004866 Homo sapiens PAC clone RP4-728H9 from 7q11.23-q21.1, complete sequence	40.1	100	0.26
00653_HN	1	BAA34445.1	(AB018268) KIAA0725 protein [Homo sapiens]	147	50	6.00E-35
00654_HN	1	J01167.1	SUSACT1S2 sea urchin (s.purpuratus) actin gene 1, 3' flanking sequence	44.1	100	0.057
00655_HN	1	AAF49072.1	(AE003514) CG14185 gene product [Drosophila melanogaster]	48.4	28	5.00E-05
00657_HH	1	AAA62413.1	(M81388) DNA-directed RNA polymerase I largest subunit [Chilo iridescent virus] gb|AAB33907.1| (S75674) DNA-depenent RNA polymerase largest subunit homolog [Chilo iridescent virus CIV, insect iridescent virus type 6, Peptide, 1051 aa]	31.3	35	6.9
00657_HN	1	AL035070.3	HS1043L13 Human DNA sequence from clone 1043L13 on chromosome 20q13.2-13.33 Contains ESTs, STSs and GSSs, complete sequence [Homo sapiens]	48.1	100	0.004
00658_HH	1	AAF46795.1	(AE003456) CG6437 gene product [Drosophila melanogaster]	121	50	6.00E-27
00658_HN	1	AAF48271.1	(AE003492) CG1998 gene product [Drosophila melanogaster]	115	44	3.00E-25
00661-HH	1	AAD43026.1	(AF100762) thyroid receptor interactor trip15 [Homo sapiens]	260	76	8.00E-69
00662_HH	1	AAG01854.1	AF289023_1 (AF289023) formiminotransferase cyclodeaminase form D [Homo sapiens]	151	45	5.00E-36
00662_HN	1	T19287	hypothetical protein C14H10.2 - Caenorhabditis elegans emb|CAA90738.2| (Z50863) weak similarity with paramyosin (Swiss Prot accession number P35418)~cDNA EST yk93b12.3 comes from this gene~cDNA EST yk95c6.5 comes from this gene~cDNA EST yk93b12.5 comes from this gene~cDNA EST yk681d12.5 comes from this gene [Caenorhabditi> emb|CAA89023.2| (Z49153) weak similarity with paramyosin (Swiss Prot accession number P35418)~cDNA EST yk93b12.3 comes from this gene~cDNA EST yk95c6.5 comes from this gene~cDNA EST yk93b12.5 comes from this gene~cDNA EST yk681d12.5 comes from this gene [Caenorhabditi>	34.4	25	0.8
00665_HH	2	CAB38462.1	(AL035632) /prediction=(method:""genefinder"", version:""084"", score:""113.36"")~/prediction=(method:""genscan"", version:""1.0"", score:""309.87"")~/match=(desc:""HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INTERGENIC REGION"", species:""Saccharom> gb|AAF45628.1| (AE003421) EG:BACN32G11.5 gene product [Drosophila melanogaster]	141	41	3.00E-33
00666_HH	3	T23195	hypothetical protein K01G5.4 - Caenorhabditis elegans emb|CAB07240.1| (Z92803) predicted using Genefinder~similar to GTP-binding protein~cDNA EST EMBL:T00705 comes from this gene; cDNA EST CEESX11R comes from this gene~cDNA EST CEESX58F comes from this gene; cDNA EST CEESX58R comes from this gene~cDNA EST CEESX11F comes >	317	90	5.00E-86
00666_HN	1	AAF58335.1	(AE003817) CG12295 gene product [Drosophila melanogaster]	37.1	21	0.12
00667_HN	1	AAF57600.1	(AE003797) CG15118 gene product [Drosophila melanogaster]	128	45	4.00E-29
00668_HH	1	AAF56990.1	(AE003772) CG7920 gene product [Drosophila melanogaster]	92.1	46	4.00E-18
00670_HN	1	AAF75772.1	AF265555_1 (AF265555) ubiquitin-conjugating BIR-domain enzyme APOLLON [Homo sapiens]	73	33	2.00E-12
00672_HN	1	AC008982.5	AC008982 Homo sapiens chromosome 19 clone LLNLF-172E10, complete sequence	40.1	100	0.88
00673_HH	1	AAF53925.1	(AE003668) CG9326 gene product [Drosophila melanogaster]	69.9	37	2.00E-11
00674_HN	2	AP001706.1	AP001706 Homo sapiens genomic DNA, chromosome 21q, section 50/105	46.1	100	0.014
00675_HH	1	AAC46896.1	(U30261) G protein beta subunit-like; Method: conceptual translation supplied by author [Schistosoma mansoni]	193	56	9.00E-49
00676_HH	1	AAD34009.1	AF148690_1 (AF148690) RNA-binding protein XlhnRNPL [Xenopus laevis]	69.9	38	7.00E-13
00676_HN	1	CAB58121.1	(AJ242971) TOLLIP protein [Mus musculus]	73.7	36	1.00E-12
00678_HH	1	T37779	probable regulator of nonsense transcript stability - fission yeast (Schizosaccharomyces pombe) emb|CAA91194.2| (Z54366) putative regulator of nonsense transcript stability [Schizosaccharomyces pombe]	69.5	37	2.00E-11
00679_HN	2	E71614	membrane transporter PFB0465c - malaria parasite (Plasmodium falciparum) gb|AAC71882.1| (AE001396) membrane transporter [Plasmodium falciparum]	76.1	31	2.00E-13
00681_HN	2	AAF81330.1	AC007767_10 (AC007767) Contains similarity to ring finger protein 14 from Homo sapiens gb|NM_004290. It contains an IBR domain PF|01485. [Arabidopsis thaliana]	43	25	0.002
00682_HN	1	AAB86528.1	(U83857) Aac11 [Homo sapiens]	116	40	2.00E-25
00683_HH	1	AAF40479.1	(AF093242) cystein protease [Clonorchis sinensis]	72.6	48	3.00E-12
00684_HH	2	BAA25400.1	(AB012667) CsCDC42 [Ciona savignyi]	274	82	5.00E-73
00684_HN	1	AAC26491.1	(AF041355) ecto-ATP-diphosphohydrolase [Gallus gallus]	89.3	39	2.00E-17
00685_HN	3	T07901	acyl CoA oxidase homolog - cucurbit gb|AAC15870.1| (AF002016) acyl CoA oxidase homolog [Cucurbita sp.]	134	43	4.00E-31
00688_HN	2	NP_037377.1	vacuolar sorting protein 4 gb|AAD49227.1|AF159063_1 (AF159063) SKD1-homolog [Homo sapiens] gb|AAG01470.1|AF282903_1 (AF282903) vacuolar protein sorting factor 4A [Homo sapiens]	190	59	8.00E-48
00689_HH	2	NP_006466.1	osteoblast specific factor 2 (fasciclin I-like) pir||S36110 osteoblast-specific factor 2 - human dbj|BAA02837.1| (D13666) osteoblast specific factor 2 [Homo sapiens]	37.5	37	0.094
00690_HN	1	prf|2019440A	Sm70 antigen [Schistosoma mansoni]	33.2	28	1.8
00692_HH	1	S51516	serine-type carboxypeptidase (EC 3.4.16.-) Z precursor - Absidia zychae dbj|BAA03966.1| (D16519) prepro-carboxypeptidase Z [Absidia zychae]	31.3	30	5.4
00692_HN	1	BAA92062.1	(AK002059) unnamed protein product [Homo sapiens]	133	48	1.00E-30
00693_HH	1	CAB65398.1	(AJ235840) NADH dehydrogenase, putative [Spigelia anthelmia]	32.8	25	2.3

00693_HN	4	T21287	hypothetical protein F23B12.5 - Caenorhabditis elegans emb|CAB01163.1| (Z77659) predicted using Genefinder~Similarity to Human dihydrolipoamide acetyltranferase component (SW:ODP2_HUMAN)~cDNA EST EMBL:Z14632 comes from this gene~cDNA EST CEESE20F comes from this gene~cDNA EST EMBL:T00798 comes from this gene~cDNA EST yk92>	123	60	1.00E-27
00694_HH	2	A46637	calnexin homolog SmIrV1 - fluke (Schistosoma mansoni) gb|AAA02575.1| (L08641) SmIrV1 protein [Schistosoma mansoni]	147	55	8.00E-35
00695_HN	3	CAB75499.1	(AL035661) dJ568C11.2 (novel protein similar to worm, plant and fly proteins) [Homo sapiens]	65.6	37	3.00E-10
00696_HH	1	AP001686.1	AP001686 Homo sapiens genomic DNA, chromosome 21q, section 30/105	46.1	93	0.014
00698_HH	1	T40646	probable protein involved in autophagy yeast apg7 homolog - fission yeast (Schizosaccharomyces pombe) emb|CAA17048.1| (AL021838) putative protein involved in autophagy yeast apg7 homolog [Schizosaccharomyces pombe]	189	56	2.00E-47
00699_HN	2	T16613	hypothetical protein K10B3.10 - Caenorhabditis elegans gb|AAB53876.1| (U49941) strong similarity to vertebrate nonerythroid spectrins [Caenorhabditis elegans]	256	80	2.00E-67
00700_HH	1	AAC47499.1	(U85806) SNAP-25 homolog [Hirudo medicinalis]	235	65	2.00E-61
00701_HH	3	CAB95193.1	(AJ131436) Ulip-like protein [Rattus norvegicus]	84.7	34	6.00E-16
00701_HN	1	AAF52430.1	(AE003614) CG11199 gene product [Drosophila melanogaster]	124	93	7.00E-28
00707_HH	1	AAA29600.1	(M93397) erythrocyte binding protein [Plasmodium falciparum]	38.3	26	0.054
00707_HN	1	S19028	protein kinase (EC 2.7.1.37) A, cAMP-dependent, catalytic chain - California sea hare emb|CAA45015.1| (X63421) catalytic subunit of protein kinase A [Aplysia californica]	232	68	2.00E-60
00708_HH	3	AAA81164.1	(U09364) paramyosin [Schistosoma japonicum]	140	45	8.00E-33
00710_HN	6	NP_035447.1	src associated in mitosis, 68 kDa pir||I49140 p62 ras-GAP associated phosphoprotein - mouse gb|AAA64997.1| (U17046) p62 ras-GAP associated phosphoprotein [Mus musculus]	83.5	61	1.00E-15
00714_HH	2	AAF78259.1	AC020576_3 (AC020576) Contains similarity to hypothetical protein F19B11.17 gi|4406763 from Arabidopsis thaliana BAC F19B11 gb|AC006836	37.9	38	0.07
00715_HN	1	NP_061291.1	cytokine inducible SH2-containing protein CIS4 gb|AAF28872.1|AF121907_1 (AF121907) cytokine inducible SH2-containing protein CIS4 [Mus musculus]	70.6	45	1.00E-11
00716_HH	2	CAA80816.1	(Z23278) ATP-binding protein [Escherichia coli]	38.7	38	0.041
00717_HN	2	NP_038658.1	polycystic kidney disease 1 homolog gb|AAC53207.1| (U70209) polycystic kidney disease 1 protein [Mus musculus]	40.6	24	0.011
00718_HN	3	AAF52202.1	(AE003608) CG3887 gene product [Drosophila melanogaster]	149	46	2.00E-35
00719_HH	1	P24638	PPAL_MOUSE LYSOSOMAL ACID PHOSPHATASE PRECURSOR (LAP) pir||S14742 acid phosphatase (EC 3.1.3.2) precursor - mouse (fragment) emb|CAA40485.1| (X57199) lysosomal acid phosphatase [Mus musculus]	112	50	2.00E-24
00719_HN	5	AAF46143.1	(AE003437) CG11700 gene product [Drosophila melanogaster]	35.2	26	0.44
00720_HN	1	NP_063920.1	neuronal guanine nucleotide exchange factor emb|CAC00698.1| (AJ238898) guanine nucleotide exchange factor [Mus musculus]	87	36	1.00E-16
00721_HH	1	AAC32982.1	(U89915) junctional adhesion molecule [Mus musculus]	36.7	28	0.16
00724_HH	1	AAF75789.1	AF271360_1 (AF271360) STE20-like kinase MST1 [Mus musculus]	179	54	1.00E-44
00724_HN	2	NP_031769.1	procollagen, type I, alpha 2 sp|Q01149|CA21_MOUSE COLLAGEN ALPHA 2(I) CHAIN PRECURSOR pir||A43291 collagen alpha 2(I) chain precursor - mouse emb|CAA41205.1| (X58251) pro-alpha-2(I) collagen [Mus musculus]	50	62	2.00E-05
00725_HN	2	S65952	[phosphorylase] phosphatase (EC 3.1.3.17) beta chain, 65K - African clawed frog	221	74	4.00E-57
00726_HH	7	AAD34588.1	(AF144713) Rab GDP dissociation inhibitor beta [Homo sapiens]	185	56	3.00E-46
00727_HN	3	T21062	hypothetical protein F17C11.10 - Caenorhabditis elegans emb|CAA96632.1| (Z72507) similarity with a domain from the chromosome segregation protein sepB~cDNA EST EMBL:M75790 comes from this gene~cDNA EST yk3g2.3 comes from this gene~cDNA EST yk3g2.5 comes from this gene~cDNA EST yk5d3.3 comes from this gene~cDNA EST yk5d3.5 >	37.1	23	0.12
00730_HH	2	P15278	FAS3_DROME FASCICLIN III PRECURSOR (FAS III) pir||A33378 fasciclin III precursor - fruit fly (Drosophila melanogaster) gb|AAA28532.1| (M27813) fasciclin III precursor [Drosophila melanogaster]	32.8	37	2.3
00731_HH	1	AAA16202.1	(L19979) sodium channel [Loligo opalescens]	34.8	29	0.61
00732_HH	1	AAF56395.1	(AE003750) CG11920 gene product [Drosophila melanogaster]	34	27	1
00733_HH	3	P54814	PRS8_MANSE 26S PROTEASE REGULATORY SUBUNIT 8 (18-56 PROTEIN) gb|AAC46996.1| (U43728) 18-56 protein [Manduca sexta]	186	63	1.00E-46
00737_HN	1	NP_002755.1	phosphoribosyl pyrophosphate synthetase 1 ref|NP_058939.1| phosphoribosyl pyrophosphate synthetase 1 sp|P09329|KPR1_HUMAN RIBOSE-PHOSPHATE PYROPHOSPHOKINASE I (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE I) (PPRIBP) (PRS-I) pir||KIHUR1 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) catalytic chain I - human pir||KIRTR1 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) catalytic chain I - rat emb|CAA33386.1| (X15331) phosphoribosylpyrophosphate synthetase (AA 1-319) [Homo sapiens] emb|CAA34555.1| (X16554) ribose-phosphate pyrophosphokinase subunit I (AA 1-318) [Rattus norvegicus] gb|AAA41959.1| (M31084) phosphoribosylpyrophosphate synthetase [Rattus norvegicus] gb|AAA41960.1| (M29392) phosphoribosylpyrophosphate synthetase (PRPS1) precursor [Rattus norvegicus] gb|AAA41963.1| (M17258) phosphoribosyl pyrophosphate synthetase I [Rattus norvegicus] dbj|BAA00733.1| (D00860) phosphoribosyl pyrophosphate synthetase subunit I [Homo sapiens] dbj|BAA84686.1| (AB025048) Sid6061p [Mus musculus]	201	80	3.00E-51
00739_HH	2	AAF64037.1	AF218314_1 (AF218314) aquaporin [Aedes aegypti]	60.5	41	1.00E-08
00739_HN	1	AL162459.2	ATF16L2 Arabidopsis thaliana DNA chromosome 3, BAC clone F16L2	42.1	100	0.22
00740_HH	1	NP_003542.1	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase) sp|P56597|NDK5_HUMAN NUCLEOSIDE DIPHOSPHATE KINASE HOMOLOG 5 (NDK-H 5) (NDP KINASE HOMOLOG 5) (NM23-H5) (TESTIS-SPECIFIC NM23 HOMOLOG) gb|AAC64358.1| (AF067724) nm23-H5 [Homo sapiens] emb|CAA75226.1| (Y14992) nucleoside-diphosphate kinase [Homo sapiens] gb|AAC69440.1| (U90450) inhibitor of p53-induced apoptosis-beta [Homo sapiens]	198	59	3.00E-50

00740_HN	1	NP_055580.1	translocase of outer mitochondrial membrane 20 (yeast) homolog sp|Q15388|OM20_HUMAN MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOMOLOG (MITOCHONDRIAL 20 KDA OUTER MEMBRANE PROTEIN) (OUTER MITOCHONDRIAL MEMBRANE RECEPTOR TOM20) (KIAA0016) pir||S66619 Mas 20 protein - human pir||S68215 Mas 20 protein - human dbj|BAA02804.1| (D13641) mitochondrial outer membrane protein 19 [Homo sapiens] gb|AAB35420.1| mitochondrial protein import receptor, huMas20p [human, fibroblast, Peptide Mitochondrial, 145 aa] gb|AAF13354.1| (AF126962) outer membrane receptor Tom20 [Homo sapiens]	58.2	38	3.00E-08
00741_HN	1	AAC40854.1	(AF032994) p18.1 [Trichoplusia ni granulovirus]	35.2	39	0.46
00742_HH	1	CAB70887.1	(AL137714) hypothetical protein [Homo sapiens]	58.9	27	3.00E-08
00745_HH	2	AAB93495.1	(U70667) Fas-ligand associated factor 1 [Homo sapiens]	114	45	7.00E-25
00747_HH	2	BAA74914.1	(AB020698) KIAA0891 protein [Homo sapiens]	33.6	32	1.4
00747_HN	5	S41224	hnRNP protein - African clawed frog gb|AAB26047.1| pre-mRNA binding K protein, hnRNP K [Xenopus laevis, Peptide, 396 aa]	101	41	5.00E-21
00749_HH	1	AAF47858.1	(AE003480) CG1308 gene product [Drosophila melanogaster]	40.2	22	0.014
00749_HN	1	NP_002699.1	protein phosphatase 1, catalytic subunit, alpha isoform sp|P08129|PP1A_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT (PP-1A) pir||PARB11 phosphoprotein phosphatase (EC 3.1.3.16) 1-alpha catalytic chain - rabbit pir||JX0157 phosphoprotein phosphatase (EC 3.1.3.16) 1-alpha catalytic chain - rat pir||JN0723 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain - human pir||I56556 protein phosphatase 1 alpha - rat pdb|1FJM|A Chain A, Protein SerineTHREONINE PHOSPHATASE-1 (Alpha Isoform, Type I) Complexed With Microcystin-Lr Toxin pdb|1FJM|B Chain B, Protein SerineTHREONINE PHOSPHATASE-1 (Alpha Isoform, Type I) Complexed With Microcystin-Lr Toxin emb|CAA32941.1| (X14832) PP1 alpha (AA 1-330) [Oryctolagus cuniculus] emb|CAA50197.1| (X70848) serine/threonine specific protein phosphatase [Homo sapiens] gb|AAA36508.1| (M63960) protein phosphatase-1 [Homo sapiens] dbj|BAA14194.1| (D90163) protein phosphatase 1, catalytic subunit [Rattus norvegicus] dbj|BAA00732.1| (D00859) protein phosphatase type 1 alpha, catalytic subunit [Rattus norvegicus] gb|AAB34333.1| (S78215) protein phosphata	344	96	5.00E-94
00755_HH	2	T00207	P109 protein - silkworm dbj|BAA23126.1| (AB008449) BmP109 [Bombyx mori]	42.6	25	0.003
00757_HH	1	AAF49042.1	(AE003514) CG17122 gene product [Drosophila melanogaster]	80.8	30	9.00E-15
00757_HN	1	NP_035491.1	serum/glucocorticoid regulated kinase gb|AAD43302.1|AF139638_1 (AF139638) serum and glucocorticoid-regulated protein kinase [Mus musculus] gb|AAF19429.1|AF205855_1 (AF205855) serum and glucocorticoid-dependent protein kinase [Mus musculus]	171	55	6.00E-42
00758_HH	1	O85291	DEGP_BUCAP PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR gb|AAC32331.1| (AF060492) periplasmic serine protease [Buchnera aphidicola]	33.2	34	1.8
00762_HH	1	T39768	probable rna-binding protein - fission yeast (Schizosaccharomyces pombe) emb|CAA03989.1| (AJ000318) putative RNA-binding protein [Schizosaccharomyces pombe] emb|CAA18401.1| (AL022304) putative rna-binding protein. [Schizosaccharomyces pombe]	36.4	20	0.21
00763_HH	1	AAF57598.1	(AE003797) enb gene product [Drosophila melanogaster]	55.8	30	3.00E-07
00767_HH	2	BAA20816.1	(AB002359) KIAA0361 [Homo sapiens]	210	62	8.00E-54
00769_HN	1	AAD03793.1	(U89800) Tc1-like transposase [Anopheles gambiae]	52.3	37	3.00E-06
00770_HH	1	AAD55415.1	AF181629_1 (AF181629) BcDNA.GH04637 [Drosophila melanogaster] gb|AAF46999.1| (AE003460) BcDNA:GH04637 gene product [alt 3] [Drosophila melanogaster]	56.6	42	2.00E-07
00771_HN	1	AAF28867.1	(AF121134) cyclophilin [Schistosoma mansoni]	75.7	54	3.00E-13
00775_HN	2	P57043	ILK2_HUMAN INTEGRIN-LINKED PROTEIN KINASE 2 (ILK-2) emb|CAB94832.1| (AJ277481) integrin-linked kinase-2 [Homo sapiens]	56.2	38	2.00E-07
00776_HH	1	NP_012151.1	159-kDa nucleoporin with coiled-coil domain and repeated motifs typical of nucleoporins; Nup159p sp|P40477|N159_YEAST NUCLEOPORIN NUP159 (NUCLEAR PORE PROTEIN NUP159) pir||S48457 nucleoporin RAT7 - yeast (Saccharomyces cerevisiae) emb|CAA86265.1| (Z38125) orf, len: 1460,CAI: 0.15 [Saccharomyces cerevisiae] gb|AAC41652.1| (L40634) nucleoporin [Saccharomyces cerevisiae]	37.5	25	0.092
00778_HH	1	Z98044.13	HS510D11 Human DNA sequence from clone RP3-510D11 on chromosome 1p36.2-36.3 Contains the H6PD (hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)) gene, STSs, GSSs and CpG Islands, complete sequence [Homo sapiens]	44.1	91	0.057
00778_HN	1	BAA86522.1	(AB033034) KIAA1208 protein [Homo sapiens]	59.7	36	2.00E-08
00779_HH	1	S46224	peroxidasin - fruit fly (Drosophila sp.) gb|AAA61568.1| (U11052) peroxidasin precursor [Drosophila melanogaster]	64	28	1.00E-09
00780_HH	1	AAA69533.1	(U25451) internalin [Listeria monocytogenes]	42.2	26	0.004
00780_HN	1	NP_055759.1	KIAA0911 protein dbj|BAA74934.1| (AB020718) KIAA0911 protein [Homo sapiens]	112	39	2.00E-24
00781_HH	1	BAA85073.1	(AB028135) ORF4S [Shigella sonnei]	34	42	1
00782_HH	1	AAF86680.1	(AF179848) unknown [Lactococcus lactis subsp. lactis]	31.3	28	6.9
00782_HN	1	AAB25835.1	(S57162) retinoblastoma binding protein 1 isoform III {C-terminal, alternatively spliced} [human, Peptide Partial, 851 aa] [Homo sapiens]	40.2	25	0.014
00783_HN	3	AAD05494.1	(AF076514) scavenger receptor cysteine-rich protein type 5 precursor [Strongylocentrotus purpuratus]	32.1	50	4
00786_HH	3	T25416	hypothetical protein T28D6.7 - Caenorhabditis elegans emb|CAB03451.1| (Z81134) predicted using Genefinder [Caenorhabditis elegans]	132	44	2.00E-30
00787_HH	1	AE003436.1	AE003436 Drosophila melanogaster genomic scaffold 142000013386054 section 20 of 35, complete sequence	48.1	100	0.004
00788_HN	1	NP_003896.1	Amyloid beta precursor protein-binding protein 1 gb|AAC50477.1| (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens] gb|AAC23784.1| (AC004638) amyloid precursor protein-binding protein 1 (APP-B1) [Homo sapiens]	81.1	67	3.00E-26
00790_HH	1	BAA74847.1	(AB020631) KIAA0824 protein [Homo sapiens]	51.5	24	6.00E-06
00791_HH	1	B71621	probable membrane associated protein PFB0190c - malaria parasite (Plasmodium falciparum) gb|AAC71827.1| (AE001379) predicted membrane associated protein [Plasmodium falciparum]	34.4	26	0.8
00792_HH	1	O44125	RL37_SCHMA 60S RIBOSOMAL PROTEIN L37 gb|AAB88508.1| (AF035770) ribosomal protein L37 [Schistosoma mansoni]	116	70	5.00E-26
00793_HN	11	P41116	RL8_XENLA 60S RIBOSOMAL PROTEIN L8 pir||S42725 ribosomal protein L8, cytosolic - African clawed frog gb|AAA18911.1| (U00920) ribosomal protein L8 [Xenopus laevis]	266	72	1.00E-70
00794_HH	1	BAA37113.1	(AB016930) Phosphatidylglycerophosphate synthase [Cricetulus griseus]	57	30	2.00E-11
00795_HH	1	AAF99574.1	AF190623_1 (AF190623) DEADSouth RNA helicase [Xenopus laevis]	151	51	5.00E-36

00797_HH	1	NP_003554.1	speckle-type POZ protein sp|O43791|SPOP_HUMAN SPECKLE-TYPE POZ PROTEIN emb|CAA04199.1| (AJ000644) SPOP [Homo sapiens]	169	72	2.00E-41
00798_HN	1	P52550	MYBA_CHICK MYB-RELATED PROTEIN A (A-MYB) pir||I50667 transforming protein A-myb - chicken emb|CAA55980.1| (X79470) A-myb [Gallus gallus]	59.7	28	2.00E-08
00799_HH	1	AAF25947.1	AF214559_1 (AF214559) RAN GTPase activating protein 1 [Arabidopsis thaliana] emb|CAB87758.1| (AL163816) RAN GTPase activating protein 1 protein [Arabidopsis thaliana]	47.3	27	1.00E-04
00801_HH	7	AAD29285.1	AF113971_1 (AF113971) paramyosin [Schistosoma japonicum]	141	54	3.00E-33
00804_HH	3	AAF55840.1	(AE003733) Cortactin gene product [Drosophila melanogaster]	53.5	24	1.00E-06
00804_HN	1	AC004028.1	AC004028 Human PAC clone RP4-800B9 from 7q11.23-q21, complete sequence [Homo sapiens]	42.1	100	0.091
00805_HH	2	AAF75839.1	AF207818_1 (AF207818) putative gap junction protein pannexin [Clione limacina]	92.1	38	4.00E-18
00806_HH	2	AAA36544.1	(M31467) ras-like protein [Homo sapiens]	241	92	4.00E-63
00806_HN	6	AL110498.1	CEY64G10A Caenorhabditis elegans cosmid Y64G10A, complete sequence	48.1	100	0.004
00807_HH	5	A49414	beta-amyloid homolog apl-1 - Caenorhabditis elegans gb|AAC46470.1| (U00240) beta-amyloid protein precursor [Caenorhabditis elegans]	107	31	7.00E-23
00808_HN	4	Q9Y0H3	RS19_MYXGL 40S RIBOSOMAL PROTEIN S19 gb|AAD34164.1|AF153049_1 (AF153049) 40S ribosomal protein S19 [Myxine glutinosa]	132	50	2.00E-30
00813_HH	1	AAF37725.1	AF238235_1 (AF238235) diaphanous protein [Entamoeba histolytica]	41.8	24	0.005
00814_HN	1	Q08084	NU6M_ALBTU NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 pir||S33145 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - door snail (Albinaria turrita) mitochondrion (fragment) emb|CAA50516.1| (X71394) ND6 [Albinaria turrita]	43.4	45	0.002
00815_HH	1	NP_065035.1	AMV253 gb|AAG02959.1|AF250284_253 (AF250284) AMV253 [Amsacta moorei entomopoxvirus]	36.4	28	0.21
00819_HH	1	NP_003442.1	zinc finger protein 177 sp|Q13360|Z177_HUMAN ZINC FINGER PROTEIN 177 gb|AAB09749.1| (U37263) KRAB zinc finger protein; Method: conceptual translation supplied by author [Homo sapiens]	38.3	28	0.054
00819_HN	3	NP_005327.1	high density lipoprotein binding protein sp|Q00341|HBP_HUMAN HIGH DENSITY LIPOPROTEIN BINDING PROTEIN (HDL-BINDING PROTEIN) pir||A44125 high density lipoprotein-binding protein, 110K - human gb|AAA35962.1| (M64098) high density lipoprotein binding protein [Homo sapiens]	153	45	1.00E-36
00820_HN	1	T41068	hypothetical protein SPCC1682.11c - fission yeast (Schizosaccharomyces pombe) emb|CAA20677.1| (AL031525) hypothetical protein [Schizosaccharomyces pombe]	32.5	34	3.1
00822_HN	1	AAF25002.1	AF156878_1 (AF156878) opioid growth factor receptor [Rattus norvegicus]	122	44	3.00E-27
00826_HH	5	AAF44848.1	AE003406_53 (AE003416) symbol=bgm; synonym=BG:DS01514.2; cDNA=method:"sim4", score:"1000.0", desc:"LD10778 Drosophila melanogaster embryo, full length mRNA sequence from BDGP"; match=method:"BLASTX", version:"2.0a19MP-WashU [05-Feb-1998] [Build sol2.5-ult> gb|AAF53368.1| (AE003642) BG:DS01514.2 gene product [Drosophila melanogaster]	93.2	39	2.00E-18
00827_HN	11	T24168	hypothetical protein R11A5.4 - Caenorhabditis elegans emb|CAB05600.1| (Z83122) predicted using Genefinder~Similarity to Haemonchus phosphoenolpyruvate carboxykinase (SW:P29190)~cDNA EST EMBL:M89103 comes from this gene; cDNA EST EMBL:M89002 comes from this gene~cDNA EST EMBL:M89064 comes from this gene; cDNA EST EMBL:M89>	178	59	4.00E-44
00828_HH	2	Q09780	KIME_SCHPO PUTATIVE MEVALONATE KINASE (MK) pir||S62440 mevalonate kinase (EC 2.7.1.36) - fission yeast (Schizosaccharomyces pombe) emb|CAA91104.1| (Z54308) putative mevalonate kinase [Schizosaccharomyces pombe] dbj|BAA25169.1| (AB000541) putative mevalonate kinase [Schizosaccharomyces pombe]	48.8	27	4.00E-05
00831_HH	1	A45182	Max-associated protein Mxi1 - human	44.5	25	7.00E-04
00832_HH	1	AAF49575.1	(AE003529) CG15715 gene product [Drosophila melanogaster]	104	67	6.00E-22
00832_HN	1	AAF54364.1	(AE003682) CG8129 gene product [alt 1] [Drosophila melanogaster]	119	46	2.00E-26
00833_HH	1	NP_064516.1	A1U protein gb|AAF80171.1|AF188240_1 (AF188240) A1U [Homo sapiens]	67.1	38	1.00E-10
00836_HH	2	CAB56523.1	(AJ249387) ornithine decarboxylase [Phaeosphaeria nodorum]	117	46	6.00E-26
00837_HN	1	NP_048295.1	ORF MSV224 putative NTPase/helicase gb|AAC97709.1| (AF063866) ORF MSV224 putative NTPase/helicase [Melanoplus sanguinipes entomopoxvirus]	30.5	28	2.2
00839_HN	1	AAF50946.1	(AE003574) CG17602 gene product [Drosophila melanogaster]	37.1	24	0.12
00841_HH	1	AAG01154.1	AF285235_1 (AF285235) quiescent cell proline dipeptidase precursor; QPP [Mus musculus]	171	55	4.00E-42
00844_HH	1	T17340	hypothetical protein DKFZp586D0624.1 - human (fragment) emb|CAB56030.1| (AL117654) hypothetical protein [Homo sapiens]	87	41	1.00E-16
00845_HN	1	P13941	CA13_RAT COLLAGEN ALPHA 1(III) CHAIN pir||S41067 collagen alpha 1(III) chain - rat emb|CAA49832.1| (X70369) pro1 collagen type III [Rattus norvegicus]	78.8	55	3.00E-14
00850_HH	1	T25137	hypothetical protein T22H2.6a - Caenorhabditis elegans emb|CAB54304.1| (Z81595) Similarity to Human granulin (SW:P28799)~cDNA EST yk470g9.3 comes from this gene~cDNA EST yk470g9.5 comes from this gene~cDNA EST yk579a12.3 comes from this gene~cDNA EST yk606e9.3 comes from this gene~cDNA EST yk643d7.3 comes from this gene~c>	87.4	38	9.00E-17
00851_HH	1	AAF52439.1	(AE003615) Nrv2 gene product [alt 1] [Drosophila melanogaster]	69.1	32	3.00E-11
00851_HN	1	CAB67164.1	(AJ271079) hypothetical protein [Oenothera elata subsp. hookeri]	77.6	31	8.00E-14
00855_HN	1	NP_060959.1	hypothetical protein ASH1 gb|AAF68983.1|AF257305_1 (AF257305) ASH1 [Homo sapiens]	34	24	1
00858_HH	7	BAA89023.1	(AB028237) ATPase6 [Pupa strigosa] gnl|NCBI_MITO|ATP6_15272 ATP synthase F0 subunit 6	63.2	30	2.00E-09
00861_HN	1	AAF46158.1	(AE003437) CG3446 gene product [Drosophila melanogaster]	65.2	34	4.00E-10
00862_HN	1	AC004936.2	AC004936 Homo sapiens PAC clone RP5-959C21 from 7p11.2-p21, complete sequence	40.1	100	0.17
00863_HN	2	NP_014838.1	possible leucine zipper; Slk19p pir||S67087 hypothetical protein YOR195w - yeast (Saccharomyces cerevisiae) emb|CAA99408.1| (Z75103) ORF YOR195w [Saccharomyces cerevisiae]	44.5	30	7.00E-04
00864_HN	2	AAF55402.1	(AE003716) CG4090 gene product [Drosophila melanogaster]	45.7	22	3.00E-04
00865_HN	2	T09127	probable erythrocyte-binding protein MAEBL - Plasmodium yoelii gb|AAC05366.1| (AF031886) erythrocyte binding protein [Plasmodium yoelii yoelii]	32.8	27	2.3
00866_HN	1	AAF45875.1	(AE003427) CG14270 gene product [Drosophila melanogaster]	57.8	27	7.00E-08
00867_HN	1	NP_056031.1	KIAA0433 protein dbj|BAA24863.1| (AB007893) KIAA0433 [Homo sapiens]	39.5	47	0.024
00868_HH	1	AAF50483.1	(AE003556) CG7962 gene product [Drosophila melanogaster]	169	59	2.00E-41

00868_HN	1	AAB39211.1	(U48395) mutant cysteine-rich FGF receptor [Gallus gallus]	83.9	29	1.00E-15
00869_HH	1	AAF54266.1	(AE003680) CG8039 gene product [Drosophila melanogaster]	62.8	38	2.00E-09
00869_HN	1	P48324	YCX2_CYAPA HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGENIC REGION (ORF182) pir||T06858 hypothetical protein 182 - Cyanophora paradoxa cyanelle gb|AAA81201.1| (U30821) orf182 gene product [Cyanophora paradoxa]	32.8	36	2.3
00871_HH	1	BAA20005.1	(D87009) putative [Homo sapiens]	75.7	31	3.00E-13
00873_HN	1	CAA05292.1	(AJ002280) shaggy-like kinase beta [Arabidopsis thaliana] emb|CAB71046.1| (AL137898) shaggy-like kinase beta [Arabidopsis thaliana]	45.7	44	2.00E-04
00874_HN	1	AAF48513.1	(AE003500) CG8959 gene product [Drosophila melanogaster]	151	43	4.00E-36
00877_HN	2	NP_013803.1	Ymr086wp sp|Q04279|YMX6_YEAST HYPOTHETICAL 105.9 KD PROTEIN IN ADH3-RCA1 INTERGENIC REGION pir||S54461 hypothetical protein YMR086w - yeast (Saccharomyces cerevisiae) emb|CAA89232.1| (Z49259) unknown [Saccharomyces cerevisiae]	32.5	27	3.1
00878_HN	1	P04068	HYEP_RABIT EPOXIDE HYDROLASE (MICROSOMAL EPOXIDE HYDROLASE) (EPOXIDE HYDRATASE) pir||S04342 epoxide hydrolase (EC 3.3.2.3), microsomal - rabbit pir||YXRBH epoxide hydrolase (EC 3.3.2.3) - rabbit gb|AAA31392.1| (M21496) microsomal epoxide hydrolase (EC 3.3.2.3) [Oryctolagus cuniculus]	126	50	1.00E-28
00882_HN	1	AC002311.1	AC002311 Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence	42.1	96	0.095
00883_HH	1	BAA31668.1	(AB014593) KIAA0693 protein [Homo sapiens]	48.8	52	3.00E-05
00883_HN	2	NP_059013.1	low Mr GTP-binding protein sp|P23640|RB27_RAT RAS-RELATED PROTEIN RAB-27A (RAB-27) (GTP-BINDING PROTEIN RAM) (RAM P25) pir||S12959 GTP-binding protein ram - rat dbj|BAA04167.1| (D17352) low Mr GTP-binding protein [Rattus sp.] prf||1702217A GTP binding protein ram [Rattus norvegicus]	208	57	4.00E-53
00884_HH	1	NP_006659.1	cytochrome P450, subfamily 46 (cholesterol 24-hydroxylase) gb|AAD41244.1|AF094480_1 (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	77.3	38	1.00E-13
00884_HN	1	BAB03525.1	(AB037869) fucolectin-3 [Anguilla japonica]	57	27	1.00E-07
00886_HH	1	AAD04345.1	(AF074960) neurogenic extracellular slit protein [Mus musculus]	44.5	25	7.00E-04
00886_HN	9	Q90705	EF2_CHICK ELONGATION FACTOR 2 (EF-2) gb|AAA87587.1| (U46663) elongation factor 2 [Gallus gallus]	283	75	7.00E-76
00887_HH	2	NP_031401.1	TAR DNA binding protein pir||I38977 TAR DNA-binding protein-43 - human gb|AAA70033.1| (U23731) TAR DNA-binding protein-43 [Homo sapiens] emb|CAB43367.1| (AL050265) hypothetical protein [Homo sapiens]	109	44	2.00E-23
00890_HH	1	T22917	hypothetical protein F58E10.3 - Caenorhabditis elegans emb|CAB04518.1| (Z81555) similar to ATP-dependent helicase (DEAD box)~cDNA EST yk436c8.5 comes from this gene; cDNA EST yk26e4.5 comes from this gene; cDNA EST yk54b11.5 comes from this gene~cDNA EST yk62h12.5 comes from this gene; cDNA EST yk63a2.5 comes from this ge>	102	63	2.00E-21
00891_HH	1	NP_003263.1	transmembrane 7 superfamily member 1 (upregulated in kidney) gb|AAC39669.1| (AF027826) putative seven pass transmembrane protein [Homo sapiens]	88.2	36	5.00E-17
00893_HH	2	AAF81283.1	(AF281663) glutathione S-transferase [Haemonchus contortus]	113	40	1.00E-24
00895_HH	1	AAF75840.1	AF207819_1 (AF207819) putative gap junction protein pannexin [Girardia tigrina]	31.3	45	6.9
00896_HH	3	NP_031922.1	pEb1 adenomatosis polyposis coli binding protein Eb1 gb|AAA96320.1| (U51196) APC-binding protein EB1 homolog [Mus musculus]	206	62	2.00E-52
00898_HH	1	BAA96029.1	(AB040938) KIAA1505 protein [Homo sapiens]	62.5	22	3.00E-09
00899_HH	1	NP_000089.1	carnitine palmitoyltransferase II precursor sp|P23786|CPT2_HUMAN CARNITINE O-PALMITOYLTRANSFERASE II, MITOCHONDRIAL PRECURSOR (CPT II) pir||A39018 carnitine O-palmitoyltransferase (EC 2.3.1.21) II, precursor - human gb|AAB59462.1| (M58581) carnitine palmitoyltransferase [Homo sapiens] gb|AAB60382.1| (U09646) carnitine palmitoyltransferase II precursor [Homo sapiens] gb|AAB60383.1| (U09648) carnitine palmitoyltransferase II precursor [Homo sapiens]	96.7	46	1.00E-19
00900_HH	2	AAF50001.1	(AE003543) CG7264 gene product [Drosophila melanogaster]	112	39	2.00E-24
00901_HH	1	T37876	probable (Xeroderma pigmentosum-group E like) DNA-binding protein - fission yeast (Schizosaccharomyces pombe) emb|CAB11219.1| (Z98597) putative (Xeroderma pigmentosum-group E like) DNA-binding protein [Schizosaccharomyces pombe]	32.1	26	4
00902_HH	2	CAB59982.1	(AJ243651) putative metal transporter [Mus musculus]	69.5	52	2.00E-11
00903_HH	1	AAD21813.1	(AF134726) NG22 [Homo sapiens]	74.5	33	7.00E-13
00905_HH	2	CAB59635.1	(Y19159) ethylene responsive receptor, ERR [Suberites domuncula]	266	79	1.00E-70
00906_HH	1	prf|1920362A	tumor suppressor gene mgl1 [Mus musculus]	66.7	32	1.00E-10
00908_HH	5	NP_005712.1	ARP3 (actin-related protein 3, yeast) homolog sp|P32391|ARP3_HUMAN ACTIN-LIKE PROTEIN 3 (ACTIN-2) pir||JQ1616 actin 2 - bovine dbj|BAA02249.1| (D12816) actin2 [Bos taurus] gb|AAB64188.1| (AF006083) Arp3 [Homo sapiens] gb|AAD51904.1| (AF127773) unknown [Homo sapiens]	245	73	3.00E-64
00910_HH	1	P25409	ALAT_RAT ALANINE AMINOTRANSFERASE (GLUTAMIC--PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE TRANSAMINASE) dbj|BAA01185.1| (D10354) alanine aminotransferase [Rattus norvegicus]	73.7	60	4.00E-13
00912_HH	1	CAB97520.1	(AJ271051) putative NADH dehydrogenase subunit 2 [Schistosoma haematobium]	31.7	34	5.3
00913_HH	2	CAA09303.1	(AJ010646) calcium ATPase [Caenorhabditis elegans]	178	55	4.00E-44
00919_HH	1	T09755	4-coumarate--CoA ligase (EC 6.2.1.12) 4CL2 - loblolly pine gb|AAA92669.1| (U12013) 4-coumarate-CoA ligase enzyme [Pinus taeda] gb|AAB42382.1| (U39404) 4-coumarate:CoA ligase [Pinus taeda] gb|AAB42383.1| (U39405) 4-coumarate:CoA ligase [Pinus taeda]	101	35	4.00E-21
00920_HH	1	CAB85475.1	(AJ277180) mod(mdg4)55.3 [Drosophila melanogaster]	34.4	28	0.8
00922_HH	1	AAB41827.1	(U39847) AO13 ankyrin [Caenorhabditis elegans]	66.7	31	4.00E-15
00924_HH	1	Q08012	DRK_DROME PROTEIN E(SEV)2B (SH2-SH3 ADAPTOR PROTEIN DRK) pir||A46444 SH2-SH3 adaptor protein drk - fruit fly (Drosophila melanogaster) gb|AAA28898.1| (L12446) downstream of receptor kinases (drk) [Drosophila melanogaster] gb|AAF58368.1| (AE003818) drk gene product [Drosophila melanogaster]	123	46	1.00E-27
00925_HH	1	P49846	T2D4_DROME TRANSCRIPTION INITIATION FACTOR TFIID 85 KDA SUBUNIT (P85) (TAFII-80) pir||A54593 transcription initiation factor TFIID subunit p85 - fruit fly (Drosophila melanogaster) gb|AAB29084.1| TFIID subunit p85=85 kda transcription factor [Drosophila, Schneider cells, embryos, Peptide, 704 aa] gb|AAC46481.1| (U06460) transcription initiation factor TFIID 85 kDa subunit [Drosophila melanogaster] gb|AAF58737.1| (AE003828) CG7704 gene product [Drosophila melanogaster]	44.9	32	5.00E-04
00926_HH	4	BAA04887.1	(D23660) ribosomal protein [Homo sapiens]	197	63	8.00E-50

00927_HH	1	P19404	NUHM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 24 KD SUBUNIT PRECURSOR pir||A30113 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 24K chain precursor - human gb|AAA75390.1| (M22538) NADH-ubiquinone reductase [Homo sapiens]	207	63	7.00E-53
00929_HH	1	NP_009167.1	calcium binding protein P22 sp|Q99653|CA22_HUMAN CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) (CALCINEURIN B HOMOLOGOUS PROTEIN) gb|AAB37770.1| (U61538) calcium-binding protein chp [Homo sapiens]	135	45	3.00E-31
00932_HH	1	AF226992.1	AF226992 Mus musculus connexin 36 gene, complete cds	44.1	100	0.018
00933_HH	1	P47615	SYT_MYCGE THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS) pir||E64241 threonine--tRNA ligase (EC 6.1.1.3) - Mycoplasma genitalium gb|AAC71602.1| (U39719) threonyl-tRNA synthetase (thrS) [Mycoplasma genitalium]	33.2	43	1.8
00936_HH	1	AAF43014.1	AF227209_1 (AF227209) AAA family protein Bor [Drosophila melanogaster] gb|AAF43016.1| (AF227210) AAA family protein Bor [Drosophila melanogaster]	99.8	33	1.00E-20
00937_HH	1	NP_033967.1	chaperonin subunit 4 (delta) sp|P80315|TCPD_MOUSE T-COMPLEX PROTEIN 1, DELTA SUBUNIT (TCP-1-DELTA) (CCT-DELTA) pir||S43060 CCT (chaperonin containing TCP-1) delta chain - mouse emb|CAA83429.1| (Z31554) CCT (chaperonin containing TCP-1) delta subunit [Mus musculus] dbj|BAA81875.1| (AB022157) chaperonin containing TCP-1 delta subunit [Mus musculus]	152	47	3.00E-36
00940_HH	1	D71608	hypothetical protein PFB0690w - malaria parasite (Plasmodium falciparum) gb|AAC71927.1| (AE001412) hypothetical protein [Plasmodium falciparum]	36	27	0.27
00944_HH	1	P16170	NCA1_XENLA NEURAL CELL ADHESION MOLECULE 1, LARGE ISOFORM PRECURSOR (N-CAM 180) [CONTAINS: N-CAM 140] pir||IJXLNL neural cell adhesion molecule long domain form precursor - African clawed frog gb|AAA49909.1| (M25696) neural cell adhesion molecule precursor [Xenopus laevis]	48.8	31	4.00E-05
00945_HH	1	CAB38969.2	(AL034556) Hypothetical protein, PFC0575w [Plasmodium falciparum]	30.9	30	9.1
00947_HH	1	Y11830.1	OVGLUTRED O.volvulus gene encoding glutathione reductase	44.1	100	0.017
00948_HH	2	AAC46909.1	(U25089) Hro-Cdc25 [Helobdella robusta]	37.1	27	0.12
00951_HH	1	T42213	m-tomosyn, isoform 130K - rat gb|AAD04756.1| (U92072) m-tomosyn [Rattus norvegicus]	74.1	30	9.00E-13
00952_HH	2	S77094	glycogen operon protein (EC 3.2.1.-) glgX-2 - Synechocystis sp. (strain PCC 6803) dbj|BAA17652.1| (D90908) glycogen operon protein GlgX [Synechocystis sp.]	37.9	25	0.07
00953_HH	4	AAD52698.1	AF091537_1 (AF091537) very low density lipoprotein binding protein precursor [Schistosoma japonicum]	123	60	9.00E-28
00955_HH	1	NP_057004.1	40S ribosomal protein S27 isoform sp|P24051|RS27_RAT 40S RIBOSOMAL PROTEIN S27 pir||R3RT27 ribosomal protein S27 - rat emb|CAA42019.1| (X59375) ribosomal protein S27 [Rattus rattus] gb|AAD20974.1| (AF070668) 40S ribosomal protein S27 isoform [Homo sapiens]	116	64	6.00E-26
00957_HH	2	BAB00612.1	(AB045982) myosin [Patinopecten yessoensis]	115	35	2.00E-25
00958_HH	1	AAB92246.1	(AF036171) homeobox-containing protein [Dictyostelium discoideum]	39.9	32	0.018
00959_HH	7	NP_060538.1	hypothetical protein FLJ10351 dbj|BAA91558.1| (AK001213) unnamed protein product [Homo sapiens]	81.5	32	5.00E-15
00965_HH	1	Q11179	YPC2_CAEEL PUTATIVE SERINE/THREONINE-PROTEIN KINASE C05D10.2 IN CHROMOSOME III gb|AAA20987.1| (U13645) similar to protein kinases [Caenorhabditis elegans]	208	59	3.00E-53
00973_HH	1	AAF50525.1	(AE003558) ESTS:149B10S gene product [Drosophila melanogaster]	101	40	7.00E-21
00980_HH	1	T20336	hypothetical protein D2013.5 - Caenorhabditis elegans emb|CAA87771.1| (Z47808) GTP-binding protein with similarity to dynamin and to interferon inducible MX proteins~cDNA EST yk10h8.3 comes from this gene~cDNA EST yk10h8.5 comes from this gene~cDNA EST yk19f3.3 comes from this gene~cDNA EST yk18c2.3 comes from this gene~>	34.8	25	0.61
00981_HH	1	T25495	hypothetical protein C03G6.15 - Caenorhabditis elegans gb|AAB52315.1| (U97008) Similar to cytochrome P450 [Caenorhabditis elegans]	45.3	32	4.00E-04
00985_HH	1	NP_064322.1	sperm tail associated protein dbj|BAA82514.1| (AB029919) sperm tail associated protein [Mus musculus]	33.2	40	1.6
00986_HH	5	AAB53370.1	(U78975) poly(ADP-ribose) glycohydrolase [Bos taurus]	32.8	33	2.3
00987_HH	1	NP_036030.1	suppressor of Lec15 homolog (C.griseus) dbj|BAA78781.1| (AB024713) Supl15h [Mus musculus]	150	48	7.00E-36
00990_HH	1	O51051	Y019_BORBU HYPOTHETICAL PROTEIN BB0019 pir||C70102 hypothetical protein BB0019 - Lyme disease spirochete gb|AAC66416.1| (AE001116) B. burgdorferi predicted coding region BB0019 [Borrelia burgdorferi]	33.2	28	1.8
00992_HH	1	AAF46516.1	(AE003448) CG15319 gene product [Drosophila melanogaster]	43.4	22	0.002
00998_HH	1	S58741	probable site-specific endonuclease - yeast (Hansenula wingei) mitochondrion	35.2	35	0.46
01001_HH	1	NP_034970.1	5,10-methylenetetrahydrofolate reductase gb|AAD20313.1| (AF105998) methylenetetrahydrofolate reductase; MTHFR [Mus musculus]	193	54	9.00E-49
01002_HH	2	T29757	protein UNC-89 - Caenorhabditis elegans gb|AAB54132.1| (AF003131) C. elegans UNC-89 (GB:U33058) (NID:g1160355) [Caenorhabditis elegans]	32.5	24	3
01005_HH	2	AAF58445.1	(AE003820) Aats-asp gene product [Drosophila melanogaster]	108	35	3.00E-23
01008_HH	1	O14173	YE57_SCHPO HYPOTHETICAL 69.4 KD PROTEIN C4D7.07C IN CHROMOSOME I pir||T38798 hypothetical protein SPAC4D7.07c - fission yeast (Schizosaccharomyces pombe) emb|CAB11279.1| (Z98602) hypothetical protein [Schizosaccharomyces pombe]	34.4	30	0.8
01009_HH	4	AAC83556.1	(AF055895) nonmuscle myosin II heavy chain A [Xenopus laevis]	63.2	27	2.00E-09
01013_HH	2	AAF87577.1	AF271209_1 (AF271209) putative t-complex polypeptide 1 delta subunit [Aedes triseriatus]	222	65	2.00E-57
01015_HH	1	AAF18300.1	AF118384_1 (AF118384) N-ethylmaleimide sensitive fusion protein [Manduca sexta]	73.7	27	1.00E-12
01021_HH	5	AAF91258.1	AF229439_1 (AF229439) zinc finger protein 289 [Mus musculus]	210	62	1.00E-53
01022_HH	1	NP_039663.1	glutaryl-Coenzyme A dehydrogenase isoform b	161	63	4.00E-39
01024_HH	1	AAD31085.1	AF078164_1 (AF078164) Ku70-binding protein [Homo sapiens]	62.8	39	5.00E-17
01025_HH	1	BAA01504.1	(D10655) dihydrolipoamide acetyltransferase [Rattus norvegicus]	148	51	4.00E-35
01026_HH	2	S42672	adhesive protein - northern horsemussel (fragments)	32.1	40	4
01029_HH	1	AAF52253.1	(AE003610) CG11024 gene product [Drosophila melanogaster]	81.1	38	7.00E-15
01031_HH	3	JC5180	serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - mouse	139	45	2.00E-32
01032_HH	1	NP_013412.1	Imh1p pir||S51441 hypothetical protein YLR309c - yeast (Saccharomyces cerevisiae) gb|AAB67359.1| (U17247) Imh1p [Saccharomyces cerevisiae]	35.2	29	0.46

01033_HH	1	T24582	hypothetical protein T06D8.9 - Caenorhabditis elegans emb|CAA88972.1| (Z49130) cDNA EST yk74a5.5 comes from this gene~cDNA EST yk74a5.3 comes from this gene~cDNA EST yk116h7.5 comes from this gene~cDNA EST yk486c7.3 comes from this gene~cDNA EST yk486c7.5 comes from this gene~cDNA EST yk484c5.3 comes from this gene~cDNA >	138	43	3.00E-32
01034_HH	2	NP_035698.1	Tcra enhancer-binding factor interacting protein 1 gb|AAC53117.1| (U89876) ALY [Mus musculus]	106	39	2.00E-22
01039_HH	1	AAD54220.1	AF142475_1 (AF142475) peroxisome targeting signal 1 receptor PEX5 [Trypanosoma brucei]	78.8	32	3.00E-14
01042_HH	1	NP_040608.1	ea59 (525) sp|P03754|VE59_LAMBD EA59 GENE PROTEIN pir||ZEBP5L Ea59 protein - phage lambda gb|AAA96561.1| (J02459) ea59 (525) [bacteriophage lambda]	33.6	30	0.65
01043_HH	2	A61034	myosin regulatory light chain, cellular - chicken	194	64	5.00E-49
01047_HH	1	prf|1313184C	chymotrypsin inhibitor [Homo sapiens]	30.9	38	9.1
01048_HH	2	P21914	DHSB_DROME SUCCINATE DEHYDROGENASE [UBIQUINONE] IRON-SULFUR PROTEIN, MITOCHONDRIAL PRECURSOR (IP) gb|AAA61925.1| (L27705) succinate dehydrogenase iron-protein subunit [Drosophila melanogaster] gb|AAF57396.1| (AE003790) SdhB gene product [Drosophila melanogaster]	224	78	4.00E-58
01050_HH	3	P16292	FA9_RABIT COAGULATION FACTOR IX (CHRISTMAS FACTOR) pir||I46712 factor IX - rabbit (fragment) gb|AAA31251.1| (M26234) factor IX [Oryctolagus cuniculus]	53.9	33	1.00E-06
01051_HH	2	AAC44336.1	(U57065) ZmaR [Bacillus cereus] gb|AAD40108.1|AF155831_2 (AF155831) zwittermicin A resistance protein [Bacillus cereus]	30.9	41	9.1
01056_HH	1	AAF59214.1	(AE003840) CG2070 gene product [Drosophila melanogaster]	90.1	41	1.00E-17
01065_HH	1	AAB71823.1	(AF003886) galactocerebrosidase [Mus musculus]	127	44	8.00E-29
01066_HH	1	T13719	calo protein - fruit fly (Drosophila melanogaster) (fragment) emb|CAA76940.1| (Y17920) CALO protein [Drosophila melanogaster]	64	24	1.00E-09
01068_HH	2	T23656	hypothetical protein M01F1.4 - Caenorhabditis elegans emb|CAA86517.1| (Z46381) Weak similarity with the Ysy6 protein (Yeast) (PIR accession number JQ0912)~cDNA EST yk10f10.3 comes from this gene~cDNA EST yk34f5.3 comes from this gene~cDNA EST yk10f10.5 comes from this gene~cDNA EST yk34f5.5 comes from this gene~cDNA EST >	64.8	29	6.00E-10
01073_HH	2	P26643	RLA1_TRYCR 60S ACIDIC RIBOSOMAL PROTEIN P1 pir||R6UTP1 acidic ribosomal protein P1 - Trypanosoma cruzi emb|CAA46159.1| (X65025) ribosomal protein P1 [Trypanosoma cruzi]	38.7	23	0.022
01076_HH	7	JC4131	glioma pathogenesis-related protein - human gb|AAA82731.1| (U16307) glioma pathogenesis-related protein [Homo sapiens]	105	48	3.00E-22
01080_HH	1	S71628	sensory transduction histidine kinase dokA - slime mold (Dictyostelium discoideum)	32.1	24	4
01085_HH	1	X02167.1	MITGTRN1 Torulopsis glabrata mitochondrial DNA for tRNA-Thr,-His and -Glu upstream of cytochrome b gene	46.1	100	0.014
01086_HH	1	AAF53987.1	(AE003669) CG8671 gene product [Drosophila melanogaster]	62.5	46	3.00E-09
01088_HH	2	T34947	hypothetical protein SC4A10.10c - Streptomyces coelicolor emb|CAB51986.1| (AL109663) hypothetical protein [Streptomyces coelicolor A3(2)]	40.6	37	0.011
01092_HH	1	T00875	hypothetical protein F17K2.15 - Arabidopsis thaliana gb|AAC06161.1| (AC003680) unknown protein [Arabidopsis thaliana]	65.2	25	4.00E-10
01095_HH	1	AL035594.7	HS67A5 Human DNA sequence from clone 67A5 on chromosome 6q22.31-22.33 Contains part of PTPRK(protein tyrosine phosphatase, receptor type, K) gene, ESTs, STSs and GSSs, complete sequence [Homo sapiens]	44.1	100	0.057
01096_HH	2	CAA63889.1	(X94180) Des-1 protein [Drosophila melanogaster] gb|AAF52318.1| (AE003612) ifc gene product [Drosophila melanogaster]	220	56	9.00E-57
01098_HH	1	NP_055382.1	breast cancer anti-estrogen resistance 1 sp|P56945|BCA1_HUMAN CRK-ASSOCIATED SUBSTRATE (P130CAS) (BREAST CANCER ANTI-ESTROGEN RESISTANCE 1 PROTEIN) emb|CAB75875.2| (AJ242987) breast cancer anti-estrogen resistance 1 protein [Homo sapiens] dbj|BAA92711.1| (AB040024) adaptor protein p130Cas [Homo sapiens]	71	48	8.00E-12
01099_HH	2	S39064	isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) gamma chain precursor - rat (fragment)	179	55	1.00E-44
01102_HH	2	T18287	protein-tyrosine kinase (EC 2.7.1.112) - slime mold (Dictyostelium discoideum) gb|AAB04999.1| (U64830) protein tyrosine kinase [Dictyostelium discoideum]	37.5	30	0.092
01107_HH	1	CAB38999.1	(AL034558) predicted using hexExon; MAL3P2.12 (PF0215c), Hypothetical protein, len: 444 aa [Plasmodium falciparum]	34.8	38	0.61
01116_HH	1	A47300	cell adhesion protein retina cognin - chicken (fragment) gb|AAA49054.1| (L11147) prolyl 4-hydroxylase [Gallus gallus]	172	70	2.00E-42
01117_HH	1	NP_032058.1	fragile X mental retardation 2 homolog pir||T30248 fragile X mental retardation protein 2 - mouse emb|CAA04821.1| (AJ001549) FMR2 protein [Mus musculus]	32.1	24	4
01120_HH	1	P08985	H2AV_DROME HISTONE H2A VARIANT pir||S08118 histone H2A.vD - fruit fly (Drosophila melanogaster) emb|CAA30370.1| (X07485) histone H2A variant (AA 1-141) [Drosophila melanogaster] emb|CAA33555.1| (X15549) histone H2A [Drosophila melanogaster] gb|AAF56631.1| (AE003758) His2Av gene product [Drosophila melanogaster]	180	85	9.00E-45
01121_HH	1	P32019	I5P2_HUMAN TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (5PTASE) gb|AAA79207.1| (M74161) inositol polyphosphate 5-phosphatase [Homo sapiens]	124	38	5.00E-28
01123_HH	2	P55745	RB21_CANFA RAS-RELATED PROTEIN RAB-21	209	61	1.00E-53
01124_HH	2	NP_057175.1	HSPC025 gb|AAD27002.1| (AF077207) HSPC021 [Homo sapiens] gb|AAD39841.1| (AF083243) HSPC025 [Homo sapiens]	163	52	1.00E-39
01126_HH	2	P15869	H1B_STRPU HISTONE H1-BETA, LATE EMBRYONIC gb|AAA30052.1| (M20314) histone H1-beta [Strongylocentrotus purpuratus]	76.5	50	2.00E-13
01128_HH	1	AAF05899.1	AF108656_1 (AF108656) prosaposin [Gallus gallus]	44.5	24	7.00E-04
01130_HH	1	T07367	thioredoxin-like protein CDSP32, chloroplast - potato emb|CAA71103.1| (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]	30.9	26	9.1
01132_HH	3	CAB70736.1	(AL137438) hypothetical protein [Homo sapiens]	106	39	2.00E-22
01135_HH	1	AP001759.1	AP001759 Homo sapiens genomic DNA, chromosome 21q, section 103/105	48.1	100	0.004
01137_HH	1	P35069	H2B3_TIGCA HISTONE H2B.3 pir||D56612 histone H2B-3 - Tigriopus californicus gb|AAC41557.1| (M84799) histone H2B-3 [Tigriopus californicus]	171	93	3.00E-42
01138_HH	1	T31603	hypothetical protein Y48C3A.u - Caenorhabditis elegans emb|CAB55118.1| (AL117203) predicted using Genefinder~cDNA EST yk139a7.3 comes from this gene~cDNA EST yk139a7.5 comes from this gene [Caenorhabditis elegans]	111	40	6.00E-24
01143_HH	1	AAC67403.1	(AF098501) Contains similarity to Pfam domain: PF00292 (PAX), Score=10.2, E-value=0.028, N=1 [Caenorhabditis elegans]	51.9	37	2.00E-08
01144_HH	1	AAD09015.1	(AF090446) 22-kDa alpha zein protein 21 [Zea mays]	33.6	36	1.4

01145_HH	1	S59310	probable membrane protein YMR317w - yeast (Saccharomyces cerevisiae)	40.2	30	0.014
01150_HH	1	NP_001090.2	prostatic acid phosphatase precursor sp|P15309|PPAP_HUMAN PROSTATIC ACID PHOSPHATASE PRECURSOR pir||JH0610 acid phosphatase (EC 3.1.3.2) ACPP precursor - human gb|AAA60021.1| (M97589) prostatic acid phosphatase [Homo sapiens] gb|AAA69694.1| (M34840) acid phosphatase [Homo sapiens] gb|AAB60640.1| (U07097) prostatic acid phosphatase [Homo sapiens]	53.1	29	2.00E-06
01153_HH	4	P12261	EF1G_ARTSA ELONGATION FACTOR 1-GAMMA (EF-1-GAMMA) pir||S00162 translation elongation factor eEF-1 gamma chain - brine shrimp gb|AAC83401.1| (M28020) elongation factor 1-gamma [Artemia sp.]	109	38	2.00E-23
01158_HH	1	S49313	protein kinase - slime mold (Dictyostelium discoideum) pir||S52076 protein kinase - slime mold (Dictyostelium discoideum) emb|CAA86053.1| (Z37981) protein kinase [Dictyostelium discoideum]	38.3	29	0.054
01164_HH	1	CAB93533.1	(AJ250014) Familial Cylindromatosis Gene [Homo sapiens]	86.2	32	2.00E-16
01165_HH	2	AL117206.1	CEY67A10A Caenorhabditis elegans cosmid Y67A10A, complete sequence	42.1	100	0.22
01166_HH	1	NP_003003.2	secreted frizzled-related protein 1 gb|AAB61576.1| (AF001900) secreted frizzled-related protein [Homo sapiens] gb|AAC12877.1| (AF056087) secreted frizzled related protein [Homo sapiens]	119	42	2.00E-26
01167_HH	2	AAF47652.1	(AE003475) CG1141 gene product [Drosophila melanogaster]	76.1	30	2.00E-13
01168_HH	1	AAF76856.1	AF231925_1 (AF231925) COPI coatomer complex, beta subunit [Mus musculus]	182	64	3.00E-45
01169_HH	1	S75793	poly(A) polymerase - Synechocystis sp. (strain PCC 6803) dbj|BAA10528.1| (D64003) polyA polymerase [Synechocystis sp.]	32.5	32	3.1
01170_HH	1	D72478	hypothetical protein APE2468 - Aeropyrum pernix (strain K1) dbj|BAA81484.1| (AP000064) 560aa long hypothetical protein [Aeropyrum pernix]	32.5	33	3.1
01173_HH	1	P40417	ERKA_DROME MITOGEN-ACTIVATED PROTEIN KINASE ERK-A (EXTRACELLULAR-REGULATED KINASE A) (ROLLED PROTEIN) pir||A46036 extracellular signal-regulated kinase (EC 2.7.1.-) DmERK-A - fruit fly (Drosophila melanogaster) gb|AAA28677.1| (M95124) MAP kinase [Drosophila melanogaster]	268	73	4.00E-71
01179_HH	1	O09110	MPK3_MOUSE DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 (MAP KINASE KINASE 3) (MAPKK 3) (MAPK/ERK KINASE 3) emb|CAA63649.1| (X93150) MAP kinase kinase 3 [Mus musculus]	132	51	3.00E-30
01180_HH	1	NP_056588.1	sperm associated antigen 6 gb|AAF35831.1|AF173866_1 (AF173866) axoneme central apparatus protein [Mus musculus]	280	82	6.00E-75
01181_HH	2	NP_031843.1	cytochrome P450, 2f2 gb|AAA37517.1| (M77497) cytochrome P-450 naphthalene hydroxylase [Mus musculus]	81.1	33	7.00E-15
01182_HH	2	NP_031620.1	calumenin sp|O35887|CALU_MOUSE CALUMENIN PRECURSOR gb|AAC53316.1| (U81829) calumenin [Mus musculus]	109	45	2.00E-23
01186_HH	23	CAA68079.1	(X99748) Y-box protein [Dugesia japonica]	261	84	3.00E-69
01189_HH	2	AAB41263.3	(U36927) rhoptry protein [Plasmodium yoelii]	44.9	29	5.00E-04
01190_HH	4	NP_055280.1	thyroid hormone slfotransferase pir||JC5885 thyroid hormone sulfotransferase (EC 2.8.2.-) B2 - human dbj|BAA24547.1| (D89479) ST1B2 [Homo sapiens]	60.1	39	1.00E-08
01192_HH	1	AC008553.4	AC008553 Homo sapiens chromosome 5 clone CTC-512C13, complete sequence	42.1	100	0.1
01199_HH	2	BAA92590.1	(AB037773) KIAA1352 protein [Homo sapiens]	106	35	1.00E-22
01200_HH	3	AAF47217.1	(AE003464) anon-60Da gene product [Drosophila melanogaster]	38.3	23	0.054
01201_HH	1	AAF03411.1	AF187851_1 (AF187851) alpha-2-fucosyltransferase Sec1 [Bos taurus]	32.8	41	2.3
01204_HH	2	NP_060294.1	hypothetical protein FLJ20445 dbj|BAA91173.1| (AK000452) unnamed protein product [Homo sapiens]	158	44	4.00E-38
01207_HH	4	S13513	heterogeneous ribonuclear particle protein A1 homolog - American bird grasshopper	189	55	1.00E-47
01209_HH	1	AAF20209.1	AF208396_1 (AF208396) Hoi-polloi [Drosophila melanogaster]	144	53	4.00E-34
01210_HH	1	AE003729.1	AE003729 Drosophila melanogaster genomic scaffold 142000013386035 section 54 of 105, complete sequence	50.1	96	0.001
01216_HH	1	B49988	hypothetical 19K protein (slyD region) - Escherichia coli gb|AAA18572.1| (L13261) GTG start codon, orf159 [Escherichia coli]	33.2	31	1.8
01217_HH	1	P34623	YO87_CAEEL HYPOTHETICAL 28.5 KD PROTEIN ZK1236.7 IN CHROMOSOME III pir||S44893 ZK1236.7 protein - Caenorhabditis elegans gb|AAA28188.1| (L13200) putative [Caenorhabditis elegans]	92.1	45	4.00E-18
01218_HH	2	P04066	FUCO_HUMAN TISSUE ALPHA-L-FUCOSIDASE PRECURSOR (ALPHA-L-FUCOSIDASE I) (ALPHA-L-FUCOSIDE FUCOHYDROLASE) gb|AAA52481.1| (M80815) alpha-L-fucosidase [Homo sapiens]	208	61	3.00E-53
01225_HH	2	AAF32311.1	AF217788_1 (AF217788) O-glycosyltransferase [Drosophila melanogaster] gb|AAF57338.1| (AE003787) BcDNA:GH04245 gene product [Drosophila melanogaster]	131	42	7.00E-30
01226_HH	2	AAF56250.1	(AE003746) CG5510 gene product [Drosophila melanogaster]	220	56	9.00E-57
01228_HH	1	A47500	Ig mu chain switch region binding protein 2 - human	125	42	4.00E-28
01231_HH	1	NP_038716.1	t-complex-associated testis expressed 1 pir||A45841 T-complex-associated-testes-expressed-1 protein - mouse gb|AAA40406.1| (M28821) Tcte-1 peptide [Mus musculus]	71.4	34	6.00E-12
01237_HH	1	CAC00661.1	(AL121772) dJ965G21.1 (Glycogen Phosphorylase, brain form (EC 2.4.1.1)) [Homo sapiens]	245	67	2.00E-64
01239_HH	3	Q12959	SP97_HUMAN PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1) pir||I38757 homolog of Drosophila discs large protein, isoform 1 - human gb|AAA50599.1| (U13897) homolog of Drosophila discs large protein, isoform 1 [Homo sapiens]	51.9	40	4.00E-06
01241_HH	3	NP_032492.1	karyopherin (importin) alpha 3 sp|O35344|IMA3_MOUSE IMPORTIN ALPHA-3 SUBUNIT (KARYOPHERIN ALPHA-3 SUBUNIT) (IMPORTIN ALPHA Q2) gb|AAC53372.1| (AF020772) importin alpha Q2 [Mus musculus]	197	61	5.00E-50
01242_HH	2	NP_004515.1	lethal giant larvae (Drosophila) homolog 2 pir||S55474 Human giant larvae homolog - human emb|CAA60780.1| (X87342) Human giant larvae homologue [Homo sapiens]	50.8	24	9.00E-06
01245_HH	1	AAF02422.1	AF103802_1 (AF103802) unknown [Homo sapiens]	55	47	5.00E-07
01247_HH	2	AAD44759.1	AF144628_1 (AF144628) SLIT2 [Mus musculus]	37.5	31	0.092
01249_HH	1	Q62761	KC11_RAT CASEIN KINASE I, GAMMA 1 ISOFORM (CKI-GAMMA 1) pir||A56711 casein kinase I (EC 2.7.1.-) gamma-1 - rat gb|AAC52200.1| (U22296) casein kinase 1 gamma 1 isoform [Rattus norvegicus]	238	78	2.00E-70
01252_HH	1	NP_055498.1	KIAA0623 gene product dbj|BAA31598.1| (AB014523) KIAA0623 protein [Homo sapiens]	90.9	39	8.00E-18
01257_HH	1	AAF16717.1	AF117595_1 (AF117595) FK506-binding protein [Manduca sexta]	160	71	6.00E-39
01264_HH	2	JC7093	Fas associated factor 1 - human gb|AAD51886.1|AF106798_1 (AF106798) fas-associated factor 1 [Homo sapiens]	56.2	26	2.00E-07

01267_HH	2	AAF59327.1	(AE003843) CG1732 gene product [Drosophila melanogaster]	116	60	2.00E-25
01270_HH	2	AAC02903.2	(AF012072) eIF4GII [Homo sapiens]	86.2	34	2.00E-16
01278_HH	1	AAB66717.1	(U90567) glutamine rich protein [Gallus gallus]	60.5	41	1.00E-08
01279_HH	1	JE0209	brain-specific angiogenesis inhibitor-associated protein 1 - human	103	44	1.00E-21
01280_HH	1	Q02963	POLG_PVYHU GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3; 6 KD PROTEIN 1 (6K1); CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NI-A) (NI> pir||JN0545 genome polyprotein - potato virus Y (isolate Hungary) gb|AAB59762.1| (M95491) polyprotein [Potato virus Y]	32.5	25	3.1
01284_HH	1	AAF56268.1	(AE003747) CG5706 gene product [Drosophila melanogaster]	172	54	2.00E-42
01287_HH	1	AAF72001.1	AF231105_1 (AF231105) beta-1,6-N-acetylglucosaminyltransferase; pBORFF3-4 [Bovine herpesvirus 4]	80.8	39	9.00E-15
01288_HH	1	AAF24343.1	AF200425_1 (AF200425) Short stop/Kakapo long isoform [Drosophila melanogaster]	178	57	3.00E-44
01289_HH	4	BAA94544.1	(AB039933) polyposis locus protein 1-like 1 (TB2 protein-like 1) [Mus musculus]	161	50	5.00E-39
01290_HH	2	P49951	CLH_BOVIN CLATHRIN HEAVY CHAIN gb|AAC48524.1| (U31757) clathrin heavy chain [Bos taurus]	305	86	1.00E-82
01293_HH	1	H55590	hypothetical protein 4 - Lyme disease spirochete plasmid cp8.3/lp21 gb|AAA19041.1| (U03641) ORF 4 [Borrelia burgdorferi]	42.6	29	0.003
01295_HH	1	AAD38574.1	AF145599_1 (AF145599) BcDNA.GH02384 [Drosophila melanogaster]	72.6	33	3.00E-12
01296_HH	4	AAB32066.1	(S72579) growth-associated protein GAP-43 homolog=igloo-S [Drosophila melanogaster, pupa, Peptide, 122 aa]	43.8	40	0.001
01300_HH	1	NP_035959.1	inosine 5'-phosphate dehydrogenase 1 sp|P50096|IMD1_MOUSE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 1 (IMP DEHYDROGENASE 1) (IMPDH-I) (IMPD 1) gb|AAA18285.1| (U00978) type I inosine monophosphate dehydrogenase [Mus musculus]	191	59	4.00E-48
01301_HH	4	T31737	hypothetical protein T21H3.3 - Caenorhabditis elegans gb|AAB65364.1| (AF016429) similar to EF-hand calcium binding proteins; most similar to calmodulin [Caenorhabditis elegans] emb|CAA10601.1| (AJ132193) calmodulin [Caenorhabditis elegans]	300	100	9.00E-81
01306_HH	3	AAF51486.1	(AE003589) CG11840 gene product [Drosophila melanogaster]	109	42	2.00E-23
01308_HH	4	NP_057048.1	CGI-38 protein gb|AAD27747.1|AF132972_1 (AF132972) CGI-38 protein [Homo sapiens]	78	33	6.00E-14
01310_HH	2	prf|2118248A	prepro-cathepsin C [Homo sapiens]	148	45	4.00E-35
01313_HH	3	AL139812.11	AL139812 Human DNA sequence from clone RP1-19N1 on chromosome Xq21.33-22.3. Contains a gene for a novel protein. Contains ESTs, STSs and GSSs, complete sequence [Homo sapiens]	40.1	100	0.88
01315_HH	1	AE003823.1	AE003823 Drosophila melanogaster genomic scaffold 142000013386047 section 33 of 52, complete sequence	42.1	100	0.22
01321_HH	1	AAF72651.1	AF259401_1 (AF259401) Ca2+-independent phospholipase A2 long form; IPLA2 [Mus musculus]	87	30	1.00E-16
01322_HH	2	CAB60875.2	(AL132880) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans]	121	44	6.00E-27
01325_HH	1	NP_002486.1	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) sp|O43181|NUYM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) gb|AAB87865.1| (AF020351) NADH:ubiquinone oxidoreductase 18 kDa IP subunit [Homo sapiens]	137	53	7.00E-32
01328_HH	1	AAD09842.1	(U41599) NADH dehydrogenase subunit F [Eichhornia crassipes]	28.6	31	8.7
01331_HH	1	AAF51605.1	(AE003591) CG5195 gene product [Drosophila melanogaster]	31.3	32	6.9
01339_HH	5	AAF61690.1	AF220365_1 (AF220365) nucleolar RNA helicase II/Gu [Mus musculus]	149	48	2.00E-35
01343_HH	1	NP_057246.1	candidate tumor suppressor p33 ING1 homolog gb|AAD48585.1| (AF110645) candidate tumor suppressor p33 ING1 homolog [Homo sapiens]	53.1	27	2.00E-06
01348_HH	1	P28173	PUR1_CHICK AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) pir||A38337 amidophosphoribosyltransferase (EC 2.4.2.14) - chicken gb|AAA62736.1| (M60069) glutamine phosphoribosylpyrophosphate amidotransferase [Gallus gallus]	195	62	3.00E-49
01349_HH	1	CAA73666.1	(Y13224) IgA1 protease [Streptococcus oralis]	34.8	43	0.61
01351_HH	1	CAB64449.1	(AJ252060) TRABID protein [Homo sapiens]	73	27	2.00E-12
01352_HH	5	AAF52881.1	(AE003628) me31B gene product [Drosophila melanogaster]	229	64	1.00E-59
01355_HH	1	AAA96439.1	(M65158) type VII collagen [Homo sapiens]	57.8	58	8.00E-08
01360_HH	1	S14470	asparagine-rich protein (clone 28C6) - Plasmodium falciparum (fragment) emb|CAA35523.1| (X17487) unnamed protein product [Plasmodium falciparum]	32.5	29	3.1
01362_HH	1	AAF21645.1	AF039412_1 (AF039412) frizzled homolog [Danio rerio]	51.2	31	7.00E-06
01363_HH	1	AC008843.5	AC008843 Homo sapiens chromosome 5 clone CTD-2156N14, complete sequence	44.1	96	0.057
01367_HH	2	AAC27663.1	(L76432) tryptophan oxygenase [Anopheles gambiae] gb|AAC27659.1| (L76433) tryptophan oxygenase [Anopheles gambiae]	165	56	3.00E-40
01370_HH	3	AAC00520.1	(AF044413) HSP70 [Schistosoma japonicum]	257	77	7.00E-68
01371_HH	1	AC006535.7	AC006535 Genomic sequence for Arabidopsis thaliana BAC T24P13 from chromosome I, complete sequence	48.1	93	0.004
01374_HH	4	A60671	tubulin alpha chain - sea urchin (Paracentrotus lividus)	294	86	5.00E-79
01376_HH	1	AAD34644.1	AF154112_1 (AF154112) transcription co-repressor Sin3 [Xenopus laevis]	73.7	27	1.00E-12
01378_HH	1	AAF48495.1	(AE003500) CG8184 gene product [Drosophila melanogaster]	32.5	35	3.1
01380_HH	1	T26642	hypothetical protein Y37D8A.22 - Caenorhabditis elegans emb|CAA21543.1| (AL032626) predicted using Genefinder~cDNA EST yk539c9.5 comes from this gene [Caenorhabditis elegans]	78.4	36	4.00E-14
01381_HH	1	AAD55746.1	AF026167_1 (AF026167) ankyrin repeat protein EMB506 [Arabidopsis thaliana]	87.8	40	7.00E-17
01382_HH	1	G71608	ATP-dept. acyl-CoA synthetase (TP) PFB0685c - malaria parasite (Plasmodium falciparum) gb|AAC71926.1| (AE001411) ATP-dept. acyl-CoA synthetase (TP) [Plasmodium falciparum]	36.7	28	0.16
01385_HH	1	Q91060	TBA_NOTVI TUBULIN ALPHA CHAIN pir||S43138 tubulin alpha chain - eastern newt emb|CAA83457.1| (Z31585) alpha-tubulin [Notophthalmus viridescens]	253	74	1.00E-66

01390_HH	1	NP_011597.1	translation initiation factor eIF2B, 71 kDa (delta) subunit; translational repressor of GCN4 protein; Gcd2p sp|P12754|E2BD_YEAST TRANSLATION INITIATION FACTOR EIF-2B DELTA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) (GUANINE NUCLEOTIDE EXCHANGE FACTOR SUBUNIT GCD2) (GCD COMPLEX SUBUNIT GCD2) pir||RGBYD2 translation regulator GCD2 - yeast (Saccharomyces cerevisiae) emb|CAA33693.1| (X15658) GCD2 gene product (AA 1 - 651) [Saccharomyces cerevisiae] emb|CAA97085.1| (Z72868) ORF YGR083c [Saccharomyces cerevisiae]	73	32	2.00E-12
01391_HH	5	P27615	LYII_RAT LYSOSOME MEMBRANE PROTEIN II (LIMP II) (85 KD LYSOSOMAL MEMBRANE SIALOGLYCOPROTEIN) (LGP85) (CD36 ANTIGEN-LIKE 2) pir||JH0241 85K lysosomal membrane sialoglycoprotein - rat gb|AAA41531.1| (M68965) lysosomal membrane protein [Rattus norvegicus] dbj|BAA01444.1| (D10587) LGP85 [Rattus sp.]	103	41	1.00E-21
01392_HH	1	AAF56560.1	(AE003754) Dak1 gene product [Drosophila melanogaster]	139	54	2.00E-32
01393_HH	1	NP_004637.1	Nephrin pir||T37190 nephrin - human gb|AAC39687.1| (AF035835) nephrin [Homo sapiens]	37.1	21	0.12
01395_HH	1	CAB77011.1	(AL159951) conserved hypothetical protein with putative coiled-coil regions [Schizosaccharomyces pombe]	34.4	23	0.8
01400_HH	1	AAG02226.1	AF292564_1 (AF292564) cytochrome P450 steroid 17alpha-hydroxylase/17,20 lyase [Felis catus]	37.1	24	0.12
01403_HH	1	P23226	MAPX_DROME 205 KDA MICROTUBULE-ASSOCIATED PROTEIN	37.5	28	0.092
01405_HH	1	AAF59316.1	(AE003843) bt gene product [Drosophila melanogaster]	68.3	31	5.00E-11
01406_HH	3	NP_055434.1	glutamate receptor, ionotropic, kainate 4 sp|Q16099|GLK4_HUMAN GLUTAMATE RECEPTOR, IONOTROPIC KAINATE 4 PRECURSOR (GLUTAMATE RECEPTOR KA-1) (KA1) (EXCITATORY AMINO ACID RECEPTOR 1) (EAA1) pir||JH0826 glutamate ionotropic receptor EAA1 chain precursor - human gb|AAB29311.1| (S67803) excitatory amino acid receptor 1, kainate receptor subunit EAA1=glutamate ionotropic receptor [human, hippocampus, Peptide, 956 aa] [Homo sapiens]	162	50	3.00E-39
01407_HH	1	AAG09240.1	AF176329_1 (AF176329) alphaCP-3 [Homo sapiens]	62.1	49	3.00E-09
01408_HH	6	NP_002622.1	phosphogluconate dehydrogenase sp|P52209|6PGD_HUMAN 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING pir||G01922 phosphogluconate dehydrogenase (decarboxylating) (EC 1.1.1.44) - human gb|AAA75302.1| (U30255) phosphogluconate dehydrogenase [Homo sapiens]	219	66	1.00E-56
01410_HH	1	AAF54271.1	(AE003680) CG8112 gene product [Drosophila melanogaster]	46.9	30	1.00E-04
01415_HH	1	P18652	KS6A_CHICK RIBOSOMAL PROTEIN S6 KINASE II ALPHA (S6KII-ALPHA) (P90-RSK) (MAP KINASE-ACTIVATED PROTEIN KINASE 1) (MAPK-ACTIVATED PROTEIN KINASE 1) (MAPKAP KINASE 1) (MAPKAPK-1) pir||A32571 ribosomal protein S6 kinase II (EC 2.7.1.-) alpha chain homolog - chicken gb|AAA21877.1| (M28488) ribosomal protein S6 kinase [Gallus gallus]	40.2	43	0.01
01416_HH	2	AAF31361.1	(AF187863) glycine amidinotransferase [Xenopus laevis]	101	42	7.00E-21
01418_HH	1	AAC47111.1	(U47278) axonemal dynein light chain p33 [Strongylocentrotus purpuratus]	213	66	9.00E-55
01422_HH	1	T00326	hypothetical protein KIAA0550 - human dbj|BAA25476.1| (AB011122) KIAA0550 protein [Homo sapiens]	50.8	62	9.00E-06
01426_HH	3	AAC39012.1	(AF044734) flotillin-1 [Drosophila melanogaster] gb|AAF58120.1| (AE003810) Flo gene product [alt 1] [Drosophila melanogaster]	169	60	1.00E-41
01428_HH	1	AAF58370.1	(AE003818) CG6016 gene product [alt 1] [Drosophila melanogaster]	71	45	2.00E-14
01435_HH	1	AAG06008.1	AE004690_8 (AE004690) ATP-binding protease component ClpA [Pseudomonas aeruginosa]	31.7	29	5.3
01438_HH	1	AAC16552.1	(AF063902) putative prenylated protein tyrosine phosphatase PRL-1 [Drosophila melanogaster] gb|AAF53506.1| (AE003650) PRL-1 gene product [Drosophila melanogaster]	55.4	44	4.00E-07
01441_HH	1	BAA92654.1	(AB037837) KIAA1416 protein [Homo sapiens]	37.9	36	0.07
01443_HH	1	BAA92185.1	(AB031543) beta-catenin [Ciona intestinalis]	57.8	27	7.00E-08
01451_HH	1	NP_058734.1	protein phosphatase type 1A (formely 2C), Mg-dependent, alpha isoform sp|P20650|P2CA_RAT PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (PP2C-ALPHA) (IA) (PROTEIN PHOSPHATASE 1A) pir||A32399 phosphoprotein phosphatase (EC 3.1.3.16) 1A - rat gb|AAA41917.1| (J04503) protein phosphatase 2c [Rattus norvegicus]	180	54	1.00E-44
01453_HH	1	AP001677.1	AP001677 Homo sapiens genomic DNA, chromosome 21q, section 21/105	42.1	100	0.22
01455_HH	1	AAF32464.1	(AC021640) putative mannose-6-phosphate isomerase [Arabidopsis thaliana]	55.8	32	3.00E-07
01460_HH	2	T40374	hypothetical protein SPBC3D6.14c - fission yeast (Schizosaccharomyces pombe) (fragment) emb|CAB09116.1| (Z95620) hypothetical protein [Schizosaccharomyces pombe]	32.5	27	3
01462_HH	1	T18426	hypothetical protein C0330w - Plasmodium falciparum emb|CAB11102.1| (Z98547) predicted using hexExon; MAL3P3.2 (PFC0330w), PDZ domain protein, len: 700 aa [Plasmodium falciparum]	35.6	26	0.32
01463_HH	1	O13923	CORO_SCHPO CORONIN-LIKE PROTEIN CRN1 pir||T38258 coronin-like protein - fission yeast (Schizosaccharomyces pombe) emb|CAB16873.1| (Z99753) yeast coronin CRN1 homolog [Schizosaccharomyces pombe]	92.8	40	2.00E-18
01464_HH	1	AF040971.1	AF040971 Eimeria tenella small subunit ribosomal RNA gene, plastid gene for plastid RNA, partial sequence	46.1	96	0.014
01468_HH	1	S18211	hypothetical protein 2 - fruit fly (Drosophila virilis) retrotransposon Ulysses emb|CAA39967.1| (X56645) ORF 2 [Drosophila virilis]	41.4	29	0.006
01473_HH	5	CAA28629.1	(X04961) hsp 108 [Gallus gallus]	219	61	1.00E-56
01475_HH	1	P42025	ACTY_HUMAN BETA-CENTRACTIN emb|CAA57691.1| (X82207) beta-centracetin [Homo sapiens]	281	84	3.00E-75
01477_HH	1	T32193	hypothetical protein T01G6.4 - Caenorhabditis elegans gb|AAC69071.1| (AF022978) contains similarity to C4-type zinc fingers [Caenorhabditis elegans]	31.3	58	6.9
01478_HH	1	AAF48357.1	(AE003495) CG15871 gene product [Drosophila melanogaster]	42.2	26	0.004
01480_HH	1	G71605	hypothetical protein PFB0825c - malaria parasite (Plasmodium falciparum) gb|AAC71954.1| (AE001419) hypothetical protein [Plasmodium falciparum]	31.3	28	6.9
01481_HH	1	F71698	hypothetical protein RP407 - Rickettsia prowazekii emb|CAA14864.1| (AJ235271) unknown [Rickettsia prowazekii]	32.5	39	3.1
01485_HH	2	AAF54109.1	(AE003674) CG2337 gene product [Drosophila melanogaster]	114	43	7.00E-25
01486_HH	2	AAF67190.1	AF252549_1 (AF252549) gamma-filamin [Homo sapiens]	74.9	35	2.00E-19
01490_HH	1	P31976	EZRI_BOVIN EZRIN (P81) (CYTOVILLIN) (VILLIN-2) pir||I45889 ezrin - bovine gb|AAA30510.1| (M98498) ezrin [Bos taurus]	161	54	6.00E-39

01492_HH	7	Q03412	UNC7_CAEEL UNC-7 PROTEIN pir||S52975 unc-7 protein - Caenorhabditis elegans pir||T24027 unc-7 protein - Caenorhabditis elegans emb|CAA79529.1| (Z19122) hypothetical polypeptide [Caenorhabditis elegans] emb|CAA94607.1| (Z70685) Identity to C.elegans UNC-7 protein (SW:UNC7_CAEEL) [Caenorhabditis elegans]	101	37	4.00E-21
01493_HH	1	S75772	hypothetical protein slr0825 - Synechocystis sp. (strain PCC 6803) dbj|BAA10507.1| (D64003) hypothetical protein [Synechocystis sp.]	62.5	38	7.00E-11
01497_HH	1	AAF13073.1	AC011621_1 (AC011621) putative retroelement pol polyprotein [Arabidopsis thaliana]	156	46	1.00E-37
01498_HH	2	AAD24794.1	AF120929_1 (AF120929) phosphoenolpyruvate carboxykinase [Schistosoma mansoni]	268	71	4.00E-71
01502_HH	3	AAB58577.1	(U87912) MAP kinase kinase protein DdMEK1 [Dictyostelium discoideum]	35.2	29	0.46
01505_HH	1	AAB00969.1	(M77233) ribosomal protein [Homo sapiens]	172	58	2.00E-42
01507_HH	1	NP_011148.1	GTP-binding protein; Ypt1p sp|P01123|YPT1_YEAST GTP-BINDING PROTEIN YPT1 (PROTEIN YP2) pir||TVBYQ2 GTP-binding protein YPT1 - yeast (Saccharomyces cerevisiae) dbj|BAA09201.1| (D50617) GTP-binding protein YPT1 [Saccharomyces cerevisiae] dbj|BAA08026.1| (D44598) GTP-BINDING PROTEIN YPT1(YP2) [Saccharomyces cerevisiae] prf||2210408C GTP-binding protein [Saccharomyces cerevisiae]	118	35	5.00E-26
01509_HH	3	CAA34683.1	(X16711) COL2A1 [Homo sapiens]	43.8	54	0.001
01510_HH	5	BAA34993.1	(AB017002) DjVLGA [Dugesia japonica]	86.6	32	2.00E-16
01512_HH	1	Q14669	TR12_HUMAN THYROID RECEPTOR INTERACTING PROTEIN 12 (TRIP12) (KIAA0045) dbj|BAA05837.1| (D28476) KIAA0045 [Homo sapiens]	165	50	2.00E-40
01514_HH	1	AAF08554.1	AC012193_3 (AC012193) putative phosphatidylinositol-4-phosphate-5-kinase [Arabidopsis thaliana]	76.5	45	2.00E-13
01517_HH	1	BAA90484.1	(AB030947) high-affinity choline transporter CHT1 [Rattus norvegicus]	165	48	3.00E-40
01518_HH	1	CAB61404.1	(AL133087) hypothetical protein [Homo sapiens]	77.3	32	1.00E-13
01521_HH	1	AAF51037.1	(AE003577) CG3714 gene product [Drosophila melanogaster]	202	57	2.00E-51
01522_HH	2	T02152	Lu-ECAM-1 protein - bovine gb|AAB86531.1| (AF001263) Lu-ECAM-1 [Bos taurus]	87.4	37	9.00E-17
01526_HH	4	Z11126.1	CEZK643 Caenorhabditis elegans cosmid ZK643, complete sequence	50.1	100	0.001
01534_HH	3	P26136	HEMA_IAMAB HEMAGGLUTININ PRECURSOR [CONTAINS: HEMAGGLUTININ HA1 CHAIN; HEMAGGLUTININ HA2 CHAIN] pir||A46339 hemagglutinin precursor - influenza A virus (strain A/Mallard/Gurjev/263/82 [H14N5])	31.3	38	6.9
01536_HH	1	Q63448	CAOQ_RAT PRISTANOYL-COA OXIDASE emb|CAA64487.1| (X95188) pristanoyl-CoA oxidase [Rattus norvegicus]	174	50	5.00E-43
01540_HH	1	CAA60050.1	(X86096) transcription factor [Homo sapiens]	176	57	2.00E-43
01541_HH	1	NP_064703.1	cyclin L ania-6a gb|AAD53184.1|AF180920_1 (AF180920) cyclin L ania-6a [Homo sapiens]	93.2	53	2.00E-18
01542_HH	1	P27591	IM23_SCHJA 23 KD INTEGRAL MEMBRANE PROTEIN (SJ23) pir||A40181 23K integral membrane protein - fluke (Schistosoma japonicum) gb|AAA29920.1| (M63706) Sj23 [Schistosoma japonicum]	67.5	35	9.00E-11
01547_HH	2	AAF48924.1	(AE003511) CG7556 gene product [Drosophila melanogaster]	51.5	21	6.00E-06
01549_HH	2	NP_003746.1	eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD) sp|O75821|IF34_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 4 (EIF-3 DELTA) (EIF3 P44) (EIF-3 RNA-BINDING SUBUNIT) (EIF3 P42) gb|AAC78728.1| (U96074) translation initiation factor eIF3 p44 subunit [Homo sapiens]	83.1	30	2.00E-15
01553_HH	1	BAA76489.1	(AB015462) maturase [Casuarina equisetifolia]	32.5	43	0.94
01554_HH	1	AAC44695.1	(AF282853) CagM [Helicobacter pylori]	37.1	26	0.12
01555_HH	2	AAF48098.1	(AE003487) CG1905 gene product [Drosophila melanogaster]	39.1	25	0.031
01556_HH	1	AL139342.7	AL139342 Human DNA sequence from clone RP5-1016N21 on chromosome 1q42.13-43, complete sequence [Homo sapiens]	44.1	100	0.057
01557_HH	2	Q39575	DYHG_CHLRE DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM pir||T08044 dynein gamma heavy chain, outer-arm - Chlamydomonas reinhardtii gb|AAA50455.1| (U15303) gamma heavy chain subunit of outer-arm dynein [Chlamydomonas reinhardtii]	155	46	3.00E-37
01558_HH	2	P39053	DYN1_MOUSE DYNAMIN-1 (DYNAMIN BREDNM19) gb|AAA37324.1| (L31397) dynamin [Mus musculus]	153	44	1.00E-36
01562_HH	1	T18451	hypothetical protein C0565w - Plasmodium falciparum emb|CAA15593.1| (AL008970) hypothetical protein, PFC0565w [Plasmodium falciparum]	34.4	21	0.8
01564_HH	8	A53665	phosphopyruvate hydratase (EC 4.2.1.11) - liver fluke	196	72	1.00E-62
01566_HH	1	AAF51067.1	(AE003578) CG10019 gene product [Drosophila melanogaster]	29.7	45	3.9
01570_HH	1	T15846	hypothetical protein C56C10.7 - Caenorhabditis elegans gb|AAA68775.1| (U29488) C56C10.7 gene product [Caenorhabditis elegans]	81.1	29	7.00E-15
01576_HH	1	NP_003918.1	methyl-CpG binding domain protein 2, isoform 1 gb|AAC68871.1| (AF072242) methyl-CpG binding protein MBD2 [Homo sapiens] gb|AAD56597.1| (AF120994) methyl-CpG binding protein 2 [Homo sapiens]	83.5	42	1.00E-15
01583_HH	1	G71949	hypothetical protein jhp0294 - Helicobacter pylori (strain J99) gb|AAD05871.1| (AE001466) putative [Helicobacter pylori J99]	32.1	44	4
01585_HH	1	AAF51059.1	(AE003578) CG3407 gene product [Drosophila melanogaster]	43.8	36	0.001
01587_HH	1	CAB63736.1	(AL133601) hypothetical protein [Homo sapiens]	110	37	1.00E-23
01588_HH	2	NP_055205.1	EBNA-2 co-activator (100kD) pir||I38968 100 kDa coactivator - human gb|AAA80488.1| (U22055) 100 kDa coactivator [Homo sapiens]	166	58	5.00E-42
01592_HH	2	AAD34769.1	(AF132181) unknown [Drosophila melanogaster] gb|AAF56930.1| (AE003771) BcDNA:LD21720 gene product [Drosophila melanogaster]	93.6	33	1.00E-18
01593_HH	1	NP_048105.1	ORF MSV034 tryptophan repeat gene family protein gb|AAC97839.1| (AF063866) ORF MSV034 tryptophan repeat gene family protein [Melanoplus sanguinipes entomopoxvirus]	32.5	36	3.1
01601_HH	1	P70052	NR21_XENLA ORPHAN NUCLEAR RECEPTOR NR2E1 (NUCLEAR RECEPTOR TLX) (TAILLESS HOMOLOG) (TLL) (XTLL) gb|AAB07732.1| (U67886) orphan nuclear receptor XTLL [Xenopus laevis]	37.1	30	0.12
01605_HH	1	T22666	hypothetical protein F54E4.4 - Caenorhabditis elegans emb|CAB01918.1| (Z79639) similar to zinc metalloprotease [Caenorhabditis elegans]	92.8	33	2.00E-18
01609_HH	1	1D0J	A Chain A, Structure Of Tnf Receptor Associated Factor 2 In Complex With A M4-1bb Peptide pdb|1D0J|B Chain B, Structure Of Tnf Receptor Associated Factor 2 In Complex With A M4-1bb Peptide pdb|1D0J|C Chain C, Structure Of Tnf Receptor Associated Factor 2 In Complex With A M4-1bb Peptide pdb|1D0J|D Chain D, Structure Of Tnf Receptor Associated Factor 2 In Complex With A M4-1bb Peptide pdb|1D0J|E Chain E, Structure Of Tnf Receptor Associated Factor 2 In Complex With A M4-1bb Peptide pdb|1D0J|F Chain F, Structure Of Tnf Receptor Associated Factor 2 In Complex With A M4-1bb Peptide	59.7	40	2.00E-08
01611_HH	1	AAF53962.1	(AE003669) Dap160 gene product [Drosophila melanogaster]	64	47	9.00E-10

<table>
<tr><td>01612_HH</td><td>2</td><td>NP_032090.1</td><td>glucosidase, alpha, acid sp|P70699|LYAG_MOUSE LYSOSOMAL ALPHA-GLUCOSIDASE PRECURSOR (ACID MALTASE) gb|AAB06943.1| (U49351) lysosomal alpha-glucosidase [Mus musculus]</td><td>109</td><td>40</td><td>2.00E-23</td></tr>
<tr><td>01614_HH</td><td>2</td><td>AAF54217.1</td><td>(AE003678) CG9615 gene product [Drosophila melanogaster]</td><td>171</td><td>48</td><td>6.00E-42</td></tr>
<tr><td>01616_HH</td><td>4</td><td>S06147</td><td>GTP-binding protein rab1B - rat prf||1515250A rab1B protein [Rattus norvegicus]</td><td>265</td><td>90</td><td>3.00E-70</td></tr>
<tr><td>01619_HH</td><td>2</td><td>AAF80999.1</td><td>(AF218039) structural polyprotein [cricket paralysis virus]</td><td>62.8</td><td>28</td><td>2.00E-09</td></tr>
<tr><td>01620_HH</td><td>1</td><td>NP_002941.1</td><td>ribophorin I sp|P04843|RIB1_HUMAN DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 67 KDA SUBUNIT PRECURSOR (RIBOPHORIN I) (RPN-I) pir||A26168 ribophorin I precursor - human emb|CAA68392.1| (Y00281) precursor [Homo sapiens]</td><td>182</td><td>56</td><td>2.00E-45</td></tr>
<tr><td>01623_HH</td><td>1</td><td>AC005875.2</td><td>AC005875 citb_188_b_12, complete sequence [Homo sapiens]</td><td>42.1</td><td>96</td><td>0.068</td></tr>
<tr><td>01629_HH</td><td>3</td><td>P13444</td><td>METL_RAT S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) (MAT-I/III) pir||S06114 methionine adenosyltransferase (EC 2.5.1.6) - rat emb|CAA33754.1| (X15734) s-adenosylmethionine synthetase [Rattus norvegicus]</td><td>236</td><td>69</td><td>1.00E-61</td></tr>
<tr><td>01631_HH</td><td>2</td><td>T18570</td><td>probable malate dehydrogenase (EC 1.1.1.37) - Caenorhabditis elegans emb|CAA22133.1| (AL033535) predicted using Genefinder~cDNA EST yk268h6.5 comes from this gene~cDNA EST yk465f2.5 comes from this gene~cDNA EST yk393g7.5 comes from this gene~cDNA EST EMBL:M88999 comes from this gene~cDNA EST yk264b4.5 comes from this gene~cDNA EST yk3> emb|CAA88951.1| (Z49127) predicted using Genefinder~cDNA EST yk268h6.5 comes from this gene~cDNA EST yk465f2.5 comes from this gene~cDNA EST yk393g7.5 comes from this gene~cDNA EST EMBL:M88999 comes from this gene~cDNA EST yk264b4.5 comes from this gene~cDNA EST yk383></td><td>157</td><td>54</td><td>7.00E-38</td></tr>
<tr><td>01632_HH</td><td>1</td><td>AP001038.2</td><td>AP001038 Homo sapiens genomic DNA, chromosome 21, clone:P178O22, ERG-ETS2 region, complete sequence</td><td>42.1</td><td>100</td><td>0.065</td></tr>
<tr><td>01636_HH</td><td>2</td><td>P05205</td><td>HP1_DROME HETEROCHROMATIN PROTEIN 1 (HP1) (NONHISTONE CHROMOSOMAL PROTEIN C1A9 ANTIGEN) pir||A39268 heterochromatin-specific chromosomal protein 1 - fruit fly (Drosophila melanogaster) gb|AAA28620.1| (M57574) heterochromatin-specific chromosomal protein HP-1 [Drosophila melanogaster] gb|AAF52618.1| (AE003620) Su(var)205 gene product [Drosophila melanogaster]</td><td>121</td><td>45</td><td>4.00E-27</td></tr>
<tr><td>01637_HH</td><td>1</td><td>AAD50328.1</td><td>AF073800_1 (AF073800) fibrillin-1 precursor [Sus scrofa]</td><td>92.8</td><td>29</td><td>2.00E-18</td></tr>
<tr><td>01638_HH</td><td>1</td><td>BAA95023.1</td><td>(AB041538) unnamed protein product [Mus musculus]</td><td>60.1</td><td>24</td><td>1.00E-08</td></tr>
<tr><td>01643_HH</td><td>1</td><td>AB032899.1</td><td>AB032899 Rattus norvegicus PIPK2 alpha mRNA for phosphatidylinositol 5-phosphate 4-kinase alpha, complete cds</td><td>44.1</td><td>100</td><td>0.057</td></tr>
<tr><td>01644_HH</td><td>6</td><td>T30338</td><td>oviductin - African clawed frog gb|AAB53972.1| (U81291) oviductin [Xenopus laevis]</td><td>78.4</td><td>33</td><td>4.00E-14</td></tr>
<tr><td>01645_HH</td><td>1</td><td>AAF54771.1</td><td>(AE003695) CG3942 gene product [Drosophila melanogaster]</td><td>32.8</td><td>29</td><td>2.3</td></tr>
<tr><td>01651_HH</td><td>1</td><td>AL117207.1</td><td>CEY60A3A Caenorhabditis elegans cosmid Y60A3A, complete sequence</td><td>44.1</td><td>100</td><td>0.057</td></tr>
<tr><td>01652_HH</td><td>3</td><td>AAB17669.1</td><td>(U72874) egg receptor for sperm [Strongylocentrotus purpuratus]</td><td>183</td><td>58</td><td>1.00E-45</td></tr>
<tr><td>01655_HH</td><td>1</td><td>P36333</td><td>ACSA_PENCH ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME) pir||JN0781 acetate--CoA ligase (EC 6.2.1.1) - Penicillium chrysogenum gb|AAC60546.1| (S54801) acetyl-coenzyme A synthetase, CoA synthetase [Penicillium chrysogenum, Peptide, 669 aa] gb|AAA02921.1| (L09598) acetyl-CoA synthetase [Penicillium chrysogenum]</td><td>105</td><td>37</td><td>3.00E-22</td></tr>
<tr><td>01656_HH</td><td>1</td><td>NP_058577.1</td><td>phosphomannomutase 2 gb|AAD02276.1| (AF043514) phosphomannomutase [Mus musculus]</td><td>154</td><td>54</td><td>6.00E-37</td></tr>
<tr><td>01659_HH</td><td>1</td><td>T41291</td><td>conserved hypothetical protein SPCC31H12.03c - fission yeast (Schizosaccharomyces pombe) emb|CAA21220.1| (AL031824) conserved hypothetical protein [Schizosaccharomyces pombe]</td><td>67.1</td><td>27</td><td>1.00E-10</td></tr>
<tr><td>01661_HH</td><td>6</td><td>AAG00542.1</td><td>AF286534_1 (AF286534) GTP-binding protein RAB11B [Rattus norvegicus]</td><td>286</td><td>90</td><td>8.00E-77</td></tr>
<tr><td>01664_HH</td><td>3</td><td>T14867</td><td>interaptin - slime mold (Dictyostelium discoideum) gb|AAC34582.1| (AF057019) interaptin [Dictyostelium discoideum]</td><td>45.7</td><td>32</td><td>3.00E-04</td></tr>
<tr><td>01665_HH</td><td>2</td><td>AAG10084.1</td><td>AF296131_1 (AF296131) diacylglycerol acyltransferase [Rattus norvegicus]</td><td>92.1</td><td>39</td><td>4.00E-18</td></tr>
<tr><td>01667_HH</td><td>3</td><td>T21358</td><td>hypothetical protein F25H5.1b - Caenorhabditis elegans emb|CAB02981.1| (Z81068) similar to LIM domain containing proteins (5 domains)~cDNA EST yk439a12.5 comes from this gene~cDNA EST yk315d3.5 comes from this gene~cDNA EST yk383d5.5 comes from this gene~cDNA EST yk396f4.5 comes from this gene [Caenorhabditis elegans]</td><td>79.6</td><td>25</td><td>2.00E-14</td></tr>
<tr><td>01669_HH</td><td>1</td><td>NP_057323.1</td><td>unconventional myosin-15 gb|AAF05903.1| (AF144094) unconventional myosin-15 [Homo sapiens]</td><td>38.3</td><td>22</td><td>0.054</td></tr>
<tr><td>01670_HH</td><td>1</td><td>NP_058052.1</td><td>enoyl coenzyme A hydratase 1, peroxisomal sp|O35459|ECH1_MOUSE DELTA3,5-DELTA2,4-DIENOYL-COA ISOMERASE PRECURSOR gb|AAB84224.1| (AF030343) ECH1p [Mus musculus]</td><td>149</td><td>50</td><td>2.00E-35</td></tr>
<tr><td>01671_HH</td><td>1</td><td>AAF48455.1</td><td>(AE003499) CG9198 gene product [Drosophila melanogaster]</td><td>84.7</td><td>32</td><td>6.00E-16</td></tr>
<tr><td>01673_HH</td><td>1</td><td>NP_058702.1</td><td>glucose-6-phosphate dehydrogenase sp|P05370|G6PD_RAT GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (G6PD) pir||S01233 glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) precursor - rat emb|CAA30355.1| (X07467) Gd (AA 1-515) [Rattus norvegicus]</td><td>179</td><td>52</td><td>2.00E-44</td></tr>
<tr><td>01677_HH</td><td>2</td><td>BAA92442.1</td><td>(AB032265) glycogen synthase kinase 3 beta [Danio rerio]</td><td>245</td><td>71</td><td>3.00E-64</td></tr>
<tr><td>01681_HH</td><td>1</td><td>Q13563</td><td>PKD2_HUMAN POLYCYSTIN 2 (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE TYPE II PROTEIN) (POLYCYSTWIN) (R48321) gb|AAC16004.1| (AF004873) autosomal dominant polycystic kidney disease type II protein [Homo sapiens]</td><td>69.5</td><td>36</td><td>2.00E-11</td></tr>
<tr><td>01683_HH</td><td>3</td><td>S23016</td><td>polypyrimidine tract-binding protein PTB-2 - human emb|CAA46443.1| (X65371) polypirimidine tract binding protein [Homo sapiens]</td><td>102</td><td>33</td><td>2.00E-21</td></tr>
<tr><td>01687_HH</td><td>1</td><td>AAC46691.1</td><td>(U23147) Contains similarity to Pfam domain: PF00097 (zf-C3HC4), Score=13.0, E-value=0.0035, N=1 [Caenorhabditis elegans]</td><td>32.1</td><td>34</td><td>4</td></tr>
<tr><td>01691_HH</td><td>1</td><td>BAA36584.1</td><td>(AB014722) rSALT-1(806) [Rattus norvegicus]</td><td>85</td><td>35</td><td>5.00E-16</td></tr>
<tr><td>01693_HH</td><td>1</td><td>NP_004832.1</td><td>ras GTPase activating protein-like gb|AAD04814.1| (AF047711) nGAP [Homo sapiens]</td><td>32.8</td><td>25</td><td>2.3</td></tr>
<tr><td>01694_HH</td><td>1</td><td>NP_057094.1</td><td>CGI-62 protein gb|AAD34057.1|AF151820_1 (AF151820) CGI-62 protein [Homo sapiens]</td><td>141</td><td>44</td><td>5.00E-33</td></tr>
<tr><td>01695_HH</td><td>1</td><td>AAD13543.1</td><td>(AF080235) reductase homolog [Streptomyces cyanogenus]</td><td>66.3</td><td>30</td><td>2.00E-10</td></tr>
<tr><td>01701_HH</td><td>1</td><td>T16915</td><td>hypothetical protein T20H4.3 - Caenorhabditis elegans gb|AAA50660.1| (U00037) similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]</td><td>274</td><td>75</td><td>5.00E-73</td></tr>
<tr><td>01703_HH</td><td>1</td><td>NP_057034.1</td><td>CGI-22 protein gb|AAD27731.1|AF132956_1 (AF132956) CGI-22 protein [Homo sapiens]</td><td>99.8</td><td>37</td><td>2.00E-20</td></tr>
<tr><td>01704_HH</td><td>7</td><td>JC5759</td><td>brain-specific serine proteinase (EC 3.4.21.-) - mouse</td><td>94.4</td><td>43</td><td>7.00E-19</td></tr>
<tr><td>01705_HH</td><td>1</td><td>BAB09014.1</td><td>(AB007645) contains similarity to unknown protein~gene_id:K8K14.1~sp|Q10058 [Arabidopsis thaliana]</td><td>113</td><td>39</td><td>2.00E-24</td></tr>
</table>

01707_HH	1	CAA96035.1	(Z71425) 116 kDa surface antigen [Mycoplasma pneumoniae]	32.5	31	3.1
01709_HH	1	CAB55278.1	(AL035461) dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) [Homo sapiens]	109	38	2.00E-23
01711_HH	1	BAA24228.1	(AB002145) CNP1 [Rana catesbeiana]	44.9	24	5.00E-04
01714_HH	1	NP_060672.1	hypothetical protein FLJ10747 dbj|BAA91786.1| (AK001609) unnamed protein product [Homo sapiens]	126	36	2.00E-28
01715_HH	1	AAC99402.1	(AF054185) proteasome subunit HSPC [Homo sapiens]	259	73	2.00E-68
01716_HH	1	C49274	protein farnesyltransferase (EC 2.5.1.-) beta subunit - bovine gb|AAB26816.1| farnesyl-protein transferase beta subunit, FTPase beta subunit=prenyl-protein transferase DPR1/RAM1 homolog [cattle, brain, Peptide, 437 aa]	101	33	5.00E-21
01718_HH	1	AAC04447.1	(AF047663) W09G12.7 gene product [Caenorhabditis elegans]	43.8	29	0.001
01732_HH	1	AC007026.3	AC007026 Homo sapiens clone DJ0751G11, complete sequence	42.1	100	0.22
01738_HH	2	AAC53545.1	(AF027570) tumor necrosis factor receptor associated factor 2A [Mus musculus]	47.6	25	8.00E-05
01740_HH	1	AJ000387.1	DMZAM Drosophila melanogaster ZAM retroelement: gag, pol and env genes	46.1	100	0.014
01743_HH	2	AAF49471.1	(AE003527) CG4729 gene product [alt 2] [Drosophila melanogaster]	125	39	2.00E-28
01754_HH	1	CAB65849.1	(AL050231) /prediction=(method:""genscan"", version:""1.0"", score:""95.02"")~/prediction=(method:""genefinder"", version:""084"")~/match=(desc:""CK01556.5prime CK Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone CK01556 5pr> gb|AAF45486.1| (AE003417) CG3038 gene product [Drosophila melanogaster]	38.7	35	0.04
01757_HH	1	NP_003895.1	zinc finger protein 259 sp|O75312|ZPR1_HUMAN ZINC-FINGER PROTEIN ZPR1 gb|AAC33514.1| (AF019767) zinc finger protein [Homo sapiens]	134	43	8.00E-31
01767_HH	1	BAA83801.1	(AB025245) coronin homolog [Xenopus laevis]	207	60	5.00E-53
01768_HH	1	AAD34754.1	(AF132166) unknown [Drosophila melanogaster] gb|AAF50077.1| (AE003545) BcDNA:LD21334 gene product [Drosophila melanogaster]	108	53	4.00E-23
01770_HH	2	AAF56122.1	(AE003742) CG6763 gene product [Drosophila melanogaster]	97.5	39	8.00E-20
01772_HH	1	S72571	hypothetical protein C35D10.5 - Caenorhabditis elegans gb|AAA62561.1| (U21324) weakly similar to S. cerevisiae CBP3 protein precursor (SP:CBP3_YEAST, P21560) [Caenorhabditis elegans]	34	19	1
01773_HH	1	T16894	hypothetical protein T19D2.2 - Caenorhabditis elegans gb|AAA83602.1| (U42846) Similar to protein-tyrosine phosphotase [Caenorhabditis elegans] gb|AAC17103.1| (AF063401) putative prenylated protein tyrosine phosphatase [Caenorhabditis elegans]	113	44	1.00E-24
01776_HH	2	NP_054908.1	adducin 1 (alpha)	125	41	2.00E-28
01777_HH	1	T28094	hypothetical protein ZK899.2 - Caenorhabditis elegans emb|CAA85502.1| (Z37140) cDNA EST EMBL:Z14481 comes from this gene~cDNA EST yk469c8.5 comes from this gene~cDNA EST yk289a6.5 comes from this gene~cDNA EST yk289a6.3 comes from this gene~cDNA EST yk469c8.3 comes from this gene~cDNA EST yk565c6.3 comes from this gene~c>	96.3	34	2.00E-19
01778_HH	2	A55314	glycine--tRNA ligase (EC 6.1.1.14) precursor - human dbj|BAA06338.1| (D30658) glycyl tRNA synthetase [Homo sapiens]	136	42	2.00E-31
01779_HH	1	T22416	hypothetical protein F49C12.12 - Caenorhabditis elegans emb|CAA92515.1| (Z68227) cDNA EST EMBL:D72691 comes from this gene~cDNA EST yk566e9.3 comes from this gene~cDNA EST yk566e9.5 comes from this gene [Caenorhabditis elegans]	64.4	35	5.00E-10
01781_HH	1	NP_033056.1	retinoblastoma binding protein 4 sp|Q60972|RB48_MOUSE CHROMATIN ASSEMBLY FACTOR 1 P48 SUBUNIT (CAF-1 P48 SUBUNIT) (RETINOBLASTOMA BINDING PROTEIN P48) (RETINOBLASTOMA-BINDING PROTEIN 4) pir||I49366 G1/S transition control protein-binding protein RbAp48 - mouse gb|AAC52275.1| (U35141) retinoblastoma-binding protein mRbAp48 [Mus musculus] prf||2201425A retinoblastoma-binding protein [Mus musculus]	301	80	4.00E-81
01783_HH	1	AAB49620.1	(U28789) PACT [Mus musculus]	78.8	36	3.00E-14
01785_HH	1	AAF48628.1	(AE003502) CG4453 gene product [Drosophila melanogaster]	42.6	43	0.003
01786_HH	1	AAD26498.1	AC007195_12 (AC007195) amidophosphoribosyltransferase [Arabidopsis thaliana]	34	33	1
01791_HH	1	AAC67569.1	(AF050654) cone transducin alpha subunit [Ambystoma tigrinum]	144	49	6.00E-34
01793_HH	1	I54367	X-linked nuclear protein - human gb|AAA20872.1| (L34363) X-linked nuclear protein [Homo sapiens] prf||2209217A ATR-X gene [Homo sapiens]	68.7	31	4.00E-11
01795_HH	1	AAD03414.1	(AF067650) sarcosine dehydrogenase [Rattus norvegicus]	240	62	7.00E-63
01796_HH	3	BAB03287.1	(AB045975) pro-alpha 1 type V/XI collagen [Chrysophrys major]	51.9	68	4.00E-06
01799_HH	1	NP_031755.1	procollagen, type XI, alpha 1 sp|Q61245|CA1B_MOUSE COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR dbj|BAA07367.1| (D38162) mouse a1(XI) collagen chain [Mus musculus]	39.9	30	0.018
01800_HH	13	AAF48419.1	(AE003497) CG9057 gene product [Drosophila melanogaster]	52.3	29	3.00E-06
01801_HH	1	BAA32385.1	(AB016720) carboxylesterase precursor [Aphis gossypii]	79.2	36	3.00E-14
01802_HH	1	NP_036412.1	SPB1 emb|CAA06749.1| (AJ005892) JM23 [Homo sapiens] gb|AAF06797.1|AF196972_2 (AF196972) JM23 protein [Homo sapiens]	122	62	6.00E-50
01805_HH	1	JW0049	protein-tyrosine-phosphatase (EC 3.1.3.48) 1 - chicken gb|AAA91186.1| (U46662) protein tyrosine phosphatase [Gallus gallus]	72.2	50	3.00E-12
01811_HH	2	AAC14372.1	(U00175) G1-like ORF's protein [Dictyostelium mucoroides]	32.8	26	2.3
01813_HH	1	Q49429	P200_MYCGE PROTEIN P200 pir||G64242 cytadherence-accessory protein (hmw1) homolog MG386 - Mycoplasma genitalium gb|AAC71613.1| (U39720) protein P200 [Mycoplasma genitalium]	36.7	23	0.16
01826_HH	1	T20010	hypothetical protein C47E12.6 - Caenorhabditis elegans emb|CAA93108.1| (Z68882) cDNA EST yk220g1.3 comes from this gene~cDNA EST yk220g1.5 comes from this gene~cDNA EST yk355a12.3 comes from this gene~cDNA EST yk355a12.5 comes from this gene~cDNA EST yk358h5.3 comes from this gene~cDNA EST yk358h5.5 comes from this gene [>	31.7	28	5.3
01827_HH	1	NP_013641.1	putative dihydroxyacetone kinase; Dak1p sp|P54838|DAK1_YEAST DIHYDROXYACETONE KINASE 1 (GLYCERONE KINASE 1) (DHA KINASE 1) pir||S48327 hypothetical protein YML070w - yeast (Saccharomyces cerevisiae) emb|CAA86250.1| (Z38114) len: 584, CAI: 0.22, similar to S14882, S14882, S14884, hypothetical proteins from Hansenula polymorpha [Saccharomyces cerevisiae]	121	44	4.00E-27
01828_HH	2	P27287	VMAT_LPMV MATRIX PROTEIN pir||MFNZLA matrix protein - La Piedad-Michoacan-Mexico virus	31.7	40	5.3
01833_HH	4	S14535	asparagine-rich protein (clone 25C4) - Plasmodium falciparum emb|CAA35522.1| (X17486) unnamed protein product [Plasmodium falciparum]	39.5	25	0.021

01836_HH	1	NP_060713.1	hypothetical protein FLJ10849 dbj|BAA91853.1| (AK001711) unnamed protein product [Homo sapiens]	233	65	1.00E-60
01840_HH	4	Q10344	TCTP_SCHPO TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) pir||S67445 IgE-dependent histamine-releasing factor homolog SPAC1F12.02c - fission yeast (Schizosaccharomyces pombe) pir||T38060 translationally controlled tumor protein homolog - fission yeast (Schizosaccharomyces pombe) emb|CAA93806.1| (Z69944) translationally controlled tumor protein homolog [Schizosaccharomyces pombe]	172	52	2.00E-42
01844_HH	1	Q9ZDH3	NUOC_RICPR NADH DEHYDROGENASE I CHAIN C (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN C) pir||E71692 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain C RP355 - Rickettsia prowazekii emb|CAA14815.1| (AJ235271) NADH DEHYDROGENASE I CHAIN C (nuoC) [Rickettsia prowazekii]	34	32	1
01845_HH	1	BAA25468.2	(AB011114) KIAA0542 protein [Homo sapiens]	45.3	20	4.00E-04
01851_HH	1	CAB60997.1	(Z69658) predicted using Genefinder~Similarity to C.elegans UNC-7 protein (SW:UNC7_CAEEL)~cDNA EST EMBL:Z14924 comes from this gene [Caenorhabditis elegans]	69.5	28	2.00E-11
01858_HH	1	AP001688.1	AP001688 Homo sapiens genomic DNA, chromosome 21q, section 32/105	46.1	100	0.014
01859_HH	2	AAF52443.1	(AE003615) CG11236 gene product [Drosophila melanogaster]	101	45	4.00E-21
01860_HH	2	NP_010076.1	phorphobilinogen deaminase (uroporphyrinogen synthase), the third step in heme biosynthesis; Hem3p sp|P28789|HEM3_YEAST PORPHOBILINOGEN DEAMINASE (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) pir||S25071 hydroxymethylbilane synthase (EC 4.3.1.8) - yeast (Saccharomyces cerevisiae) emb|CAA77804.1| (Z11745) porphobilinogen deaminase [Saccharomyces cerevisiae] emb|CAA67486.1| (X99000) hydroxymethylbilane synthase [Saccharomyces cerevisiae] emb|CAA98783.1| (Z74253) ORF YDL205c [Saccharomyces cerevisiae]	163	53	9.00E-40
01862_HH	1	NP_034536.1	hemolytic complement sp|P06684|CO5_MOUSE COMPLEMENT C5 PRECURSOR [CONTAINS: C5A ANAPHYLATOXIN] pir||C5MS complement C5 precursor - mouse gb|AAA37349.1| (M35525) complement component C5S precursor [Mus musculus]	33.2	24	1.8
01867_HH	1	AL121790.4	CNS01DSI Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-356O9 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence	42.1	93	0.22
01878_HH	3	P54611	VATE_DROME VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) (V-ATPASE 28 KDA SUBUNIT) gb|AAB09738.1| (U38198) V-ATPase subunit E [Drosophila melanogaster] gb|AAB09739.1| (U38951) vacuolar ATPase subunit E [Drosophila melanogaster] gb|AAD38593.1|AF145618_1 (AF145618) BcDNA.GH03683 [Drosophila melanogaster] gb|AAF51997.1| (AE003602) Vha26 gene product [alt 1] [Drosophila melanogaster] gb|AAF51998.1| (AE003602) Vha26 gene product [alt 2] [Drosophila melanogaster]	176	53	1.00E-43
01879_HH	2	P27545	UOG1_MOUSE UOG-1 PROTEIN pir||B39364 GDF-1 embryonic growth factor 5' hypothetical protein - mouse gb|AAA37675.1| (M62301) ORF [Mus musculus]	41.8	21	0.005
01881_HH	3	P24049	RL17_RAT 60S RIBOSOMAL PROTEIN L17 (L23) (AMINO ACID STARVATION-INDUCED PROTEIN) (ASI) pir||R5RT17 ribosomal protein L17, cytosolic - rat emb|CAA42765.1| (X60212) ribosomal protein L22 [Rattus norvegicus] emb|CAA41278.1| (X58389) ribosomal protein L17 [Rattus rattus]	212	71	2.00E-54
01884_HH	1	E71969	a/g-specific adenine glycosylase - Helicobacter pylori (strain J99) gb|AAD05709.1| (AE001452) A/G-SPECIFIC ADENINE GLYCOSYLASE [Helicobacter pylori J99]	30.9	41	9.1
01892_HH	1	AAF74745.1	AF261983_1 (AF261983) trypsin precursor Hz11 [Helicoverpa zea]	34	33	1
01893_HH	1	NP_060712.1	hypothetical protein FLJ10847 dbj|BAA91852.1| (AK001709) unnamed protein product [Homo sapiens]	73	31	2.00E-12
01896_HH	2	A71661	hypothetical protein RP563 - Rickettsia prowazekii emb|CAA15011.1| (AJ235272) unknown [Rickettsia prowazekii]	39.9	27	3.00E-04
01897_HH	1	AAF35895.1	AF229032_1 (AF229032) piL [Mus musculus]	50	32	2.00E-05
01899_HH	1	CAB96953.1	(AL365409) similar to (NP_034322.1|) sex-determination protein homolog Fem1a [Mus musculus] [Homo sapiens]	66.7	30	1.00E-10
01900_HH	1	Q16960	DYI3_ANTCR DYNEIN INTERMEDIATE CHAIN 3, CILIARY dbj|BAA06013.1| (D28863) dynein intermediate chain 3 [Anthocidaris crassispina]	277	72	4.00E-74
01901_HH	1	T00624	endo-1,4-beta-xylanase homolog T27I1.7 - Arabidopsis thaliana gb|AAC34334.1| (AC004122) Similar to endoxylanases [Arabidopsis thaliana]	36.4	28	0.18
01902_HH	1	P49071	MKK2_DROME MAP KINASE-ACTIVATED PROTEIN KINASE 2 (MAPK-ACTIVATED PROTEIN KINASE 2) (MAPKAP KINASE 2) (MAPKAPK-2) pir||JC4297 MAPK-activated protein kinase (EC 2.7.1.-) 2 - fruit fly (Drosophila melanogaster) gb|AAA86885.1| (U20757) MAP kinase activated protein kinase-2 [Drosophila melanogaster] gb|AAF46078.1| (AE003435) CG3086 gene product [Drosophila melanogaster]	196	61	1.00E-49
01903_HH	4	AAF48613.1	(AE003502) CG9947 gene product [Drosophila melanogaster]	97.9	35	6.00E-20
01905_HH	1	CAA04357.1	(AJ000870) histidine kinase [Streptococcus gordonii]	32.5	32	3.1
01911_HH	2	AAF63207.1	AF245662_1 (AF245662) ABC transporter protein white [Bombyx mori]	139	45	2.00E-32
01914_HH	1	AAF54643.1	(AE003691) CG14704 gene product [Drosophila melanogaster]	118	43	4.00E-26
01915_HH	1	AAF55685.1	(AE003727) CG16718 gene product [Drosophila melanogaster]	104	35	6.00E-22
01917_HH	1	AAB66339.1	(AF013964) low density lipoprotein-receptor related protein [Schistosoma mansoni]	74.9	30	5.00E-13
01918_HH	2	Q60803	TRA3_MOUSE TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1) (CRAF1) (TRAFAMN) pir||I49272 CD40 receptor-associated factor 1 - mouse gb|AAC52175.1| (U21050) CD40 receptor associated factor 1 [Mus musculus] prf||2107334A CRAF1 gene [Mus musculus]	49.2	47	3.00E-05
01919_HH	1	AAB40363.1	(U28444) phosphoenolpyruvate carboxykinase [Ctenocephalides felis]	280	77	8.00E-75
01923_HH	1	BAA91471.1	(AK001023) unnamed protein product [Homo sapiens]	137	42	9.00E-32
01929_HH	1	Q93714	IDHA_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE [NAD] SUBUNIT ALPHA, MITOCHONDRIAL PRECURSOR (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) pir||T22149 hypothetical protein F43G9.1 - Caenorhabditis elegans emb|CAB02111.1| (Z79755) predicted using Genefinder~Similarity to Bovine isocitrate dehydrogenase (SW:IDH3_BOVIN)~cDNA EST EMBL:Z14736 comes from this gene~cDNA EST EMBL:M75988 comes from this gene~cDNA EST yk70c9.5 comes from this gene~cDNA EST yk70c9.3 comes from th>	272	78	2.00E-72
01933_HH	1	1CZZ	C Chain C, Structure Of Tnf Receptor Associated Factor 2 In Complex With A 17-Residue Cd40 Peptide	61.7	28	5.00E-09

<table>
<tr><td>01935_HH</td><td>1</td><td>Q36424</td><td>NU4M_LOCMI NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 pir||T11474 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - migratory locust mitochondrion emb|CAA56534.1| (X80245) ND4 [Locusta migratoria] gnl|NCBI_MITO|ND4_10712 NADH dehydrogenase subunit 4</td><td>93.2</td><td>38</td><td>2.00E-18</td></tr>
<tr><td>01937_HH</td><td>1</td><td>AAG10103.1</td><td>AF233443_1 (AF233443) fibrillarin 1 [Arabidopsis thaliana] gb|AAG10152.1| (AF265547) fibrillarin 1 [Arabidopsis thaliana]</td><td>114</td><td>54</td><td>7.00E-25</td></tr>
<tr><td>01944_HH</td><td>1</td><td>NP_012535.1</td><td>U3 snoRNP protein; Mpp10p sp|P47083|MP10_YEAST U3 SMALL NUCLEOLAR RIBONUCLEOPROTEIN PROTEIN MPP10 pir||S55189 hypothetical protein YJR002w - yeast (Saccharomyces cerevisiae) emb|CAA60923.1| (X87611) ORF YJR83.5 [Saccharomyces cerevisiae] emb|CAA89524.1| (Z49502) ORF YJR002w [Saccharomyces cerevisiae]</td><td>35.2</td><td>27</td><td>0.46</td></tr>
<tr><td>01945_HH</td><td>1</td><td>AC003674.2</td><td>AC003674 Arabidopsis thaliana chromosome II section 213 of 255 of the complete sequence. Sequence from clones F12L6, F17A14, T5I7</td><td>44.1</td><td>100</td><td>0.057</td></tr>
<tr><td>01947_HH</td><td>1</td><td>AAF53626.1</td><td>(AE003655) Dhc36C gene product [Drosophila melanogaster]</td><td>33.6</td><td>26</td><td>1.4</td></tr>
<tr><td>01949_HH</td><td>2</td><td>T18819</td><td>hypothetical protein C01G10.8 - Caenorhabditis elegans emb|CAB02710.1| (Z81030) cDNA EST CEMSC45R comes from this gene~cDNA EST yk436a5.3 comes from this gene~cDNA EST yk436a5.5 comes from this gene~cDNA EST yk608h2.3 comes from this gene~cDNA EST yk608h2.5 comes from this gene~cDNA EST CESAA40F comes from this gene [Caen></td><td>100</td><td>41</td><td>1.00E-34</td></tr>
<tr><td>01951_HH</td><td>3</td><td>P35417</td><td>MYSP_ECHGR PARAMYOSIN pir||S37040 paramyosin - tapeworm (Echinococcus granulosus) emb|CAA79849.1| (Z21787) paramyosin [Echinococcus granulosus]</td><td>187</td><td>57</td><td>7.00E-47</td></tr>
<tr><td>01952_HH</td><td>1</td><td>CAB60697.1</td><td>(AL132798) putative era/thdf family GTP-binding protein [Schizosaccharomyces pombe]</td><td>46.5</td><td>29</td><td>2.00E-04</td></tr>
<tr><td>01958_HH</td><td>1</td><td>Q07167</td><td>SM16_SCHMA 16 KDA CALCIUM-BINDING PROTEIN (EGG ANTIGEN SME16) gb|AAA29859.1| (M80260) calcium-binding protein [Schistosoma mansoni]</td><td>93.6</td><td>39</td><td>1.00E-18</td></tr>
<tr><td>01959_HH</td><td>1</td><td>NP_065132.1</td><td>PIST gb|AAG00572.1|AF287894_1 (AF287894) PIST [Homo sapiens]</td><td>78</td><td>36</td><td>6.00E-14</td></tr>
<tr><td>01961_HH</td><td>1</td><td>AAB02821.1</td><td>(U58197) interleukin enhancer binding factor 2 [Homo sapiens]</td><td>138</td><td>77</td><td>5.00E-32</td></tr>
<tr><td>01963_HH</td><td>1</td><td>CAB62846.2</td><td>(AL035475) hypothetical protein [Plasmodium falciparum]</td><td>37.5</td><td>26</td><td>0.092</td></tr>
<tr><td>01978_HH</td><td>2</td><td>CAB38185.1</td><td>(AJ004938) cytoplasmic intermediate filament protein [Stylochus sp.]</td><td>150</td><td>43</td><td>1.00E-35</td></tr>
<tr><td>01979_HH</td><td>1</td><td>CAB16808.1</td><td>(Z99708) sugar transporter like protein [Arabidopsis thaliana] emb|CAB80333.1| (AL161589) sugar transporter like protein [Arabidopsis thaliana]</td><td>43.4</td><td>37</td><td>0.002</td></tr>
<tr><td>01980_HH</td><td>1</td><td>AAF19116.1</td><td>AF143461_1 (AF143461) BdrC3 [Borrelia hermsii]</td><td>44.1</td><td>24</td><td>0.001</td></tr>
<tr><td>01984_HH</td><td>3</td><td>NP_062741.1</td><td>Sid329 dbj|BAA84685.1| (AB024984) Sid329p [Mus musculus]</td><td>191</td><td>55</td><td>3.00E-48</td></tr>
<tr><td>01987_HH</td><td>1</td><td>BAA91971.1</td><td>(AK001905) unnamed protein product [Homo sapiens]</td><td>138</td><td>46</td><td>5.00E-32</td></tr>
<tr><td>01992_HH</td><td>1</td><td>AAF28950.1</td><td>AF161390_1 (AF161390) HSPC272 [Homo sapiens]</td><td>248</td><td>70</td><td>3.00E-65</td></tr>
<tr><td>01993_HH</td><td>1</td><td>A37099</td><td>myosin-light-chain kinase (EC 2.7.1.117) - chicken</td><td>32.8</td><td>35</td><td>2.3</td></tr>
<tr><td>01996_HH</td><td>1</td><td>AAD17299.1</td><td>(AF121199) thioredoxin peroxidase [Schistosoma mansoni]</td><td>212</td><td>61</td><td>2.00E-54</td></tr>
<tr><td>01997_HH</td><td>1</td><td>NP_038559.1</td><td>guanine nucleotide binding protein, beta 4 sp|P29387|GBB4_MOUSE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4) pir||RGMSB4 GTP-binding regulatory protein beta-4 chain - mouse gb|AAA37664.1| (M63658) G-protein beta subunit [Mus musculus] gb|AAA37756.1| (M87286) GTP binding protein beta subunit [Mus musculus] gb|AAB21609.1| (S86124) GTP-binding protein beta-subunit 4 [mice, brain, Peptide, 340 aa] [Mus sp.]</td><td>134</td><td>43</td><td>8.00E-31</td></tr>
<tr><td>01998_HH</td><td>1</td><td>AAF65254.1</td><td>AF221690_1 (AF221690) voltage-dependent anion channel [Squalus acanthias]</td><td>77.3</td><td>32</td><td>1.00E-13</td></tr>
<tr><td>01999_HH</td><td>1</td><td>NP_048260.1</td><td>ORF MSV189 putative core protein, Amsacta moorei EPV entomopoxvirus G1L homolog (vaccinia I7L), similar to SW:P29817 gb|AAC97767.1| (AF063866) ORF MSV189 putative core protein, Amsacta moorei EPV entomopoxvirus G1L homolog (vaccinia I7L), similar to SW:P29817 [Melanoplus sanguinipes entomopoxvirus]</td><td>32.8</td><td>24</td><td>2.3</td></tr>
<tr><td>02003_HH</td><td>1</td><td>NC_001148.1</td><td>Saccharomyces cerevisiae chromosome XVI, complete chromosome sequence</td><td>40.1</td><td>100</td><td>0.34</td></tr>
<tr><td>02012_HH</td><td>1</td><td>U39703.1</td><td>U39703 Mycoplasma genitalium section 25 of 51 of the complete genome</td><td>44.1</td><td>100</td><td>0.057</td></tr>
<tr><td>02016_HH</td><td>1</td><td>AL034423.19</td><td>HS1185N5 Human DNA sequence from clone RP5-1185N5 on chromosome 20q13.11-13.2, complete sequence [Homo sapiens]</td><td>44.1</td><td>96</td><td>0.024</td></tr>
<tr><td>02018_HH</td><td>1</td><td>AAF50023.1</td><td>(AE003544) CG11658 gene product [Drosophila melanogaster]</td><td>58.6</td><td>25</td><td>4.00E-08</td></tr>
<tr><td>02019_HH</td><td>2</td><td>AAF53464.1</td><td>(AE003647) CG15257 gene product [Drosophila melanogaster]</td><td>122</td><td>50</td><td>3.00E-27</td></tr>
<tr><td>02020_HH</td><td>1</td><td>AAF48557.1</td><td>(AE003500) CG8939 gene product [Drosophila melanogaster]</td><td>46.5</td><td>33</td><td>2.00E-04</td></tr>
<tr><td>02032_HH</td><td>1</td><td>BAA91362.1</td><td>(AK000756) unnamed protein product [Homo sapiens]</td><td>253</td><td>75</td><td>8.00E-67</td></tr>
<tr><td>02036_HH</td><td>1</td><td>AL163246.2</td><td>HS21C046 Homo sapiens chromosome 21 segment HS21C046</td><td>46.1</td><td>96</td><td>0.014</td></tr>
<tr><td>02039_HH</td><td>4</td><td>AAF49916.1</td><td>(AE003541) CG10663 gene product [Drosophila melanogaster]</td><td>39.9</td><td>58</td><td>0.018</td></tr>
<tr><td>02041_HH</td><td>1</td><td>NP_032405.1</td><td>importin beta pir||S66288 nuclear pore-targeting complex protein, 97K - mouse dbj|BAA08273.1| (D45836) nuclear pore-targeting complex component of 97kDa [Mus musculus]</td><td>159</td><td>50</td><td>2.00E-38</td></tr>
<tr><td>02043_HH</td><td>1</td><td>AL161507.2</td><td>ATCHRIV19 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 19</td><td>46.1</td><td>100</td><td>0.014</td></tr>
<tr><td>02046_HH</td><td>1</td><td>CAB46239.1</td><td>(AJ133488) SCO-spondin [Bos taurus]</td><td>32.8</td><td>50</td><td>2.3</td></tr>
<tr><td>02047_HH</td><td>1</td><td>NP_032476.1</td><td>kinesin light chain 1 gb|AAC27740.1| (AF055665) kinesin light chain 1 [Mus musculus]</td><td>96.7</td><td>32</td><td>1.00E-19</td></tr>
<tr><td>02053_HH</td><td>3</td><td>T16187</td><td>hypothetical protein F27D9.5 - Caenorhabditis elegans gb|AAA93384.1| (U49829) coded for by C. elegans cDNA yk61f5.5; coded for by C. elegans cDNA yk40b3.5; coded for by C. elegans cDNA yk129d12.5; coded for by C. elegans cDNA yk40a2.5; coded for by C. elegans cDNA yk52f10.5; coded for by C. elegans cDNA yk92b2.5; coded ></td><td>182</td><td>66</td><td>3.00E-45</td></tr>
<tr><td>02068_HH</td><td>2</td><td>AAF57563.1</td><td>(AE003796) CalpA gene product [Drosophila melanogaster]</td><td>178</td><td>50</td><td>4.00E-44</td></tr>
<tr><td>02073_HH</td><td>2</td><td>AAF78225.1</td><td>AF243514_1 (AF243514) MAK16-like protein [Schistosoma mansoni]</td><td>181</td><td>50</td><td>5.00E-45</td></tr>
<tr><td>02089_HH</td><td>2</td><td>AAF46161.1</td><td>(AE003437) CG3869 gene product [alt 1] [Drosophila melanogaster] gb|AAF46162.1| (AE003437) CG3869 gene product [alt 2] [Drosophila melanogaster]</td><td>55.4</td><td>29</td><td>4.00E-07</td></tr>
<tr><td>02090_HH</td><td>1</td><td>I51631</td><td>[phosphorylase] phosphatase (EC 3.1.3.17) 65K regulatory chain alpha-isotype - African clawed frog pir||S65953 [phosphorylase] phosphatase (EC 3.1.3.17) 65K regulatory chain isotype alpha - African clawed frog emb|CAA56713.1| (X80696) phosphorylase phosphatase [Xenopus laevis]</td><td>198</td><td>57</td><td>3.00E-50</td></tr>
<tr><td>02093_HH</td><td>2</td><td>JC4383</td><td>3'-phosphoadenosine-5'-phosphosulfate synthetase - spoonworm (Urechis caupo) gb|AAB00139.1| (L39001) PAPS synthetase [Urechis caupo]</td><td>263</td><td>73</td><td>9.00E-70</td></tr>
<tr><td>02095_HH</td><td>1</td><td>T25752</td><td>hypothetical protein F45E4.4 - Caenorhabditis elegans gb|AAB09135.1| (U70852) contains weak similarity to Salmo Gairdner (rainbow trout) SOX-LZ (GB:D61688) in one region and MAP2B (microtubule-associated protein 2) (SP:P11137) in a different region [Caenorhabditis elegans]</td><td>32.1</td><td>31</td><td>4</td></tr>
<tr><td>02100_HH</td><td>2</td><td>AAC60279.1</td><td>(U67931) ubiquitin/ribosomal protein [Gallus gallus]</td><td>123</td><td>54</td><td>7.00E-28</td></tr>
<tr><td>02104_HH</td><td>1</td><td>BAA93047.2</td><td>(AB040669) nonclathrin coat protein gamma1-COP [Bombyx mori]</td><td>179</td><td>52</td><td>2.00E-44</td></tr>
<tr><td>02107_HH</td><td>1</td><td>AAA85896.1</td><td>(U33332) orf UL154 [human herpesvirus 5]</td><td>37.5</td><td>25</td><td>0.092</td></tr>
</table>

02108_HH	1	NP_004516.1	low density lipoprotein-related protein 2 sp|P98164|LRP2_HUMAN LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN) (GLYCOPROTEIN 330) gb|AAB41649.1| (U33837) gp330 precursor [Homo sapiens]	85.4	42	3.00E-16
02111_HH	1	O93477	SAH2_XENLA ADENOSYLHOMOCYSTEINASE 2 (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE 2) (ADOHCYASE 2) emb|CAA07706.1| (AJ007835) S-adenosyl-L-homocysteine hydrolase [Xenopus laevis]	303	86	8.00E-82
02112_HH	2	NP_033977.1	CD2-associated proten gb|AAC36099.1| (AF077003) SH3 domain-containing adapter protein; CD2AP [Mus musculus]	78.8	32	3.00E-14
02114_HH	1	AAC46948.1	(U11654) mariner transposase [Chrysoperla plorabunda]	68.7	44	4.00E-11
02119_HH	4	AC004631.1	AC004631 Homo sapiens chromosome 5, PAC clone 154d1 (LBNL H113), complete sequence	48.1	90	0.004
02120_HH	1	S44455	transcription factor BTF2 chain p34 - human	51.2	32	7.00E-06
02126_HH	1	CAA12197.1	(AJ224893) SRF related protein [Dictyostelium discoideum]	34.4	35	0.8
02131_HH	1	AP001689.1	AP001689 Homo sapiens genomic DNA, chromosome 21q, section 33/105	42.1	100	0.082
02147_HH	1	CAC01616.1	(AJ278128) hypothetical protein [Mus musculus]	113	45	1.00E-24
02149_HH	2	AAD39392.1	AF124435_1 (AF124435) p55-related MAGUK protein DLG3 [Danio rerio]	59.3	60	1.00E-11
02155_HH	1	P16435	NCPR_HUMAN NADPH-CYTOCHROME P450 REDUCTASE (CPR) (P450R) pir||A60557 NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - human gb|AAG09798.1| (AF258341) NADPH-cytochrome P450 reductase [Homo sapiens]	193	60	2.00E-50
02156_HH	1	AC009487.3	AC009487 Homo sapiens clone RP11-334E15, complete sequence	44.1	100	0.057
02157_HH	1	P55063	HS73_RAT HEAT SHOCK 70 KD PROTEIN 3 (HSP70.3) pir||S41415 dnaK-type molecular chaperone Hsp70.3 - rat emb|CAA54424.1| (X77209) heat shock protein 70 [Rattus norvegicus]	141	51	3.00E-33
02159_HH	1	AAC48498.1	(U34201) cardiac triadin isoform 3 [Oryctolagus cuniculus] prf||2206439C triadin:ISOTYPE=3 [Oryctolagus cuniculus]	37.1	31	0.12
02161_HH	1	AAF13730.1	AF207550_8 (AF207550) unknown [Homo sapiens]	59.3	42	2.00E-08
02169_HH	1	P22757	HE_PARLI HATCHING ENZYME PRECURSOR (HE) (HEZ) (ENVELYSIN) (SEA-URCHIN-HATCHING PROTEINASE) pir||S12805 envelysin (EC 3.4.24.12) precursor - sea urchin (Paracentrotus lividus) emb|CAA37667.1| (X53598) pre-pro-hatching enzyme [Paracentrotus lividus]	111	61	4.00E-24
02172_HH	2	NP_000299.1	protective protein for beta-galactosidase; carboxypeptidase C; serine-type carboxypeptidase 1; cathepsin A; carboxypeptidase Y; lysosomal protective protein; carboxypeptidase L; beta-galactosidase 2 sp|P10619|PRTP_HUMAN LYSOSOMAL PROTECTIVE PROTEIN PRECURSOR (CATHEPSIN A) (CARBOXYPEPTIDASE C) pir||A31589 carboxypeptidase C (EC 3.4.16.5) precursor - human gb|AAA36476.1| (M22960) protective protein precursor [Homo sapiens]	195	58	2.00E-49
02174_HH	1	NP_003291.1	TNF receptor-associated factor 3 sp|Q13114|TRA3_HUMAN TNF RECEPTOR ASSOCIATED FACTOR 3 (CD40 RECEPTOR ASSOCIATED FACTOR 1) (CRAF1) (CD40 BINDING PROTEIN) (CD40BP) (LMP1 ASSOCIATED PROTEIN) (LAP1) pir||A55960 CD40 receptor-associated factor 1 - human gb|AAC50112.1| (U21092) CD40 receptor associated factor 1 [Homo sapiens]	69.1	39	3.00E-11
02179_HH	3	P37039	NCPR_CAVPO NADPH-CYTOCHROME P450 REDUCTASE (CPR) (P450R) pir||S27158 NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - guinea pig dbj|BAA01385.1| (D10498) NADPH-cytochrome P450 oxidoreductase [Cavia porcellus]	229	69	1.00E-59
02184_HH	1	CAB61769.1	(AL133225) putative phosphatidylserine decarboxylase proenzyme 1 precursor [Schizosaccharomyces pombe]	32.5	24	3.1
02189_HH	1	AAB62657.1	(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	70.2	30	1.00E-11
02190_HH	5	T39565	hypothetical protein SPBC16D10.01c - fission yeast (Schizosaccharomyces pombe) (fragment) emb|CAB38505.1| (AL035637) hypothetical protein [Schizosaccharomyces pombe]	71	29	8.00E-12
02192_HH	3	CAA69615.1	(Y08307) ribosomal protein S14 [Mus musculus]	198	67	3.00E-50
02197_HH	2	NP_034818.1	LIM and SH3 protein 1 sp|Q61792|LAS1_MOUSE LIM AND SH3 DOMAIN PROTEIN 1 (LASP-1) (MLN 50) emb|CAA65659.1| (X96973) Lasp-1 [Mus musculus]	134	35	8.00E-31
02198_HH	2	NP_003972.1	protein regulator of cytokinesis 1; PRC1 gb|AAC02688.1| (AF044588) protein regulating cytokinesis 1; PRC1 [Homo sapiens]	51.9	23	4.00E-06
02201_HH	1	Z78537.1	CEC09F12 Caenorhabditis elegans cosmid C09F12, complete sequence	46.1	100	0.014
02205_HH	1	AAF52657.1	(AE003621) Aats-ala gene product [Drosophila melanogaster]	249	68	1.00E-65
02207_HH	2	NP_046155.1	nonstructural polyprotein pir||T08822 nonstructural polyprotein - Rhopalosiphum padi virus gb|AAC95509.1| (AF022937) nonstructural polyprotein [Rhopalosiphum padi virus]	35.2	38	0.46
02210_HH	2	CAC00807.1	(AL390935) possible CG10064 protein [Leishmania major]	129	44	1.00E-29
02211_HH	1	Q27433	MEC2_CAEEL MECHANOSENSORY PROTEIN 2 pir||S60260 stomatin-like protein - Caenorhabditis elegans gb|AAA87551.1| (U26735) MEC-2 [Caenorhabditis elegans] gb|AAA87552.1| (U26736) MEC-2 [Caenorhabditis elegans] gb|AAA82333.1| (U41021) C. elegans mec-2 (GB:U26735) [Caenorhabditis elegans] prf||2201490A stomatin-like protein [Caenorhabditis elegans]	143	54	1.00E-33
02212_HH	1	NP_064872.1	AMV090 gb|AAG02796.1|AF250284_90 (AF250284) AMV090 [Amsacta moorei entomopoxvirus]	35.2	29	0.46
02216_HH	1	BAA13856.1	(D89195) similar to Saccharomyces cerevisiae ORF YOR091W, EMBL Accession Number Z74999 [Schizosaccharomyces pombe]	35.2	34	0.46
02217_HH	2	NP_013378.1	putative RNA helicase; Dbp9p sp|Q06218|DBP9_YEAST PROBABLE ATP-DEPENDENT RNA HELICASE DBP9 pir||S51412 hypothetical protein YLR276c - yeast (Saccharomyces cerevisiae) gb|AAB67366.1| (U17245) Ylr276cp [Saccharomyces cerevisiae]	50	40	2.00E-05
02219_HH	1	Q09624	YS89_CAEEL HYPOTHETICAL 254.3 KD PROTEIN ZK945.9 IN CHROMOSOME II pir||T28125 hypothetical protein ZK945.9 - Caenorhabditis elegans	49.6	31	2.00E-05
02220_HH	1	NP_008937.1	pre-mRNA cleavage factor Im (25kD) emb|CAA05026.1| (AJ001810) mRNA cleavage factor I 25 kDa subunit [Homo sapiens]	252	70	2.00E-66
02224_HH	3	AAF66696.1	AF145254_1 (AF145254) Sec61 alpha isoform 2 [Mus musculus]	299	86	1.00E-80
02228_HH	3	AAF54429.1	(AE003684) CG9448 gene product [Drosophila melanogaster]	212	55	2.00E-54
02232_HH	2	P11277	SPCB_HUMAN SPECTRIN BETA CHAIN, ERYTHROCYTE pir||SJHUB spectrin beta chain - human	142	41	3.00E-33
02237_HH	1	P79383	CPE1_PIG CYTOCHROME P450 2E1 (CYPIIE1) (P450-J) (P-450-J) dbj|BAA19202.1| (AB000885) Cytochrome P-450-j [Sus scrofa]	77.3	31	1.00E-13
02238_HH	7	2CTS	Citrate Synthase (E.C.4.1.3.7) - (CoA, Citrate) Complex	212	72	2.00E-54

02242_HH	2	T20630	hypothetical protein F09B12.3 - Caenorhabditis elegans emb|CAB05478.1| (Z83104) cDNA EST EMBL:T00015 comes from this gene~cDNA EST yk34c4.3 comes from this gene~cDNA EST yk34c4.5 comes from this gene~cDNA EST yk240f8.3 comes from this gene~cDNA EST yk387c8.3 comes from this gene~cDNA EST yk387c8.5 comes from this gene~cDN>	75.3	27	4.00E-13
02246_HH	1	BAA82538.1	(AB030032) ORF12 [Actinobacillus actinomycetemcomitans]	32.5	28	3.1
02247_HH	2	AAF46728.1	(AE003454) CG15668 gene product [Drosophila melanogaster]	39.9	69	2.00E-05
02248_HH	1	AC006434.5	AC006434 Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence	46.1	100	0.014
02249_HH	1	P97434	RIP3_MOUSE P116 RHO-INTERACTING PROTEIN (P116RIP) (RIP3) pir||T30868 RhoA-binding protein p116Rip - mouse gb|AAB18198.1| (U73200) p116Rip [Mus musculus]	40.6	33	0.011
02251_HH	2	NP_058843.1	cofilin 1, non-muscle sp|P45592|COF1_RAT COFILIN, NON-MUSCLE ISOFORM pir||S49101 cofilin - rat emb|CAA44694.1| (X62908) cofilin [Rattus norvegicus]	53.1	38	2.00E-06
02253_HH	1	I60079	opsin, middle-wavelength sensitive - crab-eating macaque (fragment) gb|AAB32440.1| (S76052) MW opsin=middle-wave visual pigment [Macaca fascicularis=crab-eating macaques, Peptide Partial, 126 aa]	31.7	22	5.3
02255_HH	1	AAC33482.1	(AF084574) maturation inhibited protein kinase p40 [Pisaster ochraceus]	161	54	5.00E-39
02257_HH	1	BAA11540.1	(D82082) platelet endothelial cell adhesion molecule-1 [Bos primigenius]	37.1	24	0.12
02258_HH	1	A71468	hypothetical protein CT805 - Chlamydia trachomatis (serotype D, strain UW3/Cx) gb|AAC68401.1| (AE001353) hypothetical protein [Chlamydia trachomatis]	35.2	30	0.46
02259_HH	1	AAF49399.1	(AE003526) CG9951 gene product [Drosophila melanogaster]	67.9	33	7.00E-11
02260_HH	1	NP_057305.1	dynactin p62 subunit gb|AAF03896.1|AF195120_1 (AF195120) dynactin p62 subunit [Homo sapiens] dbj|BAA91066.1| (AK000299) unnamed protein product [Homo sapiens]	146	44	2.00E-34
02272_HH	1	NP_006205.1	phytanoyl-CoA hydroxylase (Refsum disease) sp|O14832|PAHX_HUMAN PEROXISOMAL PHYTANOYL-COA ALPHA-HYDROXYLASE PRECURSOR (PHYTANIC ACID OXIDASE) gb|AAB81834.1| (AF023462) peroxisomal phytanoyl-CoA alpha-hydroxylase [Homo sapiens] gb|AAD20602.1| (AF112977) phytanoil-CoA alpha hydroxylase [Homo sapiens] gb|AAF74123.1| (AF242386) phytanoyl-CoA hydroxylase [Homo sapiens]	42.6	24	0.003
02273_HH	2	JC5507	monocarboxylate transporter 3 - chicken gb|AAB61338.1| (AF000240) monocarboxylate transporter 3 [Gallus gallus]	41.8	24	0.005
02291_HH	1	AAD21531.1	(AF073310) insulin receptor substrate-2 [Homo sapiens]	41.8	28	0.005
02298_HH	2	NP_032774.1	neuronal tyrosine/threonine phosphatase 1 sp|O09112|DUS8_MOUSE DUAL SPECIFICITY PROTEIN PHOSPHATASE 8 (NEURONAL TYROSINE THREONINE PHOSPHATASE 1) emb|CAA64772.1| (X95518) neuronal tyrosine threonine phosphatase 1 [Mus musculus]	77.3	61	1.00E-13
02301_HH	1	NP_060156.1	hypothetical protein FLJ20142 dbj|BAA90976.1| (AK000149) unnamed protein product [Homo sapiens]	89.3	31	2.00E-17
02303_HH	3	NP_036379.1	SELENOPHOSPHATE SYNTHETASE ; Human selenium donor protein sp|P49903|SPS1_HUMAN SELENIDE,WATER DIKINASE 1 (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) gb|AAA87567.1| (U34044) selenium donor protein [Homo sapiens]	166	55	2.00E-40
02307_HH	1	NP_009687.1	involved in mating pathway; Opy1p sp|P38271|OPY1_YEAST OPY1 PROTEIN (OVERPRODUCTION INDUCED PHEROMONE RESISTANT YEAST 1) pir||S45998 hypothetical protein YBR129c - yeast (Saccharomyces cerevisiae) emb|CAA53488.1| (X75891) YBR1004 [Saccharomyces cerevisiae] emb|CAA85086.1| (Z35998) ORF YBR129c [Saccharomyces cerevisiae] gb|AAB81505.1| (AF016262) overproduction induced pheromone resistant yeast 1 [Saccharomyces cerevisiae] prf||2118402D YBR1004 gene [Saccharomyces cerevisiae]	34	41	1
02313_HH	1	AAF76194.1	(AF270484) transketolase [Xenopus laevis]	142	57	4.00E-51
02314_HH	2	1YLV	A Chain A, Schiff-Base Complex Of Yeast 5-Aminolaevulinic Acid Dehydratase With Laevulinic Acid	182	54	2.00E-45
02317_HH	1	AAD04628.1	(AF109068) cytochrome P450 [Sus scrofa]	111	35	6.00E-24
02320_HH	3	AAB09671.1	(U59212) transmembrane protein [Caenorhabditis elegans]	71.8	32	4.00E-12
02321_HH	1	C70109	hypothetical protein BB0075 - Lyme disease spirochete gb|AAC66465.1| (AE001120) B. burgdorferi predicted coding region BB0075 [Borrelia burgdorferi]	34.4	25	0.8
02324_HH	1	AL353580.7	AL353580 Human DNA sequence from clone RP11-248N6 on chromosome 13, complete sequence [Homo sapiens]	46.1	100	0.014
02325_HH	1	P08253	COG2_HUMAN 72 KD TYPE IV COLLAGENASE PRECURSOR (72 KD GELATINASE) (MATRIX METALLOPROTEINASE-2) (MMP-2) (GELATINASE A) (TBE-1) pir||A28153 gelatinase A (EC 3.4.24.24) precursor - human gb|AAA52028.1| (M55593) type IV collagenase [Homo sapiens]	79.2	34	3.00E-14
02329_HH	1	AAF56345.1	(AE003749) CG13638 gene product [Drosophila melanogaster]	38.3	28	0.054
02333_HH	1	CAB88219.1	(AL352980) possible alpha collagen-related protein [Leishmania major]	34	40	1
02334_HH	2	AAF58148.1	(AE003811) Arf51F gene product [Drosophila melanogaster]	252	81	2.00E-66
02343_HH	1	NP_048021.1	orf 48 gb|AAC95573.1| (AF083424) orf 48 [Ateline herpesvirus 3]	94.4	30	5.00E-19
02344_HH	1	NP_055727.1	KIAA0940 protein dbj|BAA76784.1| (AB023157) KIAA0940 protein [Homo sapiens]	312	87	1.00E-84
02345_HH	1	CAB93524.1	(AJ271740) D-Titin [Drosophila melanogaster]	85.4	31	3.00E-16
02348_HH	1	AAF40433.1	(AF234630) IX-14 protein [Drosophila melanogaster]	114	39	7.00E-25
02350_HH	3	P34714	SPRC_CAEEL SPARC PRECURSOR (SECRETED PROTEIN ACIDIC AND RICH IN CYSTEINE) (OSTEONECTIN) (ON) (BASEMENT MEMBRANE PROTEIN BM-40) pir||A47737 osteonectin precursor - Caenorhabditis elegans gb|AAA16827.1| (L21758) osteonectin [Caenorhabditis elegans] gb|AAB88325.1| (AF036692) C. elegans osteonectin precursor OST-1 (SW:P34714) [Caenorhabditis elegans]	44.9	26	5.00E-04
02352_HH	1	BAA04489.1	(D17551) tyrosine kinase [Drosophila melanogaster]	60.1	30	1.00E-08
02353_HH	3	AF022186.2	AF022186 Cyanidium caldarium strain RK1 chloroplast, complete genome	44.1	100	0.057
02355_HH	1	P47877	IBP2_MOUSE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) pir||I48601 insulin-like growth factor binding protein-2 - mouse emb|CAA57270.1| (X81580) insulin-like growth factor binding protein-2 [Mus musculus]	44.9	40	4.00E-04
02357_HH	1	O26074	SECD_HELPY PROTEIN-EXPORT MEMBRANE PROTEIN SECD pir||F64713 protein-export membrane protein - Helicobacter pylori (strain 26695) gb|AAD08588.1| (AE000652) protein-export membrane protein (secD) [Helicobacter pylori 26695]	35.2	33	0.46
02359_HH	1	AAD46179.1	(AF153912) ORFL4R [Tanapox virus]	38.7	28	0.041
02363_HH	2	AAC47170.1	(U36377) mitogen-activated protein kinase-related protein [Plasmodium falciparum]	39.9	30	0.018
02364_HH	1	BAB11685.1	(D82983) prolidase [Mus musculus]	162	47	2.00E-39

02365_HH	3	P47836	RS4_CHICK 40S RIBOSOMAL PROTEIN S4 pir||A56537 ribosomal protein S4, cytosolic - chicken gb|AAB59946.1| (L24368) ribosomal protein S4 [Gallus gallus]	245	63	2.00E-64
02369_HH	2	NP_033970.1	chaperonin subunit 8 (theta) sp|P42932|TCPQ_MOUSE T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) pir||JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse emb|CAA85521.1| (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]	172	49	2.00E-42
02371_HH	1	NP_006003.1	endopeptidase Clp precursor; caseinolytic protease; ATP-dependent proteolytic subunit E.coli homolog sp|Q16740|CLPP_HUMAN PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT, MITOCHONDRIAL PRECURSOR (ENDOPEPTIDASE CLP) pir||S68421 ATP-dependent clp proteinase (EC 3.4.21.-) chain P - human emb|CAA90705.1| (Z50853) CLPP [Homo sapiens]	243	66	7.00E-64
02373_HH	3	AAC47429.1	(U67304) 70 kDa S6 kinase [Drosophila melanogaster]	109	44	2.00E-23
02374_HH	1	AL157906.8	AL157906 Human DNA sequence from clone RP5-896C23 on chromosome 1p22.3-31.2 Contains GSSs and STSs, complete sequence [Homo sapiens]	48.1	96	0.004
02375_HH	2	AAF60795.1	(AC024826) contains similarity to Pfam family PF00076 (RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)), score=127.3, E=2.9e-34, N=3 [Caenorhabditis elegans]	85	32	5.00E-16
02377_HH	6	BAA07652.1	(D42052) predicted protein of 548 amino acids [Homo sapiens]	181	55	4.00E-45
02378_HH	1	NP_000929.1	polymerase (RNA) II (DNA directed) polypeptide B (140kD) sp|P30876|RPB2_HUMAN DNA-DIRECTED RNA POLYMERASE II 140 KDA POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 2) (RPB2) pir||S28976 DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - human emb|CAA45124.1| (X63563) RNA polymerase II 140 kDa subunit [Homo sapiens] gb|AAB23139.1| RNA polymerase II second largest subunit, RNA polymerase B second largest subunit [human, HeLa cells, Peptide, 1174 aa]	242	73	1.00E-63
02380_HH	1	NP_013663.1	involved in secretion and RNA splicing; Rse1p sp|Q04693|YME9_YEAST HYPOTHETICAL 153.8 KD PROTEIN IN GAL80-PRP39 INTERGENIC REGION pir||S50943 hypothetical protein YML049c - yeast (Saccharomyces cerevisiae) emb|CAA87825.1| (Z47816) unknown [Saccharomyces cerevisiae]	34.8	26	0.61
02381_HH	1	AAF82124.1	(AF277893) G-protein beta-4 subunit [Mus musculus]	227	65	7.00E-59
02388_HH	5	BAA90301.2	(AB026845) kettin [Drosophila melanogaster]	84.7	39	6.00E-16
02389_HH	2	AAC27674.1	(U91326) eIF-3 p110 subunit [Homo sapiens]	74.1	32	9.00E-13
02392_HH	2	NP_037300.1	hydroxymethylbilane synthase pir||IBRTE hydroxymethylbilane synthase (EC 4.3.1.8), erythropoietic - rat emb|CAA29984.1| (X06827) porphobilinogen deaminase [Rattus norvegicus]	155	51	2.00E-37
02393_HH	1	BAA98151.1	(AB025612) CLP protease regulatory subunit CLPX-like [Arabidopsis thaliana]	46.5	44	2.00E-04
02396_HH	2	P70080	TR5H_CHICK TRYPTOPHAN 5-MONOOXYGENASE (TRYPTOPHAN 5-HYDROXYLASE) gb|AAC60036.1| (U26428) tryptophan hydroxylase [Gallus gallus]	32.8	41	2.3
02397_HH	2	H70454	conserved hypothetical protein aq_1797 - Aquifex aeolicus gb|AAC07630.1| (AE000756) hypothetical protein [Aquifex aeolicus]	32.1	41	4
02405_HH	1	AAF59198.1	(AE003840) CG1383 gene product [Drosophila melanogaster]	71.8	32	4.00E-12
02406_HH	1	T24326	hypothetical protein T01H10.3 - Caenorhabditis elegans emb|CAA91538.1| (Z67737) similar to nicotinic acetylcholine receptor [Caenorhabditis elegans]	32.5	30	3.1
02408_HH	1	AAD00079.1	(U51162) latent TGF-beta complexed protein (LTCP) [Cricetulus griseus]	108	34	5.00E-23
02410_HH	2	NP_009057.1	valosin-containing protein sp|P55072|TERA_HUMAN TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) [CONTAINS: VALOSIN] pir||T02243 probable transitional endoplasmic reticulum ATPase - human gb|AAC07984.1| (AC004472) TERA_HUMAN [Homo sapiens] gb|AAD43016.1| (AF100752) transitional endoplasmic reticulum ATPase [Homo sapiens]	301	90	3.00E-81
02411_HH	1	NP_009469.1	component of the anaphase-promoting complex; Cdc27p sp|P38042|CC27_YEAST CELL DIVISION CONTROL PROTEIN 27 pir||S45825 cell division control protein CDC27 - yeast (Saccharomyces cerevisiae) emb|CAA84905.1| (Z35845) ORF YBL084c [Saccharomyces cerevisiae]	37.5	20	0.092
02413_HH	1	AAF56060.1	(AE003740) CG17141 gene product [Drosophila melanogaster]	89.3	34	2.00E-17
02415_HH	1	CAA72123.1	(Y11253) annexin max2 [Oryzias latipes]	143	47	9.00E-34
02417_HH	1	CAA64596.1	(X95276) Clp (C?) [Plasmodium falciparum]	31.7	24	5.3
02419_HH	1	AAF45332.1	(AE003091) CG17514 gene product [Drosophila melanogaster]	83.9	34	1.00E-15
02423_HH	1	S72295	ribosomal protein S8 - Plasmodium falciparum plastid emb|CAA64585.1| (X95276) rps8 [Plasmodium falciparum]	34.4	24	0.8
02425_HH	2	prf||1413235A	beta hexosaminidase beta [Mus musculus]	47.3	25	1.00E-04
02426_HH	1	P24724	HS90_THEPA HEAT SHOCK PROTEIN 90 (HSP90) gb|AAA30132.1| (M57386) heat shock protein 90 [Theileria parva] prf||2106315A heat shock protein 90kD [Theileria parva]	32.1	25	4
02428_HH	1	Q90935	NEUS_CHICK NEUROSERPIN PRECURSOR (AXONIN-2) pir||S70647 neuroserpin precursor - chicken emb|CAA96493.1| (Z71930) neuroserpin [Gallus gallus]	37.9	22	0.07
02429_HH	1	BAA94871.1	(AB033882) protein kinase C inhibitor [Coturnix coturnix japonica] dbj|BAA94873.1| (AB033884) protein kinase C inhibitor [Anas platyrhynchos]	99.8	47	2.00E-20
02432_HH	1	AAD02817.1	(AF067126) NADP(H)-dependent ketose reductase [Bemisia argentifolii]	93.6	51	1.00E-18
02433_HH	1	AAF55633.1	(AE003725) ATPsyn-d gene product [Drosophila melanogaster]	58.6	30	4.00E-08
02435_HH	5	NP_013910.1	Ymr185wp sp|Q12751|YM48_YEAST HYPOTHETICAL 113.2 KD PROTEIN IN SSO2-HSC82 INTERGENIC REGION pir||S55132 hypothetical protein YMR185w - yeast (Saccharomyces cerevisiae) emb|CAA89918.1| (Z49808) unknown [Saccharomyces cerevisiae]	31.7	30	4.3
02439_HH	2	CAB38987.1	(AL034556) hypothetical protein, PFC0650w [Plasmodium falciparum]	31.3	27	6.9
02441_HH	1	AAD26872.1	AC007230_6 (AC007230) EST gb|T22166 comes from this gene. [Arabidopsis thaliana]	32.5	28	3.1
02442_HH	1	T26552	hypothetical protein Y22F5A.2 - Caenorhabditis elegans emb|CAA16321.1| (AL021479) Y22F5A.2 [Caenorhabditis elegans]	31.7	48	5.3
02443_HH	1	BAA33209.1	(AB005798) asense [Drosophila yakuba]	31.3	28	6.9
02444_HH	1	T41463	conserved hypothetical PFAM UPF0031 containing protein - fission yeast (Schizosaccharomyces pombe) emb|CAA22272.1| (AL034381) conserved hypothetical protein [Schizosaccharomyces pombe]	124	42	5.00E-28
02446_HH	1	P46150	MOEH_DROME MOESIN/EZRIN/RADIXIN HOMOLOG (D17 PROTEIN) gb|AAB48934.1| (L38909) moesin [Drosophila melanogaster] gb|AAF46415.1| (AE003445) Moe gene product [alt 4] [Drosophila melanogaster]	164	49	4.00E-40
02454_HH	1	CAB75578.1	(AJ230617) protein kinase C delta [Rattus norvegicus]	211	60	4.00E-54
02457_HH	4	AAB62936.1	(AF007219) PP2A inhibitor [Tetraodon fluviatilis]	181	53	4.00E-45

02460_HH	1	I70695	omega protein - human (fragment) gb|AAA36097.1| (M34516) omega protein [Homo sapiens]	31.7	44	5.3
02462_HH	1	NP_060091.1	hypothetical protein FLJ20013 dbj|BAA90888.1| (AK000020) unnamed protein product [Homo sapiens]	132	41	3.00E-30
02467_HH	1	O15442	239A_HUMAN ADULT BRAIN PROTEIN 239 (239AB)	161	54	4.00E-39
02468_HH	1	C45600	asparagine-rich blood stage antigen (clone Pfa35-2) - Plasmodium falciparum (fragment) gb|AAA29495.1| (M59474) asparagine-rich antigen Pfa35-2 [Plasmodium falciparum]	32.1	26	4
02473_HH	1	AAG10220.1	AF296765_1 (AF296765) ankyrin repeat-containing protein [Homo sapiens]	32.1	40	0.096
02474_HH	1	AAF52320.1	(AE003612) CG9093 gene product [Drosophila melanogaster]	111	50	4.00E-24
02476_HH	2	T33569	hypothetical protein R160.1 - Caenorhabditis elegans gb|AAC68739.1| (AF099001) strong similarity to C. elegans UNC-101 clathrin coat assembly protein AP50 (SW:P35603) [Caenorhabditis elegans]	244	77	5.00E-64
02478_HH	1	T15107	hypothetical protein ZC132.3 - Caenorhabditis elegans gb|AAB63926.1| (AF014939) ZC132.3 gene product [Caenorhabditis elegans]	36.4	27	0.21
02479_HH	1	BAA88322.1	(AB035707) inter-alpha-trypsin inhibitor heavy chain H1 [Oryctolagus cuniculus]	35.2	27	0.45
02481_HH	1	AAD38576.1	AF145601_1 (AF145601) BcDNA.GH02419 [Drosophila melanogaster]	213	58	7.00E-55
02485_HH	1	NP_035998.1	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase gb|AAD34174.1|AF153613_1 (AF153613) peroxisomal D3,D2-enoyl-CoA isomerase [Mus musculus]	132	39	2.00E-30
02488_HH	1	AC011470.5	AC011470 Homo sapiens chromosome 19 clone CTC-490M10, complete sequence	48.1	100	0.004
02490_HH	1	AAB88621.1	(AF035623) putative DNA helicase [Spodoptera exigua nucleopolyhedrovirus]	32.8	35	2.3
02492_HH	3	AAF50385.1	(AE003554) CG6416 gene product [alt 3] [Drosophila melanogaster]	61.3	37	6.00E-09
02494_HH	1	AE002887.1	AE002887 Drosophila melanogaster genomic scaffold 142000013385259, complete sequence	42.1	93	0.22
02496_HH	1	AAB51366.1	(U20938) No definition line found [Homo sapiens] dbj|BAA89789.1| (AB003063) dihydropyrimidine dehydrogenase [Homo sapiens]	76.9	75	1.00E-13
02497_HH	1	NP_004635.1	adaptor-related protein complex 3, beta 2 subunit gb|AAC50219.1| (U37673) beta-NAP [Homo sapiens] prf||2121258A beta-NAP protein [Homo sapiens]	252	75	2.00E-66
02499_HH	1	AAF51321.1	(AE003584) CG7289 gene product [Drosophila melanogaster]	75.3	33	4.00E-13
02503_HH	1	BAA96910.1	(AB019228) contains similarity to unknown protein~gb|AAF35955.1~gene_id:MCK7.6 [Arabidopsis thaliana]	64.8	44	6.00E-10
02504_HH	1	AAA16158.1	(M80252) norA1199 protein [Staphylococcus aureus] gb|AAA26658.1| (M97169) norA [Staphylococcus aureus]	59.3	31	2.00E-08
02508_HH	1	P48603	CAPB_DROME F-ACTIN CAPPING PROTEIN BETA SUBUNIT gb|AAB38521.1| (U35240) capping protein beta [Drosophila melanogaster] gb|AAF51349.1| (AE003585) cpb gene product [Drosophila melanogaster]	264	76	4.00E-70
02509_HH	1	CAB88361.1	(AL132960) hypothetical protein [Arabidopsis thaliana]	54.3	28	8.00E-07
02510_HH	2	AAF53299.1	(AE003640) CG9282 gene product [Drosophila melanogaster]	132	56	3.00E-30
02513_HH	1	BAA11332.1	(D78258) alkaline amylopullulanase [Bacillus sp.]	30.9	34	9.1
02517_HH	1	NP_002435.1	moesin sp|P26038|MOES_HUMAN MOESIN (MEMBRANE-ORGANIZING EXTENSION SPIKE PROTEIN) pir||A41289 moesin - human gb|AAA36322.1| (M69066) moesin B [Homo sapiens] emb|CAB46379.1| (Z98946) dJ376D21.1 (Moesin (Membrane-organizing Extension Spike protein)) [Homo sapiens]	200	60	7.00E-51
02518_HH	1	AAF66188.1	AF164401_1 (AF164401) maturase [Briza erecta]	30.1	42	2.9
02520_HH	1	AAC70891.1	(AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]	143	61	1.00E-33
02522_HH	1	BAA93706.1	(AB032605) MILI (Miwi like) [Mus musculus]	74.5	31	7.00E-13
02524_HH	1	T04260	hypothetical protein F20B18.160 - Arabidopsis thaliana emb|CAB39670.1| (AL049483) putative leucine-rich-repeat protein [Arabidopsis thaliana] emb|CAB79460.1| (AL161564) putative leucine-rich-repeat protein [Arabidopsis thaliana]	47.6	26	8.00E-05
02525_HH	3	AAF48326.1	(AE003493) CG10997 gene product [Drosophila melanogaster]	55.4	35	4.00E-07
02527_HH	1	T20986	hypothetical protein F15D4.1 - Caenorhabditis elegans emb|CAB02491.1| (Z80344) similar to helicase~cDNA EST yk330g8.5 comes from this gene~cDNA EST yk275e7.3 comes from this gene~cDNA EST yk275e7.5 comes from this gene~cDNA EST yk330g8.3 comes from this gene~cDNA EST yk633g5.3 comes from this gene~cDNA EST yk510a8.5 come> emb|CAB04949.1| (Z82079) similar to helicase~cDNA EST yk330g8.5 comes from this gene~cDNA EST yk275e7.3 comes from this gene~cDNA EST yk275e7.5 comes from this gene~cDNA EST yk330g8.3 comes from this gene~cDNA EST yk633g5.3 comes from this gene~cDNA EST yk510a8.5 come>	37.1	22	0.11
02529_HH	1	AAC70939.1	(AF070695) cytoplasmic dynein intermediate chain isoform DIC3a [Drosophila melanogaster]	86.6	43	2.00E-16
02530_HH	2	AAD45920.1	AF162224_1 (AF162224) angiopoietin-related protein 3 [Mus musculus]	36.4	24	0.21
02531_HH	1	AAF78833.1	(AF059685) cytochrome c oxidase subunit II [Uroleucon rurale]	34	30	1
02534_HH	1	O95522	YA02_HUMAN HYPOTHETICAL PROTEIN DJ1198H6.2 emb|CAA19295.1| (AL023753) dJ1198H6.2 (Melanoma Preferentially Expressed Antigen PRAME and KIAA0014 LIKE protein) [Homo sapiens]	33.2	36	1.7
02535_HH	1	E70256	immunogenic protein P37 homolog - Lyme disease spirochete plasmid K/lp36 gb|AAC66145.1| (AE000788) immunogenic protein P37, putative [Borrelia burgdorferi]	41.4	24	0.006
02537_HH	1	S20471	class V zygote-specific protein - Chlamydomonas reinhardtii gb|AAB21907.1| (S90874) cysteine-rich protein [Chlamydomonas reinhardtii, 137c, Peptide, 86 aa]	41.4	33	0.004
02542_HH	1	BAA74910.1	(AB020694) KIAA0887 protein [Homo sapiens]	107	38	7.00E-23
02545_HH	1	AAA18775.1	(U07631) beta-hexosaminidase [Mus musculus] gb|AAA18777.1| (U07721) beta-hexosaminidase alpha-subunit [Mus musculus]	177	46	7.00E-44
02546_HH	1	S40127	probable coat protein - iris severe mosaic virus (fragment) emb|CAA53541.1| (X75939) ORF [Iris severe mosaic virus] prf||2019208A nuclear inclusion protein [Iris severe mosaic virus]	30.9	33	9.1
02547_HH	1	P42687	SPK1_DUGTI TYROSINE-PROTEIN KINASE SPK-1 pir||S43532 protein-tyrosine kinase (EC 2.7.1.112) spk-1 - planarian (Dugesia tigrina) emb|CAA53058.1| (X75310) spk-1 protein [Girardia tigrina]	125	41	4.00E-28
02549_HH	2	T17237	hypothetical protein DKFZp434P106.1 - human (fragment) emb|CAB55927.1| (AL117442) hypothetical protein [Homo sapiens]	84.7	43	6.00E-16
02550_HH	1	P11418	SODC_PRIGL SUPEROXIDE DISMUTASE [CU-ZN] pir||S04623 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - blue shark pir||S45643 Cu,Zn superoxide dismutase - Blue shark	46.5	62	4.00E-12
02556_HH	1	T33150	hypothetical protein T04D1.3 - Caenorhabditis elegans gb|AAC17558.1| (AF067617) contains similarity to scr homology domain 3 (SH3) (PFam: SH3.hmm, score: 63.24) [Caenorhabditis elegans]	87.4	61	9.00E-17
02557_HH	1	AAF52139.1	(AE003606) CG1090 gene product [Drosophila melanogaster]	138	53	5.00E-32

02558_HH	1	AAF31271.1	AC022517_1 (AC022517) KIAA0876 protein [Homo sapiens]	74.9	29	5.00E-13
02564_HH	1	BAA92591.1	(AB037774) KIAA1353 protein [Homo sapiens]	51.5	42	3.00E-09
02565_HH	1	NP_004818.1	ATP-binding cassette, sub-family G (WHITE), member 2 gb|AAD09188.1| (AF103796) placenta-specific ATP-binding cassette transporter [Homo sapiens]	112	35	3.00E-24
02574_HH	2	AAF49090.1	(AE003515) CG7823 gene product [Drosophila melanogaster]	163	50	9.00E-40
02579_HH	1	B47550	bride of sevenless precursor - fruit fly (Drosophila melanogaster)	30.9	32	9.1
02580_HH	1	T09737	dehydration-induced myb-related protein Cpm7 - Craterostigma plantagineum gb|AAB58314.1| (U33917) Cpm7 [Craterostigma plantagineum]	30.9	29	9.1
02581_HH	1	A55054	calpain (EC 3.4.22.17) large chain - fruit fly (Drosophila melanogaster) emb|CAA55297.1| (X78555) calpain [Drosophila melanogaster]	203	61	8.00E-52
02582_HH	1	BAB03403.1	(AB021969) carboxypeptidase N [Mus musculus]	106	36	2.00E-22
02583_HH	1	T14306	glycine-rich protein - carrot (fragment) gb|AAB01097.1| (U47097) glycine-rich protein [Daucus carota]	37.5	36	0.092
02585_HH	1	NP_004930.1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 sp|Q92499|DDX1_HUMAN DEAD BOX PROTEIN 1 (DEAD BOX PROTEIN-RETINOBLASTOMA) (DBP-RB) emb|CAA49992.1| (X70649) member of DEAD box protein family [Homo sapiens]	125	44	2.00E-28
02588_HH	1	P43332	RU1A_DROME U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) (SEX DETERMINATION PROTEIN SNF) pir||A54279 small nuclear ribonucleoprotein D25 - fruit fly (Drosophila melanogaster) gb|AAA28441.1| (M89775) small nuclear ribonucleoprotein [Drosophila melanogaster] gb|AAA28903.1| (L29521) nuclear protein [Drosophila melanogaster] gb|AAF46017.1| (AE003433) snf gene product [Drosophila melanogaster]	167	52	6.00E-41
02589_HH	1	T22372	hypothetical protein F47H4.9 - Caenorhabditis elegans emb|CAB07208.1| (Z92786) predicted using Genefinder [Caenorhabditis elegans]	32.8	27	2.3
02591_HH	3	AAD37308.1	(AF134702) CG2 omega repeat [Plasmodium falciparum]	104	40	8.00E-22
02593_HH	2	NP_060299.1	hypothetical protein FLJ20454 dbj|BAA91180.1| (AK000461) unnamed protein product [Homo sapiens]	151	46	5.00E-36
02597_HH	1	AC012601.6	AC012601 Homo sapiens chromosome 5 clone CTC-288O10, complete sequence	44.1	100	0.057
02598_HH	1	T33801	hypothetical protein E02D9.1 - Caenorhabditis elegans gb|AAC78159.1| (AF106574) contains similarity to protein kinases (Pfam; pkinase, scores; 20.0 and 109.07) [Caenorhabditis elegans]	32.8	36	2.3
02601_HH	1	H70143	hypothetical protein BB0353 - Lyme disease spirochete gb|AAC66738.1| (AE001141) B. burgdorferi predicted coding region BB0353 [Borrelia burgdorferi]	34	25	1
02603_HH	1	T41694	hypothetical protein SPCP31B10.04 - fission yeast (Schizosaccharomyces pombe) emb|CAB58370.1| (AL121859) hypothetical protein [Schizosaccharomyces pombe]	32.5	30	3.1
02605_HH	1	AAD56281.1	AF137264_1 (AF137264) glycine decarboxylase p protein [Anas platyrhynchos]	198	56	4.00E-50
02606_HH	1	AE003516.1	AE003516 Drosophila melanogaster genomic scaffold 142000013386050 section 3 of 54, complete sequence	42.1	96	0.05
02609_HH	6	CAB51918.1	(AJ130944) apolipophorin precursor protein [Locusta migratoria]	57.4	24	1.00E-07
02614_HH	2	NP_001907.1	cytochrome c-1 pir||S00680 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor - human emb|CAA30052.1| (X06994) precursor (AA -84 to 241) [Homo sapiens]	210	63	8.00E-54
02618_HH	1	NP_039011.1	ORF FPV048 GNS1/SUR4 protein gb|AAF44392.1|AF198100_39 (AF198100) ORF FPV048 GNS1/SUR4 protein [Fowlpox virus]	112	35	3.00E-24
02619_HH	1	prf|2104271A	mlrA gene [Pyrococcus furiosus]	98.7	41	4.00E-20
02622_HH	3	AAF52334.1	(AE003612) CG9140 gene product [Drosophila melanogaster]	250	84	9.00E-66
02624_HH	1	AAA66911.1	(M14145) regulatory protein [Saccharomyces cerevisiae]	36.4	30	0.21
02626_HH	1	CAB52441.1	(AL109787) translation initiation factor-like protein [Arabidopsis thaliana] emb|CAB79786.1| (AL161577) translation initiation factor-like protein [Arabidopsis thaliana]	39.1	23	0.031
02631_HH	1	S72284	DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - Plasmodium falciparum plastid emb|CAA64574.1| (X95275) frameshift [Plasmodium falciparum]	36	23	0.27
02633_HH	4	CAA30397.1	(X07520) glpE polypeptide (AA 1-131) [Escherichia coli]	41.8	25	0.005
02635_HH	1	AP001678.1	AP001678 Homo sapiens genomic DNA, chromosome 21q, section 22/105	40.1	100	0.88
02639_HH	1	No Match				
02641_HH	1	AC007225.2	AC007225 Homo sapiens chromosome 16 clone RPCI-11_480G7, complete sequence	46.1	100	0.014
02642_HH	2	AAF57364.1	(AE003789) CG3174 gene product [Drosophila melanogaster]	111	32	5.00E-24
02645_HH	2	NP_006793.1	splicing factor 3a, subunit 3, 60kD pir||A55749 spliceosome-associated protein SAP 61 - human gb|AAA19625.1| (U08815) SAP 61 [Homo sapiens]	180	47	6.00E-45
02646_HH	1	T16944	hypothetical protein T27F7.2 - Caenorhabditis elegans gb|AAG01562.1| (U58762) Contains similarity to Pfam domain: PF00017 (SH2), Score=20.9, E-value=1.8e-06, N=1 [Caenorhabditis elegans]	57	31	1.00E-07
02647_HH	1	P13437	THIM_RAT 3-KETOACYL-COA THIOLASE MITOCHONDRIAL (BETA-KETOTHIOLASE) (ACETYL-COA ACYLTRANSFERASE) (MITOCHONDRIAL 3-OXOACYL-COA THIOLASE) pir||XURT acetyl-CoA C-acyltransferase (EC 2.3.1.16), mitochondrial - rat emb|CAA28952.1| (X05341) thiolase (AA 1-397) [Rattus norvegicus]	213	61	7.00E-55
02648_HH	1	AAF50039.1	(AE003544) CG6084 gene product [Drosophila melanogaster]	161	49	5.00E-39
02652_HH	1	AC010154.3	AC010154 Homo sapiens clone RP11-573O23, complete sequence	42.1	96	0.22
02655_HH	1	AAF75279.1	AF265353_1 (AF265353) byssal protein Dpfp1 precursor [Dreissena polymorpha]	30.9	32	6.5
02656_HH	1	P12174	MATK_MARPO PROBABLE INTRON MATURASE pir||A05034 hypothetical protein 370i - liverwort (Marchantia polymorpha) chloroplast emb|CAA28076.1| (X04465) ORF370i [Marchantia polymorpha]	32.1	30	4
02657_HH	1	BAA35095.1	(AB015981) MnhA [Staphylococcus aureus]	29.7	32	4.9
02659_HH	1	AAF86232.1	AF248650_1 (AF248650) RNA-binding protein BRUNOL-4 [Homo sapiens]	137	49	6.00E-32
02660_HH	1	T39082	hypothetical protein SPAC7D4.04 - fission yeast (Schizosaccharomyces pombe) emb|CAB16721.2| (Z99532) hypothetical protein [Schizosaccharomyces pombe]	33.2	28	1.8
02664_HH	1	NP_064955.1	AMV173 gb|AAG02879.1|AF250284_173 (AF250284) AMV173 [Amsacta moorei entomopoxvirus]	35.2	24	0.46
02666_HH	11	O42249	GBLP_ORENI GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (RECEPTOR OF ACTIVATED PROTEIN KINASE C) (RACK) gb|AAB81618.1| (AF025331) receptor for activated protein kinase C [Oreochromis niloticus]	287	79	6.00E-77
02667_HH	1	AAF53731.1	(AE003661) CG10641 gene product [Drosophila melanogaster]	35.6	45	0.28

02670_HH	1	T22938	hypothetical protein F58G11.5 - Caenorhabditis elegans emb|CAB03149.1| (Z81094) predicted using Genefinder~cDNA EST yk55e12.3 comes from this gene~cDNA EST yk55e12.5 comes from this gene~cDNA EST yk416d11.3 comes from this gene~cDNA EST yk416d11.5 comes from this gene~cDNA EST yk373c12.5 comes from this gene~cDNA EST yk44>	36	30	0.27
02673_HH	1	AAF30894.1	AE002145_2 (AE002145) unique hypothetical [Ureaplasma urealyticum]	40.6	24	0.011
02674_HH	2	A45259	desmoyokin - human (fragments)	41.4	35	0.006
02676_HH	2	O75317	UBPC_HUMAN UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 12 (UBIQUITIN THIOLESTERASE 12) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 12) (DEUBIQUITINATING ENZYME 12) (UBIQUITIN HYDROLYZING ENZYME 1) gb|AAC23551.1| (AF022789) ubiquitin hydrolyzing enzyme I [Homo sapiens]	228	68	4.00E-59
02678_HH	1	P49425	MANA_RHOMR MANNAN ENDO-1,4-BETA-MANNOSIDASE pir||T10748 mannan endo-1,4-beta-mannosidase (EC 3.2.1.78) - Rhodothermus marinus emb|CAA62442.1| (X90947) endo-1,4-beta-mannanase [Rhodothermus marinus]	30.9	34	9.1
02679_HH	2	T15598	hypothetical protein C25A11.4a - Caenorhabditis elegans gb|AAA80391.1| (U39650) C25A11.4a gene product [Caenorhabditis elegans]	32.5	26	3.1
02681_HH	1	P37818	ARG1_SCHPO ARGINASE pir||S45455 arginase (EC 3.5.3.1) - fission yeast (Schizosaccharomyces pombe) emb|CAA53236.1| (X75559) arginase [Schizosaccharomyces pombe]	107	50	9.00E-23
02682_HH	1	BAB11922.1	(AB038362) esterase D [Sus scrofa]	226	62	1.00E-58
02685_HH	1	PC4160	ribosomal protein S17 - cat (fragment) pir||2108264A ribosomal protein S17 [Mus musculus]	132	72	1.00E-30
02689_HH	1	AAF48638.1	(AE003503) CG9723 gene product [Drosophila melanogaster]	45.7	18	3.00E-04
02690_HH	1	S21399	hypothetical protein 1 (clone CBS-E8) - fruit fly (Drosophila melanogaster) (fragment) emb|CAA33737.1| (X15707) orf1 [Drosophila melanogaster]	34.4	35	0.8
02692_HH	1	CAA17432.1	(AL021939) dJ352A20.2 (aldehyde dehydrogenase family protein) [Homo sapiens]	150	45	9.00E-36
02694_HH	1	AAF45992.1	(AE003432) CG6927 gene product [Drosophila melanogaster]	54.3	26	8.00E-07
02696_HH	1	AAF45728.1	(AE003423) CG18412 gene product [Drosophila melanogaster]	37.9	36	0.07
02697_HH	1	P31383	2AAA_YEAST PROTEIN PHOSPHATASE PP2A REGULATORY SUBUNIT A (PR65)	59.7	42	2.00E-08
02699_HH	2	NP_061339.1	IFN-gamma induced sp|Q60710|MG11_MOUSE INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 pir||I49127 intracellular protein Mg11 - mouse gb|AAA66219.1| (U15635) unknown intracellular protein [Mus musculus]	120	41	7.00E-27
02701_HH	1	AC003091.1	AC003091 Human BAC clone CTA-326G4 from 7p21, complete sequence [Homo sapiens]	46.1	100	0.014
02702_HH	2	T31069	tolloid-BMP-1 like protein 1 - California sea hare gb|AAC47485.1| (U57369) TBL-1 [Aplysia californica]	90.1	32	1.00E-17
02705_HH	1	AAF23209.1	AC016795_22 (AC016795) unknown protein [Arabidopsis thaliana]	58.2	27	6.00E-08
02708_HH	1	BAA33561.1	(AB012869) natriuretic peptide receptor-A [Anguilla japonica]	185	53	3.00E-46
02709_HH	1	Q45760	C5AA_BACUD PESTICIDIAL CRYSTAL PROTEIN CRY5AA (INSECTICIDAL DELTA-ENDOTOXIN CRYVA(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (152 KDA CRYSTAL PROTEIN) pir||T18213 delta-endotoxin - Bacillus thuringiensis (fragment) gb|AAA67694.1| (L07025) delta-endotoxin [Bacillus thuringiensis]	33.6	31	1.4
02710_HH	1	AAA96260.1	(U49822) Var1p [Saccharomyces douglasii]	34.8	27	0.61
02711_HH	1	T08733	hypothetical protein DKFZp566E2346.1 - human (fragment) emb|CAB43257.1| (AL050073) hypothetical protein [Homo sapiens]	49.6	29	2.00E-05
02712_HH	1	NP_057728.1	mesenchymal stem cell protein DSC54 gb|AAF65446.1|AF242769_1 (AF242769) mesenchymal stem cell protein DSC54 [Homo sapiens]	39.9	28	0.018
02716_HH	1	Z83108.1	CEF44E5 Caenorhabditis elegans cosmid F44E5, complete sequence	42.1	100	0.22
02718_HH	2	Q63150	DPYS_RAT DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP) pir||S70581 dihydropyrimidinase - rat dbj|BAA09833.1| (D63704) dihydropyrimidinase [Rattus norvegicus]	206	58	1.00E-52
02719_HH	1	T29163	hypothetical protein C01B7.4 - Caenorhabditis elegans gb|AAA96115.1| (U53147) coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase [Caenorhabditis elegans]	43.4	37	0.002
02720_HH	1	No Match				
02721_HH	1	CAA86994.1	(Z46892) Calpain, without calmodulin-like domain [Drosophila melanogaster]	176	48	1.00E-43
02726_HH	1	AC008583.4	AC008583 Homo sapiens chromosome 16 clone CTC-566I14, complete sequence	42.1	100	0.22
02727_HH	1	T02418	hypothetical protein F27L4.9 - Arabidopsis thaliana gb|AAC17089.1| (AC004482) hypothetical protein [Arabidopsis thaliana]	28.6	40	9.5
02728_HH	1	AAF57376.1	(AE003789) CG3686 gene product [Drosophila melanogaster]	177	50	7.00E-44
02731_HH	1	T18472	hypothetical protein C0440c - Plasmodium falciparum emb|CAA15615.1| (AL008970) putative helicase [Plasmodium falciparum]	32.1	24	4
02732_HH	1	O60613	SE15_HUMAN 15 KDA SELENOPROTEIN PRECURSOR	52.7	32	2.00E-06
02738_HH	3	CAB91806.1	(AL356192) conserved hypothetical protein [Neurospora crassa]	30.9	36	8.6
02740_HH	1	AAD53398.2	AF095735_1 (AF095735) sarcosine dehydrogenase [Homo sapiens]	131	48	2.00E-35
02742_HH	2	P06012	V2A_CMVQ PROBABLE RNA-DIRECTED RNA POLYMERASE (2A PROTEIN) (RNA REPLICASE) pir||S07226 RNA replicase 2a - cucumber mosaic virus emb|CAA25494.1| (X00985) RNA 2 translation product (aa 1-839) [cucumber mosaic virus]	34.8	23	0.61
02744_HH	4	JC6539	tumor necrosis factor receptor-associated factor 5 homolog - human dbj|BAA25262.1| (AB000509) TRAF5 [Homo sapiens]	87	30	1.00E-16
02750_HH	2	CAB40403.1	(AJ010592) hypothetical protein [Guillardia theta]	42.2	35	0.004
02753_HH	1	NP_033048.1	retinaldehyde dehydrogenase 2 sp|Q62148|DHAS_MOUSE RETINALDEHYDE-SPECIFIC DEHYDROGENASE TYPE 2 (RALDH(II)) (RALDH-2) pir||S74224 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 2 - mouse emb|CAA67666.1| (X99273) retinaldehyde-specific dehydrogenas [Mus musculus]	190	64	6.00E-48
02755_HH	1	AAD15519.1	(AC006217) hypothetical protein [Arabidopsis thaliana]	43	28	0.002
02762_HH	2	AE002991.1	AE002991 Drosophila melanogaster genomic scaffold 142000013385979, complete sequence	46.1	100	0.014
02763_HH	1	NP_000715.1	calcium channel, voltage-dependent, beta 2 subunit gb|AAB53332.1| (U95019) voltage-dependent calcium channel beta-2c subunit [Homo sapiens]	152	49	3.00E-36
02767_HH	1	P15348	TOP2_DROME DNA TOPOISOMERASE II pir||S02160 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - fruit fly (Drosophila melanogaster) emb|CAA43523.1| (X61209) DNA topoisomerase type II [Drosophila melanogaster]	180	62	9.00E-45
02770_HH	1	NP_063946.1	mitochondrial ceramidase gb|AAF86240.1|AF250847_1 (AF250847) mitochondrial ceramidase [Homo sapiens]	194	54	5.00E-49
02771_HH	1	AAF17490.1	AF192787_1 (AF192787) makorin 1 [Gallus gallus]	37.9	27	0.07

02773_HH	5	AAD50021.1	AC007651_16 (AC007651) Similar to SOUL Protein [Arabidopsis thaliana]	92.1	34	4.00E-18
02774_HH	3	AAC02298.1	(AF014465) Pad1 homolog [Schistosoma mansoni]	161	86	8.00E-50
02775_HH	1	No Match				
02776_HH	5	P21531	RL3_RAT 60S RIBOSOMAL PROTEIN L3 (L4) pir||R5RT3L ribosomal protein L3 - rat emb|CAA44095.1| (X62166) ribosomal protein L3 [Rattus rattus]	229	65	1.00E-59
02778_HH	1	F71824	hypothetical protein jhp1304 - Helicobacter pylori (strain J99) gb|AAD06882.1| (AE001553) putative [Helicobacter pylori J99]	42.6	32	0.003
02781_HH	2	T25723	hypothetical protein F21F3.1 - Caenorhabditis elegans gb|AAB42278.1| (U88175) strong similarity to the carboxyl-half of peptidyl-glycine alpha-amidating monooxygenase II precursors [Caenorhabditis elegans]	150	45	1.00E-35
02782_HH	1	P40631	MLH_TETTH MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA] gb|AAC18874.1| (M87306) micronuclear linker histone polyprotein [Tetrahymena thermophila]	36.4	21	0.17
02786_HH	1	AAF46832.1	(AE003457) T3dh gene product [Drosophila melanogaster]	145	50	2.00E-34
02787_HH	1	P27592	EF1A_ONCVO ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) pir||A45618 translation elongation factor eEF-1 alpha chain - nematode (Onchocerca volvulus) gb|AAA29416.1| (M64333) elongation factor [Onchocerca volvulus]	118	76	1.00E-26
02788_HH	1	AAF58436.1	(AE003820) CG3884 gene product [Drosophila melanogaster]	61.3	33	6.00E-09
02789_HH	4	AAF61067.1	AF220548_1 (AF220548) testis enhanced gene transcript-like protein [Paralichthys olivaceus]	101	36	7.00E-21
02792_HH	1	NP_055692.1	KIAA0054 gene product; Helicase sp|P42694|Y054_HUMAN HYPOTHETICAL PROTEIN KIAA0054 dbj|BAA06147.1| (D29677) KIAA0054 [Homo sapiens]	53.1	27	2.00E-06
02796_HH	1	AAF49211.1	(AE003519) CG6841 gene product [Drosophila melanogaster]	162	48	3.00E-39
02800_HH	1	NP_003671.1	tyrosyl-tRNA synthetase gb|AAB88409.1| (U89436) tyrosyl-tRNA synthetase [Homo sapiens]	119	43	2.00E-26
02802_HH	1	AAA61946.1	(L33790) receptor protein serine/threonine kinase [Drosophila melanogaster] gb|AAF59189.1| (AE003839) sax gene product [Drosophila melanogaster]	86.6	42	2.00E-16
02803_HH	1	NP_036993.1	o6-methylguanine-DNA methyltranferase sp|P24528|MGMT_RAT METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (6-O-METHYLGUANINE-DNA METHYLTRANSFERASE) pir||XURTMC methylated-DNA--protein-cysteine S-methyltransferase (EC 2.1.1.63) - rat gb|AAA42052.1| (M76704) O-6-methylguanine-DNA methyltransferase [Rattus norvegicus] gb|AAB20187.1| (S61804) O6-methylguanine-DNA methyltransferase [rats, liver, Peptide, 209 aa] [Rattus sp.] emb|CAA38648.1| (X54862) O(6)-alkylguanine-DNA-alkyltransferase [Rattus norvegicus]	30.9	51	9.1
02804_HH	1	A54273	glucocorticoid receptor - guinea pig	32.5	30	3.1
02805_HH	1	CAB91838.1	(AL356246) hypothetical protein L1923.09 [Leishmania major]	29	42	6.4
02806_HH	1	T10542	hypothetical protein F3I3.40 - Arabidopsis thaliana emb|CAB45785.1| (AL080237) putative protein [Arabidopsis thaliana] emb|CAB80911.1| (AL161491) putative protein [Arabidopsis thaliana]	46.9	21	1.00E-05
02809_HH	2	AAF21676.1	AF051138_1 (AF051138) trispanning orphan receptor; TORE [Schistosoma mansoni]	41	38	0.008
02811_HH	1	CAA32569.1	(X14396) sodium channel protein [Drosophila melanogaster]	31.3	28	6.9
02812_HH	1	NP_001779.1	cell division cycle 10 (homologous to CDC10 of S. cerevisiae) sp|Q16181|C10H_HUMAN CDC10 PROTEIN HOMOLOG pir||JC2352 hCDC10 protein - human gb|AAB31337.1| (S72008) CDC10 homolog=hCDC10 [human, fetal lung, Peptide, 418 aa] [Homo sapiens]	189	54	2.00E-47
02814_HH	1	AAC24823.1	(AF055374) synapsin s-syn-long [Loligo pealei]	219	57	2.00E-56
02815_HH	1	NP_060877.1	putative integral membrane transporter emb|CAB81951.1| (AJ276485) integral membrane transporter protein [Homo sapiens]	51.2	73	7.00E-06
02816_HH	1	BAA14418.1	(D90452) l-caldesmon I [Homo sapiens]	32.8	33	2.3
02817_HH	1	CAB62853.1	(AL035475) hypothetical protein MAL4P2.12 [Plasmodium falciparum]	35.6	29	0.35
02818_HH	1	BAA13994.1	(D89609) choriogenin H [Oryzias latipes]	44.5	32	7.00E-04
02824_HH	2	NP_039196.1	ORF FPV233 Ankyrin repeat gene family protein gb|AAF44577.1|AF198100_224 (AF198100) ORF FPV233 Ankyrin repeat gene family protein [Fowlpox virus]	33.2	27	1.8
02825_HH	1	B71929	glutamine synthetase - Helicobacter pylori (strain J99) gb|AAD06042.1| (AE001480) GLUTAMINE SYNTHETASE [Helicobacter pylori J99]	39.9	28	0.018
02828_HH	1	O51737	MUTS_BORBU DNA MISMATCH REPAIR PROTEIN MUTS pir||D70199 DNA mismatch repair protein (mutS) homolog - Lyme disease spirochete gb|AAC67157.1| (AE001179) DNA mismatch repair protein (mutS) [Borrelia burgdorferi]	32.5	31	1.1
02830_HH	3	AAD20451.1	(AF098796) SLM-1 [Mus musculus]	88.9	37	3.00E-17
02833_HH	1	CAB75776.1	(AL157734) putative sensory transduction histidine kinase [Schizosaccharomyces pombe]	35.6	27	0.35
02836_HH	1	AF024493.1	CELF23F1 Caenorhabditis elegans cosmid F23F1	38.2	100	0.63
02837_HH	1	AL031785.1	HS478D8 Human DNA sequence from clone 478D8 on chromosome 6p24. Contains STSs and GSSs, complete sequence [Homo sapiens]	42.1	100	0.04
02838_HH	3	NP_036555.1	ribosomal protein L13a sp|P40429|R13A_HUMAN 60S RIBOSOMAL PROTEIN L13A (23 KDA HIGHLY BASIC PROTEIN) pir||S29539 ribosomal protein L13a, cytosolic - human emb|CAA40254.1| (X56932) 23 kD highly basic protein [Homo sapiens] dbj|BAA88214.1| (AB028893) ribosomal protein L13a [Homo sapiens]	244	67	4.00E-64
02840_HH	10	AAA29882.1	(L33405) fimbrin [Schistosoma mansoni]	65.2	33	4.00E-10
02842_HH	1	AAC53333.1	(AF016186) putative pheromone receptor [Rattus norvegicus]	35.6	27	0.35
02843_HH	1	NP_060401.1	hypothetical protein FLJ20699 dbj|BAA91331.1| (AK000706) unnamed protein product [Homo sapiens]	58.2	25	6.00E-08
02845_HH	3	NP_038636.1	nascent polypeptide-associated complex alpha polypeptide pir||T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse gb|AAB18732.1| (U48363) alpha-NAC, muscle-specific form gp220 [Mus musculus] gb|AAB18734.1| (U48364) alpha-NAC, muscle-specific form gp220 [Mus musculus]	129	53	1.00E-29
02847_HH	1	CAB91142.1	(AL355913) putative translation initiation factor IF-2(fragment) [Streptomyces coelicolor A3(2)]	32.8	45	2.3
02851_HH	1	NP_011604.1	Ygr090wp sp|P53254|YG2L_YEAST HYPOTHETICAL 140.5 KDA PROTEIN IN CTT1-PRP31 INTERGENIC REGION pir||S64385 probable membrane protein YGR090w - yeast (Saccharomyces cerevisiae) emb|CAA97093.1| (Z72875) ORF YGR090w [Saccharomyces cerevisiae]	34.8	66	0.61
02853_HH	1	T30807	TRAF interacting protein - Fugu rubripes emb|CAA09084.1| (AJ010317) TRAF interacting protein [Fugu rubripes]	28.6	33	8.9
02855_HH	1	AAF57235.1	(AE003781) CG11630 gene product [Drosophila melanogaster]	32.1	43	4
02857_HH	4	AAG01377.1	AF151705_1 (AF151705) adducin-like protein R1 isoform [Drosophila melanogaster]	56.6	51	2.00E-07

02858_HH	1	AAF50597.1	(AE003559) CG8616 gene product [Drosophila melanogaster]	75.7	29	3.00E-13
02863_HH	1	AAF55506.1	(AE003721) CG7957 gene product [Drosophila melanogaster] gb|AAF63336.1|AF244916_1 (AF244916) mediator transcriptional cofactor TRAP80 [Drosophila melanogaster] gb|AAG02460.1|AF289995_1 (AF289995) thyroid hormone receptor-associated protein TRAP80 [Drosophila melanogaster]	51.2	22	7.00E-06
02864_HH	1	CAB39733.1	(AJ133521) protease, reverse transcriptase, ribonuclease H, integrase [Drosophila	41	30	0.008
02865_HH	1	BAA32324.1	(AB007948) KIAA0479 protein [Homo sapiens]	101	48	5.00E-21
02867_HH	1	AP001724.1	AP001724 Homo sapiens genomic DNA, chromosome 21q, section 68/105	44.1	100	0.057
02869_HH	1	T09017	acyl-CoA-binding protein homolog T27E11.20 - Arabidopsis thaliana emb|CAB43966.1| (AL078579) putative acyl-CoA binding protein [Arabidopsis thaliana] emb|CAB81427.1| (AL161571) putative acyl-CoA binding protein [Arabidopsis thaliana]	47.6	43	8.00E-05
02870_HH	2	AAF52598.1	(AE003619) CG14472 gene product [Drosophila melanogaster]	44.5	29	7.00E-04
02871_HH	1	AAF57593.1	(AE003796) cora gene product [alt 3] [Drosophila melanogaster]	62.8	39	2.00E-09
02874_HH	1	S66572	ryanodine receptor type 3 - chicken	34	38	1
02877_HH	1	T13889	helicase II homolog - fruit fly (Drosophila sp.) gb|AAB35476.2| (S79915) His [Drosophila	37.1	30	0.12
02879_HH	1	AL157812.5	AL157812 Human DNA sequence from clone RP11-14B2 on chromosome 13, complete sequence [Homo sapiens]	40.1	100	0.88
02880_HH	1	AAF56125.1	(AE003742) pnt gene product [Drosophila melanogaster]	134	72	5.00E-31
02881_HH	1	P46825	KNLC_LOLPE KINESIN LIGHT CHAIN (KLC) gb|AAA16578.1| (L24440) kinesin light chain.[Loligo pealei]	139	64	8.00E-45
02886_HH	1	AAF13063.1	(AF187232) merozoite surface antigen 1 [Plasmodium berghei]	32.5	26	3.1
02889_HH	7	AAA24976.1	(M37913) lic2 product [Haemophilus influenzae]	35.6	62	0.35
02890_HH	1	P30736	RL15_CHITE 60S RIBOSOMAL PROTEIN L15 (YL10) pir||S26380 ribosomal protein L15.e - midge (Chironomus tentans) emb|CAA48409.1| (X68332) ribosomal YL10 protein homologue [Chironomus tentans]	201	56	5.00E-51
02892_HH	1	AL391147.1	ATF5E19 Arabidopsis thaliana DNA chromosome 5, BAC clone F5E19 (ESSA project)	46.1	91	0.014
02893_HH	1	I51244	N-methyl-D-aspartate receptor type 1 - duck dbj|BAA11898.1| (D83352) N-methyl-D-aspartate receptor type1 [Anas platyrhynchos]	97.5	41	8.00E-20
02897_HH	1	AAF22865.1	L48568_1 (L48568) maturase [Cobaea scandens]	34.8	26	0.61
02902_HH	1	AAC33859.1	(AF053059) heat shock protein 70 [Paralichthys olivaceus]	58.9	61	9.00E-17
02903_HH	1	AAD44364.1	AF111169_4 (AF111169) unknown [Homo sapiens]	70.2	44	1.00E-11
02904_HH	1	AL132898.1	CEY59A8B Caenorhabditis elegans cosmid Y59A8B, complete sequence	42.1	100	0.08
02905_HH	2	AAD50121.1	AF153362_1 (AF153362) adenylyl cyclase [Dictyostelium discoideum]	40.2	30	0.014
02907_HH	1	NP_031987.1	ets variant gene 6 (TEL oncogene) sp|P97360|ETV6_MOUSE ETS-RELATED PROTEIN TEL (ETS TRANSLOCATION VARIANT 6) emb|CAA69220.1| (Y07915) TEL protein [Mus musculus]	30.9	55	9.1
02908_HH	1	AAF50154.1	(AE003548) CG18441 gene product [Drosophila melanogaster]	58.2	78	6.00E-08
02909_HH	2	I50244	histone 3.3A - chicken gb|AAA48793.1| (M11667) histone 3.3A [Gallus gallus]	208	99	3.00E-53
02910_HH	1	AAF51245.1	(AE003583) CG3528 gene product [Drosophila melanogaster]	43	43	0.002
02915_HH	1	NP_009140.1	ribosomal protein L35 sp|P42766|RL35_HUMAN 60S RIBOSOMAL PROTEIN L35 pir||G01477 ribosomal protein L35 - human gb|AAA51648.1| (U12465) ribosomal protein L35 [Homo sapiens]	64.8	46	2.00E-10
02916_HH	1	AAF80453.1	AF162271_1 (AF162271) fibrillar collagen [Riftia pachyptila]	31.7	55	5.3
02919_HH	1	AAF50206.1	(AE003550) CG14168 gene product [Drosophila melanogaster]	61.7	44	5.00E-09
02920_HH	1	AAC47216.1	(U47862) gynecophoral canal protein [Schistosoma mansoni]	63.2	26	2.00E-09
02923_HH	2	T34212	hypothetical protein F10E7.4 - Caenorhabditis elegans gb|AAA82427.1| (U41264) coded for by C. elegans cDNA yk99a6.5; coded for by C. elegans cDNA yk72g6.5; coded for by C. elegans cDNA yk99a6.3; coded for by C. elegans cDNA yk72g6.3; coded for by C. elegans cDNA yk127a2.5; coded for by C. elegans cDNA yk127a2.3; Simila>	136	36	2.00E-31
02924_HH	2	Q23023	UN51_CAEEL SERINE/THREONINE-PROTEIN KINASE UNC-51 emb|CAA86114.1| (Z38016) serine/threonine kinase [Caenorhabditis elegans] emb|CAB60406.1| (AL117207) similar to serine/threonine protein kinase~cDNA EST yk116a11.3 comes from this gene~cDNA EST yk116a11.5 comes from this gene~cDNA EST yk153c9.5 comes from this gene~cDNA EST yk205f9.5 comes from this gene~cDNA EST yk339a1.5 comes from this g> prf||2021343A Ser/Thr kinase [Caenorhabditis elegans]	148	50	3.00E-35
02925_HH	1	P10735	RT12_DROME 40S RIBOSOMAL PROTEIN S12, MITOCHONDRIAL PRECURSOR (MT-RPS12) (TECHNICAL KNOCKOUT LOCUS PROTEIN) pir||A29622 ribosomal protein S12, mitochondrial - fruit fly (Drosophila melanogaster) gb|AAA28935.1| (M19494) tko gene product (pot.); putative [Drosophila melanogaster] emb|CAB65841.1| (AL133505) EG:BACH59J11.1 [Drosophila melanogaster] gb|AAF45781.1| (AE003424) tko gene product [Drosophila melanogaster]	144	55	7.00E-34
02926_HH	1	NP_055209.1	PTD010 protein gb|AAD44495.1| (AF078863) PTD010 [Homo sapiens]	92.8	34	2.00E-18
02928_HH	1	AAF58573.1	(AE003823) CG8877 gene product [Drosophila melanogaster]	296	83	1.00E-79
02929_HH	1	NP_002807.1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 pir||JC6523 26s proteasom p55 protein - human dbj|BAA19749.1| (AB003103) 26S proteasome subunit p55 [Homo sapiens]	146	44	2.00E-34
02930_HH	1	NP_004183.1	acetylserotonin O-methyltransferase-like emb|CAA75675.1| (Y15521) start position 1 [Homo sapiens]	111	39	4.00E-24
02931_HH	1	NP_060631.1	hypothetical protein FLJ10631 dbj|BAA91722.1| (AK001493) unnamed protein product [Homo sapiens]	201	58	4.00E-51
02933_HH	1	AAC78202.1	(AF106579) F54E2.6 gene product [Caenorhabditis elegans]	29.3	32	5
02936_HH	1	NP_038617.1	latent transforming growth factor beta binding protein 2 gb|AAB61611.1| (AF004874) latent TGF-beta binding protein-2 [Mus musculus]	34	23	1
02937_HH	1	AAB06758.1	(U66366) ORFveg109 [Dictyostelium discoideum]	34.8	26	0.61
02938_HH	1	Q90512	ODO2_FUGRU DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR (E2) (E2K) gb|AAC59779.1| (U40758) dihydrolipoamide succinyltransferase [Takifugu	110	44	1.00E-23
02939_HH	1	AAB01786.1	(U43192) myosin II heavy chain [Naegleria fowleri]	46.5	20	2.00E-04
02942_HH	1	AAF49409.1	(AE003526) CG9674 gene product [alt 1] [Drosophila melanogaster]	183	54	7.00E-46
02943_HH	1	T30976	hypothetical protein C01B10.6 - Caenorhabditis elegans gb|AAC47918.1| (U58757) C01B10.6 gene product [Caenorhabditis elegans]	35.6	34	0.35

02945_HH	2	T15521	hypothetical protein C15H9.1 - Caenorhabditis elegans gb|AAB52670.1| (U56965) Similar to NAD(P) transhydrogenase, mitochondrial; coded for by C. elegans cDNA yk27c1.5; coded for by C. elegans cDNA yk35b9.5; coded for by C. elegans cDNA yk35b9.3; coded for by C. elegans cDNA yk161c9.3; coded for by C. elegans cDNA yk161c>	153	50	1.00E-36
02947_HH	3	P81178	DHAM_MESAU ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL (ALDH CLASS 2) (ALDH1) (ALDH-E2)	170	51	7.00E-42
02948_HH	1	NP_043807.1	protease sp|P52351|VP40_HSV7J CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE) ; CAPSID ASSEMBLY PROTEIN] pir||T41955 probable proteinase - human herpesvirus 7 (strain JI) gb|AAC54715.1| (U43400) protease [Human herpesvirus 7]	35.2	24	0.46
02950_HH	2	P53994	RAB2_MOUSE RAS-RELATED PROTEIN RAB-2 emb|CAA64684.1| (X95403) GTP-binding protein [Mus musculus]	317	93	6.00E-86
02952_HH	1	AAF55639.1	(AE003725) CG11779 gene product [alt 2] [Drosophila melanogaster]	44.5	23	7.00E-04
02955_HH	2	AAF52611.1	(AE003620) CG8486 gene product [Drosophila melanogaster]	106	39	1.00E-22
02956_HH	2	G69877	fibronectin-binding protein homolog yloA - Bacillus subtilis emb|CAA04416.1| (AJ000974) putative fibronectin-binding protein [Bacillus subtilis] emb|CAB13438.1| (Z99112) similar to fibronectin-binding protein [Bacillus subtilis]	33.6	31	1.4
02957_HH	1	BAA95215.1	(AB020022) neuronal differentiation-related gene [Rattus norvegicus]	182	55	3.00E-45
02960_HH	1	CAA57212.1	(X81456) unnamed protein product [Drosophila melanogaster] gb|AAF48594.1| (AE003502) bss gene product [Drosophila melanogaster]	107	46	9.00E-23
02961_HH	1	T03632	ornithine decarboxylase (EC 4.1.1.17) - common tobacco emb|CAA71498.1| (Y10472) ornithine decarboxylase [Nicotiana tabacum]	96	33	2.00E-19
02962_HH	3	C70152	sensory transduction histidine kinase homolog - Lyme disease spirochete gb|AAC66780.1| (AE001146) sensory transduction histidine kinase, putative [Borrelia burgdorferi]	32.5	30	3.1
02963_HH	1	BAA08572.1	(D49738) cytoskeleton associated protein [Homo sapiens]	163	50	1.00E-39
02964_HH	1	NP_006453.1	HBV associated factor gb|AAD00162.1| (U67322) HBV associated factor [Homo sapiens]	108	33	4.00E-23
02965_HH	1	P20004	ACON_BOVIN ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (CITRATE HYDRO-LYASE) (ACONITASE) emb|CAA90177.1| (Z49931) aconitase [Bos taurus]	199	76	1.00E-50
02971_HH	1	AAF58643.1	(AE003826) Drip gene product [Drosophila melanogaster]	79.2	31	3.00E-14
02975_HH	1	AAF76201.1	AF270700_1 (AF270700) aFGF intracellular binding protein [Mus musculus]	93.2	36	2.00E-18
02976_HH	1	AAF54438.1	(AE003684) CG8402 gene product [Drosophila melanogaster] emb|CAB99478.1| (AJ271781) protein phosphatase 5 [Drosophila melanogaster]	240	68	7.00E-63
02978_HH	1	Q10010	YSV4_CAEEL HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III pir||T16888 hypothetical protein T19C3.4 - Caenorhabditis elegans gb|AAC46595.1| (U28412) similar to polyposis locus protein 1 (SP:DP1_HUMAN, Q00765) [Caenorhabditis elegans]	101	49	4.00E-32
02980_HH	1	NP_006657.1	RuvB (E coli homolog)-like 2 dbj|BAA76708.1| (AB024301) RuvB-like DNA helicase TIP49b [Homo sapiens] gb|AAD38073.1|AF155138_1 (AF155138) RUVBL2 protein [Homo sapiens] emb|CAB46270.1| (Y18417) erythrocyte cytosolic protein of 51 kDa, ECP-51 [Homo sapiens] emb|CAB66677.1| (AL136743) hypothetical protein [Homo sapiens] gb|AAF87087.1|AF124607_1 (AF124607) Reptin52 [Homo sapiens]	275	77	3.00E-73
02981_HH	2	P42577	FRIS_LYMST SOMA FERRITIN pir||S31358 ferritin, soma - great pond snail pir||S45603 ferritin, soma - great pond snail emb|CAA40096.1| (X56778) snail soma ferritin [Lymnaea stagnalis] gb|AAB24081.1| ferritin [Lymnaea stagnalis, soma, Peptide, 174 aa]	209	63	1.00E-53
02983_HH	3	AAF60665.1	(AC024791) contains similarity to two hypothetical proteins, one from Saccharomyces cerevisiae (GB:U28373) and one from Schizosaccharomyces pombe (GB:Z98056) [Caenorhabditis elegans]	157	54	9.00E-38
02985_HH	4	NP_055576.1	KIAA0174 gene product sp|P53990|Y174_HUMAN HYPOTHETICAL PROTEIN KIAA0174 dbj|BAA11491.1| (D79996) KIAA0174 [Homo sapiens]	217	62	5.00E-56
02987_HH	1	AAF51302.1	(AE003584) CG4263 gene product [Drosophila melanogaster]	140	42	1.00E-32
02995_HH	1	T05885	hypothetical protein F6H11.40 - Arabidopsis thaliana emb|CAA16675.1| (AL021684) predicted protein [Arabidopsis thaliana] dbj|BAB11133.1| (AB018108) contains similarity to protein arginine methyltransferase~gene_id:K14B20.3 [Arabidopsis thaliana]	118	48	5.00E-26
02996_HH	2	AAF14258.1	AF137068_1 (AF137068) cubilin [Canis familiaris]	85.8	31	3.00E-16
02997_HH	2	CAB92022.1	(AL356324) hypothetical protein [Neurospora crassa]	44.1	29	0.001
03005_HH	1	CAA71688.1	(Y10687) purine NTPase [Sulfolobus acidocaldarius]	36.7	23	0.16
03006_HH	2	AAG09686.1	AF183417_1 (AF183417) microtubule-associated proteins 1A/1B light chain 3 [Homo sapiens]	129	49	1.00E-29
03007_HH	1	T40189	probable biotin-protein ligase - fission yeast (Schizosaccharomyces pombe) emb|CAB10802.1| (Z97992) putative biotin-protein ligase [Schizosaccharomyces pombe]	65.2	25	4.00E-10
03008_HH	1	T01835	serine/threonine-specific protein kinase ARA.KIN homolog T15F16.3 - Arabidopsis thaliana gb|AAC28188.1| (AF076275) similar to protein kinases (Pfam: pkinase.hmm, score: 255.71) [Arabidopsis thaliana] emb|CAB77973.1| (AL161511) putative mitogen-activated protein kinase [Arabidopsis thaliana]	77.6	32	8.00E-14
03013_HH	1	JC4809	transcriptional factor TFIIS - African clawed frog pir||S72364 transcription elongation factor TFIIS.oA - African clawed frog emb|CAA66255.1| (X97658) TFIIS elongation factor [Xenopus laevis] dbj|BAA11672.1| (D82999) transcriptional factor [Xenopus laevis]	165	56	2.00E-40
03014_HH	1	P13230	GRP3_ARTSA GLYCINE-RICH PROTEIN GRP33 gb|AAC83400.1| (J03453) glycine-rich protein [Artemia salina]	127	48	8.00E-29
03016_HH	1	CAB40554.1	(Y17113) ribosomal protein L24 [Xenopus laevis]	109	48	1.00E-23
03023_HH	1	AAF30899.1	AE002146_5 (AE002146) MBA N-terminal paralog [Ureaplasma urealyticum]	33.6	32	1.4
03027_HH	3	AAD34244.1	AF084396_1 (AF084396) calmodulin mutant SYNCAM30 [synthetic construct]	138	47	3.00E-32
03029_HH	2	AAF52593.1	(AE003619) CG7392 gene product [alt 1] [Drosophila melanogaster] gb|AAF52594.1| (AE003619) CG7392 gene product [alt 2] [Drosophila melanogaster]	55	27	5.00E-07
03031_HH	1	BAB08310.1	(AB018107) polyubiquitin [Arabidopsis thaliana]	36	25	0.27
03032_HH	1	NP_034717.1	intersection (SH3 domain protein 1A) gb|AAD19749.1| (AF132481) Ese1L protein [Mus musculus]	105	37	3.00E-22
03033_HH	2	AAD20809.1	(AF073340) 5-aminolevulinate synthase [Strongylocentrotus droebachiensis]	213	60	7.00E-55
03035_HH	1	CAB62889.1	(AL035475) hypothetical protein, MAL4P2.48 [Plasmodium falciparum]	31.3	25	6.9
03039_HH	1	NP_006008.1	hematopoietic stem cell antigen pir||T09050 AC133 antigen - human gb|AAB92514.1| (AF027208) AC133 antigen [Homo sapiens]	48.8	37	4.00E-05
03040_HH	2	AAD42870.1	AF155104_1 (AF155104) NY-REN-28 antigen [Homo sapiens]	127	44	8.00E-29
03042_HH	1	D71148	hypothetical protein PH0398 - Pyrococcus horikoshii dbj|BAA29473.1| (AP000002) 334aa long hypothetical protein [Pyrococcus horikoshii]	37.5	33	0.092

03044_HH	3	Q9WTP7	KAD3_MOUSE GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (AK3) dbj|BAA77360.1| (AB020203) adenylate kinase isozyme 3 [Mus musculus]	142	55	2.00E-33
03045_HH	1	A60531	probable esterase D2 precursor - slime mold (Dictyostelium sp.) (strain KAx-3)	31.7	28	5.3
03047_HH	2	AAF70826.1	AF157556_1 (AF157556) meiotic asynaptic mutant 1 [Arabidopsis thaliana]	80	33	2.00E-14
03052_HH	1	D71607	VPS45-like protein (STXBP/UNC-18/SEC1 family) PFB0750w - malaria parasite (Plasmodium falciparum) gb|AAC71939.1| (AE001415) VPS45-like protein (STXBP/UNC-18/SEC1 family) [Plasmodium falciparum]	34	26	0.71
03058_HH	1	AAD13401.1	(U96887) maturase [Mastixia caudatilimba]	33.6	38	1.4
03062_HH	1	P20164	HR1B_TRIFL HEMORRHAGIC METALLOPROTEINASE HR1B (TRIMERELYSIN I) pir||A37877 hemorrhagic protein HR1B - habu	32.8	24	2.3
03066_HH	1	BAA86445.1	(AB032957) KIAA1131 protein [Homo sapiens]	34.4	34	0.8
03075_HH	1	BAA83027.1	(AB028998) KIAA1075 protein [Homo sapiens]	76.5	50	2.00E-13
03079_HH	2	AAF69696.1	AC016041_1 (AC016041) F27J15.5 [Arabidopsis thaliana]	83.5	34	1.00E-15
03081_HH	1	AAF57868.1	(AE003803) CG6546 gene product [Drosophila melanogaster]	180	51	9.00E-45
03088_HH	1	NP_060938.1	uncharacterized hematopoietic stem/progenitor cells protein MDS033 gb|AAF67646.1|AF220053_1 (AF220053) uncharacterized hematopoietic stem/progenitor cells protein MDS033 [Homo sapiens]	91.3	43	6.00E-18
03094_HH	2	CAB39000.1	(AL034558) predicted using hexExon; MAL3P2.13 (PFC0220w), Hypothetical protein, len: 1570 [Plasmodium falciparum]	33.2	28	1.8
03097_HH	2	AAF58059.1	(AE003808) CG8430 gene product [Drosophila melanogaster]	196	56	1.00E-49
03101_HH	1	A47176	probable transmembrane protein X11 - human (fragment) gb|AAA61307.1| (L04953) x11 protein [Homo sapiens]	43.4	64	0.002
03102_HH	1	AAA60089.1	(M16750) pim-1 protein [Homo sapiens]	97.9	38	6.00E-20
03104_HH	11	T09457	numb-binding protein LNXp80 - mouse gb|AAC40075.1| (AF034745) LNXp80 [Mus musculus]	53.9	29	1.00E-06
03106_HH	1	AAF85765.1	AF201894_1 (AF201894) A2 polyprotein [A-2 plaque virus]	33.2	31	1.8
03107_HH	2	T34105	hypothetical protein C17G10.8 - Caenorhabditis elegans gb|AAB93456.1| (U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]	151	46	5.00E-36
03108_HH	1	BAA99532.1	(AP002484) hypothetical protein [Oryza sativa]	31.7	36	5.3
03109_HH	1	BAB03409.1	(AP002816) Similar to Spinacia oleracea protein kinase (S42867) [Oryza sativa]	40.2	41	0.014
03111_HH	1	BAA92599.1	(AB037782) KIAA1361 protein [Homo sapiens]	42.2	37	3.00E-06
03113_HH	1	AC006001.2	AC006001 Homo sapiens clone DJ0756H11, complete sequence	46.1	100	0.014
03114_HH	1	O02623	PDK_ASCSU [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE, MITOCHONDRIAL PRECURSOR (PYRUVATE DEHYDROGENASE KINASE) gb|AAB52573.1| (U94519) pyruvate dehydrogenase kinase [Ascaris suum]	172	50	2.00E-42
03117_HH	1	AAF73122.1	AF148508_1 (AF148508) aldehyde dehydrogenase [Placopecten magellanicus] gb|AAG09204.1|AF175578_1 (AF175578) omega-crystallin; alcohol dehydrogenase [Placopecten magellanicus]	205	57	3.00E-52
03118_HH	2	CAA06695.1	(AJ005785) heat shock protein 90 [Brugia pahangi]	236	72	8.00E-62
03119_HH	1	T32185	hypothetical protein ZK994.4 - Caenorhabditis elegans gb|AAB88611.1| (AF022977) contains similarity to leucine-rich repeats (LRR) [Caenorhabditis elegans]	58.6	27	4.00E-08
03123_HH	1	AAD09237.1	(U83994) AMP-activated protein kinase beta subunit [Homo sapiens] gb|AAD00625.1| (U87276) AMP-activated protein kinase beta subunit [Homo sapiens]	67.5	34	9.00E-11
03127_HH	1	NP_006043.1	Down syndrome critical region gene 3 sp|O14972|DSR3_HUMAN DOWN SYNDROME CRITICAL REGION PROTEIN 3 dbj|BAA23225.1| (D87343) DCRA [Homo sapiens]	138	46	3.00E-32
03129_HH	1	T29201	hypothetical protein T03F1.1 - Caenorhabditis elegans gb|AAB42231.1| (U88169) similar to molybdoterin biosynthesis MOEB proteins [Caenorhabditis elegans]	175	68	3.00E-43
03130_HH	1	C71609	hypothetical protein PFB0655c - malaria parasite (Plasmodium falciparum) gb|AAC71920.1| (AE001409) hypothetical protein [Plasmodium falciparum]	34.4	25	0.8
03131_HH	1	DVHUAR	multidrug resistance protein (cell line H69AR) - human	198	56	3.00E-50
03132_HH	2	P49193	RALB_TODPA RETINAL-BINDING PROTEIN (RALBP) pir||A53057 retinal-binding protein - Japanese flying squid gb|AAB29891.1| (S68871) retinal-binding protein, RALBP [Todarodes pacificus=squid, eyes, Peptide, 343 aa]	115	44	4.00E-25
03133_HH	1	AAD45010.1	AF161594_1 (AF161594) HMG protein Tcf/Lef [Strongylocentrotus purpuratus]	110	90	1.00E-23
03135_HH	2	T13940	ankyrin - fruit fly (Drosophila melanogaster) gb|AAC37208.1| (L35601) ankyrin [Drosophila melanogaster] prf||2022340A ankyrin [Drosophila melanogaster]	74.5	32	1.00E-15
03136_HH	1	B71616	phosphatase (acid phosphatase family) PFB0380c - malaria parasite (Plasmodium falciparum) gb|AAC71865.1| (AE001391) phosphatase (acid phosphatase family) [Plasmodium falciparum]	35.2	25	0.46
03139_HH	1	BAA31670.1	(AB014595) KIAA0695 protein [Homo sapiens]	87	37	1.00E-16
03142_HH	1	T21744	hypothetical protein F35C11.5 - Caenorhabditis elegans emb|CAA90245.1| (Z49966) similar to phospholipase A2~cDNA EST yk78f12.5 comes from this gene~cDNA EST yk78f12.3 comes from this gene~cDNA EST yk363b5.3 comes from this gene~cDNA EST yk363b5.5 comes from this gene [Caenorhabditis elegans]	32.5	32	3.1
03146_HH	1	P12953	VATX_BOVIN VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (32 KD ACCESSORY PROTEIN) (P39) pir||A32123 H+-transporting ATPase (EC 3.6.1.35) polypeptide IV, vacuolar - bovine	198	73	3.00E-50
03147_HH	1	BAB00635.1	(AB036858) beta 4 galactosyltransferase [Ciona intestinalis]	142	42	3.00E-33
03148_HH	1	T18302	apsB protein - Emericella nidulans emb|CAA05918.1| (AJ003163) apsB [Aspergillus nidulans]	39.1	26	0.027
03151_HH	3	AAD52648.1	AF176010_1 (AF176010) mitochondrial carrier homolog 2 [Danio rerio]	67.5	26	9.00E-11
03152_HH	1	T25425	hypothetical protein T28F3.1 - Caenorhabditis elegans emb|CAB05302.1| (Z82285) similar to C2 domain~cDNA EST yk530g2.3 comes from this gene~cDNA EST yk115g8.3 comes from this gene~cDNA EST yk115g8.5 comes from this gene~cDNA EST yk179a4.3 comes from this gene~cDNA EST yk179a4.5 comes from this gene~cDNA EST yk187g8.3 com>	99.1	42	3.00E-20
03153_HH	1	NP_003650.1	alkylglycerone phosphate synthase precursor sp|O00116|ADAS_HUMAN ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASE PRECURSOR (ALKYL-DHAP SYNTHASE) (ALKYLGLYCERONE-PHOSPHATE SYNTHASE) emb|CAA70591.1| (Y09443) alkyl-dihydroxyacetonephosphate synthase precursor [Homo sapiens]	252	68	2.00E-66
03156_HH	1	C44863	trophozoite antigen R45 (clones R23 and R45) - malaria parasite (Plasmodium falciparum) (fragment)	97.9	39	6.00E-20
03158_HH	1	BAA75497.1	(AB019790) ezrin [Gallus gallus]	99.5	51	2.00E-20
03162_HH	1	AAB86606.1	(AF030422) acetylcholinesterase catalytic subunit precursor [Electrophorus electricus]	163	50	9.00E-40
03168_HH	2	AAF21938.1	AF111111_1 (AF111111) sperm tail protein Spag5 [Rattus norvegicus]	32.1	43	3.8

03174_HH	1	CAB87762.1	(AL163817) ankyrin-like protein [Arabidopsis thaliana]	50.8	28	9.00E-06
03180_HH	1	AAF49310.1	(AE003523) CG7460 gene product [Drosophila melanogaster]	55.4	31	4.00E-07
03184_HH	2	S51848	hypothetical protein HRD1054 - yeast (Saccharomyces cerevisiae) emb|CAA88141.1| (Z48148) Similarity with S. cerevisiae hypothetical 137.7 kD protein in subtelomeric Y' repeat region [Saccharomyces cerevisiae]	37.1	21	0.12
03186_HH	1	NP_003949.1	ring finger protein (C3HC4 type) 8 dbj|BAA31621.1| (AB014546) KIAA0646 protein [Homo sapiens] dbj|BAA33557.1| (AB012770) new zinc finger protein [Homo sapiens] emb|CAB75689.1| (AL096712) dJ744I24.1 (KIAA0646 (new zinc finger protein)) [Homo sapiens]	47.3	28	1.00E-04
03190_HH	1	A44529	succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) beta chain precursor - pig	191	63	3.00E-48
03194_HH	1	AAF54669.1	(AE003692) CG17309 gene product [alt 1] [Drosophila melanogaster]	43.8	31	0.001
03196_HH	1	S52093	hemocytin - silkworm	45.7	43	3.00E-04
03197_HH	2	AAB00542.1	(U33058) UNC-89 [Caenorhabditis elegans]	51.5	37	6.00E-06
03199_HH	5	NP_062750.1	p100 co-activator dbj|BAA84944.1| (AB021491) p100 co-activator [Mus musculus]	166	49	1.00E-40
03200_HH	2	AAD41160.1	AF042284_1 (AF042284) unknown [Homo sapiens]	165	47	2.00E-40
03201_HH	1	T26585	hypothetical protein Y32B12B.2 - Caenorhabditis elegans emb|CAA21005.1| (AL031632) cDNA EST yk47e5.3 comes from this gene~cDNA EST yk47e5.5 comes from this gene [Caenorhabditis elegans]	32.1	28	4
03203_HH	1	T28160	hypothetical protein - Plasmodium falciparum gb|AAB54058.1| (U40232) exported serine/threonine protein kinase [Plasmodium falciparum]	31.7	32	0.41
03208_HH	1	NP_004793.1	otoferlin gb|AAD26117.1|AF107403_1 (AF107403) otoferlin [Homo sapiens]	77.3	28	1.00E-13
03209_HH	1	BAA91974.1	(AK001913) unnamed protein product [Homo sapiens]	102	37	3.00E-21
03211_HH	1	AAF46272.1	(AE003441) CG12157 gene product [Drosophila melanogaster]	116	38	2.00E-25
03216_HH	1	BAA96061.1	(AB040970) KIAA1537 protein [Homo sapiens]	58.2	28	5.00E-08
03217_HH	1	AAG09063.1	AC018758_3 (AC018758) protein expressed in thyroid [Homo sapiens]	149	51	2.00E-35
03221_HH	1	AAF35954.1	(AC024128) putative transporter [Arabidopsis thaliana]	110	40	8.00E-24
03222_HH	1	CAA21379.1	(AL031866) ORF56, len=176 aa, similar to pilin precursor F17d-A, eg. Q57228 E. coli,(181 aa), 37.9% identity in 177 aa overlap, Fasta scores: opt: 287, E():2.5e-11, Escherichia coli F17d fimbrial gene cluster encoding the major fimbrial subunit protein>	32.1	30	4
03223_HH	1	NP_062494.1	NADH dehydrogenase subunit 2 sp|P48903|NU2M_CHOCR NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 pir||S59103 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - red alga (Chondrus crispus) mitochondrion emb|CAA87619.1| (Z47547) NADH dehydrogenase (ubiquinone), subunit 2 [Chondrus crispus]	36	34	0.27
03226_HH	1	AAA84868.1	(U32627) ubiquitin precursor [Candida albicans]	67.1	28	1.00E-10
03227_HH	1	BAB09287.1	(AB011476) gene_id:MDA7.9~unknown protein [Arabidopsis thaliana]	33.2	42	1.8
03231_HH	1	T20561	hypothetical protein F07H5.8 - Caenorhabditis elegans emb|CAA92662.1| (Z68314) Similarity to Mouse ultra-high-sulphur keratin (PIR Acc. No. A45910)~cDNA EST yk32c6.3 comes from this gene~cDNA EST yk32c6.5 comes from this gene [Caenorhabditis elegans]	38.7	24	0.041
03240_HH	1	AAA35601.1	(L19597) binding protein [Homo sapiens]	36.7	31	0.14
03245_HH	2	P00940	TPIS_CHICK TRIOSEPHOSPHATE ISOMERASE (TIM) pir||ISCHT triose-phosphate isomerase (EC 5.3.1.1) - chicken gb|AAA49094.1| (M11314) TIM [Gallus gallus] gb|AAA49095.1| (M11941) triosephosphate isomerase (EC 5.3.1.1) [Gallus gallus]	205	66	2.00E-52
03246_HH	1	NP_037497.1	ADP-ribosylation factor binding protein GGA1 gb|AAF05707.1|AF190862_1 (AF190862) ADP-ribosylation factor binding protein GGA1 [Homo sapiens] gb|AAF35393.1|AF233521_1 (AF233521) gamma-adaptin related protein, GGA1 [Homo sapiens] gb|AAF42847.1|AF218584_1 (AF218584) GGA1 [Homo sapiens]	173	56	8.00E-43
03249_HH	1	AAD16096.1	(AF090145) reverse transcriptase [Nasonia vitripennis]	46.1	27	2.00E-04
03251_HH	1	AAD34090.1	AF151853_1 (AF151853) CGI-95 protein [Homo sapiens] emb|CAB57295.1| (AJ132008) Phocein protein [Rattus norvegicus]	300	81	5.00E-81
03252_HH	1	S24619	pistil extensin-like protein - common tobacco emb|CAA78395.1| (Z14017) pistil extensin like protein, partial CDS [Nicotiana tabacum]	30.9	28	9.1
03255_HH	1	AAF57131.1	(AE003777) CG1746 gene product [Drosophila melanogaster]	95.2	60	4.00E-19
03256_HH	1	AAD37409.1	AF148539_1 (AF148539) major nitrogen regulatory protein [Aspergillus parasiticus]	32.1	26	3.6
03257_HH	1	AAF51151.1	(AE003581) CG17221 gene product [alt 1] [Drosophila melanogaster] gb|AAF51152.1| (AE003581) CG17221 gene product [alt 2] [Drosophila melanogaster]	94	40	9.00E-19
03261_HH	2	NP_035974.1	monoglyceride lipase emb|CAA04544.1| (AJ001118) monoglyceride lipase [Mus musculus]	105	41	3.00E-22
03262_HH	1	NP_047528.1	PP34=POLYHERON CALYX=POLYHEDRON ENVELOPE=AcMNPV o> pir||T41868 hypothetical protein, 34K - Bombyx mori nuclear polyhedrosis virus (isolate T3) gb|AAC63797.1| (L33180) PP34=POLYHERON CALYX=POLYHEDRON ENVELOPE=AcMNPV o> [Bombyx mori nuclear polyhedrosis virus]	40.2	25	0.014
03263_HH	1	AAF39787.1	(AC006624) contains similarity to Pfam family PF01019 (Gamma-glutamyltranspeptidase), Score=561.8, E=4.4e-165, N=1 [Caenorhabditis elegans]	81.9	50	4.00E-15
03264_HH	1	AF234163.1	AF234163 Hordeum vulgare starch synthase I (SSI) gene, complete cds	48.1	96	0.004
03265_HH	2	NP_060244.1	hypothetical protein FLJ20342 dbj|BAA91102.1| (AK000349) unnamed protein product [Homo sapiens]	184	53	4.00E-46
03269_HH	1	AF120318.1	MMMAHNY2 Mus musculus mahogany (mg) gene, exons and partial cds	44.1	100	0.014
03272_HH	1	AC005324.1	AC005324 Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence	48.1	96	0.004
03275_HH	2	AAF47569.1	(AE003472) alpha-Spec gene product [alt 2] [Drosophila melanogaster]	217	63	5.00E-56
03278_HH	3	S51363	actin modulator protein EWAM - earthworm (Lumbricus terrestris) emb|CAA83537.1| (Z32528) EWAM (Actin-Modulator of the Earthworm) [Lumbricus terrestris] dbj|BAA06219.1| (D29920) EWAM (actin-modulator of the earthworm) [Lumbricus terrestris]	201	58	5.00E-51
03279_HH	2	AAF01588.1	AC009895_9 (AC009895) putative cytochrome P450 [Arabidopsis thaliana]	52.7	28	2.00E-06
03284_HH	3	NP_062679.1	ubiquitin-conjugating enzyme 4 gb|AAD24572.1|AF124663_1 (AF124663) UbcM4 interacting protein 28; UIP28 [Mus musculus]	57	30	1.00E-07
03286_HH	1	CAC01162.1	(AJ298475) immunoglobulin kappa chain variable region [Homo sapiens]	34	35	1
03292_HH	2	CAA20119.1	(AL031177) dJ889M15.3 (novel protein) [Homo sapiens]	98.7	33	4.00E-20
03293_HH	1	AAF39500.1	(AE002337) tetraacyldisaccharide 4`-kinase [Chlamydia muridarum]	31.7	29	5.3
03294_HH	1	CAB60389.1	(AL132848) cDNA EST yk300e12.5 comes from this gene~cDNA EST yk39e9.5 comes from this gene [Caenorhabditis elegans]	38.7	36	5.00E-07
03305_HH	1	CAB39043.2	(AL034559) hypothetical protein, PFC1000w [Plasmodium falciparum]	30.1	34	3.1
03306_HH	1	T13954	MEGF6 protein - rat dbj|BAA32462.1| (AB011532) MEGF6 [Rattus norvegicus]	33.2	46	0.56
03315_HH	3	T16768	hypothetical protein R151.8 - Caenorhabditis elegans gb|AAA50656.1| (U00036) R151.8 gene product [Caenorhabditis elegans]	32.8	33	2.1

03322_HH	1	T39903	serine-rich protein - fission yeast (Schizosaccharomyces pombe) emb|CAA22127.1| (AL033534) hypothetical serine-rich secreted protein [Schizosaccharomyces pombe]	42.2	22	0.004
03326_HH	1	T29150	hypothetical protein F47B3.4 - Caenorhabditis elegans gb|AAB52359.1| (U97017) F47B3.4 gene product [Caenorhabditis elegans]	35.2	29	0.46
03327_HH	1	AAF59021.1	(AE003835) CG8243 gene product [Drosophila melanogaster]	205	69	3.00E-52
03328_HH	1	AAF58344.1	(AE003817) CG13337 gene product [Drosophila melanogaster]	35.6	24	0.35
03329_HH	1	AAF52438.1	(AE003615) Nrv2 gene product [alt 2] [Drosophila melanogaster]	50.4	28	1.00E-05
03331_HH	1	NP_055720.1	KIAA0838 protein dbj|BAA74861.1| (AB020645) KIAA0838 protein [Homo sapiens] gb|AAF33825.1|AF223943_1 (AF223943) glutaminase kidney isoform [Homo sapiens]	36.4	22	0.21
03332_HH	1	P42659	DPP6_BOVIN DIPEPTIDYL PEPTIDASE IV LIKE PROTEIN (DIPEPTIDYL AMINOPEPTIDASE-RELATED PROTEIN) (DIPEPTIDYLPEPTIDASE VI) (DPPX) gb|AAC41622.1| (M76428) dipeptidyl aminopeptidase-related protein [Bos taurus]	58.6	43	2.00E-11
03333_HH	1	AAF52919.1	(AE003628) CG5022 gene product [Drosophila melanogaster]	72.6	30	3.00E-12
03341_HH	1	T33320	hypothetical protein ZK1055.7 - Caenorhabditis elegans gb|AAC19265.1| (AF068721) ZK1055.7 gene product [Caenorhabditis elegans]	51.5	25	6.00E-06
03345_HH	1	NP_000427.1	3-oxoacid CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor sp|P55809|SCOT_HUMAN SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT) gb|AAB07366:1| (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]	119	48	2.00E-26
03349_HH	1	NP_036473.1	GTP-binding protein gb|AAD09830.1| (AF120334) GTP-binding protein NGB [Homo sapiens]	202	59	2.00E-51
03351_HH	3	AAC79130.1	(U86673) tegumental antigen Sm20.8 [Schistosoma mansoni] gb|AAB62067.1| (U87243) Sm 20.8 [Schistosoma mansoni] gb|AAC79131.1| (U91941) tegumental protein Sm 20.8 [Schistosoma mansoni]	55.8	35	3.00E-07
03353_HH	1	AL109913.20	HSA183K14 Human DNA sequence from clone RP11-183K14 on chromosome Xq26.3-27.3, complete sequence [Homo sapiens]	42.1	100	0.22
03359_HH	1	A70503	hypothetical protein Rv1698 - Mycobacterium tuberculosis (strain H37RV) emb|CAB10955.1| (Z98268) hypothetical protein Rv1698 [Mycobacterium tuberculosis]	34.8	27	0.61
03360_HH	1	BAA90988.1	(AK000169) unnamed protein product [Homo sapiens]	146	48	2.00E-34
03361_HH	1	BAA95668.1	(D84224) methionyl tRNA synthetase [Homo sapiens]	189	58	2.00E-47
03362_HH	1	AL136382.6	AL136382 Human DNA sequence from clone RP5-977L11 on chromosome 1p22.3-31.2 Contains part of the gene for KIAA1229 protein, ESTs, STSs and GSSs, complete sequence [Homo sapiens]	40.1	100	0.53
03365_HH	2	AAG00866.1	AF255664_1 (AF255664) major vault protein [Ictalurus punctatus]	148	49	1.00E-37
03366_HH	1	AL031265.1	CEVK04G11 Caenorhabditis elegans cosmid VK04G11, complete sequence	40.1	100	0.17
03367_HH	1	C71617	SERA antigen/papain-like proteinase with active Ser PFB0345c - malaria parasite (Plasmodium falciparum) gb|AAC71858.1| (AE001388) SERA antigen/papain-like protease with active Ser [Plasmodium falciparum]	44.9	25	5.00E-04
03368_HH	1	T19733	hypothetical protein C34F6.8 - Caenorhabditis elegans emb|CAB03943.1| (Z81479) predicted using Genefinder~similar to Isocitrate and isopropylmalate dehydrogenases~cDNA EST yk229e6.3 comes from this gene~cDNA EST yk258f7.3 comes from this gene~cDNA EST yk229e6.5 comes from this gene~cDNA EST yk258f7.5 comes from this gene>	312	85	2.00E-84
03369_HH	1	AAF47516.1	(AE003472) CG12004 gene product [Drosophila melanogaster]	178	60	3.00E-44
03371_HH	1	NP_011335.1	Protein kinase; Apg1p sp|P53104|APG1_YEAST AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 pir||S61137 probable membrane protein YGL180w - yeast (Saccharomyces cerevisiae) emb|CAA62794.1| (X91489) putative ser/thr protein kinase [Saccharomyces cerevisiae] emb|CAA96892.1| (Z72702) ORF YGL180w [Saccharomyces cerevisiae] dbj|BAA21481.1| (D29991) Apg1p [Saccharomyces cerevisiae]	36.4	31	0.21
03374_HH	3	AAC98045.1	(AC005896) unknown protein [Arabidopsis thaliana]	41.4	24	0.006
03377_HH	2	AAD41955.1	AF160864_43 (AF160864) NADH dehydrogenase subunit 4 [Tetrahymena pyriformis]	32.1	35	3.8
03380_HH	1	S68280	protein disulfide-isomerase (EC 5.3.4.1) ERp60 precursor - fruit fly (Drosophila melanogaster) gb|AAB37398.1| D-ERp60=protein disulphide isomerase isoform/multifunctional endoplasmic reticulum luminal polypeptide [Drosophila melanogaster, Peptide, 489 aa]	148	44	5.00E-35
03382_HH	1	AF165124.1	AF165124 Homo sapiens chromosome 5q31.1-q33.1 clone BAC djn082c10 containing GABRG2 gene, complete sequence	44.1	100	0.057
03384_HH	2	NP_032951.1	protein kinase C substrate 80K-H gb|AAC53183.1| (U92794) alpha glucosidase II, beta subunit [Mus musculus]	72.2	29	3.00E-12
03389_HH	1	AAB34628.1	SAP-2=ERP/NET homolog [human, placenta, Peptide, 407 aa]	120	67	7.00E-27
03390_HH	1	CAB70235.1	(AL137227) predicted using Genefinder [Caenorhabditis elegans]	34.8	30	0.61
03391_HH	1	CAB90777.1	(AL355632) homolog of yeast SLA2 protein-involved in membrane cytoskeleton assembly, cell polarization, and the internalization phase of endocytosis [Schizosaccharomyces pombe]	35.2	33	0.46
03394_HH	1	Q16959	DYI2_ANTCR DYNEIN INTERMEDIATE CHAIN 2, CILIARY dbj|BAA07539.1| (D38538) dynein intermediate chain 2 [Anthocidaris crassispina]	227	58	7.00E-59
03397_HH	1	P14088	CYPH_ECHGR PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) pir||A45000 cyclophilin - tapeworm (Echinococcus granulosus) (fragment) gb|AAA29058.1| (J04664) antigen ORF (cyclophilin) [Echinococcus granulosus]	223	68	8.00E-58
03408_HH	1	1BWR	Probing The Substrate Specificity Of The Intracellular Brain Platelet-Activating Factor Acetylhydrolase	168	49	5.00E-41
03412_HH	1	AAC60788.1	(AF022812) tetrachloroethene reductive dehalogenase catalytically active subunit [Dehalospirillum multivorans]	33.2	40	1.8
03420_HH	1	AAF49172.1	(AE003517) CG9619 gene product [Drosophila melanogaster]	78.8	42	3.00E-14
03421_HH	1	NP_064692.1	RNA binding motif, single stranded interacting protein 1 dbj|BAA77262.1| (AB026569) MSSP [Mus musculus] dbj|BAA77264.1| (AB026582) MSSP [Mus musculus]	86.6	38	1.00E-16
03422_HH	1	CAB72433.1	(AJ271216) dipeptidyl-peptidase III [Homo sapiens]	164	48	7.00E-40
03425_HH	1	AAF76887.1	(AF263458) onzin [Mus musculus]	49.6	28	2.00E-05
03429_HH	1	CAA09454.1	(AJ011003) MLL protein [Gallus gallus]	47.3	28	1.00E-04
03430_HH	1	BAA90947.1	(AK000102) unnamed protein product [Homo sapiens]	34.4	41	0.8
03434_HH	1	D70247	conserved hypothetical protein BBJ19 - Lyme disease spirochete plasmid J/lp38 gb|AAC66089.1| (AE000787) conserved hypothetical protein [Borrelia burgdorferi]	34	40	1

03437_HH	2	AAC33135.1	(AF035177) GTP-binding protein [Oncorhynchus tshawytscha]	242	91	1.00E-63
03440_HH	2	NP_004583.1	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) sp|Q12872|SFR8_HUMAN SPLICING FACTOR, ARGININE/SERINE-RICH 8 (SUPPRESSOR OF WHITE APRICOT PROTEIN HOMOLOG) gb|AAA19604.1| (U08377) similar to the Drosophila splicing regulator, suppressor-of-white-apricot: Swiss-Prot Accession Number P12297 [Homo sapiens]	68.7	37	4.00E-11
03443_HH	1	AE003765.1	AE003765 Drosophila melanogaster genomic scaffold 142000013386035 section 90 of 105, complete sequence	44.1	100	0.057
03444_HH	1	NP_033853.1	ATPase, Ca++ transporting, plasma membrane 2 gb|AAC61255.1| (AF053471) plasma membrane Ca2+-ATPase 2 [Mus musculus] dbj|BAA83104.1| (AB030737) plasma membrane Ca2+-ATPase isoform 2 [Mus musculus]	190	71	6.00E-48
03446_HH	1	AAD21873.1	(AF078907) PINCH [Drosophila melanogaster] gb|AAF54235.1| (AE003678) pin85A gene product [Drosophila melanogaster]	166	63	2.00E-40
03447_HH	2	Q09687	PCM1_SCHPO PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE C13C5.05C (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE) pir||S59642 hypothetical protein SPAC13C5.05c - fission yeast (Schizosaccharomyces pombe) pir||T37618 n-acetylglucosamine-phosphate mutase - fission yeast (Schizosaccharomyces pombe) emb|CAA90456.1| (Z50112) n-acetylglucosamine-phosphate mutase [Schizosaccharomyces pombe]	132	45	2.00E-30
03449_HH	1	P30682	GBI_LYMST GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN) pir||S27013 GTP-binding regulatory protein Gi alpha chain - great pond snail emb|CAA78807.1| (Z15095) GTP-binding protein alpha-i subunit [Lymnaea stagnalis]	196	59	2.00E-49
03455_HH	2	AAD08909.1	(AF052391) heat shock protein 70 [Trichophyton rubrum]	34.8	32	0.61
03456_HH	1	AAC72723.1	(AF059026) nuclear transcription factor 4 homolog isoform a [Aedes aegypti]	76.1	49	2.00E-13
03461_HH	1	T18429	hypothetical protein C0345w - Plasmodium falciparum emb|CAB11106.1| (Z98547) predicted using hexExon; MAL3P3.5 (PFC0345w), Hypothetical protein, len: 1712 aa [Plasmodium falciparum]	32.8	33	2.3
03465_HH	1	P81069	GABD_MOUSE GA BINDING PROTEIN BETA-2-1 CHAIN (GABP-BETA-2-1 SUBUNIT) (GABPB2-1)	68.7	35	4.00E-11
03466_HH	1	T26424	hypothetical protein Y106G6G.5 - Caenorhabditis elegans emb|CAA22056.1| (AL033508) Y106G6G.5 [Caenorhabditis elegans]	37.9	46	0.07
03468_HH	1	CAA69153.1	(Y07818) ULIP [Homo sapiens]	126	38	2.00E-28
03471_HH	1	P41951	YLK3_CAEEL PUTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME III pir||T15881 hypothetical protein D1044.3 - Caenorhabditis elegans gb|AAA50735.1| (U00065) contains EGF-like repeats; highly similar to ZC84.1; 3' exons similar to protein kinase [Caenorhabditis elegans]	65.2	25	4.00E-10
03489_HH	2	NP_055289.1	acid sphingomyelinase-like phosphodiesterase emb|CAA69328.1| (Y08134) acid sphingomyelinase-like phosphodiesterase [Homo sapiens]	116	36	2.00E-25
03491_HH	2	NP_061271.1	synaptotagmin 7 dbj|BAA85776.1| (AB026804) synaptotagmin VII [Mus musculus]	51.9	23	4.00E-06
03498_HH	3	CAA72925.1	(Y12236) Cu/Zn-superoxide dismutase [Danio rerio]	207	63	7.00E-53
03501_HH	1	CAB39023.1	(AL034559) kinesin-related protein [Plasmodium falciparum]	36.7	26	0.15
03507_HH	1	AL138758.7	AL138758 Human DNA sequence from clone RP5-824O18 on chromosome 1p11.2-13.1, complete sequence [Homo sapiens]	42.1	100	0.22
03508_HH	1	A25556	hypothetical 21.2K protein (long interspersed repetitive element) - rat emb|CAA29034.1| (X05472) ORF1 [Rattus norvegicus]	31.7	35	5.3
03509_HH	1	AAF44675.1	AF239264_1 (AF239264) cathepsin L [Fasciola gigantica]	152	49	2.00E-36
03511_HH	1	AAF70457.1	AF226273_1 (AF226273) delta-5 fatty acid desaturase [Homo sapiens]	92.8	30	2.00E-18
03514_HH	1	T14346	Herc2 protein - mouse gb|AAD08658.1| (AF071173) Herc2 [Mus musculus]	127	50	6.00E-29
03516_HH	2	NP_032887.1	polycystic kidney disease 2 emb|CAA74551.1| (Y14105) polycystin [Mus musculus]	112	35	2.00E-24
03518_HH	1	AAB96620.1	(AF017185) protein tyrosine phosphatase and tensin homolog/mutated in multiple advanced cancers protein [Rattus norvegicus]	171	58	3.00E-42
03520_HH	2	T15617	hypothetical protein C25F6.2 - Caenorhabditis elegans gb|AAA80434.1| (U39742) coded for by C. elegans cDNA yk25e5.3; coded for by C. elegans cDNA yk25e5.5; similar to repeat guanylate kinase domain of D. melanogaster lethal(1) discs large-1 tumor suppressor protein (SP:DLG1_DROME, P31007) and R. norvegicus postsynaptic>	63.6	53	1.00E-09
03525_HH	1	O35952	GLO2_RAT HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II) (ROUND SPERMATID PROTEIN RSP29) pir||JC5826 hydroxyacylglutathione hydrolase (EC 3.1.2.6) - rat gb|AAC39944.1| (U97667) RSP29 [Rattus norvegicus]	170	49	1.00E-41
03526_HH	1	AAF57776.1	(AE003801) CG5784 gene product [alt 2] [Drosophila melanogaster] gb|AAF57777.1| (AE003801) CG5784 gene product [alt 1] [Drosophila melanogaster]	138	53	4.00E-32
03527_HH	1	D71613	GAF domain protein (cyclic nt signal transduct.) PFB0510w - malaria parasite (Plasmodium falciparum) gb|AAC71891.1| (AE001399) GAF domain protein (cyclic nt signal transduct.) [Plasmodium falciparum]	34.4	33	0.57
03528_HH	1	AAF54079.1	(AE003673) BG:DS00464.1 gene product [Drosophila melanogaster]	28.6	44	8.5
03534_HH	1	AAC09360.1	(AF055010) unknown [Homo sapiens]	108	38	5.00E-23
03536_HH	1	AAC33717.1	(AF060542) HaeIV restriction/modification system [Haemophilus influenzae biogroup aegyptius]	34	23	1
03538_HH	1	AAC32270.1	(AF079459) small ras-like GTPase [Drosophila melanogaster] dbj|BAA88245.1| (AB035672) Rab7 protein [Drosophila melanogaster] gb|AAF56218.1| (AE003745) Rab7 gene product [Drosophila melanogaster] gb|AAF73041.1|AF263363_1 (AF263363) small ras-like GTPase RAB7 [Drosophila melanogaster]	252	79	2.00E-66
03539_HH	1	T18661	hypothetical protein B0035.14 - Caenorhabditis elegans emb|CAA97416.1| (Z73102) Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU)~cDNA EST yk437a1.5 comes from this gene~cDNA EST yk558g10.5 comes from this gene~cDNA EST yk655h10.5 comes from this gene [Caenorhabditis elegans]	112	35	3.00E-24
03541_HH	1	AAB47447.1	(U49262) cytoplasmic phosphoprotein [Homo sapiens]	131	70	7.00E-30
03545_HH	1	CAB60700.1	(AL132798) conserved hypothetical protein [Schizosaccharomyces pombe]	83.5	32	1.00E-15
03548_HH	1	AC008372.6	AC008372 Homo sapiens chromosome 14 clones RP11-111O16 and RP11-61F4 containing genes for nuclear receptor coactivator NCoA-62 (nuclear receptor coactivator NCoA-62) gene, complete cds; and unknown gene, complete sequence	42.1	100	0.22
03554_HH	1	CAB60891.1	(AL132885) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans] emb|CAB81910.1| (AL132889) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans]	46.5	48	2.00E-04

03560_HH	1	AL159996.7	AL159996 Human DNA sequence from clone RP11-401F12 on chromosome 9. Contains STSs and GSSs, complete sequence [Homo sapiens]	42.1	100	0.22
03562_HH	1	AAD43008.1	(AF100744) hypothetical 19.5 kDa protein [Homo sapiens]	99.5	36	2.00E-20
03563_HH	1	NP_013782.1	(putative) involved in respiration; Sov1p sp|Q04748|YMV6_YEAST HYPOTHETICAL 104.7 KD PROTEIN IN NCA1-HMS1 INTERGENIC REGION pir||S52826 hypothetical protein YMR066w - yeast (Saccharomyces cerevisiae) emb|CAA88791.1| (Z48952) unknown [Saccharomyces cerevisiae]	31.7	27	5.3
03568_HH	1	AAA88508.1	(J00738) alpha-2u globulin [Rattus norvegicus] dbj|BAA96482.1| (AB039825) alpha-2u globulin [Rattus norvegicus]	30.9	32	9.1
03571_HH	1	S54123	neurofilament protein NF70 - brown garden snail emb|CAA60122.1| (X86347) neurofilament protein NF70 [Helix aspersa]	139	50	1.00E-32
03572_HH	1	NP_013848.1	Nuclear pore membrane glycoprotein; Pom152p sp|P39685|P152_YEAST NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM152 (P150) pir||A53824 nuclear pore membrane protein POM152 - yeast (Saccharomyces cerevisiae) emb|CAA83469.1| (Z31592) POM152 [Saccharomyces cerevisiae] emb|CAA88554.1| (Z48622) Pom152p [Saccharomyces cerevisiae]	32.1	31	4
03575_HH	1	NP_043924.1	gag-pol polyprotein gb|AAC54861.1| (U26458) gag-pol polyprotein [Snakehead retrovirus]	34.4	36	0.8
03576_HH	1	prf|2101292A	G extra-large protein [Rattus norvegicus]	125	70	6.00E-32
03577_HH	1	P21358	RMAR_CANGA MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1 emb|CAA26652.1| (X02893) var1 protein (aa 1-339) [Candida utilis]	35.6	33	0.35
03583_HH	1	NP_001960.1	eukaryotic translation initiation factor 5 sp|P55010|IF5_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) gb|AAC50572.1| (U49436) translation initiation factor 5 [Homo sapiens]	178	54	4.00E-44
03584_HH	2	NP_062632.1	Ras-binding protein SUR-8 gb|AAC40175.1| (AF068921) Ras-binding protein SUR-8 [Mus musculus]	75.7	40	3.00E-13
03589_HH	1	JC4345	protein kinase (EC 2.7.1.37) gamma - rat dbj|BAA08637.1| (D49836) RAC-PK gamma [Rattus norvegicus]	186	56	1.00E-46
03590_HH	1	BAA97453.1	(AB029393) streptococcal hemagglutinin [Streptococcus gordonii]	32.5	31	1.9
03592_HH	1	AAD43133.1	AF159148_1 (AF159148) Noggin 2 [Danio rerio]	79.2	33	3.00E-14
03594_HH	1	P16967	SSRA_CANFA TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) (PGP35) pir||S08993 signal sequence receptor alpha chain precursor - dog emb|CAA35752.1| (X51367) SSRA precursor protein [Canis familiaris]	70.2	35	1.00E-11
03596_HH	2	NP_055118.1	pescadillo (zebrafish) homolog 1, containing BRCT domain gb|AAB61140.1| (U78310) pescadillo [Homo sapiens]	140	43	1.00E-32
03602_HH	1	AAF24748.1	AF137367_1 (AF137367) VPS10 domain receptor protein SORCS [Mus musculus]	51.9	35	4.00E-06
03604_HH	1	P43006	EAT2_MOUSE EXCITATORY AMINO ACID TRANSPORTER 2 (SODIUM-DEPENDENT GLUTAMATE/ASPARTATE TRANSPORTER 2) pir||A55676 excitatory amino acid transporter EEAT2 - mouse gb|AAA77673.1| (U11763) excitatory amino acid transporter 2 [Mus musculus] dbj|BAA07854.1| (D43796) glutamate transporter MGLT1 [Mus musculus] dbj|BAA23770.1| (AB007810) mGLT-1 [Mus musculus] prf||2115216A Glu transporter:ISOTYPE=MGLT1 [Mus musculus]	125	59	2.00E-28
03609_HH	1	AAF49619.1	(AE003530) CG7439 gene product [Drosophila melanogaster]	35.2	24	0.46
03610_HH	1	AAF46156.1	(AE003437) CG3842 gene product [Drosophila melanogaster]	109	42	2.00E-23
03614_HH	1	NP_033238.1	immunoglobulin S mu binding protein 2 sp|P40694|SMB2_MOUSE DNA-BINDING PROTEIN SMUBP-2 (IMMUNOGLOBULIN MU BINDING PROTEIN 2) (SMUBP-2) (CARDIAC TRANSCRIPTION FACTOR 1) (CATF1) pir||S35633 DNA-binding protein - mouse gb|AAA40143.1| (L10075) DNA-binding protein [Mus musculus]	94	39	4.00E-23
03616_HH	1	AE003781.1	AE003781 Drosophila melanogaster genomic scaffold 142000013386030 section 1 of 3, complete sequence	44.1	100	0.041
03624_HH	1	A72236	hypothetical protein TM1585 - Thermotoga maritima (strain MSB8) gb|AAD36652.1|AE001803_5 (AE001803) glycerate kinase, putative [Thermotoga maritima]	99.1	36	3.00E-20
03625_HH	1	G71660	hypothetical protein RP561 - Rickettsia prowazekii emb|CAA15009.1| (AJ235272) unknown [Rickettsia prowazekii]	32.5	27	3.1
03627_HH	1	NP_008823.1	DNA (cytosine-5-)-methyltransferase 3 beta emb|CAB53070.1| (AL035071) dJ1085F17.1.1 (ortholog of mouse DNMT3B (DNA Cytosine-5 Methyltransferase 3B1) (isoform 1)) [Homo sapiens] gb|AAD53063.1|AF156488_1 (AF156488) DNA cytosine-5 methyltransferase 3 beta 1 [Homo sapiens]	43.4	26	0.002
03628_HH	1	CAB39032.2	(AL034559) hypothetical protein, PFC0925w [Plasmodium falciparum]	35.2	48	0.46
03631_HH	1	NP_005267.1	glycerol-3-phosphate dehydrogenase 1 (soluble) sp|P21695|GPDA_HUMAN GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC (GPD-C) (GPDH-C) pir||S55920 glycerol-3-phosphate dehydrogenase (NAD+) (EC 1.1.1.8) - human gb|AAA92863.1| (L34041) L-glycerol-3-phosphate:NAD oxidoreductase [Homo sapiens] prf||2113206A alpha glycerol phosphate dehydrogenase [Homo sapiens]	176	59	1.00E-43
03636_HH	1	NP_010056.1	Septin homolog; Shs1p sp|Q07657|YD25_YEAST HYPOTHETICAL 62.6 KDA PROTEIN IN CDC13-GCS1 INTERGENIC REGION pir||S67788 hypothetical protein YDL225w - yeast (Saccharomyces cerevisiae) emb|CAA98804.1| (Z74273) ORF YDL225w [Saccharomyces cerevisiae]	33.6	26	1.4
03638_HH	1	AAF54353.1	(AE003682) CG8454 gene product [Drosophila melanogaster]	87	30	1.00E-16
03646_HH	1	T29380	hypothetical protein T14F9.1 - Caenorhabditis elegans gb|AAA91266.1| (U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; coded for by>	194	64	7.00E-49
03649_HH	1	AAF58501.1	(AE003822) CG12370 gene product [Drosophila melanogaster]	56.6	34	2.00E-07
03650_HH	3	T24694	hypothetical protein T08G11.3 - Caenorhabditis elegans emb|CAB02306.1| (Z80220) T08G11.3 [Caenorhabditis elegans]	38.3	25	0.054
03658_HH	1	NP_000099.1	dihydrolipoamide dehydrogenase precursor sp|P09622|DLDH_HUMAN DIHYDROLIPOAMIDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR pir||DEHULP dihydrolipoamide dehydrogenase (EC 1.8.1.4) precursor - human gb|AAA59527.1| (J03490) lipoamide dehydrogenase precursor old gene name 'LAD' [Homo sapiens]	213	74	1.00E-54
03661_HH	1	P12759	RSP3_CHLRE RADIAL SPOKE PROTEIN 3 pir||A31270 radial spoke protein 3 - Chlamydomonas reinhardtii emb|CAA32685.1| (X14549) spoke protein [Chlamydomonas reinhardtii]	129	46	2.00E-29
03664_HH	1	AAC51370.1	(U97698) secretory mucin MUC6 [Homo sapiens]	34	30	0.99

03665_HH	1	CAB62862.1	(AL035475) putative flap exonuclease [Plasmodium falciparum]	41	27	0.008
03666_HH	1	NP_005165.1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1 dbj|BAA03994.1| (D16561) ATP synthase gamma-subunit [Homo sapiens] dbj|BAA03997.1| (D16563) ATP synthase gamma-subunit [Homo sapiens]	148	58	3.00E-35
03670_HH	1	P37980	IPYR_BOVIN INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) pir||A45153 inorganic pyrophosphatase (EC 3.6.1.1) - bovine	209	54	2.00E-53
03673_HH	2	NP_034112.1	cathepsin C sp|P97821|CATC_MOUSE DIPEPTIDYL-PEPTIDASE I PRECURSOR (DPP-I) (DPPI) (CATHEPSIN C) (CATHEPSIN J) (DIPEPTIDYL TRANSFERASE) gb|AAB49457.1| (U89269) preprodipeptidyl peptidase I [Mus musculus] gb|AAB58400.3| (U74683) dipeptidyl peptidase I precursor [Mus musculus]	219	58	1.00E-56
03676_HH	1	AC007540.3	AC007540 Homo sapiens 12q24.1 BAC RPCI11-128P10 (Roswell Park Cancer Institute Human BAC Library) complete sequence	44.1	96	0.011
03679_HH	5	AP001710.1	AP001710 Homo sapiens genomic DNA, chromosome 21q, section 54/105	44.1	100	0.057
03681_HH	1	T37552	conserved hypothetical protein SPAC11H11.03c - fission yeast (Schizosaccharomyces pombe) emb|CAB59799.1| (AL132714) conserved hypothetical protein [Schizosaccharomyces pombe]	41.8	31	0.005
03685_HH	2	AAF51958.1	(AE003601) BcDNA:GH02439 gene product [Drosophila melanogaster]	128	35	3.00E-29
03689_HH	2	P41824	YBFH_APLCA Y-BOX FACTOR HOMOLOG (APY1) gb|AAA60373.1| (U02684) Y-Box factor [Aplysia californica]	101	64	4.00E-21
03692_HH	1	Q45825	YRI3_CORAM HYPOTHETICAL PROTEIN IN RIBF 3'REGION pir||PC4009 hypothetical protein 92 - Corynebacterium ammoniagenes (fragment) dbj|BAA07183.1| (D37967) orf-304 like gene [Corynebacterium ammoniagenes]	44.5	42	7.00E-04
03694_HH	1	BAA95045.1	(AB041561) unnamed protein product [Mus musculus]	172	56	2.00E-42
03696_HH	1	CAB46026.1	(AL023553) dJ347H13.4 (novel protein) [Homo sapiens]	76.9	50	1.00E-13
03700_HH	1	NP_035314.1	proteasome (prosome, macropain) subunit, alpha type 3 sp|O70435|PRC8_MOUSE PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) (PROTEASOME SUBUNIT K) gb|AAC12943.1| (AF055983) proteasome alpha7/C8 subunit [Mus musculus] gb|AAD50534.1|AF060089_1 (AF060089) proteasome subunit C8 [Mus musculus]	169	63	7.00E-44
03701_HH	3	NP_004893.1	splicing factor (CC1.3) pir||I55595 splicing factor - human gb|AAA16346.1| (L10910) splicing factor [Homo sapiens]	104	40	8.00E-22
03703_HH	1	P24896	NU5M_CAEEL NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 pir||S26037 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Caenorhabditis elegans mitochondrion emb|CAA38162.1| (X54252) ND5 protein (AA 1 - 527) [Caenorhabditis elegans] gnl|NCBI_MITO|ND5_10021 NADH dehydrogenase subunit 5	32.8	36	2.3
03704_HH	1	CAB62386.1	(AJ130845) pim-3 protein [Coturnix coturnix]	92.1	44	7.00E-23
03706_HH	1	BAB11140.1	(AB018108) kinesin-like calmodulin-binding protein [Arabidopsis thaliana]	39.9	25	0.018
03707_HH	1	AAF50089.1	(AE003546) CG7628 gene product [Drosophila melanogaster]	197	56	8.00E-50
03708_HH	6	AAD34973.1	AF143497_1 (AF143497) t-complex polypeptide 1 [Monodelphis domestica]	235	67	3.00E-61
03710_HH	1	O13263	SCG2_XENLA AMILORIDE-SENSITIVE SODIUM CHANNEL GAMMA-2 SUBUNIT (EPITHELIAL NA+ CHANNEL GAMMA-2 SUBUNIT) (GAMMA-2 ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 GAMMA-2 SUBUNIT) (SCNEG2) (GAMMA-2 NACH) emb|CAA72730.1| (Y12001) gamma2 subunit of epithelial sodium channel [Xenopus laevis]	40.2	25	0.014
03711_HH	2	BAA35183.1	(AB021289) epididymal secretory protein [Mus musculus]	117	40	8.00E-26
03712_HH	1	NP_012668.1	Sgm1p sp|P47166|YJ9C_YEAST HYPOTHETICAL 81.2 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION pir||S57157 hypothetical protein YJR134c - yeast (Saccharomyces cerevisiae) emb|CAA89665.1| (Z49634) ORF YJR134c [Saccharomyces cerevisiae]	38.7	25	0.041
03713_HH	1	NP_004046.1	calpain 5 gb|AAC51869.1| (U94346) calpain-like protease [Homo sapiens]	55.8	27	3.00E-07
03715_HH	3	CAA72122.1	(Y11252) annexin max1 [Oryzias latipes]	106	51	1.00E-22
03717_HH	1	T23337	hypothetical protein K05C4.2 - Caenorhabditis elegans emb|CAB04568.1| (Z81564) cDNA EST yk448c11.3 comes from this gene~cDNA EST yk158d7.5 comes from this gene~cDNA EST yk471g10.3 comes from this gene~cDNA EST yk471g10.5 comes from this gene~cDNA EST yk424a3.3 comes from this gene~cDNA EST yk424a3.5 comes from this gene~>	86.6	31	2.00E-16
03718_HH	1	P56095	AP1_KLULA AP-1-LIKE TRANSCRIPTION FACTOR gb|AAC39320.1| (AF006499) transcription factor KlYAP1 [Kluyveromyces lactis]	38.7	28	0.041
03719_HH	1	AAF55508.1	(AE003721) CG7187 gene product [Drosophila melanogaster]	157	69	9.00E-38
03721_HH	1	AAF07448.1	AE001576_7 (AE001576) conserved hypothetical protein [Borrelia burgdorferi]	36.4	29	0.19
03724_HH	3	G71609	hypothetical protein PFB0650w - malaria parasite (Plasmodium falciparum) gb|AAC71919.1| (AE001408) hypothetical protein [Plasmodium falciparum]	47.3	25	1.00E-04
03732_HH	1	NP_031670.1	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 pir||JC5670 lysosomal membrane 85K glycoprotein precursor - mouse dbj|BAA23372.1| (AB008553) mLGP85/LIMP II [Mus musculus]	111	46	5.00E-24
03734_HH	2	CAA22962.2	(AL035331) /prediction=(method:""genefinder"", version:""084"")~/prediction=(method:""genscan"", version:""1.0"")~/match=(desc:""CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-3 (ACTIVATING FACTOR 3)"", species:""HOMO SAPIENS (HUMAN)"", ranges:(query:12> emb|CAB65887.1| (AL121806) /prediction=(method:""genefinder"", version:""084"")~/prediction=(method:""genscan"", version:""1.0"")~/match=(desc:""CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-3 (ACTIVATING FACTOR 3)"", species:""Homo sapiens (Human)"", ranges:(query:13> gb|AAF45599.1| (AE003420) A3-3 gene product [Drosophila melanogaster]	36.7	24	0.14
03735_HH	2	P29314	RS9_RAT 40S RIBOSOMAL PROTEIN S9 pir||S21497 ribosomal protein S9 - rat emb|CAA47013.1| (X66370) ribosomal protein S9 [Rattus norvegicus]	287	87	4.00E-77
03736_HH	1	A45627	myosin heavy chain - nematode (Brugia malayi) gb|AAA73080.1| (M74000) [Brugia malayi myosin heavy chain gene, complete cds.], gene product	41	24	0.008
03737_HH	1	NP_005651.1	solute carrier family 35 (UDP-galactose transporter), member 2 sp|P78381|UGAT_HUMAN UDP-GALACTOSE TRANSLOCATOR (UDP-GALACTOSE TRANSPORTER) (UGT) (UDP-GAL-TR) pir||JC5022 UDP-galactose transporter, splice form 2 - human dbj|BAA13545.1| (D88146) UDP-galactose transporter 2 [Homo sapiens] dbj|BAA95614.1| (AB042425) UDP-galactose transporter 2 [Homo sapiens]	129	46	2.00E-29
03738_HH	1	CAB60144.1	(Y15953) trigger factor [Oenococcus oeni]	32.1	36	4
03739_HH	1	A69849	hypothetical protein yjdF - Bacillus subtilis emb|CAB13060.1| (Z99110) yjdF [Bacillus subtilis]	31.3	35	6.9

03740_HH	1	AAF57333.1	(AE003787) CG10417 gene product [Drosophila melanogaster]	119	51	2.00E-26
03750_HH	1	CAB66761.1	(AL136827) hypothetical protein [Homo sapiens]	118	45	5.00E-26
03751_HH	1	P80035	LIPG_CANFA TRIACYLGLYCEROL LIPASE, GASTRIC PRECURSOR (GASTRIC LIPASE) (GL) emb|CAA74198.1| (Y13899) triacylglycerol lipase [Canis familiaris]	167	54	6.00E-41
03753_HH	2	CAB41885.1	(AJ238216) supporting-cell antigen [Gallus gallus]	118	41	5.00E-26
03756_HH	1	CAB38995.1	(AL034558) predicted using hexExon; MAL3P2.8 (PFC0195w), Hypothetical protein, len: 1424 aa [Plasmodium falciparum]	39.5	37	0.024
03758_HH	1	T05322	hypothetical protein F18F4.240 - Arabidopsis thaliana emb|CAA18239.1| (AL022224) leucine rich repeat-like protein [Arabidopsis thaliana] emb|CAB79014.1| (AL161552) leucine rich repeat-like protein [Arabidopsis thaliana]	34.4	31	0.8
03759_HH	1	AAF51482.1	(AE003589) CG2789 gene product [Drosophila melanogaster]	123	45	1.00E-27
03761_HH	1	AAF47707.1	(AE003476) CG1271 gene product [Drosophila melanogaster]	92.1	28	4.00E-18
03767_HH	1	P70579	MGR8_RAT METABOTROPIC GLUTAMATE RECEPTOR 8 PRECURSOR gb|AAB09537.1| (U63288) metabotropic glutamate receptor 8 [Rattus norvegicus]	34	31	1
03768_HH	1	BAB03337.1	(AB035452) ABC transporter [Staphylococcus aureus]	33.2	26	1.8
03769_HH	1	O15532	SELW_HUMAN SELENOPROTEIN W	88.9	51	3.00E-17
03771_HH	1	NP_035699.1	tektin 1 gb|AAD13183.1| (AF081947) tektin [Mus musculus]	125	38	3.00E-28
03772_HH	1	AAF81911.1	AF279265_1 (AF279265) putative anion transporter 1 [Homo sapiens]	124	38	7.00E-28
03777_HH	1	P53442	ALF_SCHMA FRUCTOSE-BISPHOSPHATE ALDOLASE gb|AAA57567.1| (L38658) fructose 1,6 bisphosphate aldolase [Schistosoma mansoni] gb|AAB84014.1| (AF026805) fructose bisphosphate aldolase [Schistosoma mansoni]	119	76	2.00E-26
03781_HH	1	Q26481	RL5_STYCL 60S RIBOSOMAL PROTEIN L5 gb|AAC05598.1| (L78668) ribosomal protein L5 [Styela clava]	178	57	3.00E-44
03786_HH	1	AAD30269.1	AF120268_1 (AF120268) ALIEN [Homo sapiens]	249	73	2.00E-65
03787_HH	2	AAF75760.1	AF262218_2 (AF262218) putative acetyltransferase [Anabaena PCC7120]	47.3	30	1.00E-04
03789_HH	1	AAC47545.1	(U68412) fibrillar collagen [Arenicola marina]	63.6	32	1.00E-09
03797_HH	1	AAD43782.1	AF152522_1 (AF152522) protocadherin gamma B6 short form protein [Homo sapiens]	69.9	31	2.00E-11
03804_HH	1	S27270	prohormone convertase LPC2 - great pond snail emb|CAA48730.1| (X68850) LPC2 [Lymnaea stagnalis]	92.8	39	2.00E-18
03805_HH	1	CAB54435.1	(AL110487) cDNA EST yk381c11.5 comes from this gene~cDNA EST EMBL:Z14442 comes from this gene~cDNA EST yk153g7.5 comes from this gene~cDNA EST yk212f8.5 comes from this gene~cDNA EST yk254h2.5 comes from this gene~cDNA EST yk31d3.5 comes from this gene>	212	67	3.00E-54
03809_HH	1	AC004019.20	AC004019 Homo sapiens Chromosome 22q11.2 BAC Clone 357f7 In CES Region, complete sequence	40.1	100	0.52
03810_HH	2	AAF78884.1	AF168990_1 (AF168990) putative GTP-binding protein [Homo sapiens]	84.3	35	8.00E-16
03811_HH	1	P18288	TBAT_ONCMY TUBULIN ALPHA CHAIN, TESTIS-SPECIFIC pir||A56622 tubulin alpha chain, testis-specific - rainbow trout gb|AAA68904.1| (M36623) alpha-tubulin [Oncorhynchus mykiss]	264	82	4.00E-70
03812_HH	1	T13828	CREB-binding protein homolog - fruit fly (Drosophila melanogaster) gb|AAB53050.1| (U88570) CREB-binding protein homolog [Drosophila melanogaster]	164	49	4.00E-40
03814_HH	3	BAA93705.1	(AB032604) MIWI (piwi) [Mus musculus]	142	42	2.00E-33
03819_HH	1	CAB39052.1	(AL034559) hypothetical protein, PFC1055w [Plasmodium falciparum]	34.4	23	0.8
03821_HH	1	AC002302.1	HUAC002302 Homo sapiens Chromosome 16 BAC clone CIT987-SKA-345G4 ~complete genomic sequence, complete sequence	42.1	93	0.22
03823_HH	1	AL050323.4	HSJ793N16 Human DNA sequence from clone RP4-793N16 on chromosome 20, complete sequence [Homo sapiens]	42.1	100	0.074
03828_HH	1	AAF57733.1	(AE003800) Dgp-1 gene product [Drosophila melanogaster]	91.7	35	5.00E-18
03834_HH	1	AF177382.1	AF177382 Culex tritaeniorhynchus carboxylesterase b1 (Estbeta1) gene, Estbeta1-1 allele, complete cds	44.1	100	0.057
03835_HH	2	AAB94760.1	(AF039202) Hsp70/Hsp90 organizing protein; hop [Cricetulus griseus]	199	62	1.00E-50
03836_HH	1	P35605	COPP_BOVIN COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) pir||S35312 coatomer complex beta' chain - bovine emb|CAA51285.1| (X72756) beta prime cop [Bos taurus]	285	80	2.00E-76
03839_HH	2	BAA95677.1	(AB036791) prosaposin [Bos taurus]	46.9	31	1.00E-06
03840_HH	1	AAC08316.1	(AC004490) R29381_1 [Homo sapiens]	105	42	3.00E-22
03841_HH	1	AAF20064.1	AF190909_1 (AF190909) alpha-actinin 4 [Rattus norvegicus]	156	44	1.00E-37
03845_HH	2	NP_001403.1	eukaryotic translation initiation factor 1A sp|P47813|IF1A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C) gb|AAA19812.1| (L18960) protein synthesis factor [Homo sapiens]	160	71	8.00E-39
03849_HH	1	AAD12702.1	(AC006069) unknown protein [Arabidopsis thaliana]	137	46	7.00E-32
03850_HH	1	T20609	hypothetical protein F08G5.5 - Caenorhabditis elegans emb|CAA94585.1| (Z70682) Similarity to Rabbit UDP-glucuronosyltransferase (SW:UDBE_RABIT) [Caenorhabditis elegans]	32.5	31	3.1
03852_HH	1	Q10835	COGZ_XENLA COLLAGENASE 3 PRECURSOR (MATRIX METALLOPROTEINASE-13) (MMP-13) gb|AAA83996.1| (L49412) collagenase 3 [Xenopus laevis]	61.7	29	5.00E-09
03853_HH	1	AL161559.2	ATCHRIV59 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59	42.1	100	0.17
03854_HH	1	P45285	SAPA_HAEIN PEPTIDE TRANSPORT PERIPLASMIC PROTEIN SAPA PRECURSOR pir||A64134 periplasmic dipeptide transport protein dppA homolog - Haemophilus influenzae (strain Rd KW20) gb|AAC23285.1| (U32837) peptide ABC transporter, periplasmic-binding protein (sapA) [Haemophilus influenzae Rd]	31.7	30	5.3
03855_HH	1	AAB86609.1	(AF030197) vesicular acetylcholine transporter [Drosophila melanogaster]	199	71	2.00E-50
03856_HH	2	NP_061946.1	hypothetical protein dbj|BAA91403.1| (AK000869) unnamed protein product [Homo sapiens]	81.1	34	7.00E-15
03859_HH	1	O17453	PSD4_SCHMA 26S PROTEASOME REGULATORY SUBUNIT S5A	115	41	2.00E-25
03861_HH	1	AC027119.4	AC027119 Homo sapiens chromosome 3 clone RP11-113L10 map 3p, complete sequence	52	94	2.00E-04
03864_HH	1	NP_064989.1	AMV207 gb|AAG02913.1|AF250284_207 (AF250284) AMV207 [Amsacta moorei entomopoxvirus]	33.6	27	1.4
03865_HH	1	CAA44467.2	(X62582) Cellulase [Clavibacter michiganensis]	30.1	30	8
03867_HH	1	T17458	chromosome condensation protein XCAP-G - African clawed frog gb|AAD09819.1| (AF111423) chromosome condensation protein XCAP-G [Xenopus laevis]	72.6	30	2.00E-12
03868_HH	1	NP_005768.1	RNA binding motif protein 6 gb|AAC35207.1| (U50839) g16 protein [Homo sapiens] gb|AAD04160.1| (AF091264) RNA binding motif protein 6 [Homo sapiens]	69.1	38	3.00E-11

03869_HH	1	AAF58469.1	(AE003821) CG8769 gene product [Drosophila melanogaster]	35.6	29	0.35
03873_HH	1	AJ243967.1	BMY243967 Bacillus mycoides pBMY1 plasmid	42.1	100	0.22
03874_HH	1	No Match				
03880_HH	1	AAF70256.1	AF247562_1 (AF247562) Scribbler long isoform [Drosophila melanogaster] gb|AAF76322.1|AF242194_1 (AF242194) brakeless-B [Drosophila melanogaster]	60.9	47	8.00E-09
03886_HH	1	AC006499.13	AC006499 Homo sapiens chromosome 4 clone C0494H11, complete sequence	38.2	100	3.5
03887_HH	1	BAB09999.1	(AB006697) cleft lip and palate associated transmembrane protein-like [Arabidopsis thaliana]	33.6	62	1.4
03895_HH	1	A46170	tektin A1 - sea urchin (Strongylocentrotus purpuratus) gb|AAF14818.1| (M97188) tektin A1 [Strongylocentrotus purpuratus]	141	47	6.00E-33
03897_HH	3	AAF72703.1	(AF262938) gynecophoral canal protein [Schistosoma japonicum]	107	33	7.00E-23
03901_HH	1	CAB57254.1	(AJ270227) histone H2 [Entodinium caudatum]	149	60	2.00E-35
03902_HH	1	CAB60442.1	(AL132853) cDNA EST yk134e6.3 comes from this gene~cDNA EST yk134e6.5 comes from this gene [Caenorhabditis elegans]	30.1	34	9.9
03903_HH	2	AAB34914.1	peptide isomerase heavy chain	55.8	30	3.00E-07
03905_HH	1	AF289076.1	AF289076 Homo sapiens clone CTD-2372o24 chromosome 8 map 8q13, complete sequence	44.1	96	0.057
03906_HH	2	AAF54704.1	(AE003693) CG6946 gene product [alt 2] [Drosophila melanogaster] gb|AAF54705.1| (AE003693) CG6946 gene product [alt 1] [Drosophila melanogaster]	96.3	40	2.00E-19
03909_HH	2	NP_032973.1	protease (prosome, macropain) 26S subunit, ATPase 1 sp|P49014|PRS4_MOUSE 26S PROTEASE REGULATORY SUBUNIT 4 (P26S4) gb|AAB34137.1| (U39302) P26s4 [Mus musculus] dbj|BAA09341.1| (D50696) proteasomal ATPase (S4) [Rattus norvegicus]	235	82	2.00E-67
03912_HH	2	CAA09210.1	(AJ010471) RNA helicase [Arabidopsis thaliana] gb|AAD14475.1| (AC005966) Identical to gb|AJ010471 mRNA for DEAD box RNA helicase (RH22) from Arabidopsis thaliana. EST gb|Y11191 comes from this gene	33.2	42	1.8
03913_HH	1	AAC62752.1	(AF086807) fertilin alpha [Bos taurus]	31.3	33	6.9
03914_HH	1	AAC35297.1	(AF053651) cellular apoptosis susceptibility protein [Homo sapiens]	120	44	1.00E-26
03918_HH	1	AB045238.1	AB045238 Xenopus laevis XRPTPb mRNA for receptor-type protein tyrosine phosphatase beta.2 secretory variant, complete cds	38.2	100	3.5
03919_HH	1	I39005	cysteine proteinase (EC 3.4.22.-) Yama - human gb|AAB60355.1| (U13738) cysteine protease CPP32 isoform beta [Homo sapiens] gb|AAA74929.1| (U26943) Yama protein [Homo sapiens]	68.3	33	5.00E-11
03924_HH	1	NP_048269.1	ORF MSV198 MTG motif gene family protein gb|AAC97761.1| (AF063866) ORF MSV198 MTG motif gene family protein [Melanoplus sanguinipes entomopoxvirus]	34.8	42	0.61
03925_HH	2	AAF47969.1	(AE003484) CG1637 gene product [alt 3] [Drosophila melanogaster]	59.7	46	3.00E-16
03926_HH	1	T26942	hypothetical protein Y45F3A.3 - Caenorhabditis elegans emb|CAA21490.1| (AL032621) similar to Acyl-CoA dehydrogenase~cDNA EST yk104c9.5 comes from this gene~cDNA EST EMBL:M89392 comes from this gene~cDNA EST EMBL:M89303 comes from this gene~cDNA EST yk3e4.3 comes from this gene~cDNA EST yk3e4.5 comes from this gene~cDNA ES>	109	42	2.00E-23
03927_HH	1	AAF52135.1	(AE003606) CG14646 gene product [Drosophila melanogaster]	75.3	29	4.00E-13
03928_HH	1	AL121673.41	HSA305P22 Human DNA sequence from clone RP11-305P22 on chromosome 20, complete sequence [Homo sapiens]	38.2	100	3.5
03930_HH	2	AAF58520.1	(AE003822) CG8836 gene product [Drosophila melanogaster]	31.3	44	6.9
03931_HH	1	T15372	hypothetical protein C01F1.1 - Caenorhabditis elegans gb|AAB00717.1| (U58761) coded for by C. elegans cDNA yk79f12.5; coded for by C. elegans cDNA cm17c10; coded for by C. elegans cDNA yk98e4.5; coded for by C. elegans cDNA yk59d6.5; coded for by C. elegans cDNA CEESL34F; coded for by C. elegans cDNA yk98e4.3; coded for>	37.5	25	0.092
03934_HH	3	AB026643.1	AB026643 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MEE13	42.1	100	0.22
03936_HH	1	AC069558.5	AC069558 Genomic Sequence For Arabidopsis thaliana Clone T5G13 From Chromosome IV, complete sequence	42.1	100	0.22
03938_HH	1	NP_015268.1	integral membrane protein, exhibits homology to YBR161w, Hoc1p, and Och1p; Sur1p sp|P33300|SUR1_YEAST SUR1 PROTEIN pir||S41798 SUR1 protein - yeast (Saccharomyces cerevisiae) gb|AAA68909.1| (M96648) SUR1 gene product [Saccharomyces cerevisiae] dbj|BAA05628.1| (D26581) Bcl21p (multicopy suppressor) [Saccharomyces cerevisiae] gb|AAB68308.1| (U39205) Sur1p [Saccharomyces cerevisiae]	80.8	30	9.00E-15
03940_HH	2	P50143	TCPG_XENLA T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (TCP-1-GAMMA) (CCT-GAMMA) gb|AAC59783.1| (U37062) CCTgamma [Xenopus laevis]	212	72	5.00E-59
03945_HH	1	A69768	transcription antiterminator BglG family homolog ydaA - Bacillus subtilis dbj|BAA19254.1| (AB001488) PROBABLE HTH_LYSR_FAMILY TRANSCRIPTIONAL REGULATOR. [Bacillus subtilis] emb|CAB12223.1| (Z99106) similar to transcriptional antiterminator (BglG family) [Bacillus subtilis]	34.4	30	0.8
03946_HH	2	NP_061278.1	heat shock protein 40 sp|Q9QYJ3|HS41_MOUSE HEAT SHOCK 40 KDA PROTEIN 1 (HEAT SHOCK PROTEIN 40) (HSP40) dbj|BAA88083.1| (AB028272) heat shock protein 40 [Mus musculus] dbj|BAA95672.1| (AB028273) heat shock protein 40 [Mus musculus]	129	42	1.00E-29
03952_HH	1	S27015	GTP-binding regulatory protein Gs alpha chain - great pond snail	223	61	8.00E-58
03954_HH	1	AAC15706.1	(AF052191) katanin p60 subunit [Strongylocentrotus purpuratus]	219	65	1.00E-56
03955_HH	2	NP_003148.1	serine/threonine kinase 2 sp|P51957|STK2_HUMAN SERINE/THREONINE-PROTEIN KINASE NRK2 (SERINE/THREONINE KINASE 2) pir||I78885 serine/threonine-specific protein kinase (EC 2.7.1.-) STK2 - human gb|AAA36658.1| (L20321) protein serine/threonine kinase [Homo sapiens]	164	45	5.00E-40
03956_HH	1	BAA74515.1	(AB022867) cellulase [Prevotella ruminicola]	32.5	24	3.1
03959_HH	2	NP_048221.1	ORF MSV150 putative NTP pyrophosphohydrolase mutT motif homolog (vaccinia D10R), similar to SW:P32817 gb|AAC97785.1| (AF063866) ORF MSV150 putative NTP pyrophosphohydrolase mutT motif homolog (vaccinia D10R), similar to SW:P32817 [Melanoplus sanguinipes entomopoxvirus]	37.5	31	0.092
03970_HH	1	P48153	RS3_MANSE 40S RIBOSOMAL PROTEIN S3 gb|AAB05575.1| (U12708) ribosomal protein S3 [Manduca sexta]	75.3	52	1.00E-17
03974_HH	1	BAA94606.1	(AB041225) Tob2 [Mus musculus]	111	38	5.00E-24
03975_HH	1	CAA10358.1	(AJ131355) NAD(P) transhydrogenase [Strongylocentrotus purpuratus]	184	63	5.00E-53
03976_HH	1	NP_002214.1	inositol 1,4,5-triphosphate receptor, type 2 sp|Q14571|IP3S_HUMAN INOSITOL 1,4,5-TRISPHOSPHATE-BINDING PROTEIN TYPE 2 RECEPTOR (TYPE 2 INSP3 RECEPTOR) (TYPE 2 INOSITOL 1,4,5-TRISPHOSPHATE RECEPTOR) dbj|BAA05384.1| (D26350) human type 2 inositol 1,4,5-trisphosphate receptor [Homo sapiens]	36.7	34	0.031

03978_HH	1	O77210	IF4E_APLCA EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KDA SUBUNIT) gb|AAC36720.1| (AF085810) translation initiation factor eIF4E [Aplysia californica]	167	50	6.00E-41
03981_HH	1	AL163282.2	HS21C082 Homo sapiens chromosome 21 segment HS21C082	42.1	100	0.22
03983_HH	1	T13847	sno protein - fruit fly (Drosophila melanogaster) gb|AAB54001.1| (U95760) Sno [Drosophila melanogaster]	184	56	6.00E-46
03984_HH	1	AAB61676.1	(AF006663) peptidylglycine alpha-hydroxylating monooxygenase [Drosophila melanogaster] gb|AAF47127.1| (AE003462) Phm gene product [alt 2] [Drosophila melanogaster]	131	39	7.00E-30
03986_HH	1	AAF60663.1	(AC024791) contains similarity to Pfam family PF00170 (bZIP transcription factor), score=12.2, E=0.06, N=2 [Caenorhabditis elegans]	36.4	22	0.2
03989_HH	1	P24629	HS71_LYCES HEAT SHOCK COGNATE 70 KD PROTEIN 1 pir||S14949 dnaK-type molecular chaperone hsc-1 - tomato emb|CAA37970.1| (X54029) heat shock protein cognate 70 [Lycopersicon esculentum]	43.8	74	9.00E-11
03992_HH	1	T19666	hypothetical protein C33A12.13 - Caenorhabditis elegans emb|CAA92796.1| (Z68493) C33A12.13 [Caenorhabditis elegans]	34	37	1
03995_HH	2	P32876	AT91_BOVIN ATP SYNTHASE LIPID-BINDING PROTEIN P1 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C) pir||LWBOA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P1 precursor - bovine emb|CAA28845.1| (X05218) P1 subunit [Bos taurus] prf||1202261A ATP synthase proteolipid P1 [Bos taurus]	98.3	49	4.00E-20
03996_HH	1	P11638	QA1F_NEUCR QUINIC ACID UTILIZATION ACTIVATOR pir||F31277 regulatory protein qa-1F - Neurospora crassa emb|CAA32754.1| (X14603) activator [Neurospora crassa]	36.4	26	0.2
03997_HH	1	Q22498	COPG_CAEEL PROBABLE COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP) pir||T24915 hypothetical protein T14G10.5 - Caenorhabditis elegans emb|CAA93095.1| (Z68880) predicted using Genefinder~Similarity to Yeast protein transport protein SEC21 (SW:SEC21_YEAST)~cDNA EST EMBL:T00194 comes from this gene~cDNA EST EMBL:T01403 comes from this gene~cDNA EST EMBL:T02350 comes from this gene~cDNA EST EMBL:T00195 >	162	50	1.00E-39
04001_HH	3	AAF52317.1	(AE003612) eIF-4a gene product [Drosophila melanogaster]	213	67	1.00E-54
04002_HH	1	NP_001119.1	adaptor-related protein complex 1, gamma 1 subunit sp|O43747|ADG_HUMAN GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN) emb|CAA72902.1| (Y12226) gamma-adaptin [Homo sapiens]	127	42	7.00E-29
04012_HH	1	AAF53765.1	(AE003661) CG10691 gene product [Drosophila melanogaster]	223	74	1.00E-57
04016_HH	1	AAD00188.1	(U72893) TFIIE small subunit [Drosophila melanogaster] gb|AAF47880.1| (AE003480) TfIIEbeta gene product [Drosophila melanogaster]	107	35	7.00E-23
04017_HH	1	AF151389.1	AF151389 Dermatobia hominis strain Ponta Grossa tRNA-Ile gene, partial sequence; D-loop, complete sequence; and 12S ribosomal RNA, partial sequence; mitochondrial genes for mitochondrial products	44.1	100	0.057
04022_HH	1	T18497	hypothetical protein C0780w - Plasmodium falciparum	40.6	26	0.011
04028_HH	1	AAF16692.1	AF111853_1 (AF111853) PRO0750 [Homo sapiens]	159	59	2.00E-38
04031_HH	1	AL121761.5	HSJ122P22 Human DNA sequence from clone RP1-122P22 on chromosome 20 Contains STSs, GSSs and a CpG Island, complete sequence [Homo sapiens]	44.1	100	0.057
04034_HH	1	BAA81712.1	(AB006558) protein tyrosine kinase 11 [Ephydatia fluviatilis]	105	52	3.00E-22
04035_HH	1	AAF55279.1	(AE003712) CG5916 gene product [Drosophila melanogaster]	108	33	3.00E-23
04038_HH	1	NP_005125.1	protein phosphatase 4, regulatory subunit 1 gb|AAD09818.1| (AF111106) protein serine/threonine phosphatase 4 regulatory subunit 1 [Homo sapiens]	44.5	20	7.00E-04
04039_HH	4	P54675	P3K3_DICDI PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) pir||T18274 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 3 - slime mold (Dictyostelium discoideum) (fragment) gb|AAA85723.1| (U23478) phosphatidylinositol-4,5-diphosphate 3-kinase [Dictyostelium discoideum]	38.3	20	0.049
04042_HH	1	AAC33205.1	AAC33205 (AC003970) Hypothetical protein [Arabidopsis thaliana]	46.5	38	2.00E-04
04043_HH	4	T13597	hypothetical protein EG:80H7.2 - fruit fly (Drosophila melanogaster) emb|CAA19840.1| (AL031027) /prediction=(method:""genefinder"", version:""084"", score:""51.37"")~/prediction=(method:""genscan"", version:""1.0"")~/motif=(desc:""Tubulin-beta mRNA autoregulation signal"", dbase:""PROSITE"", acc:""PS00228"", method:""ppsearch"")~/match> gb|AAF45632.1| (AE003421) EG:80H7.2 gene product [Drosophila melanogaster]	53.1	26	2.00E-06
04060_HH	1	AAF43422.1	AF233321_1 (AF233321) zinc transporter like 1 [Mus musculus]	107	38	7.00E-23
04063_HH	1	NP_004425.1	echinoderm microtubule-associated protein-like gb|AAB57824.1| (U97018) HuEMAP [Homo sapiens]	196	53	2.00E-49
04065_HH	3	Q22054	RS16_CAEEL PROBABLE 40S RIBOSOMAL PROTEIN S16 pir||T24280 hypothetical protein T01C3.6 - Caenorhabditis elegans emb|CAB01658.1| (Z78413) predicted using Genefinder~Similarity to Human 40S ribosomal protein S16 (SW:RS16_HUMAN)~cDNA EST yk89g7.3 comes from this gene; cDNA EST yk97g4.3 comes from this gene; cDNA EST yk112a5.3 comes from this gene~cDNA EST yk89g7.5 comes from this >	205	70	2.00E-52
04067_HH	1	AAF27554.1	(AF179847) putative transposase [Lactococcus lactis]	32.1	30	4
04069_HH	1	Q90578	VDHA_CHICK VITAMIN D3 HYDROXYLASE-ASSOCIATED PROTEIN (VDHAP) pir||A53101 vitamin D3 hydroxylase-associated protein, mitochondrial - chicken gb|AAC59645.1| (U00694) vitamin D3 hydroxylase associated protein [Gallus gallus]	87	37	1.00E-16
04071_HH	1	I40055	positive trans-activator of capsule synthesis - Bacillus anthracis gb|AAA81894.1| (U02535) positive trans-activator of capsule synthesis [Bacillus anthracis] gb|AAF13669.1|AF188935_67 (AF188935) pXO2-64 [Bacillus anthracis]	34.8	22	0.61
04072_HH	1	CAA67697.1	(X99321) putative homologue of human EB1 [Botryllus schlosseri]	32.5	36	3.1
04073_HH	1	T13603	probable N-methyl-D-aspartate receptor - fruit fly (Drosophila melanogaster) emb|CAA19838.1| (AL031027) /prediction=(method:""genefinder"", version:""084"", score:""160.71"")~/prediction=(method:""genscan"", version:""1.0"")~/match=(desc:""GLUTAMATE [NMDA] RECEPTOR SUBUNIT ZETA 1 LONG FORM PRECURSOR (NR1)"", species:""HOMO SAPIENS (HUMAN)"", r>	171	45	3.00E-42
04076_HH	1	NP_058683.1	ATP citrate lyase sp|P16638|ACLY_RAT ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) pir||A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat gb|AAA74463.1| (J05210) ATP citrate-lyase [Rattus norvegicus]	186	70	4.00E-54
04078_HH	2	AAC04806.1	(AF037468) B subunit V-ATPase [Culex pipiens quinquefasciatus]	265	84	2.00E-70
04080_HH	1	NP_060734.1	hypothetical protein FLJ10900 dbj|BAA91891.1| (AK001762) unnamed protein product [Homo sapiens]	242	63	3.00E-63

04081_HH	1	AAF79611.1	AC027665_12 (AC027665) F5M15.17 [Arabidopsis thaliana]	67.5	31	9.00E-11
04084_HH	1	AAF22574.1	(AF140243) axin-related protein [Xenopus laevis]	34	21	1
04089_HH	1	T18582	hypothetical protein 4R79.2 - Caenorhabditis elegans emb|CAA20282.1| (AL031254) predicted using Genefinder~similar to Ras family [Caenorhabditis elegans]	141	44	6.00E-33
04093_HH	1	AAF46950.1	(AE003459) Fib gene product [Drosophila melanogaster]	208	73	4.00E-53
04096_HH	1	JC1358	thiol-endopeptidase (EC 3.4.-.-) - avirulent egg drop syndrom virus	32.8	47	0.49
04102_HH	1	NP_032421.1	itchy gb|AAB99764.1| (AF037454) ubiquitin protein ligase [Mus musculus]	170	53	7.00E-42
04105_HH	1	U53140.1	CELZC266 Caenorhabditis elegans cosmid ZC266	44.1	100	0.057
04106_HH	1	AAG08758.1	AE004950_1 (AE004950) betaine aldehyde dehydrogenase [Pseudomonas aeruginosa]	62.8	31	2.00E-09
04108_HH	1	AAC79147.1	(AC002342) Dreg-2 like protein [Arabidopsis thaliana] dbj|BAB08826.1| (AB016874) Dreg-2 like protein [Arabidopsis thaliana]	50.4	34	1.00E-05
04109_HH	1	AE002154.1	AE002154 Ureaplasma urealyticum section 55 of 59 of the complete genome	42.1	100	0.22
04118_HH	1	AP002819.1	AP002819 Oryza sativa genomic DNA, chromosome 1, PAC clone:P0501G01, complete sequence	42.1	100	0.22
04119_HH	1	CAB11139.2	(Z98551) hypothetical protein, PFC0765c [Plasmodium falciparum]	39.1	25	0.031
04131_HH	1	CAA09748.1	(AJ011706) 40S ribosomal protein S13 [Lumbricus rubellus]	141	72	4.00E-49
04134_HH	1	NP_034009.1	carnitine deficiency-associated gene expressed in ventricle 1 sp|O35594|CDV1_MOUSE CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1 (CDV-1 PROTEIN) emb|CAA71519.1| (Y10495) CDV-1R protein [Mus musculus]	103	46	9.00E-22
04136_HH	1	AAB64220.1	(U95822) putative transmembrane GTPase [Homo sapiens]	32.8	30	2.3
04138_HH	1	AAA30701.1	(L13938) phospholipase C [Bos taurus]	169	58	2.00E-41
04144_HH	1	NP_057223.1	16.7Kd protein gb|AAD44477.1| (AF078845) 16.7Kd protein [Homo sapiens]	55.4	31	4.00E-07
04148_HH	1	NP_055724.1	KIAA1036 protein dbj|BAA82988.1| (AB028959) KIAA1036 protein [Homo sapiens] gb|AAF02829.1|AC007376_1 (AC007376) KIAA1036 [Homo sapiens]	122	39	2.00E-27
04149_HH	1	AAA36018.1	(L23928) serine hydroxymethyltransferase [Homo sapiens]	232	67	2.00E-60
04155_HH	1	AAF57903.1	(AE003804) CG8946 gene product [alt 1] [Drosophila melanogaster] gb|AAF57904.1| (AE003804) CG8946 gene product [alt 2] [Drosophila melanogaster]	114	45	7.00E-25
04157_HH	1	AAF94507.1	(AE004214) sensory box sensor histidine kinase/response regulator [Vibrio cholerae]	32.5	22	3.1
04161_HH	1	NP_059429.1	stromal cell derived factor receptor 1 isoform a gb|AAD43218.1|AF109127_1 (AF109127) stromal cell-derived receptor-1 alpha [Homo sapiens]	32.1	26	4
04167_HH	1	Q11073	YT45_CAEEL HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X gb|AAB36845.1| (U23516) B0416.5 gene product [Caenorhabditis elegans]	121	41	6.00E-27
04170_HH	1	AAA83210.1	(U40484) MAP kinase [Aplysia californica]	105	67	2.00E-47
04172_HH	1	AAF54281.1	(AE003680) CG8202 gene product [Drosophila melanogaster]	67.9	26	7.00E-11
04174_HH	1	AAB08485.1	(L14329) glutathione peroxidase [Schistosoma mansoni] gb|AAC14468.1| (L37762) glutathione peroxidase [Schistosoma mansoni]	196	62	1.00E-49
04177_HH	1	T41007	atp dependent helicase - fission yeast (Schizosaccharomyces pombe) emb|CAA19304.1| (AL023776) probable atp-dependent rna helicase [Schizosaccharomyces pombe]	137	41	7.00E-32
04179_HH	1	AL163268.2	HS21C068 Homo sapiens chromosome 21 segment HS21C068	40.1	100	0.22
04180_HH	4	Q16822	PPCM_HUMAN PHOSPHOENOLPYRUVATE CARBOXYKINASE, MITOCHONDRIAL PRECURSOR [GTP] (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK-M) emb|CAA72272.1| (Y11484) phosphoenolpyruvate carboxykinase (GTP) [Homo sapiens]	149	48	2.00E-35
04187_HH	1	Q21190	UNC1_CAEEL UNC-1 PROTEIN pir||T34324 erythrocyte band 7 intergral membrane protein homolog unc-1 - Caenorhabditis elegans gb|AAC69044.1| (U55375) Erythrocyte band 7 intergral membrane protein [Caenorhabditis elegans]	75.7	55	3.00E-13
04190_HH	1	AB028619.1	AB028619 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:MQD17, complete sequence	42.1	96	0.22
04194_HH	1	AAC97963.1	(AF109907) hypothetical protein [Homo sapiens]	49.2	38	3.00E-05
04196_HH	1	AAD49861.1	AF166274_1 (AF166274) dynamin-related protein [Caenorhabditis elegans]	102	36	3.00E-21
04198_HH	1	A54521	40k egg antigen (clone 10F5) - fluke (Schistosoma mansoni)	42.6	22	0.003
04199_HH	1	AAF35425.1	(AC024090) Hypothetical protein C52E2.e [Caenorhabditis elegans]	34.8	30	0.61
04202_HH	1	Q60587	ECHB_RAT TRIFUNCTONAL ENZYME BETA SUBUNIT, MITOCHONDRIAL PRECURSOR (TP-BETA) [INCLUDES: 3-KETOACYL-COA THIOLASE (ACETYL-COA ACYLTRANSFERASE) (BETA-KETOTHIOLASE)] pir||B49681 long-chain-fatty-acid beta-oxidation multienzyme complex beta chain precursor, mitochondrial - rat dbj|BAA03940.1| (D16479) mitochondrial long-chain 3-ketoacyl-CoA thiolase beta-subunit [Rattus norvegicus]	111	76	9.00E-34
04205_HH	1	A27020	DIF-induced prestalk pDd63 protein precursor - slime mold (Dictyostelium discoideum) (fragments)	35.2	27	0.46
04210_HH	1	AAA93301.1	(U43331) HASI [Xiphophorus maculatus]	39.5	30	9.00E-10
04216_HH	1	S33814	kinesin light chain - sea urchin (Strongylocentrotus purpuratus) gb|AAA03058.1| (L10234) kinesin light chain isoform 2 [Strongylocentrotus purpuratus]	36.4	47	0.21
04218_HH	1	AF016666.1	CELB0281 Caenorhabditis elegans cosmid B0281	42.1	96	0.22
04219_HH	2	AAF70599.1	AF205066_1 (AF205066) ATP-gated ion channel receptor P2X8 [Gallus gallus]	109	37	1.00E-23
04227_HH	1	CAB77640.1	(AJ390500) ribonucleotide reductase large subunit [Candida albicans]	179	63	2.00E-44
04230_HH	1	AC024757.1	AC024757 Caenorhabditis elegans cosmid Y37E11AL, complete sequence	44.1	100	0.057
04231_HH	1	NP_009185.1	polynucleotide kinase 3'-phosphatase gb|AAD51135.1|AF126486_1 (AF126486) polynucleotide kinase-3'-phosphatase [Homo sapiens]	87	36	3.00E-19
04237_HH	1	NP_062028.1	caveolin 3 sp|P51638|CAV3_RAT CAVEOLIN-3 gb|AAC52377.1| (U31968) caveolin-3 [Rattus norvegicus]	82.3	37	2.00E-15
04238_HH	1	AAF49734.1	(AE003534) Mpcp gene product [alt 1] [Drosophila melanogaster] gb|AAF49735.1| (AE003534) Mpcp gene product [alt 2] [Drosophila melanogaster]	228	73	3.00E-59
04245_HH	1	P32161	YIIR_ECOLI HYPOTHETICAL 16.5 KD PROTEIN IN TPIA-FPR INTERGENIC REGION (O146) pir||S40864 hypothetical 16.5K protein (tpia-fpr intergenic region) - Escherichia coli gb|AAB03053.1| (L19201) ORF_o146 [Escherichia coli] gb|AAC76903.1| (AE000466) orf, hypothetical protein [Escherichia coli]	32.1	25	4
04246_HH	1	AAF54427.1	(AE003683) CG9489 gene product [alt 1] [Drosophila melanogaster]	88.9	46	3.00E-17
04253_HH	1	AAG01989.1	(AY007112) similar to Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA with GenBank Accession Number AF191298	40.2	30	0.01
04255_HH	1	AC009505.3	AC009505 Homo sapiens clone RP11-526D2, complete sequence	44.1	96	0.013
04260_HH	1	AC008109.6	AC008109 Homo sapiens chromosome 18, clone RP11-476K15, complete sequence	42.1	96	0.22

04261_HH	1	P55162	MEM2_DROME MEMBRANE-ASSOCIATED PROTEIN HEM-2 (DHEM-2) pir||S49208 transmembrane protein HEM-2 - fruit fly (Drosophila melanogaster) pir||S57832 transmembrane protein HEM-2 - fruit fly (Drosophila melanogaster) emb|CAA56332.1| (X80028) dhem2 [Drosophila melanogaster] gb|AAF51820.1| (AE003597) Hem gene product [Drosophila melanogaster]	99.1	36	3.00E-20
04263_HH	1	D75325	glutamine synthase - Deinococcus radiodurans (strain R1) gb|AAF11576.1|AE002039_6 (AE002039) glutamine synthase [Deinococcus radiodurans]	34	36	1
04265_HH	2	AAF73309.1	AF190635_1 (AF190635) ankyrin 2 [Drosophila melanogaster]	65.6	35	3.00E-10
04266_HH	1	AE003782.1	AE003782 Drosophila melanogaster genomic scaffold 142000013386030 section 2 of 3, complete sequence	46.1	100	0.014
04270_HH	1	NP_058522.1	RNA binding motif, single stranded interacting protein 1, isoform a	100	38	1.00E-20
04278_HH	1	CAA73264.2	(Y12732) sec1-like protein [Loligo pealei]	101	56	4.00E-21
04283_HH	1	P35506	KC1A_BOVIN CASEIN KINASE I, ALPHA ISOFORM (CKI-ALPHA) pir||A56406 casein kinase I (EC 2.7.1.-) alpha - bovine gb|AAA30451.1| (M76543) casein kinase I-alpha [Bos taurus] gb|AAB03992.1| (U59166) casein kinase 1 alpha [Oryctolagus cuniculus] gb|AAC35748.1| (AF042862) casein kinase 1 alpha isoform [Gallus gallus]	293	83	8.00E-79
04287_HH	3	P40829	GABT_MYCLE 4-AMINOBUTYRATE AMINOTRANSFERASE (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA TRANSAMINASE) (GLUTAMATE:SUCCINIC SEMIALDEHYDE TRANSAMINASE) (GABA AMINOTRANSFERASE) (GABA-AT) pir||S72743 4-aminobutyrate transaminase (EC 2.6.1.19) gabT - Mycobacterium leprae gb|AAA17107.1| (U00011) gabT; 4-aminobutyrate aminotransferase; B1177_F2_67 [Mycobacterium leprae] emb|CAA19078.1| (AL023591) 4-aminobutyrate aminotransferase [Mycobacterium leprae]	31.7	30	5.3
04288_HH	1	S58444	SUP35 protein - African clawed frog (fragment) gb|AAC42228.1| (L37045) SUP35 gene product [Xenopus laevis] prf||2118243A polypeptide chain releasing factor eRF3 [Xenopus laevis]	142	50	2.00E-33
04293_HH	1	AAD38595.1	AF145620_1 (AF145620) BcDNA.GH03922 [Drosophila melanogaster] gb|AAF51490.1| (AE003589) BcDNA:GH03922 gene product [Drosophila melanogaster]	38.7	28	0.041
04297_HH	1	BAA98062.1	(AB025605) contains similarity to mutator-like transposase~gene_id:F5H8.11 [Arabidopsis thaliana]	31.3	28	6.9
04300_HH	1	AAF23253.1	AC015985_11 (AC015985) putative adenosine kinase [Arabidopsis thaliana]	139	51	2.00E-32
04301_HH	1	P75062	Y040_MYCPN HYPOTHETICAL LIPOPROTEIN MG040 HOMOLOG PRECURSOR pir||S73428 probable lipoprotein D09_orf657 - Mycoplasma pneumoniae (strain ATCC 29342) gb|AAB95750.1| (AE000012) Mycoplasma pneumoniae, putative lipoprotein, MG040 homolog, from M. genitalium	31.7	26	4.8
04304_HH	1	P20678	CPH2_CHICK CYTOCHROME P450 2H2 (CYPIIH2) (P450 PCHP7) pir||A31418 cytochrome P450 2H2, hepatic - chicken gb|AAA48743.1| (M25469) cytochrome P450 [Gallus gallus]	108	37	3.00E-23
04307_HH	1	AAD32697.1	AF143846_1 (AF143846) putative nicotinic acetylcholine receptor alpha 7-1 subunit [Heliothis virescens]	94	42	9.00E-19
04308_HH	1	CAA05264.1	(AJ002234) polyprotein, cleavage products include viral coat protein and proteins with homology to an aspartic protease, reverse transcriptase and RNase H [banana streak virus]	32.5	30	3.1
04309_HH	2	NP_012685.1	Yjr151cp sp|P47179|YJ9P_YEAST HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR pir||S57180 probable membrane protein YJR151c - yeast (Saccharomyces cerevisiae) emb|CAA89684.1| (Z49651) ORF YJR151c [Saccharomyces cerevisiae]	36	23	0.27
04310_HH	1	FAFFAA	alpha-actinin - fruit fly (Drosophila melanogaster)	181	51	4.00E-45
04320_HH	3	JC6537	mda-9 protein - human gb|AAC52050.1| (AF006636) melanoma differentiation associated protein-9 [Homo sapiens]	61.7	40	5.00E-09
04323_HH	1	NP_057315.1	nemo-like kinase gb|AAD56013.1|AF180819_1 (AF180819) LAK1 protein [Homo sapiens] gb|AAF04857.1|AF197898_1 (AF197898) nemo-like kinase [Homo sapiens]	172	58	2.00E-42
04329_HH	1	O66605	LON_AQUAE ATP-DEPENDENT PROTEASE LA pir||A70322 endopeptidase La (EC 3.4.21.53) - Aquifex aeolicus gb|AAC06568.1| (AE000680) Lon protease [Aquifex aeolicus]	32.5	36	3.1
04330_HH	3	AAF49444.1	(AE003526) CG4169 gene product [Drosophila melanogaster]	55	27	5.00E-07
04333_HH	1	T23208	hypothetical protein K01H12.3 - Caenorhabditis elegans emb|CAA92473.1| (Z68218) Similarity to Drosophila DR-78 protein (PIR Acc. No. S32723) [Caenorhabditis elegans]	32.8	29	2.3
04336_HH	1	AAF47363.1	(AE003467) CG17135 gene product [Drosophila melanogaster]	37.9	31	0.07
04338_HH	1	I53498	CD40-associated protein - human pir||S68467 CD40 receptor-associated protein CAP-1 - human gb|AAA68195.1| (L38509) CD40-associated protein [Homo sapiens]	58.2	28	6.00E-08
04339_HH	1	C71874	hypothetical protein jhp0901 - Helicobacter pylori (strain J99) gb|AAD06484.1| (AE001519) putative [Helicobacter pylori J99]	53.5	33	1.00E-06
04350_HH	1	T01437	hypothetical protein R34001_1 - human gb|AAC27979.1| (AC004144) R34001_1 [Homo sapiens]	30.9	38	7.1
04353_HH	1	AAD17993.1	(AF106945) PRx IV [Rattus norvegicus]	223	71	1.00E-57
04358_HH	1	AE003775.1	AE003775 Drosophila melanogaster genomic scaffold 142000013386035 section 100 of 105, complete sequence	44.1	96	0.057
04361_HH	2	AAF62895.1	AF222689_3 (AF222689) protein arginine N-methyltransferase 1-variant 1 [Homo sapiens]	216	75	1.00E-55
04372_HH	1	P08089	M6_STRPY M PROTEIN, SEROTYPE 6 PRECURSOR pir||A26297 M6 protein - Streptococcus pyogenes gb|AAA26920.1| (M11338) M6 precursor peptide [Streptococcus pyogenes]	45.7	26	3.00E-04
04375_HH	1	I65769	smooth muscle myosin heavy chain isoform SMemb - human (fragment) gb|AAB28952.1| (S67247) smooth muscle myosin heavy chain isoform SMemb [human, umbilical cord, fetal aorta, Peptide Partial, 226 aa] [Homo sapiens]	52.7	30	2.00E-06
04382_HH	1	T08541	hypothetical protein F27B13.40 - Arabidopsis thaliana emb|CAB43655.1| (AL050352) putative protein [Arabidopsis thaliana] emb|CAB79738.1| (AL161575) putative protein [Arabidopsis thaliana]	30.9	34	9.1
04384_HH	1	CAA26090.1	(X02155) thyroglobulin [Bos taurus]	49.6	30	2.00E-05
04386_HH	1	NP_038795.2	casein kinase 1, epsilon dbj|BAA88107.2| (AB028736) casein kinase I epsilon [Mus musculus]	272	86	2.00E-72
04390_HH	1	AAF51695.1	(AE003594) AcCoAS gene product [alt 2] [Drosophila melanogaster]	104	51	1.00E-34
04400_HH	1	AC018752.4	AC018752 Homo sapiens chromosome 5 clone CTC-339F2, complete sequence	48.1	93	0.004
04406_HH	1	T26119	hypothetical protein W03C9.3 - Caenorhabditis elegans emb|CAA91357.1| (Z66516) similar to ras related protein~cDNA EST yk101c7.5 comes from this gene~cDNA EST yk101c7.3 comes from this gene~cDNA EST yk228a8.5 comes from this gene~cDNA EST yk241g4.5 comes from this gene~cDNA EST yk301h3.5 comes from this gene~cDNA EST yk	138	63	4.00E-32

04416_HH	1	NP_036265.1	coatomer protein complex, subunit gamma 2 gb|AAF14271.1|AF157833_1 (AF157833) nonclathrin coat protein gamma2-COP [Homo sapiens] gb|AAF19433.1|AF207598_1 (AF207598) coat protein gamma2-COP [Homo sapiens]	55.4	28	2.00E-09
04417_HH	1	T15892	hypothetical protein D2096.4 - Caenorhabditis elegans gb|AAA81490.1| (U40800) similar to thymidine diphosphoglucose 4,6-dehydratase [Caenorhabditis elegans]	183	52	7.00E-46
04419_HH	1	C31915	lantibiotic nisin biosynthesis protein nisB - Lactococcus lactis gb|AAA25190.1| (L16226) could encode enzyme catalyzing modification reactions [Lactococcus lactis]	35.2	25	0.46
04421_HH	1	AC007932.3	F11A17 Arabidopsis thaliana chromosome 1 BAC F11A17 sequence, complete sequence	42.1	100	0.22
04422_HH	1	Q10237	YD14_SCHPO HYPOTHETICAL 70.4 KD PROTEIN C4G9.04C IN CHROMOSOME I pir||T38863 hypothetical protein SPAC4G9.04c - fission yeast (Schizosaccharomyces pombe) emb|CAA93554.1| (Z69727) similar to yeast pre-mRNA cleavage and polyadenylation factor PCF11 [Schizosaccharomyces pombe]	35.6	31	0.31
04423_HH	1	AAC25810.1	(U80024) weak similarity to C. elegans olfactory receptor ODR-10 (GI:1235900) [Caenorhabditis elegans]	31.7	32	5.3
04425_HH	1	AAD02903.1	(AF002147) ATP synthase subunit 6 [Sarcodon imbricatus]	34	36	1
04426_HH	1	T23172	hypothetical protein K01C8.9 - Caenorhabditis elegans emb|CAA88860.1| (Z49068) similar to GTP-binding protein~cDNA EST EMBL:M89111 comes from this gene~cDNA EST yk2f7.3 comes from this gene~cDNA EST yk2f7.5 comes from this gene~cDNA EST yk63b3.5 comes from this gene~cDNA EST yk353b4.3 comes from this gene~cDNA EST yk353b>	88.2	35	5.00E-17
04428_HH	1	A55888	protein kinase RAC (EC 2.7.1.-) - fruit fly (Drosophila melanogaster) emb|CAA58499.2| (X83510) RAC protein kinase DRAC-PK85 [Drosophila melanogaster]	82.3	67	3.00E-15
04433_HH	1	P08036	RPOB_SAPOF DNA-DIRECTED RNA POLYMERASE BETA CHAIN pir||S00933 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - common soapwort chloroplast (fragment) emb|CAA30075.1| (X07026) RNA polymerase [Saponaria officinalis]	29.7	34	7.6
04435_HH	1	AAC95429.1	(AF039401) calcium-dependent chloride channel-1 [Homo sapiens]	71.4	32	6.00E-12
04438_HH	1	P81021	VGLN_CHICK VIGILIN pir||S23464 vigilin - chicken emb|CAA46387.1| (X65292) vigilin [Gallus gallus]	91.7	35	4.00E-18
04444_HH	1	AAF53440.1	(AE003646) BG:DS04929.3 gene product [Drosophila melanogaster]	82.3	31	3.00E-15
04446_HH	1	AAD38279.1	AC007789_5 (AC007789) putative CREB-binding protein [Oryza sativa]	31.3	31	6.9
04450_HH	1	Q24815	RACB_ENTHI RAS-RELATED PROTEIN RACB gb|AAC47297.1| (U29721) p21racB [Entamoeba histolytica]	101	46	5.00E-21
04451_HH	2	CAB39066.2	(AL034559) putative protein kinase [Plasmodium falciparum]	34.4	25	0.8
04455_HH	1	NP_006586.1	API5-like 1 emb|CAA75867.1| (Y15906) XAGL protein [Homo sapiens]	43	28	0.002
04456_HH	1	AE000559.1	AE000559 Helicobacter pylori 26695 section 37 of 134 of the complete genome	36.2	100	9.2
04457_HH	1	T15098	hypothetical protein T22B11.5 - Caenorhabditis elegans gb|AAB94185.1| (AF039040) Similar to 2-oxoglutarate dehydrogenase; coded for by C. elegans cDNA yk119d6.3; coded for by C. elegans cDNA yk66c8.3; coded for by C. elegans cDNA yk153a9.3; coded for by C. elegans cDNA yk154a12.3; coded for by C. elegans cDNA yk73d8.5; c>	264	73	4.00E-70
04462_HH	1	P47816	RP8_RAT ZINC FINGER PROTEIN RP-8 pir|A41257 apoptosis protein RP-8 - rat (fragment) gb|AAA42067.1| (M80601) zinc finger protein [Rattus norvegicus]	49.2	25	3.00E-05
04463_HH	1	AAF06330.1	AF192348_1 (AF192348) vitamin D response element binding protein [Saguinus oedipus]	157	45	9.00E-38
04464_HH	1	NP_004131.1	lethal giant larvae (Drosophila) homolog 1 pir||S54142 hugl protein - human pir||I38171 hugl protein - human emb|CAA60130.1| (X86371) homologue to Drosophila tumour supressor gene [Homo sapiens]	31.7	41	4.7
04472_HH	1	AAF53994.1	(AE003670) CG8665 gene product [Drosophila melanogaster]	116	43	2.00E-25
04481_HH	1	Z99110.1	BSUB0007 Bacillus subtilis complete genome (section 7 of 21): from 1194391 to 1411140	44.1	100	0.029
04484_HH	1	BAA84767.1	(AB022692) TAF-Ibeta2 [Xenopus laevis]	46.5	45	2.00E-04
04485_HH	2	AL049732.11	HSDA14C6 Human DNA sequence from clone RP6-14C6 on chromosome Xp11.21-11.23. Contains part of a putative gene for a novel protein similar to ITIH3 (pre-alpha (globulin) inhibitor, H3 polypeptide), the gene KIAA1114 for a protein similar to BCG1 and melanoma ass>	40.1	100	0.88
04487_HH	1	AAF63957.1	(AF170072) CALNUC [Spodoptera frugiperda]	92.1	34	3.00E-18
04489_HH	1	AAF46166.1	(AE003437) CG3918 gene product [Drosophila melanogaster]	45.3	24	4.00E-04
04491_HH	1	AL031676.3	HS753D4 Human DNA sequence from clone RP4-753D4 on chromosome 20q12, complete sequence [Homo sapiens]	40.1	95	0.88
04492_HH	1	AAF57486.1	(AE003792) CG9090 gene product [Drosophila melanogaster]	253	77	1.00E-66
04499_HH	4	AAF36068.1	(AC024213) Hypothetical protein B0207.5 [Caenorhabditis elegans]	34.8	29	0.55
04509_HH	1	NC_000932.1	Arabidopsis thaliana chloroplast, complete genome	40.1	100	0.15
04510_HH	1	AE003758.1	AE003758 Drosophila melanogaster genomic scaffold 142000013386035 section 83 of 105, complete sequence	38.2	100	3.5
04511_HH	1	T20993	hypothetical protein F15G9.4b - Caenorhabditis elegans gb|AAC26792.1| (AF074901) hemicentin precursor [Caenorhabditis elegans] emb|CAA87336.1| (Z47068) similar to IG (immunoglobulin) superfamily (47 domains)~cDNA EST yk556f1.5 comes from this gene [Caenorhabditis elegans] emb|CAA87345.1| (Z47070) similar to IG (immunoglobulin) superfamily (47 domains)~cDNA EST yk556f1.5 comes from this gene [Caenorhabditis elegans]	39.9	24	0.018
04514_HH	2	NP_034946.1	microrchidia gb|AAD43003.1|AF084945_1 (AF084945) microrchidia [Mus musculus]	99.8	54	2.00E-20
04515_HH	1	S72286	ribosomal protein S4 - Plasmodium falciparum plastid emb|CAA64576.1| (X95276) rps4 [Plasmodium falciparum]	31.3	30	6.9
04517_HH	1	NP_010575.1	Rtt103p pir||S70119 hypothetical protein YDR289c - yeast (Saccharomyces cerevisiae) gb|AAB64467.1| (U51031) Ydr289cp [Saccharomyces cerevisiae]	32.5	25	3
04520_HH	1	AE003630.1	AE003630 Drosophila melanogaster genomic scaffold 142000013386055 section 23 of 63, complete sequence	40.1	100	0.88
04521_HH	1	AAB40077.1	(U60498) actin [Glycine max]	118	58	5.00E-26
04524_HH	1	S63595	acyl-coenzyme A-binding protein - chicken gb|AAB36333.1| acyl-coenzyme A binding protein, ACBP [chickens, Peptide, 86 aa]	106	67	8.00E-23
04525_HH	1	AAF53253.1	(AE003639) CG5458 gene product [Drosophila melanogaster]	128	52	3.00E-29
04527_HH	1	NP_058970.1	glycerol-3-phosphate acyltransferase, mitochondrial sp|P97564|PLSB_RAT GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT) gb|AAB71605.1| (AF021348) sn-glycerol-3-phosphate acyltransferase [Rattus norvegicus]	33.6	20	1.4
04528_HH	1	P81004	POR2_XENLA VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2 (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN)	98.7	34	4.00E-20

04532_HH	1	NP_059074.1	protocadherin 14 pir||T31066 vascular cadherin-2 - mouse emb|CAA69965.1| (Y08715) vascular cadherin-2 [Mus musculus]	86.2	33	2.00E-16
04533_HH	1	AAF72203.1	AF267125_1 (AF267125) potassium transporter Trk1p [Candida albicans]	31.7	27	5.3
04534_HH	1	P98133	FBN1_BOVIN FIBRILLIN 1 PRECURSOR (MP340) pir||A55567 fibrillin I - bovine gb|AAA74122.1| (L28748) putative [Bos taurus]	106	37	2.00E-22
04536_HH	1	AAF55412.1	(AE003717) CG5419 gene product [Drosophila melanogaster]	85	31	5.00E-16
04537_HH	1	AAD28358.1	AF079967_2 (AF079967) MURF1 [Phytomonas serpens]	34.4	37	0.8
04538_HH	3	T41244	SEC14 protein homolog SPCC23B6.04c - fission yeast (Schizosaccharomyces pombe) emb|CAB51563.1| (AL109608) conserved CRAL/TRIO domain protein; SEC14 cytosolic factor family [Schizosaccharomyces pombe]	33.2	24	0.001
04540_HH	1	CAB39004.1	(AL034558) predicted using hexExon; MAL3P2.17 (PFC0240c), Hypothetical protein, len: 830 aa [Plasmodium falciparum]	44.9	28	5.00E-04
04541_HH	1	Q00383	YCF1_EPIVI HYPOTHETICAL 208 KD PROTEIN (ORF 1738) pir||S20614 conserved hypothetical protein 1738 - beechdrops plastid emb|CAA43644.1| (X61368) ORF1738 [Epifagus virginiana] gb|AAA65870.1| (M81884) ORF1738 [Epifagus virginiana]	35.6	23	0.35
04543_HH	2	CAB82750.1	(AL162351) putative protein [Arabidopsis thaliana]	41.8	25	2.00E-07
04544_HH	1	A28029	phosphoprotein phosphatase (EC 3.1.3.16) 2A catalytic chain - bovine gb|AAA30695.1| (M16968) protein phosphatase type 2A catalytic subunit [Bos taurus]	338	92	2.00E-92
04548_HH	1	AJ003128.1	MMAJ3128 Mus musculus hap1 gene homologue	40.1	95	0.59
04549_HH	1	BAB01760.1	(AP000603) MAP3K epsilon protein kinase [Arabidopsis thaliana]	37.5	40	0.092
04551_HH	2	AAD41591.1	(AF071011) myosin light chain [Schistosoma mansoni]	181	69	5.00E-45
04552_HH	1	AF172087.1	AF172087 Mus musculus major urinary protein group 1 gene, partial sequence	46.1	100	0.002
04553_HH	1	O77410	IF36_DROME PROBABLE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6 (EIF-3 P48) gb|AAC62307.1| (U89162) similar to mouse mammary tumor associated gene Int-6 product [Drosophila melanogaster] gb|AAD27850.1|AF132551_1 (AF132551) BcDNA.GM01233 [Drosophila melanogaster] gb|AAF49412.1| (AE003526) Int6 gene product [Drosophila melanogaster]	69.9	51	2.00E-19
04556_HH	3	C71622	hypothetical protein PFB0145c - malaria parasite (Plasmodium falciparum) gb|AAC71819.1| (AE001375) hypothetical protein [Plasmodium falciparum]	60.1	26	1.00E-08
04562_HH	1	T16511	hypothetical protein F59A6.1 - Caenorhabditis elegans gb|AAA83458.1| (U41994) coded for by C. elegans cDNA CEESN53F; similar to protein kinases including CDC15 in yeast [Caenorhabditis elegans]	110	40	1.00E-23
04566_HH	1	T18473	hypothetical protein C0435w - Plasmodium falciparum emb|CAA15616.1| (AL008970) hypothetical protein, PFC0435w [Plasmodium falciparum]	32.1	26	4
04567_HH	1	P54149	PMSR_BOVIN PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O) REDUCTASE) gb|AAC48539.1| (U37150) peptide methionine sulfoxide reductase [Bos taurus]	180	52	9.00E-45
04570_HH	1	NP_000178.1	homogentisate 1,2-dioxygenase; homogentisate oxidase; homogentisicase sp|Q93099|HGD_HUMAN HOMOGENTISATE 1,2-DIOXYGENASE (HOMOGENTISICASE) (HOMOGENTISATE OXYGENASE) (HOMOGENTISIC ACID OXIDASE) emb|CAA99340.1| (Z75048) homogentisate 1,2-dioxygenase [Homo sapiens] gb|AAB16836.1| (U63008) homogentisate dioxygenase [Homo sapiens] gb|AAC51650.1| (AF000573) homogentisate 1,2-dioxygenase [Homo sapiens] gb|AAC02698.1| (AF045167) homogentisate 1,2-dioxygenase; HGO [Homo sapiens]	185	52	3.00E-46
04571_HH	1	Q00083	APSA_EMENI ANUCLEATE PRIMARY STERIGMATA PROTEIN pir||A56508 anucleate primary sterigmata A (apsA) protein - Emericella nidulans emb|CAA57733.1| (X82289) anucleate primary sterigmata coiled-coil protein [Aspergillus nidulellus]	34	33	1
04575_HH	1	AL358214.10	AL358214 Human DNA sequence from clone RP11-675O23 on chromosome 10, complete sequence [Homo sapiens]	44.1	100	0.057
04580_HH	1	T21697	hypothetical protein F40E10.6 - Caenorhabditis elegans emb|CAA93657.1| (Z69790) cDNA EST yk376g11.5 comes from this gene~cDNA EST yk442f1.5 comes from this gene~cDNA EST yk455h10.5 comes from this gene~cDNA EST yk457h6.5 comes from this gene~cDNA EST yk464d8.5 comes from this gene~cDNA EST yk552f11.3 comes from this gene~> emb|CAA93669.1| (Z69792) cDNA EST yk376g11.5 comes from this gene~cDNA EST yk442f1.5 comes from this gene~cDNA EST yk455h10.5 comes from this gene~cDNA EST yk457h6.5 comes from this gene~cDNA EST yk464d8.5 comes from this gene~cDNA EST yk552f11.3 comes from this gene~>	39.9	53	0.018
04581_HH	1	AL162718.15	AL162718 Human DNA sequence from clone RP11-274H24 on chromosome 6, complete sequence [Homo sapiens]	42.1	100	0.22
04582_HH	2	P31253	UBAX_MOUSE UBIQUITIN-ACTIVATING ENZYME E1 X pir||I48756 gene Sbx protein - mouse (fragment) emb|CAA44465.1| (X62580) Sbx [Mus musculus] prf||1802391A Sby spermatogenic gene [Mus musculus]	137	46	7.00E-32
04586_HH	2	BAA91613.1	(AK001305) unnamed protein product [Homo sapiens]	69.5	24	2.00E-11
04587_HH	1	AAB40928.2	(U83085) cell division cycle protein 48 [Dictyostelium discoideum]	40.2	45	0.014
04589_HH	1	O77676	KGPA_RABIT CGMP-DEPENDENT PROTEIN KINASE 1, ALPHA ISOZYME (CGK 1 ALPHA) (CGKI-ALPHA) gb|AAC31192.1| (AF076969) cGMP-dependent protein kinase type 1 alpha [Oryctolagus cuniculus]	221	68	4.00E-57
04592_HH	1	BAA74870.1	(AB020654) KIAA0847 protein [Homo sapiens]	32.1	37	4.2
04593_HH	2	BAA09924.1	(D63874) HMG-1 [Homo sapiens]	122	37	2.00E-27
04596_HH	1	A47299	ror-related receptor RTK - Pacific electric ray gb|AAA49285.1| (L11311) receptor tyrosine kinase [Torpedo californica]	51.2	30	7.00E-06
04598_HH	1	O51750	MVIN_BORBU VIRULENCE FACTOR MVIN HOMOLOG pir||A70201 virulence factor mviN protein homolog precursor - Lyme disease spirochete gb|AAC67146.1| (AE001179) virulence factor mviN protein (mviN) (SP:P37169) [Borrelia burgdorferi]	32.5	37	3.1
04602_HH	1	P21613	KINH_LOLPE KINESIN HEAVY CHAIN pir||A35075 kinesin heavy chain - longfin squid gb|AAA29990.1| (J05258) kinesin heavy chain [Loligo pealei]	144	45	4.00E-34
04603_HH	1	AAC98027.1	(AC005990) Contains repeated region with similarity to gb|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb|Z34165 and gb|Z18788 come from this gene	34.4	31	0.8
04606_HH	1	AAF75067.1	AC007583_3 (AC007583) Similar to mitogen-activated protein kinase homolog NTF6 from tobacco gi|2499616. It contains an eukaryotic protein kinase domain PF|00069. [Arabidopsis thaliana]	101	47	4.00E-21
04615_HH	1	AF269125.1	AF269125 Neopsylla soboi individual 2 16S ribosomal RNA gene, partial sequence	46.1	93	0.014
04618_HH	1	Z92832.1	CEF31D4 Caenorhabditis elegans cosmid F31D4, complete sequence	42.1	100	0.096
04620_HH	1	AAC37263.1	(L37100) NF-YA subunit [Schistosoma mansoni]	79.2	31	3.00E-14

04621_HH	1	T02367	hypothetical protein T8F5.22 - Arabidopsis thaliana gb|AAC27151.1| (AC004512) Similar to gb|U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb|T42908, gb|AA586170 and gb|AA395125 come from this gene. [Arabidopsis thaliana]	30.9	32	9.1
04622_HH	1	AAF55427.1	(AE003718) CG5823 gene product [Drosophila melanogaster]	220	66	9.00E-57
04624_HH	1	I79272	traE protein - Escherichia coli plasmid pKM101 pir||S61379 traE protein - Escherichia coli plasmid pKM101 gb|AAA86457.1| (U09868) traE gene product [Escherichia coli]	33.2	23	1.8
04625_HH	1	T20908	hypothetical protein F14F7.3 - Caenorhabditis elegans emb|CAB04113.1| (Z81503) predicted using Genefinder~similar to cytochrome P450 [Caenorhabditis elegans]	104	43	5.00E-22
04628_HH	1	P28799	GRN_HUMAN GRANULINS PRECURSOR (ACROGRANIN)	64.8	46	5.00E-10
04630_HH	1	NP_057591.1	CDC2-related protein kinase 7 gb|AAF36401.1|AF227198_1 (AF227198) CrkRS [Homo sapiens]	45.7	50	3.00E-04
04635_HH	1	NP_000889.1	monoamine oxidase B sp|P27338|AOFB_HUMAN AMINE OXIDASE [FLAVIN-CONTAINING] B (MONOAMINE OXIDASE) (MAO-B) pir||JH0817 amine oxidase (flavin-containing) (EC 1.4.3.4) B - human gb|AAA59550.1| (M69177) monoamine oxidase B [Homo sapiens] gb|AAA59551.1| (M69135) monoamine oxidase B [Homo sapiens] gb|AAB27229.1| (S62734) monoamine oxidase B, MAO B [human, platelet, Peptide Partial, 520 aa] [Homo sapiens]	46.5	25	2.00E-04
04644_HH	1	BAA78407.1	(AB021122) translocase of inner mitochondrial membrane [Mus musculus]	53.9	24	1.00E-06
04645_HH	1	AAF28888.1	AF123303_1 (AF123303) calcium-binding transporter [Homo sapiens]	107	40	7.00E-23
04648_HH	1	T30272	hypothetical protein - sea urchin (Strongylocentrotus purpuratus) (fragment) gb|AAA85106.1| (U17377) cortical granule protein with LDL-receptor-like repeats [Strongylocentrotus purpuratus]	32.8	28	2.3
04649_HH	1	CAB64652.1	(AJ251802) GRAAL protein [Drosophila melanogaster]	113	35	1.00E-24
04652_HH	1	CAA20374.2	(AL031307) hypothetical transmembrane protein [Schizosaccharomyces pombe]	32.8	26	2.3
04653_HH	1	AAA31881.1	(L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]	37.5	22	0.092
04655_HH	2	O15127	SCA2_HUMAN SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2	93.6	32	1.00E-18
04656_HH	1	CAA74977.1	(Y14633) D4B Dopamine receptor [Cyprinus carpio]	33.6	30	1.4
04657_HH	1	NP_036260.1	chloride channel, calcium activated, family member 4 gb|AAD48398.1|AF127035_1 (AF127035) calcium-activated chloride channel protein 2 [Homo sapiens]	46.5	23	2.00E-04
04659_HH	1	NP_060762.1	hypothetical protein FLJ10989 dbj|BAA91941.1| (AK001851) unnamed protein product [Homo sapiens]	106	46	1.00E-22
04660_HH	1	P53619	COPD_BOVIN COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) emb|CAA63941.1| (X94265) coat protein delta-cop [Bos primigenius]	142	75	1.00E-57
04662_HH	1	NP_037152.1	rab geranylgeranyl transferase componenet, subunit beta sp|Q08603|PGTB_RAT GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) pir||B45977 Rab geranylgeranyl transferase component B beta subunit - rat pdb|1DCE|B Chain B, Crystal Structure Of Rab Geranylgeranyltransferase From Rat Brain pdb|1DCE|D Chain D, Crystal Structure Of Rab Geranylgeranyltransferase From Rat Brain gb|AAA41999.1| (L10416) rab geranylgeranyl transferase beta subunit [Rattus norvegicus] gb|AAB27019.1| (S62097) Rab geranylgeranyl transferase component B beta subunit, Rab GG transferase component B beta subunit [rats, brain, Peptide, 331 aa] [Rattus sp.]	226	64	1.00E-58
04663_HH	1	AAD27851.1	AF132552_1 (AF132552) BcDNA.GM01838 [Drosophila melanogaster] gb|AAF56391.1| (AE003750) OstStt3 gene product [Drosophila melanogaster]	234	76	4.00E-61
04664_HH	1	AAF48097.1	(AE003487) CG1578 gene product [Drosophila melanogaster]	156	51	2.00E-37
04677_HH	1	BAB08640.1	(AB009048) gene_id:K15E6.5~unknown protein [Arabidopsis thaliana]	75.7	43	1.00E-13
04680_HH	2	AAB99663.1	(U67604) chromosome segretation protein (smc1) [Methanococcus jannaschii]	41	29	0.007
04681_HH	1	BAA76790.1	(AB023163) KIAA0946 protein [Homo sapiens]	138	48	5.00E-32
04684_HH	1	T28810	hypothetical protein C54D1.4 - Caenorhabditis elegans gb|AAC48151.1| (U46673) Similar to aldehyde dehydrogenase [Caenorhabditis elegans]	145	45	3.00E-34
04687_HH	1	Q07598	NLTP_CHICK NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (NSL-TP) (STEROL CARRIER PROTEIN 2) (SCP-2) (STEROL CARRIER PROTEIN X) (SCP-X) (SCPX) pir||S34744 sterol carrier protein - chicken gb|AAA02488.1| (L09231) sterol carrier protein-2 [Gallus gallus]	181	55	4.00E-45
04694_HH	1	NP_001164.1	Rho GTPase activating protein 5 gb|AAA95963.1| (U17032) p190-B [Homo sapiens]	33.6	28	1.4
04697_HH	1	AAD01506.1	(AF012470) cytochrome b [Presbytis entellus]	170	50	1.00E-41
04698_HH	1	AAF52908.1	(AE003628) CG5384 gene product [Drosophila melanogaster]	166	54	2.00E-40
04699_HH	1	C71610	probable membrane associated protein PFB0615c - malaria parasite (Plasmodium falciparum) gb|AAC71912.1| (AE001406) predicted membrane associated protein [Plasmodium falciparum]	32.5	33	3.1
04700_HH	4	AAF47305.1	(AE003465) RpL19 gene product [Drosophila melanogaster]	239	69	2.00E-62
04703_HH	1	AAF46021.1	(AE003433) CG15930 gene product [Drosophila melanogaster]	41.8	23	0.005
04708_HH	3	A55035	cysteine-rich protein CRP1 - earthworm (Enchytraeus buchholzi) emb|CAA55899.1| (X79344) cysteine-rich-protein [Enchytraeus buchholzi]	43.4	39	3.00E-04
04712_HH	1	AAB95047.1	(AF040655) T24E12.10 gene product [Caenorhabditis elegans]	37.1	32	0.12
04715_HH	1	AAD17488.1	(AF051318) 28 kDa glutathione S-transferase; 28GST [Clonorchis sinensis]	36	29	0.27
04716_HH	1	BAB08083.1	(AB027295) ORF3, contains 2 coiled coil regions, putative; weakly homologous to Sccharomyces cerevisiae myosin-like protein (L01992) [Physarum polycephalum]	35.2	27	0.24
04718_HH	1	AE003733.1	AE003733 Drosophila melanogaster genomic scaffold 142000013386035 section 58 of 105, complete sequence	42.1	90	0.22
04721_HH	1	CAA18106.1	(AL022140) putative protein [Arabidopsis thaliana] emb|CAB79158.1| (AL161556) putative protein [Arabidopsis thaliana]	31.7	32	5.3
04723_HH	1	A71623	probable secreted protein PFB0115w - malaria parasite (Plasmodium falciparum) gb|AAC71813.1| (AE001373) predicted secreted protein [Plasmodium falciparum]	36	23	0.27
04728_HH	4	AAA88022.1	(L54057) deduced protein product shows significant homology to coactosin from Dictyostelium discoideum [Homo sapiens]	115	48	2.00E-25
04731_HH	1	NP_056232.1	DKFZP434I114 protein pir||T12538 hypothetical protein DKFZp434I114.1 - human emb|CAB45745.1| (AL080154) hypothetical protein [Homo sapiens]	40.6	26	0.011
04733_HH	2	AAF52107.1	(AE003605) Karybeta3 gene product [Drosophila melanogaster]	99.5	36	2.00E-20
04734_HH	1	AAF90137.1	AF274011_1 (AF274011) tetraspanin 29Fa [Drosophila melanogaster]	40.2	34	3.00E-06
04735_HH	1	AAF79711.1	AC020889_19 (AC020889) T1N15.19 [Arabidopsis thaliana]	36.4	39	0.21
04736_HH	1	BAA78268.1	(AB021506) 69.8% identical to U47 gene of strain U1102 of HHV-6 [Human herpesvirus 6]	33.6	34	1.4

04739_HH	1	AAB94785.1	(AC003972) pNORF1 [Homo sapiens] gb|AAC26788.1| (AF074016) nonsense-mediated mRNA decay trans-acting factor [Homo sapiens]	280	77	8.00E-75
04740_HH	1	AC008269.3	AC008269 Homo sapiens clone RP11-95H11, complete sequence	40.1	100	0.29
04741_HH	1	AL121781.38	HSJ1164C1 Human DNA sequence from clone RP5-1164C1 on chromosome 20. Contains (part of) two putative novel genes, ESTs, STSs and GSSs, complete sequence [Homo sapiens]	44.1	93	0.057
04746_HH	1	NP_010010.1	Ycr087wp sp|P25652|YCX7_YEAST VERY HYPOTHETICAL 19.8 KD PROTEIN IN ABP1 5'REGION pir||S19502 hypothetical protein YCR087w - yeast (Saccharomyces cerevisiae) emb|CAA42262.1| (X59720) YCR087w, len:171 [Saccharomyces cerevisiae]	34	25	0.34
04747_HH	1	AAC52262.1	(U35371) neural cell adhesion protein BIG-2 precursor [Rattus norvegicus]	62.8	32	2.00E-09
04748_HH	1	NP_010571.1	synaptonemal complex protein; Zip1p sp|P31111|ZIP1_YEAST SYNAPTONEMAL COMPLEX PROTEIN ZIP1 pir||S70115 ZIP1 protein - yeast (Saccharomyces cerevisiae) gb|AAB64474.1| (U51031) Zip1p: Synaptonemal complex protein (Swiss Prot. accession number P31111). [Saccharomyces cerevisiae]	31.7	24	5.3
04749_HH	1	CAB39005.1	(AL034558) predicted using hexExon; MAL3P2.18 (PFC0245c), Hypothetical protein, len: 3934 aa [Plasmodium falciparum]	36	27	0.27
04751_HH	1	E65008	hypothetical protein b2352 - Escherichia coli (strain K-12) gb|AAC75411.1| (AE000323) putative ligase [Escherichia coli]	30.9	45	9.1
04754_HH	1	BAA95054.1	(AB041570) unnamed protein product [Mus musculus]	213	69	8.00E-55
04756_HH	2	NP_057062.1	putative protein-tyrosine kinase gb|AAD29632.1|AF116826_1 (AF116826) putative protein-tyrosine kinase [Homo sapiens]	62.1	32	4.00E-09
04758_HH	1	Q22918	IF5_CAEEL EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) pir||T34401 hypothetical protein C37C3.2 - Caenorhabditis elegans gb|AAC25859.1| (U64857) C37C3.2 gene product [Caenorhabditis elegans]	62.8	64	3.00E-21
04759_HH	1	AAC83232.1	(AF070674) inhibitor of apoptosis protein-1 [Homo sapiens]	59.3	37	2.00E-08
04760_HH	2	AAF55156.1	(AE003708) Oscp gene product [Drosophila melanogaster]	129	37	2.00E-29
04762_HH	2	BAA81907.1	(AB029334) HrPET-1 [Halocynthia roretzi]	100	32	9.00E-21
04764_HH	2	AAB58556.3	(U85963) asparagine-rich protein [Plasmodium falciparum]	36	25	0.25
04765_HH	1	No Match				
04766_HH	2	E71606	hypothetical protein PFB0765w - malaria parasite (Plasmodium falciparum) gb|AAC71942.1| (AE001417) hypothetical protein [Plasmodium falciparum]	34.4	25	0.8
04767_HH	1	S20250	splicing factor U2AF large chain - human prf||1805352A splicing factor U2AF:SUBUNIT=large [Homo sapiens]	213	63	7.00E-55
04768_HH	1	NP_060673.1	hypothetical protein FLJ10748 dbj|BAA91787.1| (AK001610) unnamed protein product [Homo sapiens]	57	30	8.00E-09
04769_HH	2	CAB39009.1	(AL034558) predicted using hexExon; MAL3P2.22 (PFC0265c), Hypothetical protein, len: 637 aa [Plasmodium falciparum]	41.4	24	0.006
04779_HH	1	BAA92542.1	(AB037725) KIAA1304 protein [Homo sapiens]	97.5	36	8.00E-20
04785_HH	1	NP_062237.1	vesicle transport-related gb|AAC52636.1| (U57687) rsly1p [Rattus norvegicus] dbj|BAA24276.1| (D79221) vesicle transport-related protein (RA410) [Rattus norvegicus]	165	48	3.00E-40
04787_HH	1	AAA80624.1	(U23125) envelope glycoprotein [Human immunodeficiency virus type 1]	32.8	47	2.3
04789_HH	1	NP_006351.1	dendritic cell protein gb|AAC17108.1| (AF064603) GA17 protein [Homo sapiens]	52.7	26	2.00E-06
04791_HH	3	H70170	hypothetical protein BB0569 - Lyme disease spirochete gb|AAC66937.1| (AE001158) B. burgdorferi predicted coding region BB0569 [Borrelia burgdorferi]	45.3	25	4.00E-04
04794_HH	1	T42215	zonadhesin - mouse gb|AAC26680.1| (U97068) zonadhesin [Mus musculus]	37.1	25	0.12
04796_HH	1	Z50859.1	CET26C5 Caenorhabditis elegans cosmid T26C5, complete sequence	44.1	100	0.057
04798_HH	2	P47809	MPK4_MOUSE DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 4 (MAP KINASE KINASE 4) (MAPKK 4) (MAPK/ERK KINASE 4) (JNK ACTIVATING KINASE 1) (C-JUN N-TERMINAL KINASE KINASE 1) (JNK KINASE 1) (JNKK 1) (SAPK/ERK KINASE 1) (SEK1) gb|AAB81554.1| (U18310) SEK1 [Mus musculus]	191	70	3.00E-48
04799_HH	1	AAF45892.1	(AE003428) BcDNA:GH07910 gene product [alt 1] [Drosophila melanogaster]	180	61	9.00E-45
04800_HH	1	Q92796	SP02_HUMAN PRESYNAPTIC PROTEIN SAP102 (SYNAPSE-ASSOCIATED PROTEIN 102) (NEUROENDOCRINE-DLG) (NE-DLG) gb|AAB61453.1| (U49089) neuroendocrine-dlg [Homo sapiens]	61.3	41	6.00E-09
04808_HH	1	P30532	ACH5_HUMAN NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-5 CHAIN PRECURSOR emb|CAA69696.1| (Y08419) nicotinic acetylcholine receptor alpha5 subunit precursor [Homo sapiens]	123	42	9.00E-28
04815_HH	1	AAF53649.1	(AE003657) CG5758 gene product [alt 1] [Drosophila melanogaster] gb|AAF53650.1| (AE003657) CG5758 gene product [alt 2] [Drosophila melanogaster]	34	29	1
04816_HH	1	AL136294.3	CNS01DVY Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC C-2171B16 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete sequence	44.1	100	0.057
04825_HH	2	BAA99394.1	(AB035900) vacuolar calcium binding protein [Raphanus sativus]	36.4	31	0.19
04829_HH	2	AC004485.1	AC004485 Homo sapiens BAC clone CTB-118E13 from 7p15-p21, complete sequence	50.1	100	0.001
04833_HH	1	AAD09227.1	(U80927) unknown [Dictyostelium discoideum]	33.2	33	1.8
04834_HH	1	P35574	GDE_RABIT GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] pir||S38758 amylo-1,6-glucosidase (EC 3.2.1.33) / 4-alpha-glucancotransferase (EC 2.4.1.25) - rabbit gb|AAA16364.1| (L10605) amylo-1, 6-glucosidase/4-alpha-glucancotransferase [Oryctolagus cuniculus]	174	49	5.00E-43
04839_HH	1	AE003502.1	AE003502 Drosophila melanogaster genomic scaffold 142000013386053 section 19 of 30, complete sequence	46.1	100	0.014
04841_HH	1	T22523	hypothetical protein F52H3.7 - Caenorhabditis elegans emb|CAA91327.1| (Z66512) similar to galactoside-binding lectin~cDNA EST EMBL:M89116 comes from this gene~cDNA EST EMBL:M89121 comes from this gene~cDNA EST yk6f5.3 comes from this gene~cDNA EST yk6a5.3 comes from this gene~cDNA EST yk6a5.5 comes from this gene~cDNA ES	31.3	29	6.9
04843_HH	1	BAA88243.1	(AB035670) Rab4 protein [Drosophila melanogaster] gb|AAF57831.1| (AE003802) Rab4 gene product [Drosophila melanogaster]	175	70	7.00E-47

04854_HH	3	NP_009209.1	GABA(A) receptor-associated protein ref|NP_062723.1| gamma-aminobutyric acid reseptor associated protein gb|AAD02337.1| (AF044671) MM46 [Homo sapiens] gb|AAD32455.1|AF067171_1 (AF067171) ganglioside expression factor 2 homolog [Homo sapiens] gb|AAD47641.1|AF161586_1 (AF161586) GABA-A receptor-associated protein [Homo sapiens] gb|AAD47642.1|AF161587_1 (AF161587) GABA-A receptor-associated protein [Mus musculus] gb|AAD47643.1|AF161588_1 (AF161588) GABA-A receptor-associated protein [Rattus norvegicus] gb|AAG09694.1|AF183425_1 (AF183425) HT004 protein [Homo sapiens]	176	88	3.00E-46
04855_HH	1	AAF51080.1	(AE003579) CG10017 gene product [Drosophila melanogaster]	31.3	54	6.9
04860_HH	1	CAA21829.1	(AL033125) 1-evidence=predicted by content~1-method=genefinder;084~1-method_score=54.97~1- evidence_end~2-evidence=predicted by match~2-match_accession=SWISS-PROT:Q92993~2- match_description=60 KD TAT INTERACTIVE PROTEIN.~2-match_species=HOMO SAPIENS (HU> gb|AAF45923.1| (AE003430) EG:EG0007.7 gene product [Drosophila melanogaster]	240	72	7.00E-63
04862_HH	1	NP_062692.1	ADP-ribosylation factor-like protein 3 sp|Q9WUL7|ARL3_MOUSE ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 gb|AAD33067.1|AF143241_1 (AF143241) ADP-ribosylation factor-like protein 3 [Mus musculus]	240	78	6.00E-63
04863_HH	1	CAA58680.1	(X83707) protein kinase [Plasmodium falciparum]	34	21	0.92
04865_HH	1	AC006997.3	AC006997 Homo sapiens BAC clone RP11-452K21 from 7q31.1-q31.2, complete sequence	42.1	100	0.22
04869_HH	1	NP_034952.1	N-methylpurine-DNA glycosylase sp|Q04841|3MG_MOUSE DNA-3-METHYLADENINE GLYCOSYLASE (3-METHYLADENINE DNA GLYCOSIDASE) (ADPG) (3-ALKYLADENINE DNA GLYCOSYLASE) (N-METHYLPURINE-DNA GLYCOSIRASE) pir||A49003 N-methylpurine-DNA glycosirase (MPG) - mouse gb|AAA19487.1| (U10420) methyl purine glycosylase [Mus musculus] emb|CAA52615.1| (X74509) N-methylpurine-DNA glycosirase (MPG) [Mus musculus]	109	39	1.00E-23
04872_HH	1	NP_055519.1	KIAA0562 gene product pir||T00334 hypothetical protein KIAA0562 - human dbj|BAA25488.1| (AB011134) KIAA0562 protein [Homo sapiens]	101	32	5.00E-21
04874_HH	1	AAF52452.1	(AE003615) CG10354 gene product [Drosophila melanogaster]	32.1	39	0.002
04877_HH	1	NP_060616.1	hypothetical protein FLJ10581 dbj|BAA91694.1| (AK001443) unnamed protein product [Homo sapiens]	111	33	4.00E-24
04882_HH	1	NP_062751.1	inducible IKappaB kinase dbj|BAA85154.1| (AB016589) inducible IKappaB kinase [Mus musculus]	63.6	38	8.00E-11
04883_HH	1	CAB87871.1	(AL163852) palmitoyl-protein thioesterase precursor-like [Arabidopsis thaliana]	32.8	30	2.3
04884_HH	1	S54157	extensin-like protein - cowpea (fragment)	48.8	31	4.00E-05
04888_HH	1	Q20471	YWRJ_CAEEL PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X pir||T22311 hypothetical protein F46F2.2 - Caenorhabditis elegans emb|CAA93775.1| (Z69903) predicted using Genefinder~Similarity to Rat casein kinase I (SW:KC1D_RAT)~cDNA EST yk134f5.3 comes from this gene~cDNA EST yk134f5.5 comes from this gene~cDNA EST yk475f2.5 comes from this gene~cDNA EST yk502f4.5 comes from this gene [Caenorh>	34	37	1
04894_HH	1	AAF28978.1	AF161418_1 (AF161418) HSPC300 [Homo sapiens]	74.9	51	2.00E-13
04895_HH	3	T00361	hypothetical protein KIAA0678 - human (fragment) dbj|BAA31653.1| (AB014578) KIAA0678 protein [Homo sapiens]	135	41	3.00E-31
04897_HH	2	BAA86454.1	(AB032966) KIAA1140 protein [Homo sapiens]	101	36	7.00E-21
04901_HH	1	T19630	hypothetical protein C48D5.2b - Caenorhabditis elegans emb|CAB54194.1| (Z48241) cDNA EST yk651d4.3 comes from this gene~cDNA EST yk668e6.5 comes from this gene [Caenorhabditis elegans]	95.2	33	4.00E-19
04905_HH	1	AAF49822.1	(AE003538) CG10724 gene product [Drosophila melanogaster]	232	65	2.00E-60
04906_HH	1	AC005591.1	AC005591 Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence	48.1	93	0.002
04913_HH	1	NP_004332.1	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase sp|P27708|PYR1_HUMAN CAD PROTEIN [INCLUDES: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE ; ASPARTATE CARBAMOYLTRANSFERASE ; DIHYDROOROTASE] dbj|BAA11423.1| (D78586) multifunctional protein CAD [Homo sapiens]	31.3	31	6.9
04915_HH	1	AE003672.1	AE003672 Drosophila melanogaster genomic scaffold 142000013386040 section 2 of 5, complete sequence	42.1	100	0.041
04916_HH	1	AAC64182.1	(AF095445) NADP-dependent isocitrate dehydrogenase [Glycine max]	254	71	6.00E-67
04917_HH	1	AAF58060.1	(AE003808) CG8428 gene product [Drosophila melanogaster]	115	37	2.00E-25
04918_HH	1	P50880	RL3_CAEEL 60S RIBOSOMAL PROTEIN L3 pir||T19771 hypothetical protein F13B10.2 - Caenorhabditis elegans emb|CAA93269.1| (Z69337) ribosomal protein L3 [Caenorhabditis elegans] emb|CAA93268.1| (Z69336) ribosomal protein L3 [Caenorhabditis elegans] emb|CAA91277.1| (Z66495) similar to 60S ribosomal protein L3~cDNA EST EMBL:M75754 comes from this gene; cDNA EST EMBL:M88798 comes from this gene~cDNA EST EMBL:M88842 comes from this gene; cDNA EST EMBL:M88845 comes from this gene~cDNA EST EMBL:M89043 comes from this > emb|CAA90183.1| (Z49936) similar to 60S ribosomal protein L3~cDNA EST EMBL:M75754 comes from this gene; cDNA EST EMBL:M88798 comes from this gene~cDNA EST EMBL:M88842 comes from this gene; cDNA EST EMBL:M88845 comes from this gene~cDNA EST EMBL:M89043 comes from this >	37.9	38	0.07
04919_HH	1	AAF22151.1	AF133093_6 (AF133093) putative protein at the X chromosomal L1cam locus [Mus musculus]	43.4	35	0.002
04923_HH	1	BAA36494.1	(AB022023) nonmuscle myosin heavy chain B [Bos taurus]	61.3	34	6.00E-09
04924_HH	1	S75801	probable phytochrome sll0821 - Synechocystis sp. (strain PCC 6803) dbj|BAA10536.1| (D64003) hypothetical protein [Synechocystis sp.]	30.9	32	9.1
04926_HH	1	AAA88531.1	(L76203) 'Schistosoma japonicum tropomyosin'	224	72	5.00E-58
04930_HH	1	AP002047.1	AP002047 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQC3, complete sequence	44.1	100	0.057
04933_HH	1	S77450	hypothetical protein sll1078 - Synechocystis sp. (strain PCC 6803) dbj|BAA17297.1| (D90905) hypothetical protein [Synechocystis sp.]	36	26	0.27
04935_HH	1	CAB88610.1	(AL353821) glucan 1, 4-alpha-glucosidase related protein [Neurospora crassa]	39.5	31	0.024

04943_HH	1	NP_014408.1	RNA splicing factor RNA-dependent NTPase with DEAD-box motif; Prp2p sp|P20095|PR02_YEAST PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2 pir||S12334 pre-mRNA splicing protein PRP2 - yeast (Saccharomyces cerevisiae) emb|CAA39401.1| (X55936) PRP2 (RNA2) protein [Saccharomyces cerevisiae] emb|CAA39471.1| (X55999) pre RNA processing protein [Saccharomyces cerevisiae] emb|CAA54579.1| (X77395) RNA-dependent ATPase, putative [Saccharomyces cerevisiae] emb|CAA96288.1| (Z71626) ORF YNR011c [Saccharomyces cerevisiae]	169	51	2.00E-41
04944_HH	1	NP_054888.1	HSPC134 protein gb|AAF29098.1|AF161483_1 (AF161483) HSPC134 [Homo sapiens]	183	62	1.00E-45
04947_HH	1	A70157	hypothetical protein BB0458 - Lyme disease spirochete gb|AAC66838.1| (AE001151) B. burgdorferi predicted coding region BB0458 [Borrelia burgdorferi]	32.5	31	3.1
04949_HH	1	F72363	hypothetical protein - Thermotoga maritima (strain MSB8) gb|AAD35622.1|AE001729_2 (AE001729) hypothetical protein [Thermotoga maritima]	34	27	1
04951_HH	1	AAF47754.1	(AE003477) CG17723 gene product [alt 1] [Drosophila melanogaster] gb|AAF47755.1| (AE003477) CG17723 gene product [alt 2] [Drosophila melanogaster]	123	52	1.00E-27
04953_HH	1	AAF54891.1	(AE003698) CtBP gene product [alt 2] [Drosophila melanogaster] gb|AAF54892.1| (AE003698) CtBP gene product [alt 1] [Drosophila melanogaster]	240	67	6.00E-63
04956_HH	1	AL121658.2	CNS01DS8 BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 563N04 of RPCI-11 library from chromosome 2 of Homo sapiens (Human), complete sequence	48.1	100	0.004
04957_HH	3	T28798	hypothetical protein C16E9.4 - Caenorhabditis elegans gb|AAC47958.1| (U39677) strong similarity to C. elegans unc-7 protein (PID:195256) [Caenorhabditis elegans]	138	46	5.00E-32
04961_HH	1	AAF51469.1	(AE003588) CG2839 gene product [Drosophila melanogaster]	39.5	27	0.024
04962_HH	1	AC022542.4	AC022542 Homo sapiens clone RP11-537G20, complete sequence	48.1	91	0.004
04964_HH	2	JC5983	protein kinase C-interacting RBCC protein 1 - rat gb|AAC72243.1| (U48248) protein kinase C-binding protein Beta 15; RBCK1 [Rattus norvegicus]	72.6	28	3.00E-12
04965_HH	1	P19387	RPB3_HUMAN DNA-DIRECTED RNA POLYMERASE II 33 KDA POLYPEPTIDE (RPB3) (RPB33) (RPB31) gb|AAC14355.1| (AF008443) RNA polymerase II subunit hRPB33 [Homo sapiens] gb|AAC24309.1| (AC004382) RNA polymerase II subunit hRPB33 [Homo sapiens]	158	61	3.00E-38
04969_HH	2	T32472	hypothetical protein F08F1.7 - Caenorhabditis elegans gb|AAB71307.1| (AF026213) strong similarity to Saccharomyces cerevisiae endosomal P24A protein (SP:P32802) [Caenorhabditis elegans]	161	48	6.00E-39
04970_HH	2	NP_055534.1	KIAA0738 gene product dbj|BAA34458.1| (AB018281) KIAA0738 protein [Homo sapiens]	51.2	27	7.00E-06
04971_HH	1	AAB81178.1	(AF013295) developmental orphan receptor 2 [Xenopus laevis]	53.1	55	3.00E-15
04976_HH	1	AAD48152.1	(AF085806) auxin conjugate hydrolase [Arabidopsis thaliana]	33.2	42	1.8
04977_HH	1	P21522	ROA1_SCHAM HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, A2/B1 HOMOLOG pir||S14432 heterogeneous ribonuclear particle protein A1 homolog - American bird grasshopper emb|CAA38481.1| (X54670) mammalian A1, A2 /B1 hnRNP homologue [Schistocerca americana]	58.2	37	7.00E-10
04980_HH	1	CAA50980.1	(X72090) M protein [Streptococcus pyogenes]	31.7	30	5.3
04981_HH	1	AC006348.3	AC006348 Homo sapiens clone RP5-876K2, complete sequence	48.1	100	0.004
04982_HH	1	CAC00546.1	(AJ245435) guanylyl cyclase [Plasmodium falciparum]	32.8	33	2.3
04983_HH	1	NP_055475.1	KIAA0783 gene product dbj|BAA34503.1| (AB018326) KIAA0783 protein [Homo sapiens]	78.4	46	4.00E-14
04984_HH	1	AAB27916.1	Lambert-Eaton myasthenic syndrome antigen, Mys B, LEMS antigen=Ca2+ channel complexes beta-subunit homolog [human, fetal brain, Peptide, 566 aa]	44.1	33	0.001
04986_HH	2	AAF58435.1	(AE003820) CG13321 gene product [Drosophila melanogaster]	74.1	39	9.00E-13
04987_HH	4	BAA91847.1	(AK001701) unnamed protein product [Homo sapiens]	61.3	34	6.00E-09
04997_HH	1	NC_001865.1	Chlorella vulgaris chloroplast, complete genome	40.1	100	0.88
05002_HH	1	JC5443	cathepsin L-like cysteine proteinase (EC 3.4.-.-) c1 - Maize weevil dbj|BAA24442.1| (D82884) cysteine proteinase [Sitophilus zeamais]	214	60	4.00E-55
05010_HH	1	P54281	ECLC_BOVIN EPITHELIAL CHLORIDE CHANNEL PROTEIN (CALCIUM-ACTIVATED CHLORIDE CHANNEL) gb|AAC48511.1| (U36445) calcium-activated chloride channel [Bos taurus]	46.1	27	2.00E-04
05011_HH	1	AAF54180.1	(AE003677) CG2747 gene product [Drosophila melanogaster]	94.8	29	5.00E-19
05014_HH	1	Q03101	CYAG_DICDI ADENYLATE CYCLASE, GERMINATION SPECIFIC (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) gb|AAA33164.1| (M87278) adenylyl cyclase aggregation protein [Dictyostelium discoideum]	36.4	28	0.21
05015_HH	1	AAF51965.1	(AE003602) CG1239 gene product [Drosophila melanogaster]	31.7	37	5.3
05017_HH	2	NM_007826.1	Mus musculus dachshund (Drosophila) (Dach), mRNA	40.1	100	0.88
05023_HH	1	P29293	ACRO_RAT ACROSIN PRECURSOR pir||S18407 acrosin (EC 3.4.21.10) precursor - rat	32.8	33	2.3
05024_HH	1	P15398	RPA1_SCHPO DNA-DIRECTED RNA POLYMERASE I 190 KDA POLYPEPTIDE pir||JS0080 DNA-directed RNA polymerase (EC 2.7.7.6) I 189K chain - fission yeast (Schizosaccharomyces pombe) pir||T40492 dna-directed rna polymerase i 190 kd polypeptide - fission yeast (Schizosaccharomyces pombe) gb|AAA35326.1| (M37411) RNA polymerase I largest subunit [Schizosaccharomyces pombe] emb|CAA16827.1| (AL021730) dna-directed rna polymerase i 190 kd polypeptide [Schizosaccharomyces pombe]	34	39	1
05029_HH	1	P44647	PRIA_HAEIN PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y) pir||G64062 primosomal replication factor Y - Haemophilus influenzae (strain Rd KW20) gb|AAC22001.1| (U32718) primosomal protein N' (priA) [Haemophilus influenzae Rd]	34	39	1
05030_HH	1	AAC26807.1	(AF051784) 14S cohesin SMC1 subunit; SMC protein [Xenopus laevis]	36.4	23	0.21
05032_HH	1	P30397	YCX4_EUGGR HYPOTHETICAL 64.3 KD PROTEIN IN RPS3 3'REGION (ORF516) pir||S34525 hypothetical protein 516 (rps3 3' region) - Euglena gracilis chloroplast emb|CAA50104.1| (X70810) orf516~ttg start [Euglena gracilis] emb|CAA77921.1| (Z11874) ORF516 polypeptide, function unknown [Euglena gracilis]	30.9	39	9.1
05033_HH	1	T34178	hypothetical protein C49H3.6 - Caenorhabditis elegans gb|AAF99895.1| (U42436) Hypothetical protein C49H3.6 [Caenorhabditis elegans]	82.7	33	2.00E-15
05034_HH	1	AAF56856.1	(AE003768) CG11877 gene product [Drosophila melanogaster]	33.2	39	1.8
05039_HH	1	CAB60949.1	(AL132898) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans]	33.6	40	1.4
05043_HH	1	P48935	C560_CYACA SUCCINATE DEHYDROGENASE CYTOCHROME B560 SUBUNIT (SUCCINATE DEHYDROGENASE, SUBUNIT III) pir||S62755 succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) cytochrome b560 - red alga (Cyanidium caldarium) mitochondrion emb|CAA88765.1| (Z48930) succinate dehydrogenase (cytochrome b560 subunit) [Cyanidium caldarium]	35.2	26	0.42
05046_HH	1	S32821	4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) - pig	194	57	5.00E-49

05048_HH	1	Q12933	TRA2_HUMAN TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2) (TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3) pir||I38729 tumor necrosis factor type 2 receptor associated protein 3 - human gb|AAA87706.1| (U12597) tumor necrosis factor type 2 receptor associated protein 3 [Homo sapiens]	37.5	45	0.092
05049_HH	1	AAF66055.1	AF245513_1 (AF245513) interferon inducible Mx protein [Hippoglossus hippoglossus]	146	51	2.00E-34
05050_HH	1	NP_048459.1	A111R pir||T17601 hypothetical protein A111R - Chlorella virus PBCV-1 gb|AAC96479.1| (U42580) A111R [Paramecium bursaria Chlorella virus 1]	32.5	30	3.1
05052_HH	2	P21533	RL6_RAT 60S RIBOSOMAL PROTEIN L6 (NEOPLASM-RELATED PROTEIN C140) emb|CAA60588.1| (X87107) ribosomal protein L6 [Rattus norvegicus]	169	54	2.00E-41
05056_HH	1	No Match				
05059_HH	1	T25374	hypothetical protein T27E9.3 - Caenorhabditis elegans emb|CAB04875.1| (Z82059) Similarity to Xenopus cell division protein kinase 5 (SW:P51166)~cDNA EST yk101f9.3 comes from this gene~cDNA EST yk101f9.5 comes from this gene~cDNA EST yk171d8.5 comes from this gene~cDNA EST yk171d8.3 comes from this gene~cDNA EST yk367b1.3> gb|AAD37121.1|AF129111_1 (AF129111) cell division protein kinase 5 [Caenorhabditis elegans]	30.9	42	9.1
05062_HH	2	AAF50491.1	(AE003556) CG7915 gene product [Drosophila melanogaster]	181	52	5.00E-45
05063_HH	1	P94337	FTSZ_BRELA CELL DIVISION PROTEIN FTSZ emb|CAA70158.1| (Y08964) cell division protein [Brevibacterium lactofermentum]	31.7	29	5.3
05065_HH	1	AAF79914.1	AC022472_23 (AC022472) Contains a weak similarity to Rap8 (Rac-3-1) gene from Rhynchosciara americana gb|U69899. [Arabidopsis thaliana]	51.9	33	4.00E-06
05066_HH	1	NP_012128.1	Tropomyosin isoform 2; Tpm2p sp|P40414|TPM2_YEAST TROPOMYOSIN 2 pir||S48396 tropomyosin TPM2 - yeast (Saccharomyces cerevisiae) emb|CAA86140.1| (Z38059) tropomyosin [Saccharomyces cerevisiae]	41.4	28	0.001
05068_HH	1	NP_013414.1	Ylr311cp pir||S53390 probable membrane protein YLR311c - yeast (Saccharomyces cerevisiae) gb|AAB64518.1| (U20618) Ylr311cp [Saccharomyces cerevisiae]	33.2	28	1.8
05069_HH	1	NP_004038.1	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD sp|Q99437|VATO_HUMAN VACUOLAR ATP SYNTHASE 21 KD PROTEOLIPID SUBUNIT (HATPL) dbj|BAA13753.1| (D89052) proton-ATPase-like protein [Homo sapiens]	160	65	8.00E-39
05070_HH	1	AAF01247.1	AF187323_1 (AF187323) cathepsin Q [Rattus norvegicus]	35.6	30	0.086
05071_HH	1	AAA97456.1	(U32466) NADH dehydrogenase subunit 1 [Speyeria atlantis]	36	35	0.27
05073_HH	1	AAD47014.1	AF147744_4 (AF147744) transporter [Staphylococcus aureus]	33.6	26	1.4
05074_HH	1	CAB57787.1	(X13104) labial protein [Drosophila melanogaster]	34.8	30	0.61
05077_HH	1	Q57875	Y433_METJA HYPOTHETICAL PROTEIN MJ0433 pir||A64354 hypothetical protein MJ0433 - Methanococcus jannaschii gb|AAB98433.1| (U67495) M. jannaschii predicted coding region MJ0433 [Methanococcus jannaschii]	31.3	25	6.9
05079_HH	1	CAB70721.1	(AL137393) hypothetical protein [Homo sapiens]	215	59	2.00E-55
05080_HH	1	AAF54131.1	(AE003675) CG10295 gene product [alt 1] [Drosophila melanogaster] gb|AAF54132.1| (AE003675) CG10295 gene product [alt 2] [Drosophila melanogaster]	197	61	8.00E-50
05083_HH	2	AAF46696.1	(AE003453) CG9480 gene product [Drosophila melanogaster]	247	66	4.00E-65
05088_HH	1	NP_003742.1	eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD) pir||T09582 translation initiation factor eIF-3 Prt1 chain - human gb|AAB42010.1| (U62583) Prt1 homolog [Homo sapiens]	157	43	9.00E-38
05090_HH	1	AAF78930.1	(AF261917) RNA helicase II/Gu protein [Homo sapiens]	206	61	2.00E-52
05092_HH	1	NP_055488.1	KIAA0103 gene product sp|Q15006|Y103_HUMAN HYPOTHETICAL PROTEIN KIAA0103 dbj|BAA03493.1| (D14659) KIAA0103 [Homo sapiens]	183	57	1.00E-45
05093_HH	1	P20488	SYPH_BOVIN SYNAPTOPHYSIN (MAJOR SYNAPTIC VESICLE PROTEIN P38) gb|AAA30767.1| (M22967) synaptophysin [Bos taurus]	67.5	33	9.00E-11
05095_HH	1	AJ235273.1	RPXX04 Rickettsia prowazekii strain Madrid E, complete genome; segment 4/4	44.1	96	0.057
05098_HH	1	AAB97512.1	(AF005209) HsCdc7 [Homo sapiens]	35.2	40	0.46
05099_HH	1	AAD43793.1	(AF153429) CDC42 protein [Drosophila melanogaster]	54.3	69	9.00E-19
05100_HH	1	P43307	SSRA_HUMAN TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA)	119	38	2.00E-26
05102_HH	1	T18549	DNA polymerase homolog - chestnut blight fungus plasmid pUG1 emb|CAA73185.1| (Y12637) DNA polymerase [Cryphonectria parasitica]	36	25	0.25
05103_HH	1	P12341	G6PI_KLULA GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) pir||NUVKL glucose-6-phosphate isomerase (EC 5.3.1.9) - yeast (Kluyveromyces marxianus var. lactis) emb|CAA30923.1| (X12360) put. phosphoglucose isomerase (AA 1 - 557) [Kluyveromyces lactis] gb|AAB19833.1| phosphoglucose isomerase [Kluyveromyces lactis, Peptide, 557 aa]	185	55	3.00E-46
05105_HH	1	AL353995.1	ATF12B17 Arabidopsis thaliana DNA chromosome 5, BAC clone F12B17 (ESSA project)	42.1	100	0.22
05107_HH	1	NP_003741.1	eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD) sp|Q14152|IF3A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180) (EIF3 P185) (KIAA0139) dbj|BAA09488.1| (D50929) The KIAA0139 gene product is related to mouse centrosomin B. [Homo sapiens] gb|AAB41584.1| (U58046) p167 [Homo sapiens] gb|AAB80695.1| (U78311) translation initiation factor 3 large subunit [Homo sapiens]	188	55	3.00E-47
05108_HH	1	CAB94666.1	(AL359217) hypothetical protein L240.06 [Leishmania major]	31.3	42	6.9
05109_HH	1	BAA95446.1	(AB039326) acetyl-CoA transporter [Rattus norvegicus]	149	61	2.00E-35
05111_HH	1	P38040	GBG1_DROME GUANINE NUCLEOTIDE-BINDING PROTEIN GAMMA-1 SUBUNIT pir||A42155 GTP-binding regulatory protein gamma-1 chain - fruit fly (Drosophila melanogaster) gb|AAA28570.1| (M85042) G protein gamma-1 subunit [Drosophila melanogaster] gb|AAF59030.1| (AE003835) Ggamma1 gene product [Drosophila melanogaster]	36.4	48	3.00E-06
05112_HH	2	BAB12217.1	(AB047803) vasa homolog [Ciona savignyi]	165	46	3.00E-40
05113_HH	1	B75072	tyrosyl-tRNA synthetase (tyrs) PAB1728 - Pyrococcus abyssi (strain Orsay) emb|CAB49879.1| (AJ248286) tyrosyl-tRNA synthetase (tyrS) [Pyrococcus abyssi]	33.6	29	1.4
05114_HH	1	AC008403.6	AC008403 Homo sapiens chromosome 19 clone CTC-273B12, complete sequence	44.1	96	0.057
05115_HH	2	NP_012954.1	Ykr029cp sp|P36124|YK09_YEAST HYPOTHETICAL 85.5 KD PROTEIN IN SAP190-SPO14 INTERGENIC REGION pir||S38101 hypothetical protein YKR029c - yeast (Saccharomyces cerevisiae) emb|CAA82101.1| (Z28254) ORF YKR029c [Saccharomyces cerevisiae]	49.2	39	3.00E-05
05116_HH	1	AAF19255.1	AC004858_3 (AC004858) U1 small ribonucleoprotein 1SNRP homolog; match to PID:g4050087 [Homo sapiens]	124	72	7.00E-28

05118_HH	1	P21733	YCR2_BACTK HYPOTHETICAL 29.1 KD PROTEIN IN CRYB1 5'REGION (ORF2) pir||B32053 hypothetical protein 2 (cryB1 5' region) - Bacillus thuringiensis subsp. kurstaki gb|AAA83515.1| (M23723) unknown protein [Bacillus thuringiensis]	55	45	5.00E-07
05121_HH	1	T17345	hypothetical protein DKFZp586M1824.1 - human (fragment) emb|CAB56035.1| (AL117665) hypothetical protein [Homo sapiens]	41.4	30	0.006
05122_HH	1	Q04956	ATX1_PLAFA PROBABLE CATION-TRANSPORTING ATPASE 1 emb|CAA46646.1| (X65738) ATPase I [Plasmodium falciparum]	35.2	23	0.44
05125_HH	1	NP_059982.1	rTS beta protein emb|CAA61761.1| (X89602) rTSbeta [Homo sapiens]	199	54	2.00E-50
05126_HH	3	T41581	hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe) emb|CAB11610.1| (Z98951) hypothetical protein [Schizosaccharomyces pombe] emb|CAA20864.1| (AL031546) hypothetical coiled-coil protein [Schizosaccharomyces pombe]	39.9	22	0.018
05133_HH	1	AAB19602.2	(S50916) retinoic acid receptor alpha; RAR alpha [Homo sapiens]	116	49	1.00E-25
05134_HH	1	AAF48469.1	(AE003499) CG12706 gene product [Drosophila melanogaster]	38.3	25	0.054
05135_HH	1	AAF53563.1	(AE003652) CG17912 gene product [Drosophila melanogaster]	43.8	30	0.001
05136_HH	1	NP_012666.1	importin beta homolog, Kap119p; Upf1p interacting protein; Nmd5p sp|P46970|NMD5_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN 5 pir||S57155 NMD5 protein - yeast (Saccharomyces cerevisiae) emb|CAA89663.1| (Z49632) ORF YJR132w [Saccharomyces cerevisiae]	32.8	31	2.3
05140_HH	1	NP_001005.1	ribosomal protein S10 sp|P46783|RS10_HUMAN 40S RIBOSOMAL PROTEIN S10 pir||S55918 ribosomal protein S10, cytosolic - human gb|AAA85660.1| (U14972) ribosomal protein S10 [Homo sapiens] prf||2113200G ribosomal protein S10 [Homo sapiens]	103	60	1.00E-21
05143_HH	2	AAC69756.1	(AF071773) LIM-domain protein [Branchiostoma floridae]	94.4	39	7.00E-19
05147_HH	1	NP_055752.1	KIAA0966 protein dbj|BAA76810.1| (AB023183) KIAA0966 protein [Homo sapiens]	37.1	23	0.12
05150_HH	1	CAB87580.1	(AL133475) dJ357D13.3 (TTK protein kinase (PYT)) [Homo sapiens]	37.9	33	0.063
05152_HH	1	NP_055557.1	KIAA0255 gene product dbj|BAA13385.1| (D87444) Similar to S.cerevisiae EMP70 protein precursor (S25110) [Homo sapiens]	192	54	2.00E-48
05153_HH	2	AAA03704.1	(M32999) 49-kD membrane protein [Synechococcus sp.]	32.1	26	4
05154_HH	3	AAF57148.1	(AE003778) CG1607 gene product [Drosophila melanogaster]	150	50	7.00E-36
05156_HH	1	A48295	collagen 1 - marine sponge (Microciona prolifera) gb|AAA29291.1| (L14850) collagen [Microciona prolifera]	64	55	1.00E-09
05157_HH	1	AL353759.8	AL353759 Human DNA sequence from clone RP1-221C16 on chromosome 6. Contains two genes for novel histone 4 family members, two genes for novel histone 1 family members, three genes for novel histone 2B family members, a gene for a novel histone 2A family member >	46.1	100	0.014
05159_HH	1	AAC63639.1	(AC005309) unknown protein [Arabidopsis thaliana]	32.5	45	3.1
05161_HH	1	AAF51676.1	(AE003593) ko gene product [Drosophila melanogaster]	73.7	27	1.00E-12
05162_HH	1	P33946	ER21_BOVIN ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1) (P23) pir||A44394 KDEL receptor - bovine gb|AAB24941.1| KDEL receptor, p23=mERD2 product [cattle, Peptide, 212 aa]	45.7	38	3.00E-04
05167_HH	1	Q90336	MK14_CYPCA MITOGEN-ACTIVATED PROTEIN KINASE 14 (MITOGEN-ACTIVATED PROTEIN KINASE P38) (MAP KINASE P38) dbj|BAA11881.1| (D83274) mitogen-activated protein kinase (p38) [Cyprinus carpio]	205	67	3.00E-52
05168_HH	1	BAA86580.1	(AB033092) KIAA1266 protein [Homo sapiens]	108	41	5.00E-27
05169_HH	1	Q10411	YD86_SCHPO HYPOTHETICAL 222.8 KD PROTEIN C1F3.06C IN CHROMOSOME I pir||T38077 hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe) emb|CAA94624.1| (Z70690) hypothetical coiled-coil protein [Schizosaccharomyces pombe]	31.3	33	6.9
05172_HH	1	F64654	hypothetical protein HP1078 - Helicobacter pylori (strain 26695) gb|AAD08124.1| (AE000614) H. pylori predicted coding region HP1078 [Helicobacter pylori 26695]	34.4	26	0.8
05174_HH	2	CAA68255.1	(X99996) intermediate filament protein [Lineus sanguineus]	55.8	46	3.00E-07
05176_HH	1	P20785	CA16_CHICK COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR pir||A32856 collagen alpha 1(VI) chain precursor - chicken emb|CAA41062.1| (X57998) collagen alpha 1 type VI [Gallus gallus] emb|CAA45788.1| (X64458) collagen type VI alpha 1 subunit [Gallus gallus] gb|AAB59954.1| (J04598) alpha-1 type VI collagen precursor [Gallus gallus]	51.2	35	7.00E-06
05177_HH	1	AAF14284.1	AF176085_1 (AF176085) neural polypyrimidine tract binding protein [Homo sapiens]	87.4	33	9.00E-17
05178_HH	1	AAD13153.1	(AF079359) actin [Setaria digitata]	38.3	44	0.054
05181_HH	2	Q24400	MLP2_DROME MUSCLE LIM PROTEIN MLP84B emb|CAA62627.1| (X91245) muscle LIM protein [Drosophila melanogaster] gb|AAC61591.1| (AF090832) muscle LIM protein at 84B [Drosophila melanogaster] gb|AAF54063.1| (AE003672) Mlp84B gene product [alt 1] [Drosophila melanogaster] gb|AAF54064.1| (AE003672) Mlp84B gene product [alt 2] [Drosophila melanogaster]	158	48	4.00E-38
05182_HH	4	AAF48751.1	(AE003506) beta-Spec gene product [Drosophila melanogaster]	57	37	1.00E-07
05183_HH	1	AAF51799.1	(AE003596) CG7470 gene product [Drosophila melanogaster]	111	44	4.00E-24
05185_HH	1	BAA96053.1	(AB040962) KIAA1529 protein [Homo sapiens]	34.4	44	0.8
05187_HH	1	AC012156.14	AC012156 Homo sapiens 12p11-37.2-54.4 BAC RP11-433D24 (Rosewell Park Cancer Institute Human Bac Library) complete sequence	40.1	100	0.88
05188_HH	1	AAF48424.1	(AE003498) CG5627 gene product [Drosophila melanogaster]	172	48	2.00E-42
05189_HH	1	AAC83376.1	(AF101029) netrin precursor [Hirudo medicinalis]	192	47	2.00E-48
05192_HH	1	NP_033081.1	regulatory factor (trans-acting) 1 sp|P48377|RFX1_MOUSE DNA BINDING PROTEIN RFX1 pir||A55926 DNA binding protein RFX1 - mouse emb|CAA53702.1| (X76088) DNA binding protein RFX1 [Mus musculus]	236	69	8.00E-62
05193_HH	1	CAA10709.1	(AJ132583) puromycin sensitive aminopeptidase [Homo sapiens]	96.7	41	1.00E-19
05194_HH	1	T29242	hypothetical protein F48D6.2 - Caenorhabditis elegans gb|AAB00596.1| (U58732) F48D6.2 gene product [Caenorhabditis elegans]	34.8	39	0.61
05195_HH	3	AAC35289.2	(AF053538) fibrillar collagen chain FAp1 alpha [Alvinella pompejana]	100	39	9.00E-21
05196_HH	1	BAB02181.1	(AP000420) Ta11-like non-LTR retroelement protein-like; CHP-rich zinc finger protein-like [Arabidopsis thaliana]	34.4	46	0.8
05198_HH	1	AL356299.16	AL356299 Human DNA sequence from clone CTD-3216D2 on chromosome 20, complete sequence [Homo sapiens]	42.1	93	0.079
05203_HH	1	NP_004689.1	U4/U6-associated RNA splicing factor gb|AAC51926.1| (AF016370) U4/U6 small nuclear ribonucleoprotein hPrp3 [Homo sapiens]	169	54	1.00E-41

05204_HH	1	P47943	IF4A_SCHPO EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) pir||S71745 translation initiation factor eIF-4A - fission yeast (Schizosaccharomyces pombe) emb|CAA56772.1| (X80796) translation initiation factor eIF-4A [Schizosaccharomyces pombe] gb|AAB61679.1| (L40627) cell cycle control protein eIF-4A [Schizosaccharomyces pombe] emb|CAB60237.1| (AL132828) eukaryotic initiation factor 4a [Schizosaccharomyces pombe]	49.6	35	2.00E-05
05207_HH	1	AAF57579.1	(AE003796) CG7461 gene product [Drosophila melanogaster]	230	67	8.00E-60
05209_HH	1	B39066	proline-rich protein 15 - rat	34.8	43	0.61
05211_HH	1	BAA86564.1	(AB033076) KIAA1250 protein [Homo sapiens]	59.3	26	2.00E-08
05212_HH	1	AAD25919.1	AF077298_1 (AF077298) trypsin-related serine protease leydin [Homo sapiens]	34	36	1
05216_HH	1	T04867	hypothetical protein F28A21.160 - Arabidopsis thaliana emb|CAB37460.1| (AL035526) putative protein [Arabidopsis thaliana] emb|CAB78877.1| (AL161549) putative protein [Arabidopsis thaliana]	41.4	27	0.006
05217_HH	1	AE003746.1	AE003746 Drosophila melanogaster genomic scaffold 142000013386035 section 71 of 105, complete sequence	42.1	100	0.11
05218_HH	1	AB026534.1	AB026534 Lordiphosa stackelbergi gene for alcohol dehydrogenase, partial cds	44.1	100	0.057
05219_HH	1	CAA61596.1	(X89417) protein phosphatase T [Saccharomyces cerevisiae]	59.7	34	2.00E-08
05220_HH	2	NP_002700.1	protein phosphatase 1, catalytic subunit, beta isoform ref|NP_037197.1| protein phosphatase 1, catalytic subunit, beta isoform sp|P37140|PP1B_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (PP-1B) pir||S13829 phosphoprotein phosphatase (EC 3.1.3.16) 1-beta catalytic chain - rabbit pir||D32550 phosphoprotein phosphatase (EC 3.1.3.16) dis2m2 - mouse pir||S41052 phosphoprotein phosphatase (EC 3.1.3.16) 1-beta - human pir||I76571 phosphoprotein phosphatase (EC 3.1.3.16) catalytic chain 1b - rat pir||I73630 phosphoprotein phosphatase (EC 3.1.3.16) 1-beta catalytic chain - rat emb|CAA43820.1| (X61639) protein phosphatase 1 [Oryctolagus cuniculus] dbj|BAA14195.1| (D90164) protein phosphatase 1, catalytic subunit [Rattus norvegicus] gb|AAA37527.1| (M27073) protein phosphatase 1 [Mus musculus] gb|AAA85093.1| (U11005) type-1 protein phosphatase catalytic beta-subunit [Homo sapiens] emb|CAA56870.1| (X80910) protein phosphotase 1 catyltic subunit beta isoform [Homo sapiens] dbj|BAA07203.1| (D37987) Catalytic subunit of chicken gizzard type-1 delta protein phosphatase [Gallus gallus] gb|AA	305	86	3.00E-82
05221_HH	1	NP_064920.1	AMV138 gb|AAG02844.1|AF250284_138 (AF250284) AMV138 [Amsacta moorei entomopoxvirus]	32.5	25	3.1
05225_HH	1	AAB37433.1	(S82470) BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, Peptide, 342 aa] [Homo sapiens]	117	51	6.00E-26
05226_HH	1	AAF61951.2	AF237950_1 (AF237950) arginine:glycine amidinotransferase [Gallus gallus]	112	44	1.00E-24
05228_HH	1	BAA95894.1	(AP002071) Similar to Arabidopsis thaliana chromosome2 BAC F13B15; putative non-LTR retroelement reverse transcriptase. (AC006300) [Oryza sativa]	36.7	26	0.16
05232_HH	1	G75203	abc transporter, ATP-binding protein PAB0103 - Pyrococcus abyssi (strain Orsay) emb|CAB49078.1| (AJ248283) ABC transporter, ATP-binding protein [Pyrococcus abyssi]	33.6	36	1.4
05233_HH	1	P04283	YI72_DROME HYPOTHETICAL 53 KD PROTEIN IN COPIA-LIKE TRANSPOSABLE ELEMENT 17.6 pir||QXFF73 hypothetical 53K protein - fruit fly (Drosophila melanogaster) transposon 17.6	33.2	48	1.8
05234_HH	1	AC026371.9	AC026371 Homo sapiens 12 BAC RP11-59L15 (Roswell Park Cancer Institute Human BAC Library) complete sequence	42.1	100	0.1
05235_HH	1	NP_004703.1	human growth factor-regulated tyrosine kinase substrate dbj|BAA23366.1| (D84064) Hrs [Homo sapiens] gb|AAC51929.1| (U43895) hepatocyte growth factor-regulated tyrosine kinase substrate [Homo sapiens]	127	56	8.00E-29
05239_HH	1	NP_004037.1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardiac muscle sp|P25705|ATPA_HUMAN ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR pir||PWHUA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain precursor - human emb|CAA41789.1| (X59066) H(+)-transporting ATP synthase [Homo sapiens] emb|CAA46452.1| (X65460) ATP synthase alpha subunit [Homo sapiens] dbj|BAA05672.1| (D28126) ATP synthase alpha subunit [Homo sapiens] dbj|BAA03531.1| (D14710) inport precursor of human ATP synthase alpha subunit [Homo sapiens] prf||2019238A ATP synthase:SUBUNIT=alpha [Homo sapiens]	320	95	7.00E-87
05241_HH	1	U28942.1	CELF56D3 Caenorhabditis elegans cosmid F56D3	46.1	100	0.014
05244_HH	1	CAB95583.1	(AL359782) hypothetical protein, CHR1.352 [Trypanosoma brucei]	32.5	26	3.1
05249_HH	1	C55521	virS protein - Clostridium perfringens gb|AAA58950.1| (U04966) VirS [Clostridium perfringens]	30.9	30	9.1
05253_HH	1	AE003594.1	AE003594 Drosophila melanogaster genomic scaffold 142000013386036 section 4 of 9, complete sequence	42.1	100	0.14
05257_HH	1	CAB91712.1	(AL356173) kinesin-like protein Kif21a related protein [Neurospora crassa]	40.6	25	0.011
05259_HH	1	O93388	NPC2_CHICK NEUROPLASTICIN-2 gb|AAC27325.1| (AF076982) neuroplasticin-2 [Gallus gallus]	36	31	0.065
05260_HH	1	CAB92122.1	(AL096856) AtATM [Arabidopsis thaliana]	46.9	25	1.00E-04
05267_HH	1	U00036.1	CELR151 Caenorhabditis elegans cosmid R151	44.1	100	0.057
05268_HH	1	P79748	5H1D_FUGRU 5-HYDROXYTRYPTAMINE 1D RECEPTOR (5-HT-1D) (SEROTONIN RECEPTOR) (5HT1D) (F1D) emb|CAA58745.1| (X83865) serotonin receptor [Fugu rubripes]	35.2	40	0.46
05272_HH	1	AAD01499.1	(AF012424) mutant beta-glucuronidase [Felis catus]	30.9	35	9.1
05274_HH	1	CAB39025.1	(AL034559) hypothetical protein, PFC0885c [Plasmodium falciparum]	39.1	35	0.031
05275_HH	1	P45958	DNAK_MYCCA DNAK PROTEIN (HEAT SHOCK 70 KD PROTEIN) (HSP70) gb|AAB09430.1| (U51235) DnaK [Mycoplasma capricolum]	35.6	24	0.35
05279_HH	1	NP_038689.1	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (sem sp|Q60519|SM5B_MOUSE SEMAPHORIN 5B PRECURSOR (SEMAPHORIN G) (SEMA G) emb|CAA66398.1| (X97818) samaphorin G [Mus musculus]	32.1	26	4
05281_HH	1	CAB73823.1	(AL139078) putative Ni/Fe-hydrogenase small subunit [Campylobacter jejuni]	33.6	39	1.4
05288_HH	1	NP_060522.1	hypothetical protein FLJ10305 dbj|BAA91530.1| (AK001167) unnamed protein product [Homo sapiens]	137	40	9.00E-32
05289_HH	1	NP_032201.1	granulin sp|P28798|GRN_MOUSE GRANULINS PRECURSOR (ACROGRANIN) dbj|BAA03736.1| (D16195) acrogranin precursor [Mus musculus]	164	42	7.00E-40
05293_HH	1	AAB64265.1	(U97512) cytochrome oxidase II [Muscidifurax raptorellus]	36.7	36	0.16
05294_HH	1	AAC69930.1	(AC005819) putative extensin [Arabidopsis thaliana]	40.2	30	0.014

<table>
<tr><td>05296_HH</td><td>1</td><td>CAB66481.1</td><td>(AL136546) hypothetical protein [Homo sapiens]</td><td>253</td><td>70</td><td>1.00E-66</td></tr>
<tr><td>05298_HH</td><td>1</td><td>P38981</td><td>RSP4_URECA 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KD LAMININ BINDING PROTEIN) gb|AAA90978.1| (U02370) 34/67 kD laminin binding protein [Urechis caupo]</td><td>237</td><td>68</td><td>5.00E-62</td></tr>
<tr><td>05299_HH</td><td>1</td><td>Q93847</td><td>YZLL_CAEEL HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTAINING PROTEIN K04G11.4 IN CHROMOSOME X pir||T23317 hypothetical protein K04G11.4 - Caenorhabditis elegans emb|CAB01760.1| (Z78544) predicted using Genefinder~Similarity to C.elegans Guanine nucleotide binding protein (WP:C14B1.4)~cDNA EST yk567g12.3 comes from this gene~cDNA EST yk567g12.5 comes from this gene [Caenorhabditis elegans]</td><td>56.6</td><td>27</td><td>2.00E-07</td></tr>
<tr><td>05300_HH</td><td>1</td><td>CAB89292.1</td><td>(AL109915) dJ120N9.1 (KIAA0656 protein (similar to clathrin assembly lymphoid myeloid leukemia protein (CALM))) [Homo sapiens]</td><td>36.4</td><td>53</td><td>0.21</td></tr>
<tr><td>05302_HH</td><td>1</td><td>BAA34990.1</td><td>(AB016999) PRH14 [Dugesia japonica]</td><td>118</td><td>100</td><td>5.00E-26</td></tr>
<tr><td>05304_HH</td><td>1</td><td>NP_046242.1</td><td>unknown sp|O10336|Y083_NPVOP HYPOTHETICAL 91.1 KD PROTEIN (ORF86) pir||T10355 hypothetical protein 86 - Orgyia pseudotsugata nuclear polyhedrosis virus gb|AAC59085.1| (U75930) unknown [Orgyia pseudotsugata nuclear polyhedrosis virus]</td><td>34.4</td><td>35</td><td>0.26</td></tr>
<tr><td>05307_HH</td><td>1</td><td>AAC83716.1</td><td>(AF096014) antigen receptor [Ginglymostoma cirratum]</td><td>39.5</td><td>24</td><td>0.024</td></tr>
<tr><td>05314_HH</td><td>1</td><td>NP_036764.1</td><td>proline-rich protein, salivary pir||A30496 proline-rich protein 13 - rat gb|AAA42063.1| (M64792) salivary proline-rich protein [Rattus norvegicus]</td><td>34</td><td>43</td><td>1.1</td></tr>
<tr><td>05315_HH</td><td>1</td><td>AAF52394.1</td><td>(AE003613) CG9545 gene product [Drosophila melanogaster]</td><td>63.2</td><td>47</td><td>2.00E-09</td></tr>
<tr><td>05316_HH</td><td>4</td><td>AAF58366.1</td><td>(AE003818) CG6050 gene product [Drosophila melanogaster]</td><td>239</td><td>68</td><td>1.00E-62</td></tr>
<tr><td>05317_HH</td><td>1</td><td>P23116</td><td>IF3A_MOUSE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN) (CENTROSOMIN) gb|AAA90910.1| (U14172) p162 protein [Mus musculus]</td><td>171</td><td>49</td><td>6.00E-42</td></tr>
<tr><td>05321_HH</td><td>1</td><td>P17755</td><td>ENV_HV2D1 ENVELOPE POLYPROTEIN GP160 PRECURSOR [CONTAINS: EXTERIOR MEMBRANE GLYCOPROTEIN (GP120); TRANSMEMBRANE GLYCOPROTEIN (GP41)] pir||S12159 env protein - human immunodeficiency virus type 2 emb|CAA36471.1| (X52223) env gene product (AA 1-851) [Human immunodeficiency virus type 2] gb|AAA76847.1| (J04542) env [Human immunodeficiency virus type 2]</td><td>29</td><td>32</td><td>7.1</td></tr>
<tr><td>05323_HH</td><td>1</td><td>NP_002830.1</td><td>protein tyrosine phosphatase, receptor type, delta polypeptide sp|P23468|PTPD_HUMAN PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA) pir||A56178 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human gb|AAC41749.1| (L38929) protein tyrosine phosphatase delta [Homo sapiens]</td><td>41.8</td><td>29</td><td>0.005</td></tr>
<tr><td>05326_HH</td><td>2</td><td>BAA36294.1</td><td>(AB001773) PEM-6 [Ciona savignyi]</td><td>124</td><td>37</td><td>7.00E-28</td></tr>
<tr><td>05327_HH</td><td>1</td><td>AAF48171.1</td><td>(AE003489) CG11146 gene product [Drosophila melanogaster]</td><td>100</td><td>45</td><td>9.00E-21</td></tr>
<tr><td>05332_HH</td><td>1</td><td>AAF51554.1</td><td>(AE003590) CG2674 gene product [alt 2] [Drosophila melanogaster] gb|AAF51555.1| (AE003590) CG2674 gene product [alt 3] [Drosophila melanogaster]</td><td>97.5</td><td>46</td><td>2.00E-23</td></tr>
<tr><td>05334_HH</td><td>1</td><td>NP_040318.1</td><td>Non-capsid protein sp|P03133|VNCS_PAVHH NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1) (NCVP1) pir||UYPVV1 noncapsid protein NS1 - parvovirus H1 emb|CAA25689.1| (X01457) Non-capsid protein [Parvovirus H1]</td><td>30.9</td><td>41</td><td>3.2</td></tr>
<tr><td>05335_HH</td><td>1</td><td>AF281253.1</td><td>AF281253 Xenopus laevis ashwin mRNA, complete cds</td><td>38.2</td><td>100</td><td>0.73</td></tr>
<tr><td>05337_HH</td><td>1</td><td>AB015485.1</td><td>AB015485 Dugesia japonica mRNA for myosin heavy chain, partial cds</td><td>246</td><td>100</td><td>2.00E-63</td></tr>
<tr><td>05338_HH</td><td>1</td><td>AAF52389.1</td><td>(AE003613) CG9539 gene product [Drosophila melanogaster]</td><td>172</td><td>93</td><td>2.00E-42</td></tr>
<tr><td>05339_HH</td><td>1</td><td>AE003582.1</td><td>AE003582 Drosophila melanogaster genomic scaffold 142000013386046 section 8 of 16, complete sequence</td><td>42.1</td><td>100</td><td>0.22</td></tr>
<tr><td>05341_HH</td><td>1</td><td>NP_044902.1</td><td>tegument protein gb|AAB66417.1| (U97553) tegument protein [murid herpesvirus 4] gb|AAF19328.1|AF105037_60 (AF105037) 64 [murid herpesvirus 4]</td><td>28.6</td><td>37</td><td>9</td></tr>
<tr><td>05342_HH</td><td>1</td><td>CAB81620.1</td><td>(AL117352) dJ876B10.2 (novel protein (ortholog of rat EXO84)) [Homo sapiens]</td><td>67.1</td><td>29</td><td>1.00E-10</td></tr>
<tr><td>05346_HH</td><td>1</td><td>BAA95077.1</td><td>(AB041594) unnamed protein product [Mus musculus]</td><td>45.7</td><td>33</td><td>3.00E-04</td></tr>
<tr><td>05347_HH</td><td>1</td><td>AAD34760.1</td><td>(AF132172) unknown [Drosophila melanogaster] gb|AAF58742.1| (AE003828) BcDNA:LD21529 gene product [Drosophila melanogaster]</td><td>58.2</td><td>33</td><td>5.00E-08</td></tr>
<tr><td>05348_HH</td><td>1</td><td>AAF03175.1</td><td>AF110138_7 (AF110138) NADH dehydrogenase subunit 5 [Nephroselmis olivacea]</td><td>31.3</td><td>19</td><td>6.9</td></tr>
<tr><td>05350_HH</td><td>1</td><td>prf|1920343A</td><td>fibrillar collagen [Ephydatia muelleri]</td><td>63.2</td><td>29</td><td>2.00E-09</td></tr>
<tr><td>05353_HH</td><td>1</td><td>CAB72317.1</td><td>(AJ245736) aconitase [Daphnia pulex]</td><td>252</td><td>74</td><td>1.00E-66</td></tr>
<tr><td>05357_HH</td><td>1</td><td>AAB39612.1</td><td>(U67259) RING-finger protein [Helicoverpa armigera nuclear polyhedrosis virus]</td><td>43.4</td><td>25</td><td>0.002</td></tr>
<tr><td>05360_HH</td><td>3</td><td>CAA80336.1</td><td>(Z22614) ubiquitin [Tetrahymena pyriformis]</td><td>42.2</td><td>30</td><td>0.004</td></tr>
<tr><td>05364_HH</td><td>1</td><td>AAF53677.1</td><td>(AE003659) CG15160 gene product [Drosophila melanogaster]</td><td>46.9</td><td>27</td><td>1.00E-04</td></tr>
<tr><td>05367_HH</td><td>1</td><td>P39429</td><td>TRA2_MOUSE TNF RECEPTOR ASSOCIATED FACTOR 2 (TRAF2) pir||I61512 TNF receptor associated factor 2 - mouse gb|AAC37662.1| (L35303) TNF receptor associated factor 2 [Mus musculus] gb|AAF59928.1| (AF233332) tumor necrosis factor receptor-associated factor [Mus musculus]</td><td>87</td><td>48</td><td>1.00E-16</td></tr>
<tr><td>05371_HH</td><td>2</td><td>T28677</td><td>rhoptry protein - Plasmodium yoelii gb|AAA21304.1| (L27838) rhoptry protein [Plasmodium yoelii]</td><td>51.5</td><td>23</td><td>5.00E-06</td></tr>
<tr><td>05372_HH</td><td>1</td><td>AAF51035.1</td><td>(AE003577) CG3702 gene product [Drosophila melanogaster]</td><td>231</td><td>65</td><td>3.00E-60</td></tr>
<tr><td>05373_HH</td><td>1</td><td>AP001718.1</td><td>AP001718 Homo sapiens genomic DNA, chromosome 21q, section 62/105</td><td>42.1</td><td>100</td><td>0.22</td></tr>
<tr><td>05375_HH</td><td>1</td><td>P30652</td><td>YOW6_CAEEL HYPOTHETICAL 23.7 KD PROTEIN ZK643.6 IN CHROMOSOME III pir||S23244 hypothetical protein ZK643.6 - Caenorhabditis elegans emb|CAA77472.1| (Z11126) ZK643.6 [Caenorhabditis elegans]</td><td>42.2</td><td>33</td><td>8.00E-04</td></tr>
<tr><td>05376_HH</td><td>1</td><td>AL389887.7</td><td>AL389887 Human DNA sequence from clone RP11-54F22 on chromosome X, complete sequence [Homo sapiens]</td><td>38.2</td><td>100</td><td>3.5</td></tr>
<tr><td>05379_HH</td><td>2</td><td>NP_000968.1</td><td>ribosomal protein L13 sp|P26373|RL13_HUMAN 60S RIBOSOMAL PROTEIN L13 (BREAST BASIC CONSERVED PROTEIN 1) pir||S23753 ribosomal protein L13, cytosolic - human emb|CAA45963.1| (X64707) BBC1 [Homo sapiens]</td><td>159</td><td>52</td><td>2.00E-38</td></tr>
<tr><td>05380_HH</td><td>1</td><td>AAF37351.1</td><td>AF192387_1 (AF192387) feline leukemia virus subgroup C receptor [Felis catus]</td><td>120</td><td>44</td><td>7.00E-27</td></tr>
<tr><td>05383_HH</td><td>1</td><td>BAA87879.1</td><td>(AB035353) Drab5 [Drosophila melanogaster] dbj|BAA88244.1| (AB035671) Rab5 protein [Drosophila melanogaster] gb|AAF51265.1| (AE003583) Rab5 gene product [Drosophila melanogaster]</td><td>258</td><td>76</td><td>2.00E-68</td></tr>
<tr><td>05384_HH</td><td>1</td><td>P50886</td><td>RL22_XENLA 60S RIBOSOMAL PROTEIN L22 emb|CAA63927.1| (X94243) ribosomal protein homologue to human L22 [Xenopus laevis]</td><td>68.3</td><td>40</td><td>3.00E-11</td></tr>
<tr><td>05385_HH</td><td>1</td><td>Q58611</td><td>YC14_METJA HYPOTHETICAL PROTEIN MJ1214 gb|AAB99215.1| (U67562) type I restriction-modification enzyme 1, R subunit [Methanococcus jannaschii]</td><td>36.7</td><td>31</td><td>0.16</td></tr>
<tr><td>05387_HH</td><td>1</td><td>NP_036272.1</td><td>solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10 emb|CAB59892.1| (AJ131613) dicarboxylate carrier protein [Homo sapiens] emb|CAB60007.1| (AJ131612) dicarboxylate carrier protein [Homo sapiens]</td><td>177</td><td>61</td><td>7.00E-44</td></tr>
<tr><td>05388_HH</td><td>1</td><td>BAA84069.1</td><td>(AB028498) Flamingo [Drosophila melanogaster]</td><td>78.8</td><td>30</td><td>3.00E-14</td></tr>
</table>

05390_HH	2	T18438	hypothetical protein C0415c - Plasmodium falciparum emb|CAB11117.1| (Z98547) predicted using hexExon; MAL3P3.16 (PFC0415c), Hypothetical protein, len: 1533 aa [Plasmodium falciparum]	37.5	29	0.092
05391_HH	1	T18402	asparagine/aspartate rich protein - Plasmodium falciparum (fragment) emb|CAA70130.1| (Y08926) AARP1 protein [Plasmodium falciparum]	30.9	23	9.1
05393_HH	1	AAF51754.1	(AE003595) CG7166 gene product [Drosophila melanogaster]	38.7	27	0.041
05397_HH	1	AAF56315.1	(AE003748) CG13625 gene product [Drosophila melanogaster]	34	29	0.001
05399_HH	1	AAF45694.1	(AE003422) EG:86E4.4 gene product [Drosophila melanogaster]	103	48	1.00E-21
05400_HH	1	AAF26129.1	AC011620_5 (AC011620) unknown protein [Arabidopsis thaliana]	31.7	27	5.3
05405_HH	1	NP_064618.1	x 006 protein gb|AAF87317.1|AF168715_1 (AF168715) x 006 protein [Homo sapiens]	80.8	34	9.00E-15
05419_HH	1	NP_034493.1	glutathione transferase zeta 1 (maleylacetoacetate isomerase) gb|AAD43846.1|AF093418_1 (AF093418) maleylacetoacetate isomerase [Mus musculus]	178	53	3.00E-44
05421_HH	1	AAF55190.1	(AE003708) CG5073 gene product [Drosophila melanogaster]	118	39	5.00E-26
05422_HH	1	T21371	hypothetical protein F25H8.3 - Caenorhabditis elegans emb|CAA93287.1| (Z69360) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517)~cDNA EST EMBL:M89266 comes from this gene~cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans] emb|CAA93288.1| (Z69361) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517)~cDNA EST EMBL:M89266 comes from this gene~cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]	69.9	33	2.00E-11
05423_HH	1	A29872	phosphorylase kinase (EC 2.7.1.38) catalytic chain, skeletal muscle - mouse gb|AAA39926.1| (M16216) phosphorylase kinase, gamma-subunit [Mus musculus]	138	45	3.00E-32
05425_HH	2	T26818	hypothetical protein Y41E3.7 - Caenorhabditis elegans emb|CAB09005.2| (Z95559) cDNA EST yk236d4.5 comes from this gene~cDNA EST yk171f4.5 comes from this gene~cDNA EST yk329g6.5 comes from this gene~cDNA EST CEMSH45R comes from this gene~cDNA EST yk504e1.5 comes from this gene~cDNA EST yk544e10.5 comes from this gene~cDN>	65.2	29	4.00E-10
05428_HH	1	AC005220.1	AC005220 Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence	42.1	100	0.22
05429_HH	1	NM_007561.1	Mus musculus bone morphogenic protein receptor, type II (serine/threonine kinase) (Bmpr2), mRNA	40.1	100	0.18
05430_HH	1	P16237	HMDH_SCHMA 3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (HMG-COA REDUCTASE) pir||A34416 hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) - fluke (Schistosoma mansoni) gb|AAA29896.1| (M27294) 3-hydroxy-3-methylglutaryl coenzyme A reductase [Schistosoma mansoni]	150	49	7.00E-36
05432_HH	1	AAC24364.1	(AF065393) putative G-binding protein [Homo sapiens]	225	68	3.00E-58
05433_HH	1	AAD43714.1	(AF152320) protocadherin gamma A11 [Homo sapiens]	42.2	33	0.004
05435_HH	1	AAD44341.1	AF160970_1 (AF160970) prominin [Danio rerio]	41	26	0.008
05436_HH	1	AAF07792.1	AC010704_17 (AC010704) hypothetical protein [Arabidopsis thaliana]	57	26	1.00E-07
05438_HH	1	AAF71814.1	(AF105091) maturase [Bruguiera sexangula]	33.6	24	1.4
05442_HH	1	CAC04447.1	(AL391572) conserved hypothetical protein [Neurospora crassa]	44.9	39	5.00E-04
05444_HH	1	AC008126.9	AC008126 Homo sapiens 12 BAC RPCI11-90E9 (Roswell Park Cancer Institute Human BAC Library) complete sequence	42.1	96	0.22
05449_HH	1	JE0293	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 8B, cAMP-specific - human (fragment)	36.4	29	0.21
05451_HH	1	S13043	methylmalonyl-CoA mutase (EC 5.4.99.2) - mouse	212	60	2.00E-54
05457_HH	1	BAA81705.1	(AB006551) G protein a subunit 9 [Ephydatia fluviatilis]	30.9	40	9.1
05458_HH	1	AF152364.1	AF152364 Homo sapiens constitutive fragile region FRA3B sequence	40.1	100	0.88
05551_HH	1	AAD19219.1	(AF053083) ubiquitin-like protein SMT3 [Drosophila melanogaster] gb|AAF31702.1|AF218862_1 (AF218862) Smt3 [Drosophila melanogaster] gb|AAF52470.1| (AE003615) smt3 gene product [Drosophila melanogaster]	87.8	71	1.00E-21
05552_HH	1	AAF57676.1	(AE003799) Pepck gene product [Drosophila melanogaster]	189	53	1.00E-47
05553_HH	1	NP_057316.1	ST2V protein pir||JC7109 ST2V protein - human dbj|BAA85894.1| (AB029084) ST2V [Homo sapiens]	33.2	35	1.8
05556_HH	2	NP_036370.2	sir2-like 1 gb|AAD40849.2|AF083106_1 (AF083106) sirtuin type 1 [Homo sapiens]	101	47	7.00E-21
05557_HH	1	A45605	mature-parasite-infected erythrocyte surface antigen MESA - Plasmodium falciparum	33.2	34	1.8
05558_HH	1	CAB90834.1	(AJ250837) putative transposase [Streptococcus dysgalactiae]	33.6	27	1.4
05561_HH	1	NP_004362.1	coatomer protein complex, subunit alpha; xenin sp|P53621|COPA_HUMAN COATOMER ALPHA SUBUNIT (ALPHA-COAT PROTEIN) (ALPHA-COP) (HEPCOP) (HEP-COP) [CONTAINS: XENIN (XENOPSIN-RELATED PEPTIDE); PROXENIN] pir||ERHUAH coatomer complex alpha chain homolog - human gb|AAB70879.1| (U24105) coatomer protein [Homo sapiens]	162	49	2.00E-39
05563_HH	1	CAA08995.1	(AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]	112	37	3.00E-24
05569_HH	2	AAF44685.1	AF239824_1 (AF239824) GTP-binding protein Mx2 [Canis familiaris]	152	48	2.00E-36
05574_HH	1	AAF58018.1	(AE003807) CG3615 gene product [Drosophila melanogaster]	115	33	3.00E-25
05580_HH	1	AE003638.1	AE003638 Drosophila melanogaster genomic scaffold 142000013386055 section 31 of 63, complete sequence	44.1	100	0.057
05582_HH	1	P75551	OPPF_MYCPN OLIGOPEPTIDE TRANSPORT ATP-BINDING PROTEIN OPPF pir||S73939 oligopeptide transport ATP-binding protein oppF - Mycoplasma pneumoniae (strain ATCC 29342) gb|AAB96261.1| (AE000058) Mycoplasma pneumoniae, oligopeptide transport ATP-binding protein OppF; similar to Swiss-Prot Accession Number P24137 and P23366, from B. subtilis	30.9	30	8
05586_HH	1	NP_006506.1	SET domain and mariner transposase fusion gene gb|AAC52012.1| (U80776) orf; encodes putative chimeric protein with SET domain in N-terminus with similarity to several other human, Drosophila, nematode and yeast proteins [Homo sapiens]	88.2	48	2.00E-22
05587_HH	1	NP_034894.1	mannosidase 2, alpha B1 sp|O09159|MA2B_MOUSE LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN) pir||T42385 alpha-mannosidase (EC 3.2.1.24) - mouse gb|AAC78560.1| (AF044192) lysosomal alpha-mannosidase [Mus musculus]	99.8	36	2.00E-20
05588_HH	1	AAF50868.1	(AE003569) CG1532 gene product [Drosophila melanogaster]	148	48	3.00E-35
05590_HH	1	AAF53652.1	(AE003657) CG15154 gene product [Drosophila melanogaster]	42.2	47	0.004
05592_HH	1	CAA64971.1	(X95669) thdF [Borrelia burgdorferi] emb|CAA06004.1| (AJ003222) thdF [Borrelia burgdorferi]	31.7	24	5.3
05596_HH	2	A49674	flightless-I homolog - human (fragment) gb|AAC03568.1| (U01184) flightless-I homolog [Homo sapiens]	108	34	4.00E-23

05597_HH	2	NP_012089.1	Yhr217cp sp|P38898|YH17_YEAST HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION pir||S48998 hypothetical protein YHR217c - yeast (Saccharomyces cerevisiae) gb|AAB69740.1| (U00029) Yhr217cp [Saccharomyces cerevisiae]	38.7	30	0.041
05598_HH	1	AAF07441.1	AE001575_42 (AE001575) hypothetical protein [Borrelia burgdorferi] gb|AAF07486.1|AE001576_45 (AE001576) hypothetical protein [Borrelia burgdorferi] gb|AAF07658.1|AE001580_43 (AE001580) hypothetical protein [Borrelia burgdorferi]	30.9	38	9.1
05601_HH	1	AAD38284.1	AC007789_10 (AC007789) putative polyprotein [Oryza sativa]	103	36	1.00E-21
05609_HH	1	No Match				
05612_HH	1	AAD38661.1	AF145686_1 (AF145686) BcDNA.LD24639 [Drosophila melanogaster] gb|AAF52387.1| (AE003613) BcDNA:LD24639 gene product [Drosophila melanogaster]	121	45	6.00E-27
05616_HH	1	NP_036251.1	cell cycle related kinase gb|AAC98920.1| (AF035013) cell cycle related kinase [Homo sapiens] gb|AAF43778.1|AF113130_1 (AF113130) cyclin-dependent protein kinase H [Homo sapiens]	215	73	2.00E-55
05617_HH	2	AAF46338.1	(AE003443) Traf2 gene product [Drosophila melanogaster]	51.2	26	7.00E-06
05618_HH	1	AAA85261.1	(U13152) guanine nucleotide-binding protein beta 5 [Mesocricetus auratus]	161	45	4.00E-39
05621_HH	1	NP_048276.1	ORF MSV205 tryptophan repeat gene family protein gb|AAC97756.1| (AF063866) ORF MSV205 tryptophan repeat gene family protein [Melanoplus sanguinipes entomopoxvirus]	32.5	33	1.2
05625_HH	1	NP_049991.1	orf203 gp emb|CAA64932.1| (X95646) putative immunity function, homology to orf 258 of lactococcal bacteriophage BK5-t [Streptococcus thermophilus bacteriophage Sfi21] gb|AAD44096.1|AF115103_26 (AF115103) orf203 gp [Streptococcus thermophilus bacteriophage Sfi21]	37.5	36	0.092
05631_HH	1	AAF48792.1	(AE003507) Dhc16F gene product [Drosophila melanogaster]	123	44	9.00E-28
05640_HH	1	Q04832	HEXP_LEIMA DNA-BINDING PROTEIN HEXBP (HEXAMER-BINDING PROTEIN) pir||A47156 hexamer-binding protein HEXBP - Leishmania major gb|AAA29245.1| (M94390) HEXBP DNA binding protein [Leishmania major]	131	36	7.00E-30
05641_HH	1	G70338	conserved hypothetical protein aq_423 - Aquifex aeolicus gb|AAC06703.1| (AE000689) hypothetical protein [Aquifex aeolicus]	39.5	31	0.024
05642_HH	1	No Match				
05645_HH	1	NP_009998.1	protein kinase; Ssk22p sp|P25390|SS22_YEAST SERINE/THREONINE PROTEIN KINASE SSK22 pir||S19488 probable membrane protein YCR073c - yeast (Saccharomyces cerevisiae) emb|CAA42271.1| (X59720) YCR073c, len:1314 [Saccharomyces cerevisiae]	31.3	23	6.9
05646_HH	1	T14328	protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type, GMC1 precursor - rat gb|AAC34801.1| (AF063249) glomerular mesangial cell receptor protein-tyrosine phosphatase precursor [Rattus norvegicus]	44.1	30	0.001
05648_HH	1	T18499	hypothetical protein C0770c - Plasmodium falciparum emb|CAB11138.1| (Z98551) putative kinesin-related protein [Plasmodium falciparum]	35.6	34	0.35
05650_HH	1	AC018721.1	AC018721 Arabidopsis thaliana chromosome II section 217 of 255 of the complete sequence. Sequence from clones F27I1, T7M7, T3G21	38.2	100	3.5
05652_HH	1	CAA09077.2	(AJ010306) smoothelein L1, large isoform [Homo sapiens]	34	42	0.2
05653_HH	1	AAB16964.1	(U67921) collagen-like protein [Bacillus thuringiensis subsp. israelensis]	64.4	30	7.00E-10
05655_HH	1	AAD26852.1	AF123074_2 (AF123074) cytoplasmic dynein intermediate chain 1 [Homo sapiens]	36.4	28	0.21
05656_HH	1	AL117334.29	HSJ687F11 Human DNA sequence from clone RP4-687F11 on chromosome 20. Contains part of one or two novel genes, a pseudogene similar to MMS2 and chicken CROC-1B, ESTs, STSs, GSSs and a putative CpG island, complete sequence [Homo sapiens]	42.1	100	0.093
05659_HH	3	O02414	DYL1_ANTCR DYNEIN LIGHT CHAIN LC6, FLAGELLAR OUTER ARM dbj|BAA20525.1| (AB004830) outer arm dynein LC6 [Anthocidaris crassispina]	166	86	1.00E-40
05663_HH	1	CAA15711.1	(AL009196) /prediction=(method:""genefinder"", version:""084"", score:""150.41"")~/prediction=(method:""genscan"", version:""1.0"")~/match=(desc:""HEAT-SHOCK PROTEIN 110 KD (KIAA0201)"", species:""HOMO SAPIENS (HUMAN)"", ranges:(query:12688..12861, tar> gb|AAF45769.1| (AE003423) EG:25E8.1 gene product [Drosophila melanogaster]	78.4	34	4.00E-14
05671_HH	1	AAB48046.1	(U88294) carnitine palmitoyltransferase I [Rattus norvegicus]	97.5	38	8.00E-20
05672_HH	5	AAF57403.1	(AE003790) CG9446 gene product [Drosophila melanogaster]	221	66	3.00E-57
05673_HH	1	AAB35697.2	(S79797) enzymatic glycosylation-regulating gene [Rattus norvegicus]	72.6	41	3.00E-12
05676_HH	1	AAF46200.1	(AE003438) C3G gene product [Drosophila melanogaster]	34	23	1
05677_HH	1	AF266075.1	AF266075 Onychogomphus forcipatus large subunit ribosomal RNA gene, partial sequence; tRNA-Valine gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	42.1	100	0.22
05680_HH	1	AC011904.3	AC011904 Homo sapiens clone CTD-3244O18, complete sequence	40.1	100	0.31
05683_HH	1	P10733	SEVE_DICDI SEVERIN pir||A28517 severin - slime mold (Dictyostelium discoideum) gb|AAA33250.1| (J03515) severin [Dictyostelium discoideum]	80.4	38	1.00E-14
05684_HH	1	T25851	hypothetical protein T01B11.5 - Caenorhabditis elegans gb|AAB38002.1| (U80931) similar to cation transporters [Caenorhabditis elegans]	32.5	28	3.1
05685_HH	1	AAD43761.1	AF152500_1 (AF152500) protocadherin beta 7 [Homo sapiens]	57.8	27	7.00E-08
05686_HH	1	AAA03341.1	(U02032) ribosomal protein L23a [Homo sapiens]	150	57	9.00E-36
05688_HH	1	AC004401.2	AC004401 Arabidopsis thaliana chromosome II section 131 of 255 of the complete sequence. Sequence from clones T20K9, F21P24	40.1	95	0.2
05689_HH	1	AF055914.1	AF055914 Crithidia fasciculata tryparedoxin peroxidase (TryP) gene, complete cds	42.1	100	0.22
05691_HH	1	P35813	P2CA_HUMAN PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (PP2C-ALPHA) (IA) (PROTEIN PHOSPHATASE 1A) pir||S22423 phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - human pdb|1A6Q| Crystal Structure Of The Protein SerineTHREONINE Phosphatase 2c At 2 A Resolution gb|AAB21784.1| (S87759) protein phosphatase 2C alpha, PP2Calpha [human, Peptide, 382 aa] [Homo sapiens]	181	52	5.00E-45
05697_HH	3	T18372	repeat organellar protein - Plasmodium chabaudi gb|AAC63403.1| (U43145) repeat organellar protein [Plasmodium chabaudi]	40.2	23	0.014
05700_HH	1	NM_004713.1	Homo sapiens serologically defined colon cancer antigen 1 (SDCCAG1) mRNA	46.1	93	0.014
05705_HH	1	AAF51814.1	(AE003597) Ddx1 gene product [Drosophila melanogaster]	138	41	5.00E-32
05706_HH	1	AAF46670.1	(AE003453) CG4030 gene product [Drosophila melanogaster]	35.6	28	0.35
05707_HH	1	AF047449.1	AF047449 Gallus gallus microsatellite repeat region	42.1	96	0.22
05709_HH	1	CAA08835.1	(AJ009799) ABC transporter protein [Gallus gallus]	132	44	2.00E-30
05711_HH	1	AAF53729.1	(AE003661) CG10639 gene product [Drosophila melanogaster]	154	66	2.00E-38
05714_HH	1	CAB94755.1	(AJ272079) APOBEC-1 stimulating protein [Homo sapiens]	230	65	6.00E-60
05716_HH	1	A47392	chromodomain-helicase-DNA-binding protein, CHD-1 - mouse	60.5	25	1.00E-08

05717_HH	1	P81156	GOX_PENAG GLUCOSE OXIDASE (GLUCOSE OXYHYDRASE) (GOD) (BETA-D-GLUCOSE:OXYGEN 1-OXIDO-REDUCTASE) pdb|1GPE|A Chain A, Glucose Oxidase From Penicillium Amagasakiense pdb|1GPE|B Chain B, Glucose Oxidase From Penicillium Amagasakiense	30.9	41	9.1
05720_HH	1	T18524	scavenger receptor cysteine-rich protein homolog srcrm2 - Geodia cydonium emb|CAA75175.1| (Y14953) SRCR domain, membrane form 2 [Geodia cydonium]	78.4	48	5.00E-14
05723_HH	1	BAA35092.1	(AB015894) neural specific sr protein NSSR 1 [Mus musculus]	82.7	42	2.00E-15
05726_HH	1	CAA68369.1	(Y00222) delta protein [Drosophila melanogaster]	55	44	5.00E-07
05727_HH	1	AL355838.2	CNS051C1 Human chromosome 14 DNA sequence IN PROGRESS BAC R-705B14 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete	38.2	100	3.5
05728_HH	1	AAF49618.1	(AE003530) CG7739 gene product [Drosophila melanogaster]	34	35	1
05730_HH	1	S22804	replication licensing factor MCM3 - mouse (fragment)	276	84	1.00E-73
05732_HH	1	BAA95977.1	(AB040886) KIAA1453 protein [Homo sapiens]	58.2	33	6.00E-08
05739_HH	1	Q05116	MPK1_XENLA DUAL SPECIFICITY MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAP KINASE KINASE 1) (MAPKK 1) (ERK ACTIVATOR KINASE 1) (MAPK/ERK KINASE 1) (MEK1) pir||S36186 mitogen-activated protein kinase kinase (EC 2.7.1.-) 1 - African clawed frog dbj|BAA02860.1| (D13700) MAP kinase kinase [Xenopus laevis]	120	59	1.00E-26
05742_HH	1	AF167979.1	AF167979 Dictyostelium discoideum protein phosphatase 2A B55 regulatory subunit (pppD) mRNA, complete cds	46.1	100	0.014
05743_HH	2	AAC18911.1	(U86634) metalloproteinase-disintegrin-like protein [Agkistrodon contortrix laticinctus]	42.2	28	0.004
05744_HH	1	F64405	methyl coenzyme M reductase (EC 1.8.-.-) I alpha chain - Methanococcus jannaschii	31.3	68	6.9
05745_HH	1	AAF46317.1	(AE003442) CG2256 gene product [Drosophila melanogaster]	108	41	4.00E-23
05753_HH	1	AE001274.1	AE001274 Leishmania major chromosome 1, complete sequence	44.1	100	0.057
05755_HH	1	AL109914.16	HSBA27F12 Human DNA sequence from clone RP11-27F12 on chromosome 6p22.3-24. Contains STSs and GSSs, complete sequence [Homo sapiens]	48.1	100	0.004
05756_HH	1	AAD04729.1	(AC005531) similar to lymphocyte early activation antigen AIM/CD69; similar to Q07108 (PID:g584906) [Homo sapiens]	50	25	2.00E-05
05757_HH	1	AC005050.2	AC005050 Homo sapiens BAC clone CTB-30L5 from 7q22, complete sequence	44.1	100	0.057
05758_HH	1	AAB03481.1	(U60562) amelogenin [Rattus norvegicus]	36	24	0.27
05762_HH	1	T16475	hypothetical protein F56C9.10 - Caenorhabditis elegans gb|AAB08719.1| (U00063) F56C9.10 gene product [Caenorhabditis elegans]	36	22	0.27
05763_HH	1	AAD28329.1	AF080446_2 (AF080446) adenylosuccinate lyase [Plasmodium chabaudi adami]	31.3	28	3
05764_HH	1	T20080	hypothetical protein C49F8.2 - Caenorhabditis elegans emb|CAA94126.1| (Z70206) Similarity to Hamster moncarboxylate transporter (SW:MOT1_CRILO)~cDNA EST yk14d9.3 comes from this gene~cDNA EST yk294c8.3 comes from this gene~cDNA EST yk294c8.5 comes from this gene~cDNA EST yk219b11.5 comes from this gene	35.2	31	0.43
05765_HH	1	BAA95789.1	(AB009883) KED [Nicotiana tabacum]	48.4	30	5.00E-05
05766_HH	2	T20830	hypothetical protein F13D12.7 - Caenorhabditis elegans emb|CAA88948.1| (Z49127) similar to guanine nucleotide-binding protein beta subunit~cDNA EST yk64c5.5 comes from this gene~cDNA EST yk64c5.3 comes from this gene~cDNA EST yk148a4.5 comes from this gene~cDNA EST yk211a1.5 comes from this gene~cDNA EST yk265d8.5 comes f>	81.1	91	7.00E-15
05769_HH	1	NP_062664.1	neuroendocrine-specific Golgi protein p55 isoform 1 gb|AAD11801.1| (AF107844) neuroendocrine-specific Golgi protein p55 [Rattus norvegicus] gb|AAD11803.1| (AF107845) neuroendocrine-specific Golgi protein p55 [Rattus norvegicus] gb|AAD11805.1| (AF107847) neuroendocrine-specific Golgi protein p55 isoform 1 [Mus musculus] gb|AAF63227.1|AF105254_1 (AF105254) neuroendocrine secretory protein 55 [Rattus norvegicus]	36.4	29	0.21
05770_HH	1	NP_002069.2	golgi autoantigen, golgin subfamily a, 4 gb|AAC50434.1| (U41740) trans-Golgi p230 [Homo sapiens] prf||2211333A peripheral membrane protein p230 [Homo sapiens]	52.7	46	2.00E-06
05778_HH	1	AE002742.1	AE002742 Drosophila melanogaster genomic scaffold 142000013385944, complete sequence	42.1	100	0.22
05784_HH	1	AAF60937.1	(AC024882) contains similarity to a large family of C. elegans hypothetical proteins; see (GB:AF000299, Z81540 and Z98851) [Caenorhabditis elegans]	31.7	34	5.3
05787_HH	1	S74632	hypothetical protein slr1774 - Synechocystis sp. (strain PCC 6803) dbj|BAA16784.1| (D90900) hypothetical protein [Synechocystis sp.]	37.1	31	0.12
05789_HH	1	JC1235	transcription factor BTF3a - human	78	45	4.00E-26
05790_HH	1	NP_014986.1	RNA polymerase I subunit 190 (alpha); Rpa190p sp|P10964|RPA1_YEAST DNA-DIRECTED RNA POLYMERASE I 190 KD POLYPEPTIDE (A190) pir||S67250 DNA-directed RNA polymerase (EC 2.7.7.6) I 190K chain - yeast (Saccharomyces cerevisiae) emb|CAA65029.1| (X95720) O6276 [Saccharomyces cerevisiae] emb|CAA99665.1| (Z75249) ORF YOR341w [Saccharomyces cerevisiae]	33.6	32	1.4
05792_HH	1	AAB71410.1	(AF020432) eukaryotic translation initiation factor XeIF-4AIII [Xenopus laevis]	94.4	71	2.00E-30
05795_HH	1	AC018637.3	AC018637 Human Chromosome 7 clone RP11-175P8, complete sequence [Homo sapiens]	46.1	100	0.014
05796_HH	1	AP002745.1	AP002745 Oryza sativa genomic DNA, chromosome 1, PAC clone:P0489G09, complete sequence	42.1	100	0.22
05797_HH	3	NP_057739.1	GA-binding protein transcription factor, beta subunit 2 (47kD), isoform gamma 2 pir||I38744 nuclear respiratory factor-2 subunit gamma 2 - human gb|AAA65710.1| (U13048) nuclear respiratory factor-2 subunit gamma 2 [Homo sapiens]	63.2	38	2.00E-09
05799_HH	1	AL115423.1	CNS01CEP Botrytis cinerea strain T4 cDNA library under conditions of nitrogen	42.1	100	0.22
05800_HH	1	O08710	THYG_MOUSE THYROGLOBULIN PRECURSOR gb|AAB53204.1| (U76389) thyroglobulin [Mus musculus]	59.7	33	2.00E-08
05801_HH	1	P45479	PPT_RAT PALMITOYL-PROTEIN THIOESTERASE PRECURSOR (PALMITOYL-PROTEIN HYDROLASE) pir||A54717 palmitoyl-protein thioesterase precursor - rat gb|AAA59358.1| (L34262) palmitoyl-protein thioesterase [Rattus norvegicus]	178	57	4.00E-44
05802_HH	1	AAC53193.1	(U92456) WW domain binding protein 6; WBP6/SRPK-1 [Mus musculus]	176	77	2.00E-43
05809_HH	1	Q28955	PNAD_PIG PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA) pir||A55768 asparaginyl-peptide amidohydrolase (EC 3.5.1.-) - pig gb|AAA65019.1| (U17062) protein N-terminal asparagine amidohydrolase [Sus scrofa]	60.9	38	8.00E-09
05812_HH	1	AAF73757.1	AF149768_1 (AF149768) NADH dehydrogenase 3 [Bombyx mori] gnl|NCBI_MITO|ND3_15423 NADH dehydrogenase subunit 3	38.7	56	0.041

05816_HH	1	S70554	calcineurin A homolog CnnA14D splice form I - fruit fly (Drosophila melanogaster) gb|AAC47079.1| (U30493) CnnA14D(I) [Drosophila melanogaster]	101	61	8.00E-38
05817_HH	1	T28953	hypothetical protein F28A12.3 - Caenorhabditis elegans gb|AAC47988.1| (U64851) F28A12.3 gene product [Caenorhabditis elegans]	39.1	36	0.031
05820_HH	1	T04876	hypothetical protein F18F4.20 - Arabidopsis thaliana emb|CAA16600.1| (AL021637) downy mildew resistance-like protein [Arabidopsis thaliana] emb|CAB78992.1| (AL161551) downy mildew resistance-like protein [Arabidopsis thaliana]	41.4	28	0.006
05822_HH	1	AC012147.7	AC012147 Mus musculus, clone RP23-191A4, complete sequence	40.1	100	0.88
05823_HH	1	P39854	CAPE_STAAU CAPE PROTEIN gb|AAA64644.1| (U10927) CapE [Staphylococcus	36.7	28	0.16
05825_HH	1	AAF47970.1	(AE003484) CG1637 gene product [alt 2] [Drosophila melanogaster]	161	47	4.00E-39
05826_HH	2	NP_057508.1	cisplatin resistance-associated overexpressed protein dbj|BAA91981.1| (AK001925) unnamed protein product [Homo sapiens]	75.7	59	2.00E-23
05827_HH	1	AAC63909.1	(AF022228) sarco/endoplasmic reticulum-type Ca-2+-ATPase [Placopecten magellanicus]	293	86	6.00E-79
05828_HH	1	NP_001179.1	BCL2-antagonist/killer 1 sp|Q16611|BAK_HUMAN BCL-2 HOMOLOGOUS ANTAGONIST/KILLER (APOPTOSIS REGULATOR BAK) pir||S58873 Bak protein - human gb|AAA74466.1| (U16811) Bak protein [Homo sapiens] gb|AAA93066.1| (U23765) Bak protein [Homo sapiens] emb|CAA58997.1| (X84213) bcl-2 homologue [Homo sapiens] emb|CAB65626.1| (Z93017) dJ291J10.1 (BCL2-antagonist/killer 1) [Homo sapiens] prf||2110382A bak gene [Homo sapiens] prf||2110383A bak gene [Homo sapiens] prf||2110384A bak gene [Homo sapiens]	41	19	0.008
05829_HH	1	AL109865.36	HSG120K12 Human DNA sequence from clone GS1-120K12 on chromosome 1q25.3-31.2. Contains the gene for ring finger protein DING or BAP-1, an FTH1 (ferritin, heavy polypeptide 1) pseudogene, the 3' end of the gene for a novel protein similar to archaeal, yeast and w>	46.1	100	0.014
05830_HH	1	AAF48133.1	(AE003488) CG1796 gene product [Drosophila melanogaster]	129	68	3.00E-29
05835_HH	1	NP_061235.1	WW domain binding protein 4 gb|AAC34810.1| (AF071184) formin binding protein 21 [Mus musculus]	33.2	36	1.8
05836_HH	1	AL049874.3	CNS0000Q Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-1042B17 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence	42.1	90	0.22
05844_HH	1	P31018	EF1A_ENTHI ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) gb|AAA29096.1| (M92073) elongation factor-1 alpha [Entamoeba histolytica]	96.7	54	1.00E-19
05847_HH	1	AAC79839.1	(AF080468) putative glycogen storage disease type 1b protein [Rattus norvegicus]	77.3	29	1.00E-13
05848_HH	1	AAF78249.1	AF276997_1 (AF276997) tricarboxylate carrier-like protein [Rattus norvegicus]	206	58	2.00E-52
05849_HH	1	S68306	pol polyprotein, truncated - red flour beetle retrotransposon Woot gb|AAC47271.1| (U09586) protease, reverse transcriptase and RNase H [Tribolium castaneum]	32.1	41	4
05850_HH	1	AC009044.3	AC009044 Homo sapiens chromosome 16 clone RP11-190D6, complete sequence	40.1	100	0.88
05851_HH	1	CAB88187.1	(AL352972) putative transmembrane transport protein [Streptomyces coelicolor A3(2)]	32.1	33	4
05855_HH	1	BAA22437.1	(D32066) BMP receptor [Xenopus laevis]	137	47	7.00E-32
05856_HH	1	AF266101.1	AF266101 Sympetrum vulgatum large subunit ribosomal RNA gene, partial sequence; tRNA-Valine gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence; mitochondrial genes for mitochondrial products	40.1	92	0.88
05857_HH	1	P55260	ANX4_RAT ANNEXIN IV (LIPOCORTIN IV) (36 KDA ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP36) dbj|BAA07399.1| (D38224) ZAP 36/annexin IV [Rattus norvegicus]	113	54	1.00E-24
05859_HH	1	NP_062350.1	fatty acid-Coenzyme A ligase, long chain 4 emb|CAB95965.1| (AJ243502) Acyl-CoA synthetase, long chain [Mus musculus]	137	47	9.00E-32
05862_HH	11	NP_055701.1	hypothetical protein emb|CAA10008.1| (AJ012409) hypothetical protein [Homo sapiens]	100	61	9.00E-21
05863_HH	1	AAF58011.1	(AE003807) Vha44 gene product [alt 1] [Drosophila melanogaster]	143	46	9.00E-34
05865_HH	1	Z98884.11	HS467L1 Human DNA sequence from clone RP3-467L1 on chromosome 1p36.21-36.33. Contains the 3' part of gene KIAA0833, the VAMP3 gene for vesicle-associated membrane protein 3 (cellubrevin), the PER3 gene for period (Drosophila) homolog 3 and the gene for urotens>	42.1	100	0.22
05868_HH	1	NC_001134.1	Saccharomyces cerevisiae chromosome II, complete chromosome sequence	40.1	100	0.88
05870_HH	1	AAF56763.1	(AE003763) CG5514 gene product [Drosophila melanogaster]	34.4	36	0.8
05871_HH	1	CAB73116.1	(AL139076) putative integral membrane protein [Campylobacter jejuni]	32.1	33	4
05873_HH	1	AAC83350.1	(AF089730) potassium channel subunit [Rattus norvegicus]	152	61	3.00E-36
05876_HH	1	CAB70660.1	(AL137259) hypothetical protein [Homo sapiens]	90.1	37	1.00E-17
05878_HH	1	AAF47943.1	(AE003482) CG7479 gene product [Drosophila melanogaster]	124	58	7.00E-28
05879_HH	1	AAB38008.1	(U80959) putative outer membrane protein [Borrelia burgdorferi]	42.6	26	0.003
05881_HH	1	P92176	ACT2_LUMTE ACTIN 2 pir||JC5228 actin 2 - earthworm (Lumbricus terrestris) emb|CAA65365.1| (X96516) Actin [Lumbricus terrestris] emb|CAA65362.1| (X96513) Actin [Lumbricus terrestris]	177	58	7.00E-44
05882_HH	1	AC006312.8	AC006312 Homo sapiens chromosome 9, clone hRPK.401_G_18, complete sequence	40.1	100	0.56
05883_HH	1	T27132	hypothetical protein Y53C12B.5a - Caenorhabditis elegans pir||T42238 transcription factor MAB-3 homolog - Caenorhabditis elegans gb|AAC38956.1| (AF022388) putative transcription factor MAB-3 [Caenorhabditis elegans] emb|CAB16489.1| (Z99278) predicted using Genefinder~similar to DM DNA binding domain~cDNA EST yk69b1.5 comes from this gene [Caenorhabditis elegans]	70.6	31	1.00E-11
05884_HH	1	NP_006283.1	tumor susceptibility gene 101 sp|Q99816|TS101_HUMAN TUMOR SUSCEPTIBILITY GENE 101 PROTEIN gb|AAC52083.1| (U82130) tumor susceptibility protein [Homo	139	42	2.00E-32
05892_HH	1	AF174095.1	AF174095 Homo sapiens clone sc77u-09 immunoglobulin heavy chain variable region (IgH) mRNA, partial cds	40.1	100	0.88
05893_HH	1	NP_031719.1	chromogranin A sp|P26339|CMGA_MOUSE CHROMOGRANIN A PRECURSOR (CGA) [CONTAINS: PANCREASTATIN; BETA-GRANIN; WE-14] pir||A39868 chromogranin A precursor - mouse gb|AAA37457.1| (M64278) chromogranin A [Mus musculus]	36	32	0.27
05894_HH	1	NP_001331.1	cylicin 2 sp|Q14093|CYL2_HUMAN CYLICIN II (MULTIPLE-BAND POLYPEPTIDE II) pir||I37271 cylicin II - human emb|CAA86752.1| (Z46788) human cylicin II [Homo sapiens]	35.6	36	0.35
05895_HH	1	AAF48351.1	(AE003495) CG1375 gene product [Drosophila melanogaster]	31.7	37	5.3
05900_HH	2	AAC38975.1	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]	36.7	23	0.16
05902_HH	1	NP_044881.1	helicase-primase emb|CAA70277.1| (Y09060) DNA helicase-primase compelx component [murine herpesvirus 68] gb|AAB66409.1| (U97553) helicase-primase [murid herpesvirus 4] gb|AAF19308.1|AF105037_40 (AF105037) 44 [murid herpesvirus 4]	31.7	26	5.3
05906_HH	1	CAA08994.1	(AJ010090) MAP3K alpha protein kinase [Arabidopsis thaliana]	39.5	38	0.022

05912_HH	1	U33021.1	CEU33021 Culex erraticus clone EUH2333 putative 5.8S rRNA gene, complete sequence, 18S rRNA and 28S rRNA genes, partial sequence, and internal transcribed spacers 1 and	42.1	100	0.22
05914_HH	1	AAF46005.1	(AE003433) CG5086 gene product [Drosophila melanogaster]	34	28	1
05920_HH	1	NC_001993.1	Melanoplus sanguinipes entomopoxvirus, complete genome	42.1	100	0.22
05923_HH	1	T32833	hypothetical protein F33H12.6 - Caenorhabditis elegans gb|AAB95006.1| (AF040649) contains similarity to helicases [Caenorhabditis elegans]	38.7	36	0.041
05927_HH	1	NP_062831.1	CTP synthase II gb|AAF91241.1|AF226667_1 (AF226667) CTP synthetase isoform [Homo sapiens]	212	59	2.00E-54
05933_HH	2	AAG01031.1	AF290981_1 (AF290981) ornithine decarboxylase [Danio rerio]	74.9	55	5.00E-13
05934_HH	1	G71615	phospholipase A2-like a/b fold hydrolase PFB0410c - malaria parasite (Plasmodium falciparum) gb|AAC71871.1| (AE001393) phospholipase A2-like a/b fold hydrolase [Plasmodium falciparum]	32.1	32	4
05935_HH	1	AAA74396.1	(U30468) cytochrome c oxidase subunit IV [Urechis caupo]	61.3	44	2.00E-12
05936_HH	1	AAF27140.1	AC016529_3 (AC016529) hypothetical protein [Arabidopsis thaliana]	56.2	28	2.00E-07
05941_HH	1	AC005549.1	AC005549 Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence	44.1	96	0.057
05943_HH	1	AAA96074.1	(U51995) F07G6.3 gene product [Caenorhabditis elegans]	34.8	22	0.61
05944_HH	1	NP_055643.1	KIAA0737 gene product dbj|BAA34457.1| (AB018280) KIAA0737 protein [Homo sapiens]	47.3	32	1.00E-04
05948_HH	1	CAA06918.1	(AJ006219) clathrin-associated protein [Drosophila melanogaster] gb|AAF14247.1|AF110231_1 (AF110231) clathrin-associated adaptor complex AP-1 medium chain [Drosophila melanogaster] gb|AAF54399.1| (AE003683) AP-47 gene product [Drosophila melanogaster]	252	69	2.00E-66
05949_HH	2	AAF59384.1	(AE003846) CG11059 gene product [Drosophila melanogaster]	108	37	4.00E-23
05952_HH	1	AAF19031.1	AF206661_1 (AF206661) neuronal tetraspanin [Gallus gallus]	105	40	4.00E-22
05953_HH	2	P12262	EF1B_ARTSA ELONGATION FACTOR 1-BETA (EF-1-BETA) pir||A24806 translation elongation factor eEF-1 beta chain - brine shrimp gb|AAC83402.1| (M35636) elongation factor 1-beta [Artemia salina] prf||1212288A elongation factor 1beta [Artemia salina]	62.5	45	1.00E-14
05954_HH	1	AAF52579.1	(AE003619) CG7093 gene product [Drosophila melanogaster]	37.5	31	0.092
05958_HH	1	NP_005476.1	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 2 gb|AAD29855.1|AF083068_1 (AF083068) NAD+ ADP-ribosyltransferase 3 [Homo sapiens]	185	54	2.00E-46
05964_HH	2	T31613	hypothetical protein Y50E8A.i - Caenorhabditis elegans	36.4	35	0.21
05967_HH	1	AF226710.1	AF226710 Mus musculus tryptase 4 gene, complete cds	40.1	95	0.88
05969_HH	1	AAB48482.1	(U87224) contactin associated protein [Rattus norvegicus] gb|AAC53342.1| (AF000114) paranodin [Rattus norvegicus]	34	25	1
05971_HH	1	AAF58440.1	(AE003820) CG17019 gene product [Drosophila melanogaster]	36.4	24	0.21
05973_HH	1	BAA86446.1	(AB032958) KIAA1132 protein [Homo sapiens]	47.6	28	8.00E-05
05976_HH	1	JC5638	pH-sensing regulatory factor - human dbj|BAA22632.1| (AB001328) pH-sensing regulatory factor of peptide transporter [Homo sapiens]	112	47	2.00E-24
05979_HH	1	NP_054779.1	MCT-1 protein dbj|BAA86055.1| (AB034206) MCT-1 [Homo sapiens]	219	61	2.00E-56
05981_HH	1	AC024877.1	CELY95B8A Caenorhabditis elegans cosmid Y95B8A, complete sequence	46.1	93	0.014
05985_HH	1	NP_001139.1	ankyrin 2, neuronal sp|Q01484|ANK2_HUMAN ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID) pir||S37431 ankyrin 2, neuronal long splice form - human prf||2003319A ankyrin B:ISOTYPE=440kD [Homo sapiens]	37.5	37	0.092
05986_HH	1	P44974	YA05_HAEIN HYPOTHETICAL PROTEIN HI1005 pir||I64163 hypothetical protein HI1005 - Haemophilus influenzae (strain Rd KW20) gb|AAC22666.1| (U32781) conserved hypothetical protein [Haemophilus influenzae Rd]	34.4	25	0.8
05988_HH	1	NP_038827.1	arginine-tRNA-protein transferase 1 gb|AAD12365.1| (AF079097) arginine-tRNA-protein transferase 1-2p; ATE1-2p [Mus musculus]	62.1	48	4.00E-09
05989_HH	1	AC000098.1	YUP8H12 Arabidopsis thaliana chromosome 1 YAC yUP8H12 complete sequence	40.1	100	0.88
05991_HH	1	AAF36051.1	(AC024206) Hypothetical protein Y74C9A.5 [Caenorhabditis elegans]	32.5	42	3.1
05994_HH	1	NP_000326.1	sodium channel, voltage-gated, type V, alpha polypeptide (long (electrocardiographic) QT syndrome 3) sp|Q14524|CIN5_HUMAN SODIUM CHANNEL PROTEIN, CARDIAC MUSCLE ALPHA-SUBUNIT (HH1) pir||A38195 sodium channel protein hHI, cardiac - human gb|AAA58644.1| (M77235) sodium channel alpha subunit [Homo sapiens]	35.6	39	0.35
05995_HH	1	AAG08586.1	AE004933_2 (AE004933) conserved hypothetical protein [Pseudomonas aeruginosa]	51.9	34	4.00E-06
05999_HH	1	AAF86207.1	(AF238892) VrrB [Bacillus anthracis]	31.3	35	6.9
06004_HH	1	NP_005727.1	ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha) ref|NP_058556.1| actin-related protein 1 homolog A (yeast) sp|P42024|ACTZ_HUMAN ALPHA-CENTRACTIN (CENTRACTIN) (CENTROSOME-ASSOCIATED ACTIN HOMOLOG) (ACTIN-RPV) (ARP1) pir||S29075 centractin - dog pir||S29089 alpha-centractin - human emb|CAA78701.1| (Z14978) actin-related protein [Homo sapiens] gb|AAB23391.1| actin-related protein, actin-RPV=dynactin complex major component [human, N-Tera teratocarcinoma, Peptide, 376 aa] gb|AAC15824.1| (S45367) centractin [Canis familiaris] emb|CAA57690.1| (X82206) alpha-centractin [Homo sapiens] dbj|BAA24423.1| (AB010297) actin-related protein 1 alpha-isoform [Mus musculus] prf||1818359A centractin [Canis familiaris]	240	73	7.00E-63
06005_HH	1	NP_032808.1	paired box gene 5 sp|Q02650|PAX5_MOUSE PAIRED BOX PROTEIN PAX-5 (B-CELL SPECIFIC TRANSCRIPTION FACTOR) (BSAP) gb|AAA37325.1| (M97013) transcription factor [Mus musculus]	190	80	8.00E-48
06008_HH	1	NM_016777.1	Mus musculus nuclear autoantigenic sperm protein (histone-binding) (Nasp), mRNA	38.2	100	3.5
06009_HH	1	No Match				
06010_HH	1	Q11208	PPOL_SARPE POLY [ADP-RIBOSE] POLYMERASE (PARP) (ADPRT) (NAD(+) ADP-RIBOSYLTRANSFERASE) (POLY[ADP-RIBOSE] SYNTHETASE) pir||S42208 NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - flesh fly (Sarcophaga peregrina) dbj|BAA03943.1| (D16482) poly(ADP-ribose) polymerase [Sarcophaga peregrina]	149	53	2.00E-35
06012_HH	1	H70450	lipoprotein NlpD fragment - Aquifex aeolicus gb|AAC07590.1| (AE000754) lipoprotein NlpD fragment [Aquifex aeolicus]	30.9	27	9.1
06014_HH	1	AAF52426.1	(AE003614) GRHR gene product [Drosophila melanogaster]	39.9	27	0.018
06015_HH	1	AAF60863.1	(AC006815) contains similarity to Pfam family 3' exoribonuclease (PF01138), score=33, E=2.3e-06, N=1 [Caenorhabditis elegans]	178	52	4.00E-44
06025_HH	1	NP_057083.1	CGI-45 protein gb|AAD34040.1|AF151803_1 (AF151803) CGI-45 protein [Homo sapiens]	110	52	8.00E-24
06027_HH	1	NP_032474.1	kinesin family member 5B sp|Q61768|KINH_MOUSE KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) gb|AAB53940.1| (U86090) kinesin heavy chain [Mus musculus]	41	27	0.008

06034_HH	1	P12216	CCSA_TOBAC CYTOCHROME C BIOGENESIS PROTEIN CCSA pir||A05213 cytochrome c-type synthesis protein homolog - common tobacco chloroplast emb|CAA77395.1| (Z00044) c-type cytochrome synthesis protein [Nicotiana tabacum] prf||1211235CN ORF 313 [Nicotiana tabacum]	30.9	33	9.1
06036_HH	1	P52709	SYTC_CAEEL PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIGASE) (THRRS) pir||T19994 hypothetical protein C47D12.6 - Caenorhabditis elegans emb|CAA93762.1| (Z69902) predicted using Genefinder~Similarity to Human threonyl-tRNA synthetase (SW:SYTC_HUMAN)~cDNA EST EMBL:M89192 comes from this gene~cDNA EST EMBL:M89296 comes from this gene~cDNA EST yk29d3.3 comes from this gene~cDNA EST yk29d3.5 comes from thi>	270	78	9.00E-72
06040_HH	2	NP_037434.1	elongation factor-2 kinase sp|O00418|EF2K_HUMAN ELONGATION FACTOR 2 KINASE (EEF-2 KINASE) (EEF-2K) (CALCIUM/CALMODULIN-DEPENDENT EUKARYOTIC ELONGATION FACTOR-2 KINASE) gb|AAB58270.1| (U93850) elongation factor-2 kinase [Homo sapiens]	203	73	1.00E-51
06041_HH	1	AL356596.2	CNS05TDF Human chromosome 14 DNA sequence IN PROGRESS BAC R-354G16 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence	44.1	96	0.057
06043_HH	1	NP_038470.1	stomatin-like protein 2 gb|AAF09142.1|AF190167_1 (AF190167) membrane associated protein SLP-2 [Homo sapiens] gb|AAF91466.1|AF282596_1 (AF282596) stomatin-like protein 2 [Homo sapiens]	141	65	3.00E-33
06048_HH	1	AL136381.12	AL136381 Human DNA sequence from clone RP5-905H16 on chromosome 1p22.1-22.3, complete sequence [Homo sapiens]	42.1	100	0.22
06049_HH	1	Q03745	C1EB_BACTA PESTICIDIAL CRYSTAL PROTEIN CRY1EB (INSECTICIDAL DELTA-ENDOTOXIN CRYIE(B)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (134 KDA CRYSTAL PROTEIN) gb|AAA22346.1| (M73253) cryIE(b) [Bacillus thuringiensis]	33.6	66	1.4
06051_HH	1	S48158	glycosylation-inhibiting factor - bovine gb|AAB32021.1| p12a isoform=macrophage migration-inhibitory factor [cattle, Peptide, 114 aa]	94.8	42	4.00E-19
06053_HH	1	AAF51355.1	(AE003585) CG14352 gene product [Drosophila melanogaster]	31.3	31	5.1
06055_HH	1	BAA34985.1	(AB016994) PRH4 [Dugesia japonica]	58.2	33	5.00E-08
06056_HH	1	Q16975	KPC2_APLCA CALCIUM-INDEPENDENT PROTEIN KINASE C (APL II) gb|AAA27771.1| (M94884) protein kinase C [Aplysia californica] prf||1716374B protein kinase C II [Aplysia californica]	101	41	7.00E-21
06061_HH	2	AAF54422.1	(AE003683) CG9492 gene product [Drosophila melanogaster]	222	60	2.00E-57
06064_HH	1	CAA22835.1	(AL035245) /prediction=(method:""genefinder"", version:""084"", score:""51.86"")~/prediction=(method:""genscan"", version:""1.0"") [Drosophila melanogaster] gb|AAF45701.1| (AE003422) EG:BACH6115.1 gene product [Drosophila melanogaster]	34.4	29	0.8
06065_HH	1	NP_004701.1	synaptogyrin 2 sp|O43760|SNG2_HUMAN SYNAPTOGYRIN 2 (CELLUGYRIN) emb|CAA05325.1| (AJ002308) synaptogyrin 2 [Homo sapiens]	136	41	1.00E-31
06072_HH	1	CAB62867.1	(AL035475) hypothetical protein, MAL4P2.26 [Plasmodium falciparum]	32.5	30	2.2
06077_HH	1	AAF52089.1	(AE003605) CG1129 gene product [Drosophila melanogaster]	153	59	8.00E-37
06078_HH	1	AAC28787.1	(AF047722) adenylate kinase [Trypanosoma brucei rhodesiense]	53.5	24	1.00E-06
06080_HH	1	AAF51993.1	(AE003602) CG2919 gene product [Drosophila melanogaster]	39.9	27	0.018
06081_HH	1	AAD05297.1	(AF082511) putative glucose/galactose binding protein precursor MglB [Treponema denticola]	32.1	35	4
06082_HH	1	AAA62102.1	(L10328) high affinity ribose transport protein [Escherichia coli]	32.1	58	4
06083_HH	1	AAD43813.1	AF164349_1 (AF164349) Na,K-ATPase alpha-4 subunit [Mus musculus]	256	79	1.00E-67
06095_HH	2	AAC72364.1	(AF093575) surface antigen ariel1 [Entamoeba histolytica]	41.8	38	0.005
06103_HH	1	A41609	dnaK-type molecular chaperone - Cryptomonas sp. chloroplast (strain Phi)	39.9	30	0.014
06105_HH	1	CAA32191.1	(X14031) protein phosphatase X (203 AA) [Oryctolagus cuniculus]	242	80	2.00E-63
06107_HH	1	T32961	hypothetical protein C11D2.4 - Caenorhabditis elegans gb|AAC02573.1| (AF045640) C11D2.4 gene product [Caenorhabditis elegans]	128	38	4.00E-29
06108_HH	1	AAF39361.1	(AE002320) glycogen phosphorylase [Chlamydia muridarum]	33.6	29	1.4
06109_HH	1	AC068658.3	AC068658 Homo sapiens chromosome 5 clone CTC-228N24, complete sequence	48.1	96	0.004
06111_HH	1	P55735	SC13_HUMAN SEC13-RELATED PROTEIN	178	58	4.00E-44
06113_HH	1	AAF49047.1	(AE003514) Clc gene product [Drosophila melanogaster]	56.2	26	2.00E-07
06114_HH	1	NP_042523.1	ORF putative L1 emb|CAA54856.1| (X77858) ORF putative L1 [Human papillomavirus type 59]	33.2	25	1.8
06115_HH	1	AC069298.8	AC069298 Homo sapiens chromosome 3 clone RP11-56K23, complete sequence	38.2	100	3.5
06116_HH	1	AAF46127.1	(AE003436) CG4222 gene product [Drosophila melanogaster]	194	57	7.00E-49
06119_HH	1	P01474	CX2_NAJME CYTOTOXIN 2 (CYTOTOXINS V-II-2 AND V-II-3) pir||H3NJ2W cytotoxin 2 - forest cobra	38.7	55	0.022
06123_HH	1	AE003612.1	AE003612 Drosophila melanogaster genomic scaffold 142000013386055 section 5 of 63, complete sequence	42.1	100	0.15
06127_HH	1	BAA21390.1	(AB004534) miosis-specific transcription factor [Schizosaccharomyces pombe] dbj|BAA25402.1| (AB012695) forkhead/HNF3 homologue [Schizosaccharomyces pombe]	34.8	25	0.61
06130_HH	1	S57218	twitchin - Caenorhabditis elegans (fragment)	51.2	29	7.00E-06
06131_HH	1	CAB42096.1	(AJ132045) shAT2 protein [Theileria annulata]	36.4	28	0.18
06133_HH	1	BAA23524.1	(D38036) Truncated TSH receptor [Rattus sordidus]	34	40	1
06135_HH	1	S09142	ND5 intron 1 protein - Podospora anserina mitochondrion	30.5	27	2.3
06140_HH	1	Q92777	SYN2_HUMAN SYNAPSIN II gb|AAC28368.1| (AF077671) synapsin IIa [Homo sapiens]	34.4	28	0.8
06141_HH	1	AL008634.1	HS396D17 Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence [Homo sapiens]	40.1	100	0.88
06145_HH	1	NP_035311.1	pleckstrin homology, Sec7 and coiled/coil domains 2 gb|AAB41444.1| (U83896) Rat homologues of yeast sec7p [Rattus norvegicus] dbj|BAA33429.1| (AB013466) cytohesin 2 [Mus musculus] gb|AAC77924.1| (AF079971) cytohesin-2 [Mus musculus]	103	35	1.00E-21
06151_HH	1	AAD40880.1	AF154826_1 (AF154826) insulin receptor substrate [Drosophila melanogaster] gb|AAD43005.1|AF092046_1 (AF092046) insulin receptor substrate [Drosophila melanogaster] gb|AAF52882.1| (AE003628) flp gene product [Drosophila melanogaster]	36	29	0.27
06152_HH	1	T40696	hypothetical protein SPBC83.07 - fission yeast (Schizosaccharomyces pombe) emb|CAB36869.1| (AL035536) hypothetical protein [Schizosaccharomyces pombe]	29	40	6.7
06154_HH	1	T00065	hypothetical protein KIAA0442 - human (fragment) dbj|BAA23714.1| (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]	29.7	34	4
06156_HH	1	AAF52796.1	(AE003625) CG15828 gene product [Drosophila melanogaster]	33.6	36	1.4

06157_HH	1	T39943	hypothetical protein SPBC23E6.09 - fission yeast (Schizosaccharomyces pombe) emb|CAA18877.1| (AL023287) tpr domain protein [Schizosaccharomyces pombe]	42.2	27	0.004
06164_HH	1	CAA69646.1	(Y08359) ethylene response sensor protein [Rumex palustris] gb|AAB68819.1| (U63291) ethylene receptor [Rumex palustris]	32.8	44	2.3
06166_HH	1	CAA07196.1	(AJ006701) putative serine/threonine protein kinase [Homo sapiens]	40.2	58	0.014
06167_HH	3	F22845	hypothetical protein 6 - Trypanosoma brucei mitochondrion	40.6	27	0.011
06170_HH	1	AAA29873.1	(L00992) essential myosin light chain [Schistosoma mansoni]	196	64	1.00E-49
06171_HH	1	BAB03453.1	(AB046539) cysteine-rich protease inhibitor [Mus musculus]	120	37	7.00E-27
06173_HH	1	Q18179	YXX5_CAEEL PUTATIVE NEUROPEPTIDE Y RECEPTOR (NPY-R) pir||T15622 hypothetical protein C25G6.5 - Caenorhabditis elegans gb|AAA82357.1| (U41028) similar to neuropeptide Y receptor type 1 (NYP1-R) and other family 1 G-protein coupled receptors [Caenorhabditis elegans]	96.3	43	2.00E-19
06176_HH	1	P11620	YPT1_SCHPO YPT1-RELATED PROTEIN 1 pir||S10025 GTP-binding protein ypt1 - fission yeast (Schizosaccharomyces pombe) emb|CAA36319.1| (X52099) ypt1 [Schizosaccharomyces pombe] emb|CAB66454.1| (AL136536) ypt1-related protein 1 [Schizosaccharomyces pombe]	62.5	37	3.00E-09
06179_HH	1	NP_011031.1	Nucleoporin similar to Nup157p and to mammalian Nup155p; Nup157p sp|P40064|N157_YEAST NUCLEOPORIN NUP157 (NUCLEAR PORE PROTEIN NUP157) pir||S50608 hypothetical protein YER105c - yeast (Saccharomyces cerevisiae) gb|AAB64660.1| (U18839) Nup157p: nucleoporin [Saccharomyces cerevisiae]	32.1	36	4
06183_HH	1	AAF52137.1	(AE003606) CG1084 gene product [Drosophila melanogaster]	71	33	8.00E-12
06184_HH	1	AC002381.1	AC002381 Human BAC clone CTB-20D2 from 7q22, complete sequence [Homo sapiens]	42.1	100	0.22
06187_HH	1	AC007364.2	AC007364 Homo sapiens BAC clone RP11-329H24 from 2, complete sequence	40.1	92	0.22
06189_HH	1	AAF04108.1	AF188360_1 (AF188360) filamin A [Drosophila melanogaster]	70.2	27	1.00E-11
06190_HH	1	CAB51772.1	(Z97187) swiss cheese protein [Drosophila melanogaster]	36	29	0.27
06192_HH	1	NP_011450.1	glycosyltransferase; Alg2p sp|P43636|ALG2_YEAST GLYCOSYLTRANSFERASE ALG2 pir||S64069 ALG2 protein precursor - yeast (Saccharomyces cerevisiae) emb|CAA96768.1| (Z72587) ORF YGL065c [Saccharomyces cerevisiae]	31.7	36	5.3
06196_HH	1	NP_013887.1	Predicted 758 amino acid polypeptide with poly-glutamine and poly-asparagine domains; Mss11p sp|Q03825|YM38_YEAST HYPOTHETICAL 85.0 KD PROTEIN IN HLJ1-SMP2 INTERGENIC REGION pir||S54522 hypothetical protein YMR164c - yeast (Saccharomyces cerevisiae) emb|CAA89800.1| (Z49705) unknown [Saccharomyces cerevisiae]	41.8	25	0.005
06200_HH	1	BAA91475.1	(AK001034) unnamed protein product [Homo sapiens]	102	41	2.00E-21
06201_HH	1	NP_006650.1	gamma-tubulin complex protein 2 gb|AAC39728.1| (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]	70.6	26	9.00E-12
06202_HH	1	T24703	hypothetical protein T08G3.6 - Caenorhabditis elegans emb|CAB05796.1| (Z83238) T08G3.6 [Caenorhabditis elegans]	30.5	51	7.1
06206_HH	1	CAA34473.1	(X16454) carcinoembryonic antigen subdomain B [Homo sapiens]	30.5	35	6
06209_HH	1	NP_060943.1	uncharacterized hypothalamus protein HT012 dbj|BAA91215.1| (AK000508) unnamed protein product [Homo sapiens] gb|AAF67006.1|AF155649_1 (AF155649) hypothetical 15 kDa protein [Homo sapiens] gb|AAF67651.1|AF220186_1 (AF220186) uncharacterized hypothalamus protein HT012 [Homo sapiens]	90.9	34	8.00E-18
06210_HH	1	AL133335.29	AL133335 Human DNA sequence from clone RP5-1162C3 on chromosome 20 Contains the prefoldin 4 (PFDN4) gene (C-1), two CpG islands, ESTs, STSs and GSSs, complete sequence [Homo sapiens]	38.2	100	0.69
06216_HH	1	P34612	YOG3_CAEEL HYPOTHETICAL 17.5 KD PROTEIN ZK112.3 IN CHROMOSOME III pir||S44891 ZK112.3 protein - Caenorhabditis elegans gb|AAA28186.1| (L14324) putative [Caenorhabditis elegans]	30.1	42	2.9
06217_HH	1	AAD25542.1	AF134591_1 (AF134591) P-type ATPase 2 [Cryptosporidium parvum]	31.7	26	5.3
06220_HH	1	NP_057437.1	rec dbj|BAA88923.1| (AB023584) reduced expression in cancer [Homo sapiens]	122	62	3.00E-27
06229_HH	1	S55036	tyrosine-rich hydroxyproline-rich glycoprotein - parsley (fragment)	32.1	37	0.76
06230_HH	1	T29265	hypothetical protein C01G8.7 - Caenorhabditis elegans gb|AAB37645.1| (U80439) coded for by C. elegans cDNA yk7c8.5; coded for by C. elegans cDNA yk133b3.5; coded for by C. elegans cDNA yk65a4.5; coded for by C. elegans cDNA yk7c8.3; coded for by C. elegans cDNA CEESQ66F; coded for by C. elegans cDNA yk65a4.3; coded for >	30.9	59	5.1
06232_HH	1	CAB89878.1	(AL354632) hypothetical protein [Schizosaccharomyces pombe]	30.1	45	6.2
06235_HH	1	AC002062.1	F20P5 Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence	42.1	100	0.067
06238_HH	1	BAA97048.1	(AB041881) cytoplasmic dynein heavy chain [Rattus norvegicus]	148	44	3.00E-35
06240_HH	1	AF192134.1	AF192134 Mus musculus surfactant protein-D gene, complete cds	46.1	100	0.006
06241_HH	1	AAF67472.1	AF150732_1 (AF150732) protein tyrosine phosphatase [Homo sapiens]	86.2	35	2.00E-16
06244_HH	1	AAF13869.1	AF179359_1 (AF179359) cyclin-dependent kinase inhibitor [Caenorhabditis elegans]	37.5	26	0.092
06245_HH	2	AAF57974.1	(AE003806) CG5065 gene product [Drosophila melanogaster]	120	52	1.00E-26
06249_HH	3	AAF59637.1	(AC024755) Hypothetical protein Y34B4A.b [Caenorhabditis elegans]	30.9	38	9.1
06258_HH	1	NP_044474.1	UL5 sp|P28277|HELI_HSV2H PROBABLE HELICASE emb|CAB06765.1| (Z86099) UL5 [human herpesvirus 2]	32.1	36	4
06259_HH	1	AC022522.2	AC022522 T28K15, complete sequence [Arabidopsis thaliana]	42.1	96	0.22
06260_HH	1	O16005	OPSD_SEPOF RHODOPSIN gb|AAC26329.1| (AF000947) rhodopsin [Sepia officinalis]	36.4	34	0.083
06262_HH	1	AAB05596.1	(U57816) SH2/SH3 adaptor protein [Drosophila melanogaster]	57.4	52	1.00E-07
06263_HH	1	P12115	KAD_CYPCA ADENYLATE KINASE (ATP-AMP TRANSPHOSPHORYLASE) pir||KICAC adenylate kinase (EC 2.7.4.3), cytosolic - common carp	92.1	76	4.00E-18
06266_HH	1	NP_064341.1	deoxyribonuclease DLAD gb|AAF05082.1|AF128888_1 (AF128888) deoxyribonuclease DLAD [Mus musculus]	100	36	1.00E-20
06269_HH	1	AAF46510.1	(AE003447) CG12141 gene product [Drosophila melanogaster]	218	61	3.00E-56
06270_HH	1	AL033522.1	HS451B21 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, complete sequence [Homo sapiens]	42.1	100	0.22
06275_HH	1	AL353580.7	AL353580 Human DNA sequence from clone RP11-248N6 on chromosome 13, complete sequence [Homo sapiens]	40.1	95	0.88
06276_HH	1	AAC46985.1	(U30874) cyclophilin B [Schistosoma mansoni] prf||2208425A B-like cyclophilin [Schistosoma mansoni]	80.4	51	6.00E-15
06282_HH	1	Q61084	M3K3_MOUSE MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 3 (MAPK/ERK KINASE KINASE 3) (MEK KINASE 3) (MEKK 3) gb|AAB03535.1| (U43187) MEK Kinase 3 [Mus musculus]	135	42	3.00E-31

06284_HH	1	AC016955.15	AC016955 Homo sapiens 3 BAC RP11-21I16 (Roswell Park Cancer Institute Human BAC Library) complete sequence	61.9	94	2.00E-07
06285_HH	1	AL121981.17	HS1061C18 Human DNA sequence from clone RP5-1061C18 on chromosome 1p36.22-36.33, complete sequence [Homo sapiens]	46.1	96	0.014
06286_HH	1	AL161516.2	ATCHRIV28 Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28	40.1	100	0.4
06287_HH	1	NP_034759.1	kinesin-associated protein 3 dbj|BAA08902.1| (D50367) KAP3B [Mus musculus]	194	60	5.00E-49
06288_HH	1	T16345	hypothetical protein F42C5.9 - Caenorhabditis elegans gb|AAA81487.1| (U40799) coded for by C. elegans cDNA CESAA62F; coded for by C. elegans cDNA CEESL37R; coded for by C. elegans cDNA CEESV61F; coded for by C. elegans cDNA CEESX16F; coded for by C. elegans cDNA CEESL37F; coded for by C. elegans cDNA CEESX39F; short re>	75.3	30	4.00E-13
06289_HH	1	NP_014725.1	Yor082cp pir||S66967 probable membrane protein YOR082c - yeast (Saccharomyces cerevisiae) emb|CAA99276.1| (Z74990) ORF YOR082c [Saccharomyces cerevisiae]	32.8	28	2.3
06291_HH	1	AAD31508.1	AF140785_1 (AF140785) Rho GTPase [Schistosoma mansoni]	185	54	2.00E-46
06293_HH	1	BAA94076.1	(AB035495) ubiquitin-activating enzyme E1 [Carassius auratus]	205	60	2.00E-52
06296_HH	2	AAF86276.1	AF275948_1 (AF275948) ABCA1 [Homo sapiens]	108	47	3.00E-23
06297_HH	1	T04026	probable ubiquitin / ribosomal protein S27a - rice gb|AAA74960.1| (L31941) ribosomal protein-linked ubiquitin [Oryza sativa]	34.8	44	4.00E-05
06300_HH	1	AAF05807.1	AF193903_30 (AF193903) ATP synthase F1 subunit alpha [Cafeteria roenbergensis]	31.3	27	6.9
06301_HH	1	AAF43421.1	AF233291_1 (AF233291) epsin-like protein [Drosophila melanogaster]	193	57	9.00E-49
06302_HH	1	Q45705	C8BA_BACUK PESTICIDIAL CRYSTAL PROTEIN CRY8BA (INSECTICIDAL DELTA-ENDOTOXIN CRYVIIIB(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (134 KDA CRYSTAL PROTEIN) gb|AAA21118.1| (U04365) CryIII delta-endotoxin [Bacillus thuringiensis]	31.3	27	6.9
06306_HH	1	NP_012623.1	cyclin F box protein; Grr1p sp|P24814|GRR1_YEAST GRR1 PROTEIN pir||A41529 GRR1 protein - yeast (Saccharomyces cerevisiae) gb|AAA34652.1| (M59247) putative [Saccharomyces cerevisiae] emb|CAA89617.1| (Z49590) ORF YJR090c [Saccharomyces cerevisiae] gb|AAB39313.1| (L47993) ORF YJR090c [Saccharomyces cerevisiae]	36.7	33	0.16
06308_HH	1	CAA06314.1	(AJ005052) PMP1 protein [Podocoryne carnea]	68.3	32	5.00E-11
06309_HH	3	NP_057681.1	protein kinase MEKK2b gb|AAF63496.1|AF239798_1 (AF239798) protein kinase MEKK2b [Homo sapiens]	76.5	35	2.00E-13
06311_HH	1	NP_011516.1	Ygr002cp sp|P53201|YG12_YEAST HYPOTHETICAL 55.2 KD PROTEIN IN ERP6-TFG2 INTERGENIC REGION pir||S64291 hypothetical protein YGR002c - yeast (Saccharomyces cerevisiae) emb|CAA96985.1| (Z72787) ORF YGR002c [Saccharomyces cerevisiae]	36.4	27	0.21
06313_HH	1	T30844	serine-repeat antigen 5 precursor - Plasmodium vivax gb|AAB41489.1| (U51723) V-SERA 5 [Plasmodium vivax]	31.3	21	6.9
06317_HH	1	P27950	NDK_GINCI NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE) gb|AAA49312.1| (M63964) nucleoside diphosphate kinase [Ginglymostoma cirratum]	201	62	3.00E-51
06326_HH	2	NP_048116.1	ORF MSV045 hypothetical protein gb|AAC97618.1| (AF063866) ORF MSV045 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	56.6	39	2.00E-07
06333_HH	3	AAC38955.1	(U73123) radial spokehead [Strongylocentrotus purpuratus]	158	46	4.00E-38
06334_HH	1	Z93304.2	MTAD93304 A.daguerrei mitochondrial 16S rRNA gene (partial)	52	96	2.00E-04
06335_HH	1	T17227	hypothetical protein DKFZp434A236.1 - human (fragment) emb|CAB55917.1| (AL117428) hypothetical protein [Homo sapiens]	250	70	7.00E-66
06336_HH	1	Q20970	SYM_CAEEL PROBABLE METHIONYL-TRNA SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS) pir||T22898 hypothetical protein F58B3.5 - Caenorhabditis elegans emb|CAA97803.1| (Z73427) Similarity to Yeast methionyl-tRNA synthetase (SW:SYMC_YEAST)~cDNA EST yk9d5.5 comes from this gene~cDNA EST yk11b4.5 comes from this gene~cDNA EST yk9d5.3 comes from this gene~cDNA EST yk11b4.3 comes from this gene~cDNA EST yk112d5.5 comes fr>	150	58	1.00E-35
06337_HH	1	JE0237	apolipoprotein E receptor 2 precursor - mouse	30.9	41	9.1
06340_HH	1	S37003	transposase (clone 11.9) - bean leaf beetle transposon mariner (fragment) gb|AAA28280.1| (L10460) transposase [Cerotoma trifurcata]	47.6	47	3.00E-08
06344_HH	1	AAF06035.1	(L35321) class VII unconventional myosin [Dictyostelium discoideum]	36.7	27	0.15
06347_HH	1	AAF80634.1	AC069251_27 (AC069251) F2D10.21 [Arabidopsis thaliana]	31.7	37	5.3
06348_HH	1	AAF55650.1	(AE003725) CG5269 gene product [Drosophila melanogaster] gb|AAF61273.1|AF246993_1 (AF246993) phosphatidylinositol transfer protein [Drosophila melanogaster]	181	56	5.00E-45
06351_HH	2	NP_002152.1	isoleucine-tRNA synthetase ref|NP_038203.1| isoleucine-tRNA synthetase gb|AAA80153.1| (U04953) isoleucyl-tRNA synthetase [Homo sapiens]	115	40	2.00E-25
06352_HH	1	Q19877	RS23_CAEEL PROBABLE 40S RIBOSOMAL PROTEIN S23 pir||T21497 hypothetical protein F28D1.7 - Caenorhabditis elegans emb|CAA94601.1| (Z70684) Similarity to Human 40S ribosomal protein S23 (SW:RS23_HUMAN)~cDNA EST EMBL:M80070 comes from this gene; cDNA EST EMBL:T02217 comes from this gene~cDNA EST CEMSH25R comes from this gene; cDNA EST yk90c3.3 comes from this gene~cDNA EST yk90c3.5>	251	88	3.00E-66
06354_HH	1	P02399	RLA2_ARTSA 60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12) pir||R8SS12 ribosomal protein L12eI - brine shrimp	82.3	41	2.00E-15
06356_HH	1	AAF53146.1	(AE003634) CG6734 gene product [Drosophila melanogaster]	86.6	39	2.00E-16
06357_HH	1	AL022334.1	HS569D19 Human DNA sequence from clone RP4-569D19 on chromosome 22q13.1 Contains 3' part of a novel gene similar to mouse Ras, Dexamethasone-induced 1 (Ras-related protein, RASD1, DEXRAS1) and the last exon of the MB gene for Myoglobin, ESTs, STSs and GSSsh, c>	56	94	8.00E-06
06359_HH	1	T00356	hypothetical protein KIAA0690 - human (fragment) dbj|BAA31665.1| (AB014590) KIAA0690 protein [Homo sapiens]	43.4	26	0.002
06361_HH	1	Q60446	H105_CRIGR HEAT-SHOCK PROTEIN 105 KDA (HEAT SHOCK 110 KDA PROTEIN) (KIAA0201) pir||A57513 heat shock protein 110k - Chinese hamster emb|CAA87768.1| (Z47807) heat-shock protein 110 kDa [Cricetulus griseus]	81.9	30	4.00E-15
06362_HH	1	AAF47730.1	(AE003477) CG12734 gene product [Drosophila melanogaster]	43	34	0.002
06363_HH	1	NP_048574.1	A226R pir||T17717 hypothetical protein A226R - Chlorella virus PBCV-1 gb|AAC96594.1| (U42580) A226R [Paramecium bursaria Chlorella virus 1]	31.3	30	6.9

06364_HH	1	NP_005041.1	ATP-binding cassette, sub-family D (ALD), member 4 sp|O14678|ABD4_HUMAN ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 4 (PEROXISOMAL MEMBRANE PROTEIN 69) (PMP69) (PEROXISOMAL MEMBRANE PROTEIN 1-LIKE) (PXMP1-L) (P70R) pir||JC5604 ABC-transporting peroxisomal membrane protein 69 - human gb|AAB83967.1| (AF009746) peroxisomal membrane protein 69 [Homo sapiens] emb|CAA74699.1| (Y14318) peroxisomal ABC-transporter [Homo sapiens]	87.4	35	9.00E-17
06365_HH	1	AAB09439.1	(U53177) Psmras1 [Schistosoma mansoni]	248	78	2.00E-65
06367_HH	1	AAA66077.1	(U24436) transposase [Mayetiola destructor]	44.9	41	5.00E-04
06368_HH	1	NP_036951.1	acyl Coenzyme A dehydrogenase, long chain sp|P15650|ACDL_RAT ACYL-COA DEHYDROGENASE, LONG-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (LCAD) pir||A34252 long-chain-acyl-CoA dehydrogenase (EC 1.3.99.13) precursor - rat gb|AAA40668.1| (J05029) long chain acyl-CoA dehydrogenase precursor (EC 1.3.99.2) [Rattus norvegicus] gb|AAA41514.1| (L11276) long chain acyl-CoA dehydrogenase [Rattus norvegicus] prf||1704376A long chain acyl-CoA dehydrogenase [Rattus norvegicus]	233	69	1.00E-60
06370_HH	1	AAF76898.1	AF274033_1 (AF274033) apetala2 domain-containing protein [Atriplex hortensis]	38.3	29	0.054
06372_HH	1	NP_031790.1	v-crk avian sarcoma virus CT10 oncogene homolog-like sp|P47941|CRKL_MOUSE CRK-LIKE PROTEIN pir||S58352 SH2/SH3 adaptor protein - mouse emb|CAA62220.1| (X90648) SH2/SH3 adaptor protein [Mus musculus]	52.7	37	2.00E-06
06378_HH	1	AAF21799.1	AF090429_2 (AF090429) beta-glucosidase precursor [Azospirillum irakense]	29.3	45	5.3
06382_HH	1	No Match				
06383_HH	1	CAA66885.1	(X98225) gastrin-binding protein [Rattus norvegicus]	153	51	1.00E-36
06386_HH	1	G72580	hypothetical protein APE1926 - Aeropyrum pernix (strain K1) dbj|BAA80932.1| (AP000062) 155aa long hypothetical protein [Aeropyrum pernix]	37.1	63	0.12
06387_HH	1	AC006021.2	AC006021 Homo sapiens PAC clone RP5-1129L24 from 7q32-q34, complete sequence	38.2	100	3.5
06388_HH	1	NP_001524.1	heterogeneous nuclear ribonucleoprotein L sp|P14866|ROL_HUMAN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN L (HNRNP L) pir||A33616 heterogeneous ribonuclear particle protein L - human emb|CAA34261.1| (X16135) L protein (AA 1-558) [Homo sapiens] prf||1604358A nuclear RNP protein L [Homo sapiens]	48.4	31	5.00E-05
06390_HH	1	P25867	UBC1_DROME UBIQUITIN-CONJUGATING ENZYME E2-17 KDA (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (EFFETE PROTEIN) pir||S19157 ubiquitin-conjugating enzyme - fruit fly (Drosophila melanogaster) emb|CAA44453.1| (X62575) ubiquitin-conjugating enzyme [Drosophila melanogaster] gb|AAF55093.1| (AE003706) eff gene product [alt 2] [Drosophila melanogaster] gb|AAF55094.1| (AE003706) eff gene product [alt 1] [Drosophila melanogaster]	275	85	3.00E-73
06397_HH	1	AAF30907.1	AE002147_8 (AE002147) unique hypothetical membrane lipoprotein [Ureaplasma urealyticum]	32.8	27	2.3
06398_HH	1	AAC31662.1	(U95740) Unknown gene product [Homo sapiens]	41.8	30	0.005
06400_HH	1	AAB61226.1	(AF002987) snail homolog [Ciona intestinalis]	29	39	6.8
06404_HH	1	P48444	COPD_HUMAN COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) pir||A56750 archain - human emb|CAA57071.1| (X81197) archain [Homo sapiens]	133	42	1.00E-30
06408_HH	1	AE003486.1	AE003486 Drosophila melanogaster genomic scaffold 142000013386053 section 3 of 30, complete sequence	40.1	100	0.88
06413_HH	2	CAB38986.2	(AL034556) hypothetical protein, PFC0590c [Plasmodium falciparum]	34.8	28	0.61
06414_HH	1	T31844	hypothetical protein C02E7.7 - Caenorhabditis elegans gb|AAC24166.1| (AF016446) similar to C. elegans cuticlin 2 precursor CUT-2 (SP:P34682) [Caenorhabditis elegans]	33.6	57	0.26
06415_HH	1	AAF55785.1	(AE003731) CG4159 gene product [Drosophila melanogaster]	46.1	50	2.00E-04
06417_HH	1	BAB08321.1	(AB018107) gene_id:K12B20.23~pir||T06152~similar to unknown protein [Arabidopsis thaliana]	31.7	35	5.3
06419_HH	1	AE003532.1	AE003532 Drosophila melanogaster genomic scaffold 142000013386050 section 19 of 54, complete sequence	42.1	100	0.22
06422_HH	1	PN0607	cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - pig (fragment) gb|AAB28132.1| cytochrome c oxidase subunit VIIc (N-terminal) [swine, intestine, Peptide, 47 aa]	36.4	42	0.038
06431_HH	1	T00070	hypothetical protein KIAA0532 - human (fragment) dbj|BAA25458.1| (AB011104) KIAA0532 protein [Homo sapiens]	66.3	33	2.00E-10
06442_HH	1	AAB50226.1	(U79302) unknown [Homo sapiens]	35.6	37	0.35
06445_HH	2	T18440	hypothetical protein C0425w - Plasmodium falciparum emb|CAB11121.1| (Z98547) predicted using hexExon; MAL3P3.18 (PFC0425w), Hypothetical protein, len: 4551 aa [Plasmodium falciparum]	42.6	25	0.003
06446_HH	1	S63617	cymH protein - Klebsiella oxytoca emb|CAA60007.1| (X86014) cymH [Klebsiella oxytoca]	34	44	1
06450_HH	1	P77296	YBET_ECOLI HYPOTHETICAL 20.9 KDA PROTEIN IN LEUS-GLTL INTERGENIC REGION pir||E64799 ybeT protein - Escherichia coli gb|AAB40848.1| (U82598) hypothetical protein [Escherichia coli] gb|AAC73748.1| (AE000169) orf, hypothetical protein [Escherichia coli] dbj|BAA35294.1| (D90704) Hypothetical protein SPAC24B11.10c [Escherichia coli] dbj|BAA35299.1| (D90705) Hypothetical protein SPAC24B11.10c [Escherichia coli]	51.5	38	6.00E-06
06452_HH	1	AAF81225.1	AF257318_1 (AF257318) SH3-containing protein SH3GLB1 [Homo sapiens]	64	28	1.00E-09
06454_HH	1	T40953	hypothetical protein SPCC1393.05 - fission yeast (Schizosaccharomyces pombe) emb|CAB38161.1| (AL035592) hypothetical protein [Schizosaccharomyces pombe]	34.4	22	0.8
06455_HH	1	AAF56564.1	(AE003754) CG6090 gene product [Drosophila melanogaster]	145	64	2.00E-34
06456_HH	1	AAD55263.1	AF176784_1 (AF176784) eps8 binding protein [Rattus norvegicus]	92.8	45	2.00E-18
06458_HH	1	AAF36008.1	(AC024200) contains similarity to Pfam family PF00687 (Ribosomal_L1 L1P family of ribosomal proteins), score=233.0, E=4.3e-66, N=1 [Caenorhabditis elegans]	217	62	6.00E-56
06459_HH	1	AAD42033.1	(AF075293) agglutinin-like protein 6 [Candida albicans]	33.6	37	1.4
06460_HH	1	AAD37366.1	AF144258_1 (AF144258) AP180-like adaptor protein [Caenorhabditis elegans]	212	59	3.00E-54
06461_HH	2	F75103	probable purine NTPase PAB0812 - Pyrococcus abyssi (strain Orsay) emb|CAB50131.1| (AJ248286) purine NTPase, putative [Pyrococcus abyssi]	41	22	0.008
06464_HH	1	AAG00604.1	AF291437_1 (AF291437) neuronal leucine-rich repeat protein-3 [Rattus norvegicus]	30.9	34	9.1
06465_HH	1	NP_005789.1	ret finger protein 2 sp|O60858|LEU5_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 (B-CELL CHRONIC LYMPHOCYTIC LEUKEMIA TUMOR SUPPRESSOR LEU5) emb|CAA12136.1| (AJ224819) tumor suppressor [Homo sapiens] gb|AAF91315.1|AF241850_1 (AF241850) ret finger protein 2 [Homo sapiens]	57.4	39	1.00E-07
06468_HH	1	AAA46630.1	(M35233) M-T8 gene product [Myxoma virus]	29.7	38	8.2
06469_HH	1	CAB81621.1	(AL117352) dJ876B10.3 (novel protein similar to C. elegans T19B10.6 (Tr:Q22557)) [Homo sapiens]	83.1	50	2.00E-15

06472_HH	1	P24603	OPSD_LOLFO RHODOPSIN pir||S14332 rhodopsin - northern European squid emb|CAA40108.1| (X56788) rhodopsine [Loligo forbesi]	52.7	32	6.00E-08
06474_HH	1	AAF23187.1	AF099924_2 (AF099924) C. elegans Ca2+/calmodulin-dependent protein kinase I (GB:AB021864); contains similarity to Pfam domain PF00069 (pkinase), Score=262.3, E-value=2e-75, N=1 [Caenorhabditis elegans]	187	62	7.00E-47
06475_HH	1	BAA91316.1	(AK000668) unnamed protein product [Homo sapiens]	44.1	23	0.001
06477_HH	1	AAF96570.1	(AE004396) sugar transporter family protein [Vibrio cholerae]	29.7	40	6.4
06478_HH	1	T29871	hypothetical protein F32B5.7 - Caenorhabditis elegans gb|AAB54209.1| (AF003148) weak similarity to rat and mouse sperm outer dense fiber protein [Caenorhabditis elegans]	56.2	28	2.00E-07
06480_HH	1	NP_036256.1	chord domain-containing protein 1 gb|AAF18437.1|AF192466_1 (AF192466) CHORD containing protein-1 [Homo sapiens]	139	41	2.00E-32
06481_HH	1	AAC51842.1	(AF000995) ubiquitous TPR motif, Y isoform [Homo sapiens]	32.1	34	4
06484_HH	1	AAF49848.1	(AE003539) CG11274 gene product [Drosophila melanogaster]	49.6	42	2.00E-05
06485_HH	1	D71917	toxin-like outer membrane protein jhp0556 - Helicobacter pylori (strain J99) gb|AAD06134.1| (AE001488) putative vacuolating cytotoxin (VacA) paralog [Helicobacter pylori J99]	36.7	26	0.16
06490_HH	1	AAF55874.1	(AE003734) CG6056 gene product [Drosophila melanogaster]	267	90	5.00E-71
06496_HH	1	Q09305	YQQ2_CAEEL HYPOTHETICAL 41.7 KD PROTEIN F10B5.2 IN CHROMOSOME II pir||T20689 hypothetical protein F10B5.2 - Caenorhabditis elegans emb|CAA88309.1| (Z48334) F10B5.2 [Caenorhabditis elegans]	61.3	35	1.00E-15
06497_HH	1	No Match				
06499_HH	1	AAD31501.1	AF138808_1 (AF138808) serum opacity factor precursor [Streptococcus pyogenes]	34	42	0.51
06501_HH	2	AAB70839.1	(AF019980) ZipA [Dictyostelium discoideum]	70.2	26	1.00E-11
06505_HH	1	NP_063927.1	heat shock protein hsp40-3 gb|AAC35861.1| (AF088983) heat shock protein hsp40-3 [Mus musculus] gb|AAC64141.1| (AF092536) heat shock protein hsp40-3 [Mus musculus]	95.6	61	3.00E-19
06508_HH	1	T29144	partial CDS - Caenorhabditis elegans gb|AAB18318.1| (U64854) partial CDS [Caenorhabditis elegans]	69.5	27	2.00E-11
06512_HH	1	NP_003461.1	Herpes virus-associated ubiquitin-specific protease sp|Q93009|UBP7_HUMAN UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (UBIQUITIN THIOLESTERASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DEUBIQUITINATING ENZYME 7) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) emb|CAA96580.1| (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]	33.2	43	1.8
06515_HH	1	T28908	hypothetical protein T26C11.2 - Caenorhabditis elegans gb|AAC48211.1| (U41017) repetitive region; weakly similar to E. gracilis major membrane skeletal protein (PIR:A43417) [Caenorhabditis elegans]	30.1	30	3
06522_HH	1	AAF44970.1	AE003406_175 (AE003416) hypothetical protein [Drosophila melanogaster] gb|AAF53487.1| (AE003649) BG:DS02252.1 gene product [Drosophila melanogaster]	47.3	23	1.00E-04
06523_HH	1	L15359.1	YSJATPTRN Yarrowia lipolytica mitochondrial ATP synthase subunits 6, 8, 9 (atp 6,8,9), tRNA-Met, cytochrome oxidase subunit 3 (cox3) gene, exons 1-2, NADH oxidoreductase (ubiquinone) subunit 4, tRNA-Trp, tRNA-Thr, tRNA-Pro	54	94	6.00E-05
06524_HH	1	AAF49616.1	(AE003530) CG6498 gene product [Drosophila melanogaster]	62.8	47	2.00E-09
06527_HH	1	NP_012143.1	(putative) invovled in control of DNA replication; Sim1p sp|P40472|SIM1_YEAST SIM1 PROTEIN pir||S49886 probable membrane protein YIL123w - yeast (Saccharomyces cerevisiae) emb|CAA86869.1| (Z46833) unknown [Saccharomyces cerevisiae]	36.4	34	0.21
06528_HH	1	S25299	extensin precursor - tomato gb|AAA34164.1| (M76671) extensin (class II) [Lycopersicon esculentum]	32.8	41	1.4
06529_HH	1	AAF08702.1	AF155120_1 (AF155120) ubiquitin-conjugating enzyme variant Kua [Homo sapiens]	43	58	0.002
06530_HH	1	U94410.1	DDU94410 Dictyostelium discoideum plasmid Ddp6 Rep protein (rep) gene, complete cds	44.1	100	0.057
06535_HH	1	NP_011793.1	Ygr277cp sp|P53332|YG51_YEAST HYPOTHETICAL 34.3 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION pir||S64612 hypothetical protein YGR277c - yeast (Saccharomyces cerevisiae) emb|CAA97307.1| (Z73062) ORF YGR277c [Saccharomyces cerevisiae]	39.9	57	0.018
06541_HH	1	S43427	intermediate filament protein - Sloane's squid gb|AAA16612.1| (L10112) intermediate filament protein [Ommastrephes sloanei]	34	50	1
06542_HH	2	Q9ZYM7	NU5M_RHISA NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 pir||T11161 NADH dehydrogenase 5 - hardbacked tick (Rhipicephalus sanguineus) mitochondrion gb|AAD05525.1| (AF081829) NADH dehydrogenase 5 [Rhipicephalus sanguineus] gnl|NCBI_MITO|ND5_15045 NADH dehydrogenase subunit 5	31.7	41	3.1
06545_HH	1	AAF37203.1	AF198254_1 (AF198254) mRNA-binding protein CRDBP [Homo sapiens]	54.7	28	6.00E-07
06551_HH	1	CAB61364.1	(AL133034) hypothetical protein [Homo sapiens]	127	58	2.00E-33
06556_HH	1	CAB73530.1	(AL139077) putative integral membrane protein [Campylobacter jejuni]	34.8	24	0.61
06559_HH	1	AAF49900.1	(AE003541) CG10620 gene product [Drosophila melanogaster]	100	35	9.00E-21
06562_HH	1	T34496	hypothetical protein ZK1248.14 - Caenorhabditis elegans gb|AAC71095.1| (U29244) ZK1248.14 gene product [Caenorhabditis elegans]	84.7	32	6.00E-16
06563_HH	1	NP_061241.1	semaF cytoplasmic domain associated protein 1 gb|AAC72311.1| (AF061263) semaF cytoplasmic domain associated protein 1 [Mus musculus] gb|AAD12262.1| (AF104358) synectin [Mus musculus]	107	37	7.00E-23
06567_HH	1	P08714	HEMA_VACCI HEMAGGLUTININ PRECURSOR pir||HNVZVV hemagglutinin precursor - vaccinia virus gb|AAA48251.1| (M14783) hemagglutinin precursor [Vaccinia virus]	31.7	32	5.3
06570_HH	1	P41383	TBA2_PATVU TUBULIN ALPHA-2/ALPHA-4 CHAIN pir||S42033 tubulin alpha chain - common limpet emb|CAA54712.1| (X77618) alpha tubulin [Patella vulgata] emb|CAA55978.1| (X79468) alpha tubulin 2 [Patella vulgata]	237	85	5.00E-62
06572_HH	1	CAA56732.1	(X80759) cdc2-related protein kinase 1 [Plasmodium falciparum]	33.6	42	1.4
06575_HH	1	T20853	hypothetical protein F13G3.1 - Caenorhabditis elegans emb|CAA95789.1| (Z71259) similar to Zinc finger, C2H2 type [Caenorhabditis elegans]	57.4	46	5.00E-08
06576_HH	1	AAF51870.1	(AE003599) CG11137 gene product [Drosophila melanogaster]	153	52	1.00E-36
06579_HH	1	AL032649.1	CEY55D9A Caenorhabditis elegans cosmid Y55D9A, complete sequence	46.1	100	0.014
06580_HH	1	AAF49764.1	(AE003536) CG6833 gene product [Drosophila melanogaster]	34.4	22	0.8
06581_HH	1	AAF52198.1	(AE003608) CG8895 gene product [alt 4] [Drosophila melanogaster]	69.5	28	2.00E-11
06582_HH	1	CAC05730.1	(AL391743) eif-2alpha kinase [Schizosaccharomyces pombe]	33.2	31	1.8
06584_HH	1	NP_060549.1	hypothetical protein FLJ10379 dbj|BAA91577.1| (AK001241) unnamed protein product [Homo sapiens]	147	46	6.00E-35
06586_HH	1	AAB98510.1	(U67501) polyferredoxin (mvhB) [Methanococcus jannaschii]	35.6	28	0.35
06588_HH	1	P31370	POU1_DUGJA POU DOMAIN PROTEIN 1 (DJPOU1) pir||JQ2010 transcription factor POU-1 - planarian (Dugesia japonica) dbj|BAA02308.1| (D12924) ORF 1 [Dugesia japonica]	335	100	2.00E-91

06590_HH	1	AP000499.1	AP000499 Homo sapiens genomic DNA, chromosome 3p21.3, clone:603 to 320, anti-oncogene region, section 2/3	44.1	100	0.057
06591_HH	1	BAB02799.1	(AB024034) gb|AAF53066.1~gene_id:MDC11.13~similar to unknown protein [Arabidopsis thaliana]	38.7	34	0.022
06592_HH	1	T11704	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pieris rapae mitochondrion (fragment) dbj|BAA28201.1| (AB013161) NADH dehydrogenase subunit 5 [Pieris rapae]	73	43	2.00E-12
06595_HH	1	AAF74615.1	AF244780_1 (AF244780) integrase [Oryza officinalis]	51.9	43	4.00E-06
06596_HH	1	CAA28542.1	(X04851) lymphocyte LCa (AA 1-213) [Bos taurus] prf||1304303B clathrin LCa [Bos	84.7	30	6.00E-16
06600_HH	1	NP_055560.1	KIAA0233 gene product dbj|BAA13240.1| (D87071) similar to C.elegans protein encoded in cosmid T20D3 (Z68220). [Homo sapiens]	164	42	4.00E-40
06604_HH	1	P95539	CATE_PSEPU CATALASE HPII gb|AAB40866.1| (U82622) stationary-phase inducible catalase C [Pseudomonas putida]	34	45	1
06606_HH	1	AAF51344.1	(AE003585) Eno gene product [Drosophila melanogaster]	61.7	50	1.00E-11
06607_HH	1	P55862	MCM5_XENLA DNA REPLICATION LICENSING FACTOR MCM5 (CDC46 HOMOLOG) (X.CDC46) gb|AAC60224.1| (U44048) MCM5/CDC46p [Xenopus laevis]	181	53	5.00E-45
06610_HH	1	AL031116.1	HS87808 Human DNA sequence from clone 87808 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence [Homo sapiens]	42.1	100	0.22
06611_HH	1	AAD10205.1	(AF047020) alpha-methylacyl-CoA racemase [Homo sapiens]	132	51	2.00E-30
06612_HH	1	S39295	beta-adaptin 1 - fruit fly (Drosophila melanogaster) emb|CAA53509.1| (X75910) beta-adaptin Drosophila 1 [Drosophila melanogaster] gb|AAF49013.1| (AE003513) Bap gene product [Drosophila melanogaster]	249	75	1.00E-65
06613_HH	1	S61535	nucleotide-binding head-stalk protein 183K - Giardia lamblia emb|CAA56212.1| (X79815) HPSR2 - heavy chain potential motor protein [Giardia intestinalis] prf||2120344A nucleotide-binding head stalk protein [Giardia intestinalis]	55	24	4.00E-07
06615_HH	1	NP_032410.1	inositol polyphosphate-1-phosphatase sp|P49442|INPP_MOUSE INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (IPPASE) (IPP) gb|AAA97574.1| (U27295) inositol polyphosphate 1-phosphatase [Mus musculus]	31.7	57	5.3
06619_HH	1	NP_064656.1	Cdc42 GTPase-activating protein gb|AAD38043.1|AF151363_1 (AF151363) Cdc42 GTPase-activating protein [Mus musculus]	67.1	31	1.00E-10
06622_HH	1	AC024183.4	AC024183 Homo sapiens clone RP11-268K13, complete sequence	40.1	100	0.88
06628_HH	1	CAB16830.1	(Z99708) hypothetical protein [Arabidopsis thaliana] emb|CAB80329.1| (AL161589) hypothetical protein [Arabidopsis thaliana]	33.2	37	1.8
06630_HH	1	AE001416.1	AE001416 Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence	46.1	89	0.014
06631_HH	1	S29170	annexin VII - mouse	33.2	65	0.34
06632_HH	1	O83642	DNLJ_TREPA DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [NAD+]) pir||H71300 probable DNA ligase (lig) - syphilis spirochete gb|AAC65609.1| (AE001238) DNA ligase (lig) [Treponema pallidum]	32.1	21	4
06633_HH	1	NM_008408.1	Mus musculus intergral membrane protein 1 (Itm1), mRNA	40.1	100	0.88
06634_HH	1	NP_009204.1	B-cell associated protein gb|AAB51324.1| (U47924) B-cell receptor associated protein [Homo sapiens] gb|AAC36005.1| (AC002397) BAP [Mus musculus] gb|AAD38042.1|AF150962_1 (AF150962) repressor of estrogen receptor activity [Homo sapiens] gb|AAF17231.1|AF126021_1 (AF126021) B-cell receptor-associated protein BAP37 [Homo sapiens] gb|AAF44345.1|AF178980_1 (AF178980) D-prohibitin [Homo sapiens]	151	60	4.00E-36
06635_HH	2	P42704	L130_HUMAN 130 KD LEUCINE-RICH PROTEIN (LRP 130) (GP130) gb|AAA67549.1| (M92439) leucine-rich protein [Homo sapiens]	51.2	22	7.00E-06
06638_HH	1	AAF97960.1	AC000103_10 (AC000103) F21J9.15 [Arabidopsis thaliana]	30.5	59	1.1
06639_HH	3	AAC23536.1	(U52151) polyketide synthase PKSL2 [Aspergillus parasiticus]	34	29	1
06640_HH	1	P37880	SYR_CRILO ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE) (ARGRS) pir||JN0870 arginine--tRNA ligase (EC 6.1.1.19) - Chinese hamster emb|CAA45012.1| (X63415) arginine--tRNA ligase [Cricetulus longicaudatus]	193	57	1.00E-48
06642_HH	1	AAF32327.1	AF218817_1 (AF218817) Dbest [Drosophila melanogaster] gb|AAF54503.1| (AE003686) CG6264 gene product [Drosophila melanogaster]	116	42	1.00E-25
06643_HH	1	T23056	hypothetical protein H06O01.2 - Caenorhabditis elegans emb|CAB07481.1| (Z92970) predicted using Genefinder~Similarity to Mouse chromodomain-helicase-DNA-binding protein (SW:P40201)~cDNA EST yk11a2.3 comes from this gene~cDNA EST yk9a3.3 comes from this gene~cDNA EST yk9a3.5 comes from this gene~cDNA EST yk11a2.5 comes fro>	29	35	7.2
06646_HH	1	A54748	cap-binding protein 80 - human	55.4	28	4.00E-07
06649_HH	1	AF154637.1	AF154637 Nicotiana tabacum clone PR12 mRNA sequence	38.2	100	0.76
06650_HH	1	NP_012755.1	cAMP-dependent protein kinase catalytic subunit; Tpk3p sp|P05986|KAPC_YEAST CAMP-DEPENDENT PROTEIN KINASE TYPE 3 (PKA 3) pir||OKBYC3 protein kinase (EC 2.7.1.37), cAMP-dependent, catalytic chain 3 - yeast (Saccharomyces cerevisiae) emb|CAA81521.1| (Z26878) unknown [Saccharomyces cerevisiae] emb|CAA82008.1| (Z28166) ORF YKL166c [Saccharomyces cerevisiae] prf||2118403N ORF [Saccharomyces cerevisiae]	85.4	35	3.00E-16
06655_HH	1	BAA21708.1	(D84315) rab11 [Drosophila melanogaster] dbj|BAA87880.1| (AB035354) Drab11 [Drosophila melanogaster] gb|AAF55850.1| (AE003733) Rab11 gene product [Drosophila melanogaster]	187	51	5.00E-47
06657_HH	1	O79437	NU5M_RABIT NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 pir||T11490 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - rabbit mitochondrion emb|CAA04857.1| (AJ001588) NADH dehydrogenase subunit 5 [Oryctolagus cuniculus] gnl|NCBI_MITO|ND5_13726 NADH dehydrogenase subunit 5	29.7	43	7.3
06658_HH	1	AC007090.3	AC007090 Homo sapiens clone DJ0701O19, complete sequence	44.1	100	0.057
06659_HH	1	BAA74927.1	(AB020711) KIAA0904 protein [Homo sapiens]	187	60	5.00E-47
06661_HH	1	NP_057170.1	map kinase phosphatase-like protein MK-STYX gb|AAD36983.1|AF069762_1 (AF069762) map kinase phosphatase-like protein MK-STYX [Homo sapiens]	146	44	2.00E-34
06663_HH	1	Z95114.19	HS212A2 Human DNA sequence from clone CTA-212A2 on chromosome 22q12 Contains the gene for TNF-inducible protein CG12-1 (similar to apolipoprotein L), the 3' end of the APOL2 gene for apolipoprotein L 2, MTCO2 (Cytochrome c oxidase subunit II), MTATP8 (ATP synt>	42.1	100	0.22
06664_HH	2	AAF54380.1	(AE003682) CG8144 gene product [Drosophila melanogaster]	123	39	1.00E-27

06672_HH	1	NP_064830.1	AMV048 gb|AAG02754.1|AF250284_48 (AF250284) AMV048 [Amsacta moorei entomopoxvirus]	41.4	24	0.006
06674_HH	1	NP_004969.1	potassium voltage-gated channel, Shaw-related subfamily, member 4 sp|Q03721|CIKG_HUMAN VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.4 (KSHIIIC) gb|AAA57263.1| (M64676) potassium channel protein [Homo sapiens]	92.4	37	3.00E-18
06675_HH	1	AAB62537.1	(AF001363) protein phosphatase-1 [Herdmania curvata]	150	92	7.00E-36
06677_HH	1	T22350	hypothetical protein F47B8.1 - Caenorhabditis elegans emb|CAB01201.1| (Z77662) predicted using Genefinder [Caenorhabditis elegans]	31.7	41	5.3
06678_HH	1	NP_013008.1	nuclear pore protein; Nup133p sp|P36161|N133_YEAST NUCLEOPORIN NUP133 (NUCLEAR PORE PROTEIN NUP133) pir||S38160 NUP133 protein - yeast (Saccharomyces cerevisiae) emb|CAA81633.1| (Z27116) ORF YKR402 [Saccharomyces cerevisiae] emb|CAA82161.1| (Z28307) ORF YKR082w [Saccharomyces cerevisiae] emb|CAA56372.1| (X80066) Nup133p [Saccharomyces cerevisiae]	35.2	22	0.46
06682_HH	1	No Match				
06683_HH	1	P05044	SORC_CRILO SORCIN (22 KD PROTEIN) (CP-22) (V19) pir||A25706 sorcin - Chinese hamster emb|CAA28354.1| (X04656) 22-kd protein (AA 1-198) [Cricetulus longicaudatus]	77.6	39	8.00E-14
06686_HH	1	AC015973.2	AC015973 Homo sapiens clone RP11-366C6, complete sequence	42.1	100	0.22
06689_HH	2	AAF04790.1	(AF154067) ribosomal protein S6 [Aedes aegypti]	139	53	1.00E-32
06690_HH	1	NP_060768.1	hypothetical protein FLJ11006 dbj|BAA91951.1| (AK001868) unnamed protein product [Homo sapiens]	86.2	32	2.00E-16
06693_HH	1	P26937	SP4G_BACSU STAGE IV SPORULATION PROTEIN FB pir||S18438 sporulation protein spoIVFB - Bacillus subtilis emb|CAA42107.1| (X59528) sporulation protein [Bacillus subtilis] emb|CAB14757.1| (Z99118) protease [Bacillus subtilis]	31.7	23	5.3
06694_HH	1	P07545	VIRG_AGRT5 VIRG REGULATORY PROTEIN pir||S03760 virG protein - Agrobacterium tumefaciens plasmid pTiC58 emb|CAA68595.1| (Y00535) virG [Agrobacterium tumefaciens] gb|AAD15211.1| (M36786) virulence protein [Plasmid pTiC58] dbj|BAA87777.1| (AB016260) Probable virG gene [Agrobacterium tumefaciens]	32.5	35	3.1
06696_HH	1	AAC36188.1	(AC005314) putative pre-mRNA splicing factor RNA helicase [Arabidopsis thaliana]	163	50	9.00E-40
06698_HH	1	AAD43770.1	AF152510_1 (AF152510) protocadherin gamma A3 short form protein [Homo sapiens]	30.9	30	9.1
06699_HH	1	NP_031786.1	carnitine acetyltransferase sp|P47934|CACP_MOUSE CARNITINE O-ACETYLTRANSFERASE (CARNITINE ACETYLASE) (CAT) pir||S52782 carnitine acetyltransferase - mouse emb|CAA59971.1| (X85983) carnitine acetyltransferase [Mus musculus]	122	41	3.00E-27
06701_HH	1	AAF50218.1	(AE003551) CG16707 gene product [Drosophila melanogaster]	46.9	47	1.00E-04
06703_HH	1	P18845	ACH3_CARAU NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3) pir||B37014 nicotinic acetylcholine receptor alpha-3 chain precursor - goldfish emb|CAA37985.1| (X54051) nicotinic acetylcholine receptor subunit alpha-3 precursor (512 AA) [Carassius auratus]	80	33	2.00E-14
06706_HH	1	A42239	adenylate cyclase (EC 4.6.1.1) germination stage - slime mold (Dictyostelium discoideum)	31.7	30	5.3
06707_HH	1	AAD55434.1	AF181648_1 (AF181648) BcDNA.GH12558 [Drosophila melanogaster] gb|AAF52789.1| (AE003625) BcDNA:GH12558 gene product [Drosophila melanogaster]	109	41	1.00E-23
06711_HH	2	R5FF2E	acidic ribosomal protein P1 - fruit fly (Drosophila melanogaster) emb|CAA68557.1| (Y00504) rp21C [Drosophila melanogaster]	54.3	36	8.00E-07
06712_HH	1	T02388	hypothetical protein F4I1.14 - Arabidopsis thaliana gb|AAC16082.1| (AC004521) hypothetical protein [Arabidopsis thaliana]	30.9	60	9.1
06713_HH	1	P53458	ACT5_DIPDE ACTIN 5 gb|AAA82603.1| (U27836) actin [Diphyllobothrium dendriticum]	49.2	38	3.00E-05
06714_HH	1	AAF53750.1	(AE003661) CG10492 gene product [Drosophila melanogaster]	80.4	30	1.00E-14
06716_HH	1	T02837	long chain fatty acyl-CoA synthetase homolog LCFACAS5 - Leishmania major gb|AAC24660.1| (AE001274) LCFACAS5; L5701.2 [Leishmania major]	30.5	36	9.6
06717_HH	1	AAF71926.1	AF260530_1 (AF260530) Dscam [Drosophila melanogaster]	47.6	26	8.00E-05
06718_HH	1	BAA82147.1	(AB025269) compared with human FXR2 mRNA;GenBank Accession Number U31501 [Mus musculus]	128	44	4.00E-29
06724_HH	1	AAB96334.1	(U80823) casein kinase I alpha LS [Gallus gallus]	56.2	71	2.00E-07
06725_HH	1	AAC24728.1	(U70880) BLu protein testis isoform [Homo sapiens]	86.6	35	2.00E-16
06727_HH	1	NP_062129.1	purinergic receptor P2X, ligand-gated ion channel, 7 sp|Q64663|P2X7_RAT P2X PURINOCEPTOR 7 (ATP RECEPTOR) (P2X7) (PURINERGIC RECEPTOR) (P2Z RECEPTOR) emb|CAA65131.1| (X95882) P2X7 [Rattus norvegicus]	101	36	5.00E-21
06729_HH	1	AAD52645.2	AF176007_1 (AF176007) mitochondrial carrier homolog 1 isoform a [Mus musculus domesticus] dbj|BAA92861.1| (AB040292) mitochondrial carrier homolog isoform a [Mus musculus]	36.7	38	0.16
06730_HH	1	A72491	hypothetical protein APE2568 - Aeropyrum pernix (strain K1) dbj|BAA81585.1| (AP000064) 221aa long hypothetical protein [Aeropyrum pernix]	34.4	39	0.8
06739_HH	1	T12956	hypothetical protein T6H20.50 - Arabidopsis thaliana emb|CAB51173.1| (AL096859) putative protein [Arabidopsis thaliana]	31.3	34	6.9
06742_HH	1	AAC09350.1	(AF054989) unknown [Homo sapiens]	83.5	42	2.00E-27
06743_HH	1	CAB63558.1	(AL031746) putative ABC transporter [Plasmodium falciparum]	32.1	48	4
06744_HH	1	AAF55374.1	(AE003715) CG8907 gene product [Drosophila melanogaster]	42.2	29	0.004
06747_HH	1	NP_056596.1	nucleosome assembly protein 1-like 1 sp|P28656|NPL1_MOUSE NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1 (NAP-1 RELATED PROTEIN) (BRAIN PROTEIN DN38) pir||JS0707 nucleosome assembly protein 1 - mouse dbj|BAA02142.1| (D12618) nucleosome assembly protein-1 [Mus musculus]	103	44	1.00E-21
06750_HH	1	AC009486.3	AC009486 Homo sapiens clone RP11-333O1, complete sequence	44.1	100	0.057
06752_HH	1	NP_064371.1	intestinal cell kinase gb|AAF37277.1|AF225918_1 (AF225918) intestinal cell kinase [Mus musculus]	226	70	1.00E-58
06753_HH	1	CAB61122.1	(AL132950) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans] emb|CAB81995.1| (AL132902) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans]	32.1	42	0.78
06754_HH	1	AF179378.1	AF179378 Mycoplasma fermentans orfG1 gene (partial cds), Insertion sequence IS1630G and orfG2 gene (partial cds)	42.1	96	0.12
06755_HH	1	NP_051057.1	ribosomal protein S14 sp|P56804|RR14_ARATH CHLOROPLAST 30S RIBOSOMAL PROTEIN S14 dbj|BAA84383.1| (AP000423) ribosomal protein S14 [Arabidopsis thaliana]	30.9	28	9.1
06756_HH	1	AF051403.1	AF051403 Caenorhabditis elegans fibulin-1 precursor (FBLN1) gene, alternatively spliced products, complete cds	44.1	100	0.057
06758_HH	1	NP_057120.1	CGI-93 protein gb|AAD34088.1|AF151851_1 (AF151851) CGI-93 protein [Homo sapiens]	61.3	33	6.00E-09

06762_HH	1	CAA62831.1	(X91637) BRG1 protein [Gallus gallus]	216	71	1.00E-55
06763_HH	1	AAF68997.1	AF257517_1 (AF257517) eIF2 alpha subunit [Danio rerio]	175	51	4.00E-43
06764_HH	1	S60122	probable RNA/ssDNA-binding protein HMD1 - yeast (Saccharomyces cerevisiae) dbj|BAA07154.1| (D37935) RNA binding protein [Saccharomyces cerevisiae] prf||2201484A dosage-dependent suppressor [Saccharomyces cerevisiae]	34	46	0.63
06769_HH	1	AAB50222.1	(U79294) unknown [Homo sapiens]	97.1	34	1.00E-19
06771_HH	1	AP001714.1	AP001714 Homo sapiens genomic DNA, chromosome 21q, section 58/105	40.1	100	0.88
06774_HH	5	AAC98911.1	(AF029222) Sm29 [Schistosoma mansoni]	45.3	30	4.00E-04
06777_HH	1	AL031667.18	HS620E11 Human DNA sequence from clone RP4-620E11 on chromosome 20q11.2-12, complete sequence [Homo sapiens]	40.1	95	0.88
06782_HH	2	NP_062761.1	SEC23B (S. cerevisiae) gb|AAF08301.1| (AF200326) SEC23B protein [Mus musculus]	179	49	2.00E-44
06784_HH	1	T32733	AMPA glutamate receptor interacting protein GRIP - rat gb|AAB51689.1| (U88572) AMPA receptor interacting protein GRIP [Rattus norvegicus]	39.1	33	0.029
06785_HH	3	P49020	P24_CRIGR COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR gb|AAA82925.1| (U26264) CHOp24 [Cricetulus griseus]	187	62	5.00E-47
06795_HH	1	NP_062769.1	DnaJ homolog dbj|BAA88309.1| (AB028861) mDj11 [Mus musculus]	108	36	3.00E-23
06800_HH	1	T07719	aldose 1-epimerase homolog T23J7.130 - Arabidopsis thaliana emb|CAB41863.1| (AL049746) aldose 1-epimerase-like protein [Arabidopsis thaliana]	83.1	46	2.00E-15
06802_HH	1	A46194	neurofilament protein NF-220, high-molecular-weight splice form - longfin squid gb|AAA29991.1| (M94389) neurofilament protein [Loligo pealei]	69.5	58	8.00E-19
06808_HH	1	P52480	KPY2_MOUSE PYRUVATE KINASE, M2 ISOZYME	202	58	2.00E-51
06810_HH	1	AC007639.5	AC007639 Homo sapiens chromosome 17, clone hRPK.57_A_1, complete sequence	40.1	95	0.88
06812_HH	1	T20349	hypothetical protein D2023.3 - Caenorhabditis elegans emb|CAB02875.1| (Z81052) D2023.3 [Caenorhabditis elegans]	36.4	33	0.21
06817_HH	1	T32839	hypothetical protein T04B8.1 - Caenorhabditis elegans gb|AAB95007.1| (AF040650) T04B8.1 gene product [Caenorhabditis elegans]	30.9	37	9.1
06818_HH	1	AAF30888.1	AE002144_2 (AE002144) unique hypothetical ATP/GTP-binding protein [Ureaplasma urealyticum]	35.2	26	0.46
06819_HH	1	No Match				
06822_HH	1	AAF65409.1	AF238313_1 (AF238313) developmental protein DG1037 [Dictyostelium discoideum]	32.1	29	4
06825_HH	1	CAB55506.1	(AL117268) malate dehydrogenase [Leishmania major]	29	48	7.4
06828_HH	1	NP_002652.1	phospholipase C, gamma 2 (phosphatidylinositol-specific) sp|P16885|PIP5_HUMAN 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC-IV) pir||S02004 phospholipase C (EC 3.1.4.3), phosphoinositol-specific - human emb|CAA32194.1| (X14034) phospholipase C (AA 1 - 1252) [Homo sapiens] gb|AAA60112.1| (M37238) phospholipase C [Homo sapiens]	34	28	1
06829_HH	1	S48472	probable membrane protein YIL100c-a - yeast (Saccharomyces cerevisiae) emb|CAA86280.1| (Z38125) orf, len: 112, CAI: 0.07, overlapped by orf 36949..36826 qv [Saccharomyces cerevisiae]	31.7	36	5.3
06835_HH	1	CAA04196.1	(AJ000641) flice [Mus musculus]	54.3	37	8.00E-07
06836_HH	1	AAF71307.1	AF231339_1 (AF231339) bHLH-PAS transcription factor MOP9 [Homo sapiens]	38.3	25	0.054
06839_HH	1	AAC24520.1	(AF055287) molybdenum cofactor biosynthetic protein [Aspergillus nidulans]	171	54	3.00E-42
06842_HH	1	CAA91110.1	(Z54312) ttg start codon; product similar to CylM; probably involved in serine/threonine dehydration and lanthionine formation [Lactobacillus sakei]	30.9	28	9.1
06846_HH	1	NP_002993.1	succinate dehydrogenase complex, subunit D precursor; succinate dehydrogenase ubiquinone cytochrome B small subunit sp|O14521|DHSD_HUMAN SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT, MITOCHONDRIAL PRECURSOR (CYBS) (SUCCINATE-UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) (QPS2) (CII-4) (SUCCINATE DEHYDROGENASE COMPLEX SUBUNIT D) (SUCCINATE-UBIQUINONE OXIDOREDUCTASE CYT> dbj|BAA22054.1| (AB006202) cytochrome b small subunit of complex II [Homo sapiens] dbj|BAA81889.1| (AB026906) small subunit of cytochrome b of succinate dehydrogenase [Homo sapiens]	56.2	33	2.00E-07
06850_HH	1	T15905	hypothetical protein E04F6.5 - Caenorhabditis elegans gb|AAA68357.1| (U28943) coded for by C. elegans cDNA cm11f3; similar to isovaleryl-CoA dehydrogenase [Caenorhabditis elegans]	34.8	29	0.61
06855_HH	1	BAA92713.1	(AP001389) ESTs AU033035(S1515),D39871(S1515) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence; putative glucan synthase (AC006223) [Oryza sativa]	32.1	29	4
06857_HH	1	NP_064505.1	UDP-glucose:glycoprotein glucosyltransferase 1 gb|AAF66232.1|AF227905_1 (AF227905) UDP-glucose:glycoprotein glucosyltransferase 1 precursor [Homo sapiens]	54.7	46	2.00E-07
06858_HH	1	AC015448.4	AC015448 Arabidopsis thaliana chromosome I BAC T14L22 genomic sequence, complete sequence	42.1	100	0.22
06862_HH	1	BAA22403.1	(AB004540) serotonin receptor-like planarian receptor 4 [Dugesia japonica]	324	92	5.00E-88
06866_HH	1	A57087	cell division control protein cdc15 - fission yeast (Schizosaccharomyces pombe)	42.2	31	0.003
06867_HH	1	AC004936.2	AC004936 Homo sapiens PAC clone RP5-959C21 from 7p11.2-p21, complete sequence	40.1	100	0.16
06869_HH	2	AAF55974.1	(AE003738) CG7073 gene product [Drosophila melanogaster]	125	53	4.00E-48
06870_HH	1	G71690	hypothetical protein RP341 - Rickettsia prowazekii emb|CAA14801.1| (AJ235271) unknown [Rickettsia prowazekii]	32.1	38	4
06873_HH	1	AAF76432.1	AF272661_1 (AF272661) alpha 4 type V collagen [Rattus norvegicus]	78	37	6.00E-14
06874_HH	1	AAD25933.1	AF085279_6 (AF085279) protein phosphatase 2C [Arabidopsis thaliana] gb|AAF18732.1|AC018721_7 (AC018721) protein phosphatase 2C (AthPP2C5) [Arabidopsis thaliana]	32.1	45	3.6
06882_HH	1	O42248	GBLP_BRARE GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (RECEPTOR OF ACTIVATED PROTEIN KINASE C) (RACK) gb|AAB81617.1| (AF025330) receptor for activated protein kinase C [Danio rerio]	82.3	32	3.00E-15
06884_HH	1	T24515	hypothetical protein T05D4.2 - Caenorhabditis elegans emb|CAB03292.1| (Z81115) T05D4.2 [Caenorhabditis elegans]	32.5	25	3.1
06885_HH	1	AF263003.1	AF263003 Ditylum brightwellii clone Dbr3 microsatellite sequence	42.1	100	0.14
06889_HH	1	AAF73811.1	AF154039_1 (AF154039) surface protein PspC [Streptococcus pneumoniae]	37.5	23	0.083
06893_HH	1	AAF49761.1	(AE003536) CG6807 gene product [Drosophila melanogaster]	37.5	41	0.092
06894_HH	1	AAF44722.1	AF155135_1 (AF155135) novel retinal pigment epithelial cell protein [Homo sapiens]	35.6	22	0.35
06897_HH	1	AC022127.4	AC022127 Homo sapiens chromosome 5 clone CTD-2151N11, complete sequence	42.1	96	0.087

06905_HH	1	T15803	hypothetical protein C44B7.10 - Caenorhabditis elegans gb|AAA68341.1| (U28928) coded for by C. elegans cDNA yk20f6.3; coded for by C. elegans cDNA cm14f1; coded for by C. elegans cDNA cm12f2; coded for by C. elegans cDNA yk20f6.5; coded for by C. elegans cDNA cm06a2 [Caenorhabditis elegans]	153	75	4.00E-55
06913_HH	1	NP_042749.1	pEP424R gb|AAA65285.1| (U18466) pEP424R [African swine fever virus] prf||2113434BF EP424R gene [African swine fever virus]	31.3	43	6.9
06914_HH	1	P54633	TALA_DICDI FILOPODIN (TALIN HOMOLOG) pir||A57036 talin - slime mold (Dictyostelium discoideum)	32.1	23	4
06924_HH	1	AAB86567.1	(AF030966) unknown [Schistosoma mansoni]	51.2	25	7.00E-06
06926_HH	1	CAB64379.1	(AJ251163) dynamin B [Dictyostelium discoideum]	38.7	27	0.041
06929_HH	1	AAB49970.2	(U72937) putative DNA dependent ATPase and helicase [Homo sapiens]	34.4	24	0.8
06931_HH	1	NP_015346.1	Ypr021cp pir||S54495 probable carrier protein YPR021c - yeast (Saccharomyces cerevisiae) emb|CAA89275.1| (Z49274) unknown [Saccharomyces cerevisiae] emb|CAA95017.1| (Z71255) unknown [Saccharomyces cerevisiae]	32.8	30	2.3
06935_HH	1	prf|2123443A	cathepsin C [Schistosoma mansoni]	194	64	4.00E-49
06938_HH	1	AAF48230.1	(AE003491) CG4330 gene product [Drosophila melanogaster]	127	44	8.00E-29
06939_HH	1	Q98892	G55A_CHICK NEURITE INHIBITOR GP55-A PRECURSOR (OBCAM PROTEIN GAMMA ISOFORM) emb|CAB41420.1| (Y08170) OBCAM protein gamma isoform [Gallus gallus]	35.6	30	0.35
06940_HH	1	T18466	hypothetical protein C0470w - Plasmodium falciparum emb|CAA15609.1| (AL008970) putative valyl tRNA synthetase [Plasmodium falciparum]	32.8	40	2.3
06943_HH	3	T18427	hypothetical protein C0335c - Plasmodium falciparum emb|CAB11104.1| (Z98547) predicted using hexExon; MAL3P3.3 (PFC0335c), Hypothetical protein, len: 3725 aa [Plasmodium falciparum]	46.9	25	1.00E-04
06945_HH	1	T00080	hypothetical protein KIAA0522 - human (fragment) dbj|BAA25448.1| (AB011094) KIAA0522 protein [Homo sapiens]	67.1	29	1.00E-10
06946_HH	1	D72653	hypothetical protein APE0656 - Aeropyrum pernix (strain K1) dbj|BAA79628.1| (AP000060) 464aa long hypothetical protein [Aeropyrum pernix]	30.9	60	8.4
06948_HH	1	AAF59198.1	(AE003840) CG1383 gene product [Drosophila melanogaster]	119	39	2.00E-26
06949_HH	1	AC019226.4	AC019226 Homo sapiens clone RP11-567F11, complete sequence	44.1	100	0.057
06952_HH	1	AC005213.1	AC005213 Homo sapiens chromosome 5, BAC clone 84E9 (LBNL H120), complete sequence	48.1	100	0.001
06954_HH	1	T31070	notch homolog - sea urchin (Lytechinus variegatus) gb|AAB82088.1| (AF000634) notch homolog [Lytechinus variegatus]	34.8	23	0.61
06955_HH	1	O02485	YDJ1_CAEEL HYPOTHETICAL 35.6 KDA PROTEIN ZK1073.1 IN CHROMOSOME X pir||T27688 hypothetical protein ZK1073.1 - Caenorhabditis elegans emb|CAA92227.1| (Z68135) cDNA EST yk56h9.5 comes from this gene~cDNA EST yk90d6.5 comes from this gene~cDNA EST yk85h7.3 comes from this gene~cDNA EST yk90d6.3 comes from this gene~cDNA EST yk140a6.5 comes from this gene~cDNA EST yk493b4.3 comes from this gene~cDNA ES>	67.1	32	1.00E-10
06959_HH	1	CAB62858.1	(AL035475) hypothetical protein MAL4P2.17 [Plasmodium falciparum]	50.8	30	8.00E-06
06968_HH	1	AAF51548.1	(AE003590) CG3164 gene product [Drosophila melanogaster]	69.9	55	2.00E-11
06975_HH	1	NP_064518.1	lysophosphatidic acid acyltransferase-delta gb|AAF80338.1|AF156776_1 (AF156776) lysophosphatidic acid acyltransferase-delta [Homo sapiens]	127	40	6.00E-29
06982_HH	1	Q05975	RAB2_LYMST RAS-RELATED PROTEIN RAB-2 pir||S38341 GTP-binding protein rab2 - great pond snail emb|CAA51234.1| (X72689) RAB2 [Lymnaea stagnalis]	324	94	5.00E-88
06984_HH	1	AAF51586.1	(AE003591) BcDNA:GH08385 gene product [Drosophila melanogaster]	35.2	29	0.46
06985_HH	1	NP_050182.1	B4 gb|AAD49620.1|AF157706_7 (AF157706) B4 [Human herpesvirus 6B]	37.1	27	0.12
06989_HH	1	T04426	hypothetical protein T18B16.20 - Arabidopsis thaliana emb|CAA16762.1| (AL021711) putative protein [Arabidopsis thaliana] emb|CAB78907.1| (AL161550) putative protein [Arabidopsis thaliana]	42.6	27	0.003
06991_HH	1	B70208	conserved hypothetical protein BBA10 - Lyme disease spirochete plasmid A/lp54 gb|AAC66233.1| (AE000790) conserved hypothetical protein [Borrelia burgdorferi]	30.5	35	2.3
06995_HH	1	AL020989.2	HS192P9 Human DNA sequence from clone RP1-192P9 on chromosome Xp11.23-11.4 Contains a pseudogene similar to rat Plasmolipin, ESTs and GSSs, complete sequence [Homo sapiens]	52	100	2.00E-04
06998_HH	1	NP_009521.1	Ybl032wp sp|P38199|YBD2_YEAST HYPOTHETICAL 41.7 KD PROTEIN IN RIB1-AAC2 INTERGENIC REGION pir||S45766 hypothetical protein YBL032w - yeast (Saccharomyces cerevisiae) emb|CAA84852.1| (Z35793) ORF YBL032w [Saccharomyces cerevisiae] emb|CAA54496.1| (X77291) YBL0418 [Saccharomyces cerevisiae]	32.1	34	4
07002_HH	1	NP_036087.1	old astrocyte specifically induced substance dbj|BAA75670.1| (AB017614) OASIS protein [Mus musculus]	73	37	2.00E-12
07004_HH	1	NP_060930.1	uncharacterized bone marrow protein BM046 gb|AAF67633.1|AF217522_1 (AF217522) uncharacterized bone marrow protein BM046 [Homo sapiens]	42.2	33	0.004
07005_HH	1	Q20502	HUTH_CAEEL PROBABLE HISTIDINE AMMONIA-LYASE (HISTIDASE) pir||T22333 histidine ammonia-lyase (EC 4.3.1.3) - Caenorhabditis elegans emb|CAA91982.1| (Z68004) Similairty to mouse histidine ammonia-lyase protein (PIR Acc. No. A46128)~cDNA EST EMBL:Z14639 comes from this gene~cDNA EST yk16g3.3 comes from this gene~cDNA EST yk8d9.3 comes from this gene~cDNA EST yk8d9.5 comes from this gene~cDNA EST yk3>	41.8	28	0.005
07006_HH	1	AAF57078.1	(AE003775) CG1340 gene product [Drosophila melanogaster]	52.3	37	3.00E-06
07007_HH	1	AB007774.2	AB008218S2 Homo sapiens gene for cystatin A, exon 2, 3, and complete cds	38.2	100	3.5
07011_HH	1	Q27409	FP1_MYTGA ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1) pir||S68957 adhesive plaque protein precursor - Mytilus galloprovincialis dbj|BAA09851.1| (D63778) adhesive plaque protein [Mytilus galloprovincialis]	52.7	46	2.00E-06
07012_HH	1	CAB45309.1	(AJ132244) multidrug resistance protein 2 (MRP2) [Homo sapiens]	93.6	32	1.00E-18
07014_HH	1	AAF48979.1	(AE003512) CG14220 gene product [Drosophila melanogaster]	36.7	41	0.16
07021_HH	1	T25024	hypothetical protein Y102A5A.1 - Caenorhabditis elegans emb|CAB04744.1| (Z81593) cDNA EST yk430g8.5 comes from this gene~cDNA EST yk8h4.3 comes from this gene~cDNA EST yk383c8.5 comes from this gene~cDNA EST yk20d4.5 comes from this gene~cDNA EST yk247d1.5 comes from this gene~cDNA EST yk8h4.5 comes from this gene~cDNA EST> emb|CAA19440.1| (AL023822) cDNA EST yk430g8.5 comes from this gene~cDNA EST yk8h4.3 comes from this gene~cDNA EST yk383c8.5 comes from this gene~cDNA EST yk20d4.5 comes from this gene~cDNA EST yk247d1.5 comes from this gene~cDNA EST yk8h4.5 comes from this gene~cDNA E>	59.7	29	2.00E-08

07022_HH	1	JE0110	Dis3p protein - human	92.4	45	2.00E-22
07023_HH	1	S61455	flagellar hook protein flgE - Helicobacter mustelae (fragment)	32.8	32	2.3
07026_HH	1	CAA19655.1	(AL023893) /prediction=(method:""genefinder"", version:""084"")~/prediction=(method:""genscan"", version:""1.0"")~/motif=(desc:""Eukaryotic putative RNA-binding region RNP-1 signature"", dbase:""PROSITE"", acc:""PS00030"", method:""ppsearch"")~/match=(> gb|AAF45613.1| (AE003420) EG:132E8.1 gene product [Drosophila melanogaster]	67.1	45	1.00E-10
07027_HH	1	AAB37626.1	(U80437) Contains similarity to Pfam domain: PF00397 (WW_rsp5_WWP), Score=25.3, E-value=8.3e-06, N=1 [Caenorhabditis elegans]	30.9	27	9.1
07028_HH	1	AL353810.9	AL353810 Human DNA sequence from clone RP11-261H15 on chromosome 9, complete sequence [Homo sapiens]	44.1	100	0.057
07031_HH	1	BAA95482.1	(AB026999) glia maturation factor beta [Cyprinus carpio]	141	46	6.00E-33
07038_HH	1	CAA33483.1	(X15443) gamma-glutamyltranspeptidase (AA 1-568) [Rattus sp.]	167	46	6.00E-41
07040_HH	1	AAA29892.1	(M87799) 28kDa glutathione-S transferase [Schistosoma haematobium]	66.7	48	4.00E-19
07042_HH	1	AAF49951.1	(AE003542) Nrx gene product [Drosophila melanogaster]	65.2	45	4.00E-10
07044_HH	1	NP_008945.1	Nedd-4-like ubiquitin-protein ligase; WW domain-containing protein 2 gb|AAC51325.1| (U96114) WWP2 [Homo sapiens]	231	65	4.00E-60
07046_HH	1	BAA97309.1	(AB019236) mitochondrial carrier protein-like [Arabidopsis thaliana]	33.6	34	1.4
07048_HH	1	NP_011145.1	multicopper oxidase, type 1 integral membrane protein; Fet5p sp|P43561|FET5_YEAST IRON TRANSPORT MULTICOPPER OXIDASE FET5 PRECURSOR pir||S56214 probable membrane protein YFL041w - yeast (Saccharomyces cerevisiae) dbj|BAA09199.1| (D50617) YFL041W [Saccharomyces cerevisiae] dbj|BAA08024.1| (D44598) unknown [Saccharomyces cerevisiae] prf||2210408A ORF 4121orfR003 [Saccharomyces cerevisiae]	37.1	27	0.12
07062_HH	1	NP_005111.1	trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit) gb|AAD22033.1| (AF117755) thyroid hormone receptor-associated protein complex component TRAP230 [Homo sapiens]	32.5	29	3.1
07063_HH	1	AAF55542.1	(AE003721) CG7671 gene product [Drosophila melanogaster]	44.9	26	5.00E-04
07064_HH	1	I59402	NAB1 - rat gb|AAC52236.1| (U17253) NAB1 [Rattus norvegicus]	77.6	47	5.00E-17
07065_HH	1	BAA25883.1	(D88669) RNA-dependent RNA polymerase [Bryopsis cinicola]	36.4	36	0.21
07070_HH	1	Q07327	ROP_DROME ROP PROTEIN pir||S33578 rop protein - fruit fly (Drosophila melanogaster) emb|CAA47658.1| (X67218) Rop [Drosophila melanogaster] emb|CAA47659.1| (X67219) Rop [Drosophila melanogaster]	54.7	34	6.00E-07
07071_HH	1	H71427	hypothetical protein - Arabidopsis thaliana emb|CAB10394.1| (Z97340) transcription factor like protein [Arabidopsis thaliana] emb|CAB78657.1| (AL161543) transcription factor like protein [Arabidopsis thaliana]	32.5	40	3.1
07075_HH	1	A75014	hypothetical protein PAB1262 - Pyrococcus abyssi (strain Orsay) emb|CAB50551.1| (AJ248288) hypothetical protein [Pyrococcus abyssi]	32.8	30	2.3
07077_HH	1	AF286472.1	AF286471S2 Homo sapiens retinitis pigmentosa GTPase regulator (RPGR) gene, exon ORF15 partial cds	36.2	95	4
07079_HH	1	P34673	YO23_CAEEL HYPOTHETICAL 23.3 KDA PROTEIN ZK688.3 IN CHROMOSOME III pir||S44919 ZK688.3 protein - Caenorhabditis elegans gb|AAA28230.1| (L16621) coded for by C. elegans cDNAs GenBank:T01366 and T00450; putative [Caenorhabditis elegans]	117	50	8.00E-26
07080_HH	1	Z77249.1	HS358H7 Human DNA sequence from PAC 358H7 on chromosome X	40.1	100	0.22
07082_HH	1	CAB39033.1	(AL034559) hypothetical protein, PFC0930c [Plasmodium falciparum]	32.8	23	2.3
07083_HH	1	P80478	C560_PORPU SUCCINATE DEHYDROGENASE CYTOCHROME B560 SUBUNIT (SUCCINATE DEHYDROGENASE, SUBUNIT III) pir||T11245 probable succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) chain 3 - red alga (Porphyra purpurea) mitochondrion gb|AAD03124.1| (AF114794) succinate:cytochrome c oxidoreductase subunit 3 [Porphyra purpurea]	32.5	30	3.1
07084_HH	1	AAF57087.1	(AE003775) CG11316 gene product [Drosophila melanogaster]	30.1	42	3.2
07087_HH	1	NP_048252.1	ORF MSV181 hypothetical protein gb|AAC97690.1| (AF063866) ORF MSV181 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	33.6	22	1.4
07089_HH	1	AAC31918.1	(AF079447) myosin heavy chain kinase C [Dictyostelium discoideum]	30.9	37	1.9
07091_HH	1	AAF21700.1	AF051995_1 (AF051995) maturase K [Orobanche hederae]	38.7	37	0.041
07093_HH	1	T03044	hypothetical protein 008L - Chilo iridescent virus gb|AAB94418.1| (AF003534) hypothetical protein 008L [Chilo iridescent virus]	30.5	52	2.4
07096_HH	1	Q16943	VP33_APLCA VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPTOBREVIN BINDING PROTEIN (VAP-33) pir||A57245 VAMP-binding protein VAP-33 - California sea hare gb|AAC46883.1| (U36779) vesicle-associated membrane protein/synaptobrevin binding protein [Aplysia californica]	38.7	37	0.041
07100_HH	1	CAC01820.1	(AL391146) putative protein [Arabidopsis thaliana]	38.7	26	0.041
07103_HH	1	AAB47253.1	(U83280) 39 kDa antigen [Leishmania donovani]	30.9	26	9.1
07105_HH	1	AAC17967.1	(AF023450) Down syndrome cell adhesion molecule [Homo sapiens]	51.2	28	7.00E-06
07107_HH	1	BAA76831.1	(AB023204) KIAA0987 protein [Homo sapiens]	74.5	40	7.00E-13
07113_HH	1	NP_064381.1	hypothetical protein MNCb-2146 dbj|BAA95065.1| (AB041581) unnamed protein product [Mus musculus]	125	40	3.00E-28
07123_HH	1	P00489	PHS2_RABIT GLYCOGEN PHOSPHORYLASE, MUSCLE FORM (MYOPHOSPHORYLASE) pir||A24302 glycogen phosphorylase (EC 2.4.1.1) - rabbit pir||PHRBG glycogen phosphorylase (EC 2.4.1.1), muscle - rabbit	182	56	6.00E-46
07124_HH	1	NP_065038.1	AMV256 gb|AAG02962.1|AF250284_256 (AF250284) AMV256 [Amsacta moorei entomopoxvirus]	33.6	20	1.4
07127_HH	2	T00337	hypothetical protein KIAA0568 - human (fragment) dbj|BAA25494.1| (AB011140) KIAA0568 protein [Homo sapiens]	39.9	24	0.017
07128_HH	1	AC021045.2	AC021045 Arabidopsis thaliana chromosome I BAC T9L6 genomic sequence, complete sequence	42.1	100	0.22
07129_HH	1	P93376	ACT6_TOBAC ACTIN 103 gb|AAB40091.1| (U60495) actin [Nicotiana tabacum]	77.3	35	1.00E-13
07131_HH	1	S47282	merozoite surface antigen 1 - Plasmodium falciparum (strain RO-71) (fragment) emb|CAA84558.1| (Z35329) merozoite surface antigen 1 gene, 3+-end [Plasmodium falciparum]	35.6	22	0.35
07134_HH	1	P35610	ACAT_HUMAN STEROL O-ACYLTRANSFERASE (CHOLESTEROL ACYLTRANSFERASE) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) pir||A48026 sterol O-acyltransferase (EC 2.3.1.26) - human gb|AAC37532.2| (L21934) acyl-coenzyme A: cholesterol acyltransferase [Homo sapiens]	58.6	57	4.00E-08

07138_HH	1	Q09826	SD23_SCHPO SDS23 PROTEIN (MOC1 PROTEIN) pir||T40589 CBS-domain protein Sds23p - fission yeast (Schizosaccharomyces pombe) dbj|BAA13172.1| (D86840) Sds23 [Schizosaccharomyces pombe] dbj|BAA13486.1| (D87870) MOC1 [Schizosaccharomyces pombe] emb|CAA22817.1| (AL035216) CBS-domain protein Sds23p [Schizosaccharomyces pombe]	35.6	41	0.35
07139_HH	1	NP_003878.1	ADP-ribosylation factor[arf]-directed GTPase activating protein pir||T00050 hypothetical protein KIAA0400 - human dbj|BAA23696.1| (AB007860) KIAA0400 [Homo sapiens]	136	45	2.00E-31
07140_HH	1	JE0284	Mm-1 cell derived transplantability-associated 1b - Human dbj|BAA32568.1| (AB006746) hMmTRA1b [Homo sapiens] gb|AAC99413.1| (AF098642) phospholipid scramblase 1; plasma membrane phospholipid scramblase [Homo sapiens] gb|AAF80593.1| (AF224492) phospholipid scramblase 1 [Homo sapiens]	129	59	2.00E-29
07143_HH	1	T30547	major surface glycoprotein - Pneumocystis carinii (fragment) gb|AAC34982.1| (AF038556) variant region of major surface glycoprotein [Pneumocystis carinii f. sp. hominis]	34.8	24	0.61
07144_HH	1	AC016903.3	AC016903 Homo sapiens clone RP11-259I20, complete sequence	44.1	100	0.057
07145_HH	1	BAA19101.1	(AB000407) DNA topoisomerase I [Gallus gallus]	98.7	48	1.00E-32
07148_HH	1	AAF36069.1	(AC024213) Hypothetical protein C34G6.1 [Caenorhabditis elegans]	47.6	29	8.00E-05
07151_HH	1	T13576	hypothetical protein EG:52C10.5 - fruit fly (Drosophila melanogaster) emb|CAA22949.1| (AL035311) 1-evidence=predicted by content~1-method=genefinder;084~1-method_score=133.73~1- evidence_end~2-evidence=predicted by match~2-match_accession=SWISS-PROT:P34756~2- match_description=PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB1 (EC 2.>	36.7	29	0.16
07152_HH	1	O57561	RL1X_SALSA 60S RIBOSOMAL PROTEIN L18A gb|AAC03021.1| (AF045188) ribosomal protein L18a [Salmo salar]	115	58	1.00E-43
07157_HH	1	AAF21133.1	L81170_1 (L81170) putative [Rattus norvegicus]	104	40	5.00E-22
07160_HH	1	AAF46816.1	(AE003456) CG5625 gene product [alt 2] [Drosophila melanogaster] gb|AAF46817.1| (AE003456) CG5625 gene product [alt 1] [Drosophila melanogaster]	43	31	3.00E-06
07164_HH	1	CAA07066.1	(AJ006487) propionyl-CoA carboxylase [Homo sapiens]	277	81	5.00E-74
07168_HH	1	S72296	ribosomal protein L6 - Plasmodium falciparum plastid emb|CAA64586.1| (X95276) rpl6 [Plasmodium falciparum]	34.4	32	0.8
07169_HH	1	AAF56487.1	(AE003752) BcDNA:LD22548 gene product [Drosophila melanogaster]	76.5	32	2.00E-13
07170_HH	1	AAD30230.1	AC007202_12 (AC007202) T8K14.13 [Arabidopsis thaliana]	30.9	24	9.1
07172_HH	1	B71620	monosaccharide transporter PFB0210c - malaria parasite (Plasmodium falciparum) gb|AAC71831.1| (AE001381) monosaccharide transporter [Plasmodium falciparum] emb|CAA10374.1| (AJ131457) hexose transporter 1 [Plasmodium falciparum] gb|AAD23958.1|AF101827_1 (AF101827) putative sugar transporter [Plasmodium falciparum]	32.8	38	2.2
07173_HH	1	AAF47599.1	(AE003473) CG5691 gene product [Drosophila melanogaster]	30.5	30	9.5
07176_HH	1	AAF50573.1	(AE003559) CG8591 gene product [Drosophila melanogaster]	31.3	38	6.9
07181_HH	1	BAA88963.1	(AB025319) Yb-E5R [Yaba monkey tumor virus]	35.2	24	0.46
07182_HH	1	G64556	flagellin B homolog - Helicobacter pylori (strain 26695) gb|AAD07364.1| (AE000548) flagellin B homolog (fla) [Helicobacter pylori 26695]	30.9	48	9.1
07183_HH	1	Q10074	YAN9_SCHPO HYPOTHETICAL 73.1 KDA PROTEIN C3H1.09C IN CHROMOSOME I pir||T38741 major facilitator protein homolog - fission yeast (Schizosaccharomyces pombe) emb|CAA92262.1| (Z68144) putative amino acid transpoter [Schizosaccharomyces pombe]	33.6	45	1.4
07187_HH	1	NP_064792.1	AMV010 gb|AAG02716.1|AF250284_10 (AF250284) AMV010 [Amsacta moorei entomopoxvirus]	34.4	38	0.8
07191_HH	1	AAB35413.1	kalicludine 1, AsKC1 [Anemonia sulcata=sea anemones, toxin, Peptide, 58 aa]	69.1	60	1.00E-11
07195_HH	1	AAF55345.1	(AE003714) CG14905 gene product [Drosophila melanogaster]	116	36	1.00E-25
07199_HH	1	NP_048099.1	ORF MSV028 hypothetical protein gb|AAC97844.1| (AF063866) ORF MSV028 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	38.7	34	0.041
07202_HH	1	NP_064387.1	kidney predominant protein NCU-G1 dbj|BAA92527.1| (AB027141) kidney predominant protein [Mus musculus] dbj|BAA95676.1| (AB027142) kidney predominant protein [Mus musculus]	36	26	0.27
07203_HH	1	NP_011001.1	Yer078cp sp|P40051|YEQ8_YEAST HYPOTHETICAL 58.0 KD PEPTIDASE IN PTP3-ILV1 INTERGENIC REGION pir||S50581 hypothetical protein YER078c - yeast (Saccharomyces cerevisiae) gb|AAB64633.1| (U18839) Yer078cp [Saccharomyces cerevisiae]	34	27	1
07206_HH	1	AAF60432.1	(AC006709) Hypothetical protein Y119C1A.1 [Caenorhabditis elegans]	34.4	38	0.46
07208_HH	1	AE003658.1	AE003658 Drosophila melanogaster genomic scaffold 142000013386055 section 51 of 63, complete sequence	40.1	100	0.88
07212_HH	1	I38361	TRPC1 protein - human	33.2	35	1.8
07214_HH	1	T18296	myosin heavy chain - Entamoeba histolytica gb|AAB48065.1| (L03534) myosin heavy chain [Entamoeba histolytica]	34.4	30	0.8
07216_HH	1	CAA04360.1	(AJ000871) histidine kinase [Streptococcus mitis]	33.6	30	1.4
07219_HH	1	AAC95157.1	(AF100165) polo-like kinase kinase 1; xPlkk1 [Xenopus laevis]	75.7	36	3.00E-13
07220_HH	1	AAD37094.1	AF106539_3 (AF106539) LicD2 [Streptococcus pneumoniae]	62.5	34	3.00E-09
07222_HH	1	NP_004522.1	molybdenum cofactor synthesis 2 gb|AAD13297.1| (AF117815) molybdopterin synthase large subunit [Homo sapiens] gb|AAD14599.1| (AF091871) molybdopterin-synthase large subunit [Homo sapiens] gb|AAF67478.1|AF155659_1 (AF155659) molybdenum cofactor biosysthesis protein E [Homo sapiens]	83.5	34	1.00E-15
07227_HH	1	AAF36143.1	AF151057_1 (AF151057) HSPC223 [Homo sapiens]	131	43	5.00E-30
07228_HH	1	AAB51432.1	(L63543) endodermin [Xenopus laevis]	165	45	2.00E-40
07231_HH	1	AAF35233.1	(AF224669) mannosidase, beta A, lysosomal [Homo sapiens]	102	37	2.00E-21
07234_HH	1	NP_032481.1	kallikrein 3, plasma sp|P26262|KAL_MOUSE PLASMA KALLIKREIN PRECURSOR (PLASMA PREKALLIKREIN) (KININOGENIN) (FLETCHER FACTOR) pir||KQMSPL plasma kallikrein (EC 3.4.21.34) precursor - mouse gb|AAA63393.1| (M58588) plasma kallikrein [Mus musculus]	73.7	52	1.00E-12
07236_HH	1	NP_032755.1	neural plakophilin-related arm-repeat protein pir||T42209 neural plakophilin related arm-repeat protein NPRAP - mouse gb|AAB82409.1| (U90331) arm-repeat protein NPRAP/neurojungin [Mus musculus]	37.1	38	0.12
07237_HH	1	AAF52507.1	(AE003617) CG5155 gene product [Drosophila melanogaster]	119	50	2.00E-26
07240_HH	1	P51824	ARF1_SOLTU ADP-RIBOSYLATION FACTOR 1 pir||S36453 ADP-ribosylation factor 1 - potato emb|CAA52468.1| (X74461) ADP-ribosylation factor 1 [Solanum tuberosum]	133	72	2.00E-33
07241_HH	1	prf||2205380A	spike protein [Canine coronavirus]	35.2	31	0.46
07244_HH	1	AAC51324.1	(U96113) WWP1 [Homo sapiens]	111	60	4.00E-43

07246_HH	1	AAB49975.1	(U86404) egl [Drosophila melanogaster]	53.1	42	2.00E-06
07248_HH	1	CAB44357.1	(AJ006776) IF2 protein [Homo sapiens]	165	53	2.00E-40
07250_HH	1	AAF51376.1	(AE003586) CG5574 gene product [Drosophila melanogaster]	33.6	40	1.4
07251_HH	1	BAA89358.1	(AB034736) gyrase B [Flavobacterium psychrophilum]	36.4	29	0.21
07254_HH	1	NP_034830.1	low density lipoprotein receptor sp|P35951|LDLR_MOUSE LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR) emb|CAA79581.1| (Z19521) low density lipoprotein receptor [Mus musculus]	95.6	44	3.00E-19
07258_HH	1	CAA64088.1	(X94355) D3L [Cowpox virus] emb|CAA72553.1| (Y11842) C3L [Cowpox virus]	36.4	23	0.21
07261_HH	1	AAF56327.1	(AE003749) CG13630 gene product [Drosophila melanogaster]	89.3	46	2.00E-17
07266_HH	1	NP_037223.1	tumor necrosis factor receptor sp|P22934|TNR1_RAT TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI) (P55) pir||GQRTT1 tumor necrosis factor receptor 1 precursor - rat gb|AAA42256.1| (M63122) tumor necrosis factor receptor [Rattus norvegicus]	31.7	28	5.3
07272_HH	1	NP_004948.1	folylpolyglutamate synthase pir||A46281 tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) - human gb|AAA35852.1| (M98045) folylpolyglutamate synthetase [Homo sapiens]	157	51	5.00E-38
07273_HH	1	AAF47507.1	(AE003472) CG7852 gene product [Drosophila melanogaster]	151	44	4.00E-36
07279_HH	1	AL121838.4	CNS01DSP Human chromosome 14 DNA sequence IN PROGRESS BAC C-2068J7 of library CalTech-D from chromosome 14 of Homo sapiens (Human), complete	38.2	100	1.2
07284_HH	1	AAB47565.1	(U87449) opsin [Gallus gallus]	42.6	25	0.003
07289_HH	1	AAF53968.1	(AE003669) CG9248 gene product [alt 1] [Drosophila melanogaster] gb|AAF53969.1| (AE003669) CG9248 gene product [alt 2] [Drosophila melanogaster]	108	32	4.00E-23
07294_HH	1	AAF50767.1	(AE003565) CG5146 gene product [Drosophila melanogaster]	30.9	40	9.1
07295_HH	1	BAB09084.1	(AB025628) gene_id:MNJ7.17~pir||E71441~strong similarity to unknown protein [Arabidopsis thaliana]	32.1	35	3.9
07296_HH	1	T29404	hypothetical protein C16C8.4 - Caenorhabditis elegans gb|AAB37860.1| (U80452) short region of similarity to ubiquitin [Caenorhabditis elegans]	39.9	30	0.018

APPENDIX C

List of the ascidian EST clones derived from the ocellus and otolith cells

Summary

As I showed in the Chapter 3, we sequenced EST clones from the cDNA libraries of ascidian ocellus and otolith cell. Here, I attached the whole list of the sequenced clones that was used in this thesis. The list contains 485 of the total non-redundant clones from the ocellus cell cDNA library (Table C.1) and 505 of those from the otolith cell cDNA library (Table C.2). These lists contained the frequency and annotation of each clone using the 3'- and 5'-ESTs. The methods and results were described in chapter 3.

Table C-1: List of EST clones of the Ascidian ocellus cell

		analyses based on 3' ESTs					analyses based on 5' ESTs				
clone ID	frequency	accession No.	homologous sequence which showed the highest E-value	score	identity (%)	E-value	accession No.	homologous sequence which showed the highest E-value	score	identity (%)	E-value
00074_Ci_oc	17	NP_194721.1	| putative protein [Arabidopsis thaliana] >gi|7486224|pir||T08553 hypothetical protein F27B13.160 - Arabidopsis thaliana >gi|4914416|emb|CAB43667.1| (AL050352) putative protein [Arabidopsis thaliana] >gi|7269891|emb|CAB79750.1| (AL161575) putative protein [Arabidopsis thaliana]	32.1	30	5.7	No Match				
00002_Ci_oc	113	NP_282581.1	| putative sugar transferase [Campylobacter jejuni] >gi|11347152|pir||H81289 probable sugar transferase Cj1440c [imported] - Campylobacter jejuni (strain NCTC 11168) >gi|6968869|emb|CAB73864.1| (AL139078) putative sugar transferase [Campylobacter jejuni]	32.1	36	5.7					
00004_Ci_oc	1	NP_042278.1	| ribosomal protein S2 [Prototheca wickerhamii] >gi|1173299|sp|P46741|RT02_PROWI MITOCHONDRIAL RIBOSOMAL PROTEIN S2 >gi|7521644|pir||T11947 ribosomal protein S2 - Prototheca wickerhamii mitochondrion >gi|467879|gb|AAD12666.1| (U02970) ribosomal protein S2 [Prototheca wickerhamii]	32.8	35	3.3					
00005_Ci_oc	1	AAK94066.1	(AF401656) MAGI-1C beta [Homo sapiens]	38.3	28	0.076					
00007_Ci_oc	1	NP_143088.1	| hypothetical protein [Pyrococcus horikoshii] >gi|7519019|pir||F71061 hypothetical protein PH1188 - Pyrococcus horikoshii >gi|3257605|dbj|BAA30288.1| (AP000005) 484aa long hypothetical protein [Pyrococcus horikoshii]	31.7	30	7.4					
00014_Ci_oc	1	No Match									
00015_Ci_oc	1	P39195	ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY	37.5	78	0.028	P39195	ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY	37.5	66	0.027
00019_Ci_oc	1	No Match									
00021_Ci_oc	7	AAF48428.1	(AE003498) CG9091 gene product [Drosophila melanogaster]	103	64	1.00E-21	AAF48428.1	(AE003498) CG9091 gene product [Drosophila melanogaster]	104	57	8.00E-22
00023_Ci_oc	1	P49165	RL4_URECA 60S RIBOSOMAL PROTEIN L4 (L1) >gi|7440596|pir||T12048 ribosomal protein L4 - spoonworm (Urechis caupo) >gi|929961|gb|AAA74021.1| (U30495) ribosomal protein [Urechis caupo]	195	65	4.00E-49					
00029_Ci_oc	1	No Match									
00031_Ci_oc	1	AAG28381.1	AF191308_1 (AF191308) coagulation factor V [Sus scrofa]	46.9	31	2.00E-04					
00033_Ci_oc	1	No Match					No Match				
00036_Ci_oc	1	No Match									
00037_Ci_oc	1	No Match									
00043_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.9	No Match				
00044_Ci_oc	1	T40933	hypothetical protein SPCC1322.02 - fission yeast (Schizosaccharomyces pombe) >gi|4176542|emb|CAA22855.1| (AL035259) hypothetical protein [Schizosaccharomyces pombe]	31.3	33	9.7					
00045_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.6					
00046_Ci_oc	2	AAB52915.1	(U72543) ubiquitin-like/S30 ribosomal fusion protein [Sus scrofa]	145	53	4.00E-34	AAB52915.1	(U72543) ubiquitin-like/S30 ribosomal fusion protein [Sus scrofa]	104	49	1.00E-21
00047_Ci_oc	2	P21571	ATPR_RAT ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (F6) >gi|92098|pir||JC1167 coupling factor 6 precursor - rat >gi|203530|gb|AAA40954.1| (M73030) coupling factor 6 [Rattus norvegicus] >gi|599963|emb|CAA38369.1| (X54510) mitochondrial oxidative phosphorylation coupling factor 6 [Rattus norvegicus]	70.6	45	1.00E-11	P21571	ATPR_RAT ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (F6) pir||JC1167 coupling factor 6 precursor - rat gb|AAA40954.1| (M73030) coupling factor 6 [Rattus norvegicus] emb|CAA38369.1| (X54510) mitochondrial oxidative phosphorylation coupling factor 6 [Rattus norvegicus]	71	43	1.00E-11
00050_Ci_oc	1	No Match					CAA10856.2	(AJ222584) maturase-like protein [Euglena viridis]	32.8	33	3.3
00051_Ci_oc	2	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	52.3	69	5.00E-06					
00531_Ci_oc	28	T18423	hypothetical protein C0150w - malaria parasite (Plasmodium falciparum)	33.2	31	1.8	AAA81404.2	(U40414) Hypothetical protein F53B3.1 [Caenorhabditis elegans]	33.6	36	1.4
00053_Ci_oc	2	AAF61072.1	AF220553_1 (AF220553) 40S ribosomal protein S15A [Paralichthys olivaceus]	226	86	2.00E-58	AAF61072.1	AF220553_1 (AF220553) 40S ribosomal protein S15A [Paralichthys olivaceus]	240	86	1.00E-62
00054_Ci_oc	3	AAB66305.1	(U82663) cytoplasmic actin CyII [Heliocidaris erythrogramma]	180	100	1.00E-44					
00543_Ci_oc	4	R5HU23	ribosomal protein L23 - human	166	66	2.00E-40	R5HU23	ribosomal protein L23 - human	219	80	3.00E-56
00058_Ci_oc	5	AAD54776.1	AF134852_1 (AF134852) acidic ribosomal phophoprotein P0 [Danio rerio]	129	50	3.00E-29					
00421_Ci_oc	17	No Match					No Match				
00060_Ci_oc	1	No Match									
00061_Ci_oc	1	NP_113516.1	| hypothetical protein [Guillardia theta] >gi|12580767|emb|CAC27085.1| (AJ010592) hypothetical protein [Guillardia theta]	34.4	34	1.1					
00062_Ci_oc	1	CAA09747.1	(AJ011705) 40S ribosomal protein S10 [Lumbricus rubellus]	34.4	93	0.053					
00524_Ci_oc	6	AAK77710.1	AF369029_41 (AF369029) ORF41 [white spot syndrome virus]	31.7	31	7.4					
00065_Ci_oc	1	JQ0948	A5 antigen precursor - African clawed frog >gi|222963|dbj|BAA01260.1| (D10467) A5-protein [Xenopus laevis]	37.1	48	0.17					
00066_Ci_oc	1	NP_192837.1	| putative retrotransposon polyprotein [Arabidopsis thaliana] >gi|7486142|pir||T04294 hypothetical protein F25I24.200 - Arabidopsis thaliana >gi|4539373|emb|CAB40067.1| (AL049525) putative retrotransposon polyprotein [Arabidopsis thaliana] >gi|7267797|emb|CAB81200.1| (AL161518) putative retrotransposon polyprotein [Arabidopsis thaliana]	31.7	46	7.4					

00067_Ci_oc	1	AAA32122.1	(M20379) cytochrome c oxidase III [Trypanosoma brucei] >gi|447158|prf||1913438A cytochrome c oxidase [Trypanosoma brucei]	33.2	24	2.5					
00069_Ci_oc	1	T12117	polyprotein - fava bean dsRNA replicon >gi|3184156|emb|CAA04392.1| (AJ000929) ORFA+B [Vicia faba]	31.7	45	7.4					
00072_Ci_oc	1	No Match					NP_326275.1	predicted coding region [Mycoplasma pulmonis] emb|CAC13617.1| (AL445564) predicted coding region [Mycoplasma pulmonis]	31.3	35	8.8
00073_Ci_oc	1	AAF53297.1	(AE003640) CG9293 *gene product* [Drosophila melanogaster]	136	63	3.00E-31					
00075_Ci_oc	1	No Match					No Match				
00076_Ci_oc	1	T25945	hypothetical protein ZC196.5 - Caenorhabditis elegans >gi|1938470|gb|AAB52295.1| (U97007) ZC196.5 gene product [Caenorhabditis elegans]	32.1	29	5.7					
00077_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.63					
00078_Ci_oc	2	AAK38173.1	AF104915_1 (AF104915) protein serine/threonine kinase-1 [Plasmodium falciparum]	62.1	41	5.00E-09	T30272	hypothetical protein - sea urchin (Strongylocentrotus purpuratus) (fragment) gb|AAA85106.1| (U17377) cortical granule protein with LDL-receptor-like repeats [Strongylocentrotus purpuratus]	66	25	4.00E-10
00088_Ci_oc	1	BAB68391.1	(AB058682) opsin [Ciona intestinalis]	240	99	1.00E-62					
00089_Ci_oc	1	AAB94313.1	(U82990) envelope glycoprotein [Human immunodeficiency virus type 1]	31.7	32	6.3	No Match				
00091_Ci_oc	1	NP_200212.1	| flavonol 3-O-glucosyltransferase-like protein [Arabidopsis thaliana] >gi|10177263|dbj|BAB10731.1| (AB007644) flavonol 3-O-glucosyltransferase-like protein [Arabidopsis thaliana]	30.9	41	9.5					
00092_Ci_oc	1	AAF46988.1	(AE003460) CG3496 gene product [Drosophila melanogaster] >gi|13111554|gb|AAK12372.1|AF281363_1 (AF281363) virilizer [Drosophila melanogaster]	29	60	9.4					
00093_Ci_oc	1	No Match					No Match				
00094_Ci_oc	2	AAK95183.1	AF402809_1 (AF402809) 40S ribosomal protein S2 [Ictalurus punctatus]	95.2	71	6.00E-19					
00099_Ci_oc	1	No Match					XP_047891.2	*pre-mRNA splicing SR protein rA4 [Homo sapiens]*	29.3	47	7.7
00100_Ci_oc	2	T21339	hypothetical protein F25D7.5 - Caenorhabditis elegans >gi|3876262|emb|CAB01698.1| (Z78418) similar to EGF-like domain [Caenorhabditis elegans]	32.8	28	1.8	CAA25317.1	(X00729) poss. precursor polypeptide [Cowpea mosaic virus]	30.5	26	9
00101_Ci_oc	1	BAA97980.1	(AB045355) ORF2 [Ralstonia solanacearum]	176	85	9.00E-44	BAA97980.1	(AB045355) ORF2 [Ralstonia solanacearum]	186	80	9.00E-47
00237_Ci_oc	18	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.1	No Match				
00106_Ci_oc	2	NP_038243.1	COX3_15273| cytochrome c oxidase subunit III [Halocynthia roretzi] >gi|6566118|dbj|BAA88254.1| (AB024528) Cytochrome oxidase subunit III [Halocynthia roretzi]	136	50	2.00E-31					
00109_Ci_oc	1	T21259	hypothetical protein F22D6.5 - Caenorhabditis elegans >gi|3876247|emb|CAA95814.1| (Z71262) contains similarity to Pfam domain: PF00069 (Eukaryotic protein kinase domain), Score=166.8, E-value=1.2e-46, N=2~cDNA EST yk109g8.5 comes from this gene~cDNA EST yk14h12.3 comes from this gene~cDNA EST yk44f1.3 comes from this gene~cDNA EST y>	41.4	36	0.009					
00111_Ci_oc	1	BAA86200.1	(AB033282) nucleolin like protein CiRGG1 [Ciona intestinalis]	53.1	100	3.00E-06					
00112_Ci_oc	3	AAF57560.1	(AE003796) RpL11 gene product [Drosophila melanogaster]	250	84	9.00E-69	AAF57560.1	(AE003796) RpL11 *gene product [Drosophila melanogaster]*	252	85	3.00E-67
00125_Ci_oc	3	AAF78063.1	AF266749_1 (AF266749) ribsomal protein S29 [Culex pipiens quinquefasciatus]	87.8	68	9.00E-17					
00118_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2.4	P26270	PRSC_DROME 26S PROTEASOME REGULATORY SUBUNIT S12 (PROTEASOME SUBUNIT P40) (MOV34 PROTEIN) gb|AAA28695.1| (M64643) Mov34 [Drosophila melanogaster]	30.1	40	4.2
00769_Ci_oc	2	BAB25295.1	(AK007837) putative [Mus musculus] >gi|12842769|dbj|BAB25724.1| (AK008531) putative [Mus musculus] >gi|12845615|dbj|BAB26822.1| (AK010286) *putative [Mus musculus] >gi|13992534|emb|CAC38113.1|* (AJ307670) ribosmal protein L27a [Mus musculus]	199	66	3.00E-50					
00122_Ci_oc	1	No Match									
00126_Ci_oc	1	S62680	ubiquitin/ribosomal protein S27a fusion protein - Emericella nidulans	39.5	40	0.033	AAA36788.1	(M10939) pro-ubiquitin [Homo sapiens]	187	67	9.00E-47
00128_Ci_oc	1	XP_044615.1	| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] >gi|14759117|ref|XP_044612.1| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] >gi|14759129|ref|XP_044614.1| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] >gi|14786070|ref|XP_027333.1| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] >gi|14786073|ref|XP_027331.1| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] >gi|14786076|ref|XP_027332.1| ribosomal protein L36 [Homo sapiens] >gi|16117794|ref|NP_056229.2| ribosomal protein L36; 60S ribosomal protein L36 [Homo sapiens] >gi|16117796|ref|NP_378669.1| ribosomal *protein L36; 60S ribosomal protein L36 [Homo sapiens]* >gi|7388073|sp|Q9Y3U8|RL36_HUMAN 60S RIBOSOMAL PROTEIN L36 >gi|7441099|pir||T08720 ribosomal protein L36 - human >gi|4886451|emb|CAB43374.1| (AL050273) *hypothetical protein [Homo* sapiens] >gi|12804381|gb|AAH03052.1|AAH03052 (BC003052) ribosomal protein L36 [Homo sapiens] >gi|12833572|dbj|BAB22575.1| (AK003115) putative [Mus musculus] >gi|13436380|gb|AAH04971.1|AAH04971	121	68	6.00E-27	XP_044615.1	similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] ref|XP_044612.1| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] ref|XP_044614.1| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] ref|XP_027333.1| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] ref|XP_027331.1| similar to ribosomal protein L36 (H. sapiens) [Homo sapiens] ref|XP_027332.1| ribosomal protein L36 [Homo sapiens] ref|NP_056229.2| ribosomal protein L36; 60S ribosomal protein L36 [Homo sapiens] ref|NP_378669.1| ribosomal protein L36; 60S ribosomal protein L36 [Homo sapiens] sp|Q9Y3U8|RL36_HUMAN 60S RIBOSOMAL PROTEIN L36 pir||T08720 ribosomal protein L36 - human emb|CAB43374.1| (AL050273) hypothetical protein [Homo sapiens] gb|AAH03052.1|AAH03052 (BC003052) *ribosomal protein L36 [Homo sapiens] dbj|BAB22575.1|* (AK003115) putative [Mus musculus] gb|AAH04971.1|AAH04971 (BC004971) ribosomal protein L36 [Homo sapiens]	122	68	2.00E-27
00129_Ci_oc	1	AAH00047.1	AAH00047 (BC000047) Similar to ribosomal protein L8 [Homo sapiens]	66	70	7.00E-11					

00130_Ci_oc	2	NP_001011.1	| ribosomal protein S16; 40S ribosomal protein S16 [Homo sapiens] >gi|14764310|ref|XP_046112.1| ribosomal protein S16 [Homo sapiens] >gi|15306480|ref|XP_053077.1| ribosomal protein S16 [Homo sapiens] >gi|133807|sp|P17008|RS16_HUMAN 40S RIBOSOMAL PROTEIN S16 >gi|70918|pir||R3HU16 ribosomal protein S16, cytosolic - human >gi|70919|pir||R3RT16 ribosomal protein S16, cytosolic [validated] - rat >gi|57714|emb|CAA35662.1| (X17665) ribosomal protein S16 (AA 1-146) [Rattus rattus] >gi|338447|gb|AAA60583.1| (M60854) RPS16 [Homo sapiens] >gi|12846181|dbj|BAB27062.1| (AK010613) putative [Mus musculus] >gi|12846230|dbj|BAB27083.1| (AK010641) putative [Mus musculus] >gi|12846934|dbj|BAB27368.1| (AK011060) putative [Mus musculus] >gi|12859587|dbj|BAB31702.1| (AK019400) putative [Mus musculus] >gi|13279236|gb|AAH04324.1|AAH04324 (BC004324) ribosomal protein S16 [Homo sapiens] >gi|14044116|gb|AAH07977.1|AAH07977 (BC007977) ribosomal protein S16 [Homo sapiens]	138	76	2.00E-54	AAK11731.1	(AY027434) ribosomal protein S16 [Heteropneustes fossilis]	138	79	6.00E-32
00131_Ci_oc	1	CAC36098.1	(AJ310911) putative ribosomal protein L14 [Takifugu rubripes] >gi|13559250|emb|CAC36099.1| (AJ310912) putative ribosomal protein L14 [Takifugu rubripes]	137	47	1.00E-31	CAC36098.1	(AJ310911) putative ribosomal protein L14 [Takifugu rubripes] emb|CAC36099.1| (AJ310912) putative ribosomal protein L14 [Takifugu rubripes]	136	48	3.00E-31
00136_Ci_oc	1	No Match									
00138_Ci_oc	1	XP_008390.1	| gap junction protein, alpha 7, 45kD (connexin 45) [Homo sapiens]	132	58	4.00E-30	NP_200107.1	putative protein [Arabidopsis thaliana] dbj|BAB10443.1| (AB009055) dbj|BAA94533.1~gene_id:MXC20.18~similar to unknown protein [Arabidopsis thaliana]	32.5	56	4.3
00139_Ci_oc	1	AAA92980.1	(L39838) endoglucanase 3 [Fibrobacter succinogenes]	30.5	37	7.3					
00140_Ci_oc	7	P23403	RS20_XENLA 40S RIBOSOMAL PROTEIN S20 (S22) >gi|85846|pir||A37974 ribosomal protein S20, cytosolic - African clawed frog >gi|214758|gb|AAA49953.1| (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]	181	77	5.00E-45	P23403	RS20_XENLA 40S RIBOSOMAL PROTEIN S20 (S22) pir||A37974 ribosomal protein S20, cytosolic - African clawed frog gb|AAA49953.1| (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]	203	83	2.00E-51
00141_Ci_oc	1	NP_035473.1	| SEC61, gamma subunit (S. cerevisiae); Sec61, gamma subunit [Mus musculus] >gi|7657546|ref|NP_055117.1| Sec61 gamma; protein transport protein SEC61 gamma subunit [Homo sapiens] >gi|14741787|ref|XP_044650.1| Sec61 gamma [Homo sapiens] >gi|585962|sp|P38384|S61G_HUMAN PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT >gi|631518|pir||S42412 protein translocation complex sec61 gamma chain, endoplasmic reticulum - dog >gi|459748|gb|AAA19705.1| (L25086) Sec61-complex gamma-subunit [Canis familiaris] >gi|506792|gb|AAA19431.1| (U11027) Sec61 protein complex gamma subunit [Mus musculus] >gi|4092056|gb|AAC99401.1| (AF054184) Sec61 gamma [Homo sapiens] >gi|12849107|dbj|BAB28210.1| (AK012393) putative [Mus musculus] >gi|12849524|dbj|BAB28376.1| (AK012644) putative [Mus musculus] >gi|14550465|gb|AAH09480.1|AAH09480 (BC009480) SEC61, gamma subunit (S. cerevisiae) [Homo sapiens] >gi|740572|prf||2005371B Sec61 protein:SUBUNIT=gamma [Canis familiaris]	88.5	67	3.00E-17					
00142_Ci_oc	1	BAA95101.1	(AB041649) unnamed protein product [Mus musculus]	34.4	29	1.1					
00143_Ci_oc	1	NP_053027.1	| EpsG [Lactococcus lactis subsp. cremoris] >gi|2072444|gb|AAC45234.1| (AF036485) EpsG [Lactococcus lactis subsp. cremoris]	32.8	47	3.3					
00144_Ci_oc	1	No Match									
00145_Ci_oc	1	AAF13755.1	AF117351_12 (AF117351) unknown [Zymomonas mobilis]	31.3	25	9.7					
00146_Ci_oc	1	NP_224031.1	| UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE [Helicobacter pylori J99] >gi|6707717|sp|Q9ZJJ4|MURB_HELPJ UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (UDP-N-ACETYLMURAMATE DEHYDROGENASE) >gi|7465441|pir||B71823 udp-n-acetylenolpyruvoylglucosamine reductase - Helicobacter pylori (strain J99) >gi|4155918|gb|AAD06886.1| (AE001554) UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE [Helicobacter pylori J99]	30.5	48	7.2	AAD47860.1	AF171685_1 (AF171685) envelope glycoprotein [Porcine reproductive and respiratory syndrome virus]	31.3	50	3.2
00147_Ci_oc	2	AAF82581.3	(AF272885) regulatory protein HrpX [Xanthomonas oryzae pv. oryzicola]	32.5	38	4	I51638	F-cadherin - African clawed frog emb|CAA59679.1| (X85330) F-cadherin [Xenopus laevis]	31.3	36	9.7
00148_Ci_oc	1	No Match									
00149_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	50	57	2.00E-05	NP_246871.1	unknown [Pasteurella multocida] gb|AAK04016.1| (AE006230) unknown [Pasteurella multocida]	32.5	51	2.1
00553_Ci_oc	5	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.6	No Match				
00151_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.64	No Match				
00152_Ci_oc	1	NP_346146.1	| hypothetical protein [Streptococcus pneumoniae TIGR4] >gi|15903595|ref|NP_359145.1| Hypothetical protein [Streptococcus pneumoniae R6] >gi|14973203|gb|AAK75786.1| (AE007464) hypothetical protein [Streptococcus pneumoniae TIGR4] >gi|15459217|gb|AAL00356.1| (AE008523) Hypothetical protein [Streptococcus pneumoniae R6]	29.7	39	9	P55303	CATR_ASPNG CATALASE R pir||S37384 catalase (EC 1.11.1.6) R - Aspergillus niger emb|CAA80669.1| (Z23138) catR [Aspergillus niger] gb|AAA68206.1| (L15474) catalase [Aspergillus niger]	30.9	31	5.6
00736_Ci_oc	2	AAK95168.1	AF401596_1 (AF401596) ribosomal protein L39 [Ictalurus punctatus]	99.1	86	2.00E-20	AAK95168.1	AF401596_1 (AF401596) ribosomal protein L39 [Ictalurus punctatus]	99.1	86	2.00E-20

00155_Ci_oc	1	AAA03341.1	(U02032) ribosomal protein L23a [Homo sapiens]	215	75	3.00E-55	NP_207117.1	arginyl-tRNA synthetase (argS) [Helicobacter pylori 26695] sp|P56128|SYR_HELPY ARGINYL-TRNA SYNTHETASE (ARGININE--TRNA LIGASE) (ARGRS) pir||G64559 arginine--tRNA ligase (EC 6.1.1.19) - Helicobacter pylori (strain 26695) gb|AAD07388.1| (AE000550) arginyl-tRNA synthetase (argS) [Helicobacter pylori 26695]	31.7	46	4.4
00156_Ci_oc	1	NP_006295.1	| deleted in split-hand/split-foot 1 region [Homo sapiens] >gi|6677941|ref|NP_033195.1| split hand/foot deleted gene 1 [Mus musculus] >gi|14749104|ref|XP_044488.1| deleted in split-hand/split-foot 1 region [Homo sapiens] >gi|7531100|sp|Q13437|DSS1_HUMAN DELETED IN SPLIT HAND/SPLIT FOOT PROTEIN 1 (SPLIT HAND/FOOT DELETED PROTEIN 1) >gi|7512379|pir||G02284 deleted in split hand/split foot 1 - human >gi|1209724|gb|AAA91179.1| (U41515) Method: conceptual translation supplied by author [Homo sapiens] >gi|1209726|gb|AAA91180.1| (U41626) Method: conceptual translation supplied by author [Mus musculus]	63.6	44	2.00E-09	CAC00723.1	(AJ250752) olfactory receptor class I [Xenopus laevis]	32.8	35	3.3
00158_Ci_oc	1	NP_001976.1	| electron-transfer-flavoprotein, beta polypeptide; electron-transferring-flavoprotein, beta polypeptide; Electron transfer flavoprotein, beta polypeptide [Homo sapiens] >gi|11424346|ref|XP_008953.1| electron-transfer-flavoprotein, beta polypeptide [Homo sapiens] >gi|585110|sp|P38117|ETFB_HUMAN ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-ETF) >gi|479194|pir||S32482 electron transfer flavoprotein beta chain - human >gi|2781203|pdb|1EFV|B Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution >gi|297902|emb|CAA50441.1| (X71129) electron transfer flavoprotein beta subunit [Homo sapiens]	161	61	7.00E-39					
00160_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.89					
00161_Ci_oc	3	NP_077799.1	| hypothetical protein MGC8159 [Mus musculus] >gi|12805613|gb|AAH02286.1|AAH02286 (BC002286) Unknown (protein for MGC:8159) [Mus musculus]	48	28	9.00E-05					
00162_Ci_oc	5	A61144	probable flagellar protein (clone FCT-F8-4) - Trypanosoma cruzi (fragment)	36.7	83	0.22	S12206	hypothetical protein 2 (rRNA external transcribed spacer) - mouse	44.1	55	0.001
00163_Ci_oc	1	No Match					T25827	hypothetical protein K12D9.12 - Caenorhabditis elegans gb|AAG24169.1| (U80030) Hypothetical protein K12D9.12 [Caenorhabditis elegans]	31.7	29	7.3
00164_Ci_oc	1	P13272	UCRI_BOVIN UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) [CONTAINS: UBIQUINOL-CYTOCHROME C REDUCTASE 8 KDA PROTEIN (COMPLEX III SUBUNIT IX)] >gi|1070400|pir||A34660 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) Rieske iron-sulfur protein precursor [validated] - bovine >gi|299558|gb|AAB26197.1| (S58789) Rieske iron-sulfur [Bos taurus]	42.2	51	0.004					
00167_Ci_oc	1	No Match									
00168_Ci_oc	1	XP_050217.1	| RNA binding protein [Homo sapiens] >gi|14747087|ref|XP_050216.1| hypothetical protein XP_050216 [Homo sapiens]	141	77	5.00E-38					
00169_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	33.2	55	0.68	No Match				
00170_Ci_oc	1	P16305	GAA6_MOUSE GAMMA-AMINOBUTYRIC-ACID RECEPTOR ALPHA-6 SUBUNIT PRECURSOR (GABA(A) RECEPTOR) >gi|5813766|gb|AAD52004.1|U77411_4 (U77411) GABAA receptor alpha 6 subunit [Mus musculus] >gi|11055259|gb|AAG28024.1|AF256197_1 (AF256197) GABA-A receptor alpha-6 subunit protein long splice variant [Mus musculus] >gi|11055261|gb|AAG28025.1|AF256198_1 (AF256198) GABA-A receptor alpha-6 subunit protein long splice variant [Mus musculus]	50.4	57	2.00E-05					
00171_Ci_oc	1	BAB25321.1	(AK007871) putative [Mus musculus]	60.1	68	2.00E-08					
00603_Ci_oc	2	No Match					AAC14171.1	(AF050425) T cell receptor beta chain CDR3 [Mus musculus]	30.9	30	7.3
00173_Ci_oc	5	P02350	RS3A_XENLA 40S RIBOSOMAL PROTEIN S3A (S1A) >gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed frog >gi|65091|emb|CAA40592.1| (X57322) ribosomal protein S1a [Xenopus laevis]	195	79	3.00E-49					
00174_Ci_oc	2	T23759	hypothetical protein M117.2 - Caenorhabditis elegans >gi|3878744|emb|CAA98138.1| (Z73910) predicted using Genefinder~Identity to C.elegans 14-3-3-like protein (SW:1433_CAEEL), contains similarity to Pfam domain: PF00244 (14-3-3 proteins), Score=497.0, E-value=4.5e-146, N=1~cDNA EST EMBL:T00100 comes from this gene; cDNA EST EMBL:T0>	57.8	68	1.00E-07	AAF46439.1	(AE003446) CG4350 gene product [Drosophila melanogaster]	30.5	44	4.1
00176_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2.8	T38957	probable GPR/FUN34 family protein - fission yeast (Schizosaccharomyces pombe) emb|CAB10857.1| (Z98056) putative GPR/FUN34 family protein [Schizosaccharomyces pombe]	32.5	41	0.83
00177_Ci_oc	1	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	46.5	75	3.00E-04					
00178_Ci_oc	1	BAA25882.1	(D88669) capsid protein [Bryopsis cinicola]	31.7	35	7.4					
00507_Ci_oc	8	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9
00180_Ci_oc	3	NP_174360.1	| putative reticuline oxidase-like protein [Arabidopsis thaliana] >gi|4587529|gb|AAD25760.1|AC007060_18 (AC007060) Strong similarity to F19I3.2 gi|3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb|AC004238. EST gb|H76902 comes from this gene	34.4	30	1.1					

00181_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9					
00182_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.7					
00184_Ci_oc	6	CAA73906.1	(Y13578) calmodulin [Ciona intestinalis]	131	93	9.00E-30					
00185_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.98	No Match				
00186_Ci_oc	1	AAK18771.1	(AF260996) chitin synthase [Glomus intraradices]	32.5	32	4.3					
00905_Ci_oc	8	NP_149817.1	| 354L [Chilo iridescent virus] >gi|15042435|gb|AAK82215.1|AF303741_356 (AF303741) 354L [Chilo iridescent virus]	31.7	44	6.1	AAF13046.1	AF157641_2 (AF157641) putative Ni/Fe hydrogenase small subunit precursor [Desulfitobacterium dehalogenans]	32.5	40	4.2
00188_Ci_oc	1	P15541	AMPN_RABIT AMINOPEPTIDASE N (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA ANTIGEN CD13) >gi|544755|gb|AAB29534.1| (S68687) aminopeptidase N; APN [Oryctolagus cuniculus] >gi|737584|prf||1923196A aminopeptidase N [Oryctolagus cuniculus]	31.3	43	9.7					
00189_Ci_oc	1	P55389	Y4CG_RHISN PROBABLE DNA-INVERTASE Y4CG >gi|2182332|gb|AAB92422.1| (AE000068) Y4cG [Rhizobium sp. NGR234]	79.6	79	5.00E-15	P55389	Y4CG_RHISN PROBABLE DNA-INVERTASE Y4CG gb|AAB92422.1| (AE000068) Y4cG [Rhizobium sp. NGR234]	86.2	83	6.00E-17
00190_Ci_oc	1	NP_298110.1	| hypothetical protein [Xylella fastidiosa 9a5c] >gi|11292771|pir||G82759 hypothetical protein XF0820 [imported] - Xylella fastidiosa (strain 9a5c) >gi|9105720|gb|AAF83630.1|AE003921_10 (AE003921) hypothetical protein [Xylella fastidiosa 9a5c]	44.9	38	3.00E-04	NP_298110.1	hypothetical protein [Xylella fastidiosa 9a5c] pir||G82759 hypothetical protein XF0820 [imported] - Xylella fastidiosa (strain 9a5c) gb|AAF83630.1|AE003921_10 (AE003921) hypothetical protein [Xylella fastidiosa 9a5c]	44.9	38	2.00E-04
00191_Ci_oc	1	T18440	hypothetical protein C0425w - malaria parasite (Plasmodium falciparum) >gi|3649772|emb|CAB11121.1| (Z98547) hypothetical protein, PFC0425w [Plasmodium falciparum]	32.5	32	4.3					
00570_Ci_oc	14	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.2	NP_196884.1	putative protein [Arabidopsis thaliana] dbj|BAB11108.1| (AB005230) gene_id:MAC12.25~pir||S77419~similar to unknown protein [Arabidopsis thaliana] gb|AAL08242.1| (AY056386) AT5g13800/MAC12_25 [Arabidopsis thaliana]	31.7	33	5.9
00193_Ci_oc	1	NP_421067.1	| phosphoglucomutase/phosphomannomutase family protein [Caulobacter crescentus] >gi|13423775|gb|AAK24235.1| (AE005896) phosphoglucomutase/phosphomannomutase family protein [Caulobacter crescentus]	126	76	1.00E-28	NP_421067.1	phosphoglucomutase/phosphomannomutase family protein [Caulobacter crescentus] gb|AAK24235.1| (AE005896) phosphoglucomutase/phosphomannomutase family protein [Caulobacter crescentus]	125	76	1.00E-28
00199_Ci_oc	1	T22493	hypothetical protein F52B5.3 - Caenorhabditis elegans >gi|3877406|emb|CAA99855.1| (Z75541) contains similarity to Pfam domain: PF00271 (Helicases conserved C-terminal domain), Score=15.7, E-value=0.0013, N=1; PF01424 (R3H domain), Score=70.5, E-value=1.2e-17, N=1~cDNA EST yk17a7.3 comes from this gene~cDNA EST yk28d3.3 comes from th>	33.6	35	1.9					
00397_Ci_oc	5	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9	T21620	hypothetical protein F32A11.6 - Caenorhabditis elegans emb|CAB04229.1| (Z81521) contains similarity to Pfam domain: PF00642 (Zinc finger C-x8-C-x5-C-x3-H type (and similar).), Score=65.4, E-value=1.3e-17, N=2 [Caenorhabditis elegans]	32.5	18	4.3
00260_Ci_oc	12	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.5	No Match				
00205_Ci_oc	1	AAD25102.1	(AF139590) ribosomal protein L17 [Dicentrarchus labrax]	41	28	0.007	BAB28415.1	(AK012694) putative [Mus musculus]	113	76	1.00E-24
00207_Ci_oc	1	P10922	H10_MOUSE HISTONE H1' (H1.0) (H1(0)) >gi|2118973|pir||I49150 histone H1.0 - mouse >gi|897830|gb|AAA69911.1| (U18295) histone H1(0) [Mus musculus] >gi|13277924|gb|AAH03830.1|AAH03830 (BC003830) Similar to H1 histone family, member 0 [Mus musculus] >gi|15079307|gb|AAH11493.1|AAH11493 (BC011493) Similar to H1 histone family, member 0 [Mus musculus]	90.9	53	1.00E-17	BAB64304.1	(AB030839) beta-conglycinin alpha-subunit [Glycine max]	31.7	34	7.4
00208_Ci_oc	3	NP_067461.2	| beta-carotene 15, 15'-dioxygenase; beta,beta-carotene 15,15'-dioxygenase [Mus musculus] >gi|11320970|gb|AAG33982.1|AF271298_1 (AF271298) beta-carotene 15,15'-dioxygenase [Mus musculus] >gi|11990268|emb|CAB92531.2| (AJ278064) beta,beta-carotene 15,15'-dioxygenase [Mus musculus]	86.6	51	2.00E-16					
00209_Ci_oc	1	NP_036005.1	| proteasome (prosome, macropain) 26S subunit, non-ATPase, 13; 26S proteasome subunit p40.5 [Mus musculus] >gi|5453129|gb|AAD43443.1|AF107838_1 (AF107838) 26S proteasome subunit p40.5 [Mus musculus]	120	58	1.00E-26					
00211_Ci_oc	1	No Match									
00214_Ci_oc	1	NP_008855.1	| splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) [Homo sapiens] >gi|730773|sp|Q07955|SFR1_HUMAN SPLICING FACTOR, ARGININE/SERINE-RICH 1 (PRE-MRNA SPLICING FACTOR SF2, P33 SUBUNIT) (ALTERNATIVE SPLICING FACTOR ASF-1) >gi|105293|pir||A40040 alternative splicing factor ASF-1 - human >gi|179075|gb|AAA35565.1| (M72709) alternative [Homo sapiens] >gi|338047|gb|AAA03476.1| (M69040) SF2p33 [Homo sapiens]	107	78	1.00E-22					
00215_Ci_oc	1	B71612	hypothetical protein PFB0555c - malaria parasite (Plasmodium falciparum) >gi|3845215|gb|AAC71900.1| (AE001402) hypothetical protein [Plasmodium falciparum]	30.5	38	6	B71612	hypothetical protein PFB0555c - malaria parasite (Plasmodium falciparum) gb|AAC71900.1| (AE001402) hypothetical protein [Plasmodium falciparum]	30.5	38	5.9
00216_Ci_oc	1	A48925	mannose receptor precursor, macrophage - mouse	48.4	30	7.00E-05					
00218_Ci_oc	1	No Match									
00220_Ci_oc	1	BAA00447.1	(D00570) open reading frame (251 AA) [Mus musculus]	32.5	29	4.3					

00221_Ci_oc	1	No Match									
00222_Ci_oc	1	NP_005639.1	| elongin C; transcription elongation factor B, polypeptide 1 [Homo sapiens] >gi|11426593|ref|XP_005275.1| elongin C [Homo sapiens] >gi|12018254|ref|NP_072115.1| elongation factor SIII p15 subunit [Rattus norvegicus] >gi|16162599|ref|XP_056058.1| hypothetical protein XP_056058 [Homo sapiens] >gi|4930145|pdb|1VCB|B Chain B, The Vhl-Elonginc-Elonginb Structure >gi|4930148|pdb|1VCB|E Chain E, The Vhl-Elonginc-Elonginb Structure >gi|4930151|pdb|1VCB|H Chain H, The Vhl-Elonginc-Elonginb Structure >gi|4930154|pdb|1VCB|K Chain K, The Vhl-Elonginc-Elonginb Structure >gi|497780|gb|AAA41.109.1| (L29259) elongation factor SIII p15 subunit [Rattus norvegicus] >gi|551606|gb|AAA67650.1| (L34587) RNA polymerase II elongation factor SIII, p15 subunit [Homo sapiens] >gi|12848087|dbj|BAB27825.1| (AK011757) putative [Mus musculus] >gi|12848402|dbj|BAB27939.1| (AK011958) putative [Mus musculus] >gi|12849959|dbj|BAB28546.1| (AK012909) putative [Mus musculus] >gi|12850234|dbj|BAB28641.1| (AK013089) putative [Mus musculus] >gi|14318612|gb|AAH09104.1|AAH09104 (BC009104) transcription	195	82	3.00E-49	NP_005639.1	elongin C; transcription elongation factor B, polypeptide 1 [Homo sapiens] ref|XP_005275.1| elongin C [Homo sapiens] ref|NP_072115.1| elongation factor SIII p15 subunit [Rattus norvegicus] ref|XP_056058.1| hypothetical protein XP_056058 [Homo sapiens] pdb|1VCB|B Chain B, The Vhl-Elonginc-Elonginb Structure pdb|1VCB|E Chain E, The Vhl-Elonginc-Elonginb Structure pdb|1VCB|H Chain H, The Vhl-Elonginc-Elonginb Structure pdb|1VCB|K Chain K, The Vhl-Elonginc-Elonginb Structure gb|AAA41109.1| (L29259) elongation factor SIII p15 subunit [Rattus norvegicus] gb|AAA67650.1| (L34587) RNA polymerase II elongation factor SIII, p15 subunit [Homo sapiens] dbj|BAB27825.1| (AK011757) putative [Mus musculus] dbj|BAB27939.1| (AK011958) putative [Mus musculus] dbj|BAB28546.1| (AK012909) putative [Mus musculus] dbj|BAB28641.1| (AK013089) putative [Mus musculus] gb|AAH09104.1|AAH09104 (BC009104) transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C) [Mus musculus] gb|AAH13809.1|AAH13809 (BC013809) Similar to transcription elongation factor B (SIII), polypeptide	195	82	3.00E-49
00227_Ci_oc	2	AAD16877.1	(AF104059) ribosomal protein S15 [Salmo salar]	208	72	3.00E-53	AAD16877.1	(AF104059) ribosomal protein S15 [Salmo salar]	207	71	7.00E-53
00228_Ci_oc	1	NP_033556.1	| X-linked nuclear protein; alpha thalassemia/mental retardation syndrome (X-linked) [Mus musculus] >gi|5915738|sp|Q61687|ATRX_MOUSE TRANSCRIPTIONAL REGULATOR ATRX (X-LINKED NUCLEAR PROTEIN) (HETEROCHROMATIN PROTEIN 2) (HP1 ALPHA-INTERACTING PROTEIN) (HP1-BP38 PROTEIN) >gi|3002558|gb|AAC08741.1| (AF026032) ATRX protein [Mus musculus]	51.5	36	8.00E-06	NP_213526.1	putative protein [Aquifex aeolicus] pir||B70367 hypothetical protein aq_765 - Aquifex aeolicus gb|AAC06926.1| (AE000706) putative protein [Aquifex aeolicus]	32.5	35	4.1
00232_Ci_oc	1	NP_075622.1	| ribosomal protein S19 [Mus musculus] >gi|133857|sp|P17074|RS19_RAT 40S RIBOSOMAL PROTEIN S19 >gi|71019|pir||R3RT19 ribosomal protein S19, cytosolic [validated] - rat >gi|57716|emb|CAA36003.1| (X51707) ribosomal protein S19 (AA 1-145) [Rattus rattus] >gi|7648818|gb|AAF65683.1|AF216207_1 (AF216207) ribosomal protein S19 [Mus musculus] >gi|12850925|dbj|BAB28898.1| (AK013524) putative [Mus musculus] >gi|12858583|dbj|BAB31370.1| (AK018725) putative [Mus musculus]	213	69	2.00E-54	NP_075622.1	ribosomal protein S19 [Mus musculus] sp|P17074|RS19_RAT 40S RIBOSOMAL PROTEIN S19 pir||R3RT19 ribosomal protein S19, cytosolic [validated] - rat emb|CAA36003.1| (X51707) ribosomal protein S19 (AA 1-145) [Rattus rattus] gb|AAF65683.1|AF216207_1 (AF216207) ribosomal protein S19 [Mus musculus] dbj|BAB28898.1| (AK013524) putative [Mus musculus] dbj|BAB31370.1| (AK018725) putative [Mus musculus]	212	71	2.00E-54
00234_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.8	No Match				
00236_Ci_oc	1	No Match									
00238_Ci_oc	1	AAD40001.1	AF150095_1 (AF150095) small zinc finger-like protein [Ciona intestinalis]	182	98	2.00E-49	AAD40001.1	AF150095_1 (AF150095) small zinc finger-like protein [Ciona intestinalis]	179	97	1.00E-48
00239_Ci_oc	1	NP_112327.1	| ribosomal protein L10a [Rattus norvegicus] >gi|13642763|ref|XP_017704.1| ribosomal protein L10a [Homo sapiens] >gi|15431288|ref|NP_009035.3| ribosomal protein L10a; 60S ribosomal protein L10a [Homo sapiens] >gi|1709974|sp|P52859|R10A_RAT 60S RIBOSOMAL PROTEIN L10A >gi|2143564|pir||JC4677 ribosomal protein L10a, cytosolic [validated] - rat >gi|1370289|emb|CAA63732.1| (X93352) ribosomal protein L10a [Rattus norvegicus] >gi|4490422|emb|CAB38627.1| (AL022721) dJ109F14.2 (60S Ribosomal Protein RPL10A) [Homo sapiens] >gi|13905016|gb|AAH06791.1|AAH06791 (BC006791) ribosomal protein L10a [Homo sapiens] >gi|15030214|gb|AAH11366.1|AAH11366 (BC011366) Similar to ribosomal protein L10a [Homo sapiens]	220	68	8.00E-57					
00240_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.6	NP_191128.1	putative protein [Arabidopsis thaliana] pir||T47708 hypothetical protein F1I16.100 - Arabidopsis thaliana emb|CAB81594.1| (AL161667) putative protein [Arabidopsis thaliana]	32.5	30	2.1
00243_Ci_oc	1	No Match					No Match				
00249_Ci_oc	3	AAK09383.1	AF321768_1 (AF321768) ribosomal protein S3a [Ophiophagus hannah]	188	61	4.00E-47					
00250_Ci_oc	1	No Match					No Match				
00252_Ci_oc	3	P41383	TBA2_PATVU TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi|542502|pir||S42033 tubulin alpha chain - common limpet >gi|454315|emb|CAA54712.1| (X77618) alpha tubulin [Patella vulgata] >gi|496495|emb|CAA55978.1| (X79468) alpha tubulin 2 [Patella vulgata]	108	100	8.00E-41					
00253_Ci_oc	2	BAA00448.1	(D00570) open reading frame (196 AA) [Mus musculus]	31.3	22	9.7					
00256_Ci_oc	1	No Match									
00258_Ci_oc	1	O13966	ACON_SCHPO ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (CITRATE HYDRO-LYASE) (ACONITASE) >gi|7490068|pir||T38347 aconitate hydratase - fission yeast (Schizosaccharomyces pombe) >gi|2330789|emb|CAB11263.1| (Z98601) aconitate hydratase [Schizosaccharomyces pombe]	44.9	58	1.00E-10					
00262_Ci_oc	4	D71614	hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum) >gi|3845190|gb|AAC71881.1| (AE001396) hypothetical protein [Plasmodium falciparum]	66.7	56	2.00E-10	D71614	hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum) gb|AAC71881.1| (AE001396) hypothetical protein [Plasmodium falciparum]	66.7	50	2.00E-10
00265_Ci_oc	1	No Match					No Match				
00270_Ci_oc	3	AAB19650.1	retinaldehyde-binding protein, CRALBP [cattle, Peptide, 316 aa]	129	50	3.00E-29					
00273_Ci_oc	1	No Match					D71614	hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum) gb|AAC71881.1| (AE001396) hypothetical protein [Plasmodium falciparum]	66.7	50	2.00E-10
00277_Ci_oc	2	CAB46918.2	(AJ242946) hyaluronan synthase [Streptococcus uberis]	34	30	1.5					

00107_Ci_oc	2	BAA11765.1	(D83069) ADT/ATP translocase [Halocynthia roretzi]	115	80	6.00E-25					
00279_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.6	No Match				
00281_Ci_oc	2	AAB03641.1	(U22295) unknown protein [Drosophila melanogaster]	40.6	35	0.015					
00282_Ci_oc	1	JC4338	tryptophan dimethylallyltransferase (EC 2.5.1.34) - ergot fungus >gi|1005418|gb|AAC18893.1| (L39640) dimethylallyl-trans-transferase [Claviceps fusiformis] >gi|1585797|prf||2202167A Trp(dimethylallyl) synthase [Claviceps purpurea]	34.4	38	1.1					
00283_Ci_oc	1	No Match									
00284_Ci_oc	1	BAB13725.1	(AB049118) transcription factor HpLim1 [Hemicentrotus pulcherrimus]	51.9	70	6.00E-06					
00290_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	3.1	No Match				
00291_Ci_oc	1	P26692	DCMA_METSO CARBON MONOXIDE DEHYDROGENASE ALPHA SUBUNIT >gi|150036|gb|AAA72934.1| (M55280) carbon monoxide dehydrogenase alpha subunit [Methanosaeta concilii]	30.5	30	6.3					
00293_Ci_oc	1	B53234	vicilin-like storage protein Glb1-L, embryo - maize >gi|22284|emb|CAA41809.1| (X59083) vicilin-like embryo storage protein [Zea mays]	31.7	47	1.7	B53234	vicilin-like storage protein Glb1-L, embryo - maize emb|CAA41809.1| (X59083) vicilin-like embryo storage protein [Zea mays]	31.7	47	1.8
00294_Ci_oc	1	NP_220165.1	| hypothetical protein [Chlamydia trachomatis] >gi|7468790|pir||E71488 hypothetical protein CT647 - Chlamydia trachomatis (serotype D, strain UW3/Cx) >gi|3329096|gb|AAC68824.1| (AE001335) hypothetical protein [Chlamydia trachomatis]	32.8	50	3.3					
00296_Ci_oc	1	NP_215831.1	| murA [Mycobacterium tuberculosis H37Rv] >gi|15840766|ref|NP_335803.1| UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium tuberculosis CDC1551] >gi|1709182|sp|Q10604|MURA_MYCTU UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (ENOYLPYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE) (EPT) >gi|7448136|pir||G70775 UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) - Mycobacterium tuberculosis >gi|1235980|emb|CAA65472.1| (X96711) UDP-N-acetylglucosamine enolpyruvyl transferase [Mycobacterium tuberculosis] >gi|3261575|emb|CAA97748.1| (Z73419) murA [Mycobacterium tuberculosis H37Rv] >gi|13880959|gb|AAK45617.1| (AE007009) UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Mycobacterium tuberculosis CDC1551]	30.1	35	4.6	No Match				
00299_Ci_oc	1	No Match					AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9
00302_Ci_oc	1	AAK29781.1	AF258619_1 (AF258619) creatine kinase [Ciona intestinalis]	193	86	2.00E-48					
00305_Ci_oc	4	AAK95156.1	AF401584_1 (AF401584) *ribosomal protein L29 [Ictalurus punctatus]*	91.3	75	5.00E-18	AAK95156.1	AF401584_1 (AF401584) ribosomal protein L29 [Ictalurus punctatus]	97.5	78	8.00E-20
00307_Ci_oc	1	BAB21828.1	(AB051524) KIAA1737 protein [Homo sapiens]	34	51	0.53	NP_038816.1	frequently rearranged in advanced T-cell lymphomas 3 [Mus musculus] gb|AAD42076.1|AF148857_1 (AF148857) FRAT3 [Mus musculus]	34	35	0.76
00720_Ci_oc	5	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	37.1	41	0.093	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	35.6	38	0.25
00311_Ci_oc	2	CAC14409.1	(AL132898) Y59A8B.9 [*Caenorhabditis elegans*]	65.2	49	6.00E-10					
00313_Ci_oc	1	No Match									
00316_Ci_oc	1	NP_195032.1	| putative protein [Arabidopsis thaliana] >gi|7486212|pir||T05314 hypothetical protein F26P21.180 - Arabidopsis thaliana >gi|3688187|emb|CAA21215.1| (AL031804) *putative protein [Arabidopsis* thaliana] >gi|7270253|emb|CAB80023.1| (AL161582) putative protein [Arabidopsis thaliana]	207	62	7.00E-53	AAF50009.1	(AE003543) CG10907 gene product [Drosophila melanogaster]	171	63	6.00E-42
00317_Ci_oc	1	XP_038290.2	| hypothetical protein XP_038290 [Homo sapiens] >gi|12835352|dbj|BAB23233.1| (AK004239) putative [Mus musculus] >gi|12847445|dbj|BAB27573.1| (AK011367) putative [Mus musculus] >gi|12850284|dbj|BAB28660.1| (AK013120) putative [Mus musculus] >gi|14042661|dbj|BAB55342.1| (AK027750) unnamed protein product [Homo sapiens]	118	75	7.00E-26					
00318_Ci_oc	1	P79382	GST1_PIG MICROSOMAL GLUTATHIONE S-TRANSFERASE 1 (MICROSOMAL GST-1) (MICROSOMAL GST-I) >gi|1840393|dbj|BAA19201.1| (AB000884) glutathione S-transferase [Sus scrofa]	60.5	41	9.00E-09	P79382	GST1_PIG MICROSOMAL GLUTATHIONE S-TRANSFERASE 1 (MICROSOMAL GST-1) (MICROSOMAL GST-I) dbj|BAA19201.1| (AB000884) glutathione S-transferase [Sus scrofa]	59.3	45	2.00E-08
00320_Ci_oc	1	BAB18575.1	(AB037688) patched-2 [Xenopus laevis]	31.3	35	9.7					
00323_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.2	No Match				
00324_Ci_oc	1	CAC19490.1	(AJ009699) putative ribosomal protein L27 [Stichodactyla helianthus]	95.2	68	6.00E-19					
00325_Ci_oc	1	NP_057284.1	| U6 snRNA-associated Sm-like protein LSm8 [Homo sapiens] >gi|14753215|ref|XP_027184.1| U6 snRNA-associated Sm-like protein LSm8 [Homo sapiens] >gi|10720071|sp|O95777|LSM8_HUMAN U6 SNRNA-ASSOCIATED SM-LIKE PROTEIN LSM8 >gi|4309884|gb|AAD15542.1| (AC006389) similar to Schizosaccharomyces pombe splicing factor; similar to PID:3395591 [Homo sapiens] >gi|5919157|gb|AAD56232.1|AF182294_1 (AF182294) U6 snRNA-associated Sm-like protein LSm8 [Homo sapiens] >gi|12803805|gb|AAH02742.1|AAH02742 (BC002742) U6 snRNA-associated Sm-like protein LSm8 [Homo sapiens]	87.8	68	1.00E-16					

00327_Ci_oc	1	P26007	ITA6_CHICK INTEGRIN ALPHA-6 PRECURSOR (VLA-6) >gi|104740|pir||A38457 integrin alpha-6 chain precursor - chicken >gi|63542|emb|CAA39909.1| (X56559) integrin alpha 6 subunit [Gallus gallus]	37.5	29	0.13					
00329_Ci_oc	1	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	43.4	61	0.002	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	43.4	61	0.002
00331_Ci_oc	2	NP_036526.2	| prefoldin 2 [Homo sapiens] >gi|14723987|ref|XP_041939.1| prefoldin 2 [Homo sapiens] >gi|14723996|ref|XP_041940.1| hypothetical protein XP_041940 [Homo sapiens] >gi|12643887|sp|Q9UHV9|PFD2_HUMAN PREFOLDIN SUBUNIT 2 (PROTEIN HSPC231) >gi|6563248|gb|AAF17218.1|AF117237_1 (AF117237) prefoldin subunit 2 [Homo sapiens] >gi|15214670|gb|AAH12464.1|AAH12464 (BC012464) prefoldin 2 [Homo sapiens]	60.1	60	2.00E-08					
00332_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.8	No Match				
00333_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	36	44	0.17	AAF55583.1	(AE003723) CG7708 gene product [Drosophila melanogaster]	30.1	44	9.8
00335_Ci_oc	2	AAK37484.1	(AF322122) teosinte branched1 protein [Coix lacryma-jobi]	34.4	37	1.1					
00336_Ci_oc	2	BAB32661.1	(AB055884) 60S ribosomal protein L35 [Sus scrofa]	142	65	3.00E-33	BAB32661.1	(AB055884) 60S ribosomal protein L35 [Sus scrofa]	158	68	5.00E-38
00337_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.69					
00340_Ci_oc	1	NP_052312.1	| ORF C2 [Ralstonia solanacearum] >gi|3402498|dbj|BAA32220.1| (AB015669) ORF C2 [Ralstonia solanacearum]	33.2	38	2.5					
00344_Ci_oc	1	No Match									
00346_Ci_oc	1	No Match					B71600	variant-specific surface protein 1 homolog PFB1055c - malaria parasite (Plasmodium falciparum) gb|AAC71996.1| (AE001434) PfEMP1 [Plasmodium falciparum]	38.3	42	0.075
00348_Ci_oc	1	XP_006170.4	| proteasome (prosome, macropain) 26S subunit, ATPase, 3 [Homo sapiens] >gi|14250524|gb|AAH08713.1|AAH08713 (BC008713) Unknown (protein for MGC:8487) [Homo sapiens]	202	91	3.00E-51					
00351_Ci_oc	1	NP_419576.1	| sensory box histidine kinase FixL [Caulobacter crescentus] >gi|13421994|gb|AAK22744.1| (AE005751) sensory box histidine kinase FixL [Caulobacter crescentus]	77.6	44	9.00E-14	NP_419576.1	sensory box histidine kinase FixL [Caulobacter crescentus] gb|AAK22744.1| (AE005751) sensory box histidine kinase FixL [Caulobacter crescentus]	77.6	43	9.00E-14
00352_Ci_oc	1	T29757	protein UNC-89 - Caenorhabditis elegans >gi|2088675|gb|AAB54132.1| (AF003131) Hypothetical protein C09D1.1 [Caenorhabditis elegans]	40.6	45	0.015					
00353_Ci_oc	1	1POE	A Chain A, Phospholipase A2 (E.C.3.1.1.4) Complex With The Transition-State Analogue >gi|443192|pdb|1POE|B Chain B, Phospholipase A2 (E.C.3.1.1.4) Complex With The Transition-State Analogue >gi|443190|pdb|1POD| Phospholipase A2 (E.C.3.1.1.4) >gi|6573592|pdb|1DB4|A Chain A, Human S-Pla2 In Complex With Indole 8 >gi|442665|pdb|1BBC| Phospholipase A2 (Phosphatidylcholine 2-Acylhydrolase) (E.C.3.1.1.4) >gi|6573488|pdb|1DCY|A Chain A, Crystal Structure Of Human S-Pla2 In Complex With Indole 3 Active Site Inhibitor >gi|6573593|pdb|1DB5|A Chain A, Human S-Pla2 In Complex With Indole 6 >gi|1127283|pdb|1AYP|A Chain A, Phospholipase A2 (E.C.3.1.1.4) Complexed With An Acylamino Phospholipid Analogue >gi|1127284|pdb|1AYP|B Chain B, Phospholipase A2 (E.C.3.1.1.4) Complexed With An Acylamino Phospholipid Analogue >gi|1127285|pdb|1AYP|C Chain C, Phospholipase A2 (E.C.3.1.1.4) Complexed With An Acylamino Phospholipid Analogue >gi|1127286|pdb|1AYP|D Chain D, Phospholipase A2 (E.C.3.1.1.4) Complexed With An Acylamino Phospholipid Analogue >gi|1127287|pdb|1AYP|E Chain E, Pl	97.9	43	9.00E-20					
00428_Ci_oc	8	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.7	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.7
00356_Ci_oc	1	AAK52067.1	AF368032_1 (AF368032) QM protein [Heliothis virescens]	237	69	9.00E-62					
00358_Ci_oc	1	BAA32526.1	(AB003502) Guanine Nucleotide Regulatory Protein [Mus musculus]	32.5	33	2.9	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	4.9
00361_Ci_oc	1	AAH04900.1	AAH04900 (BC004900) ribosomal protein L13a [Homo sapiens]	208	68	3.00E-53					
00362_Ci_oc	2	XP_041170.1	| hypothetical protein XP_041170 [Homo sapiens] >gi|433501|emb|CAA53152.1| (X75383) TFIIA [Homo sapiens] >gi|727195|dbj|BAA03603.1| (D14886) TFIIA-37 [Homo sapiens]	101	70	1.00E-20					
00365_Ci_oc	1	AAK95134.1	AF401562_1 (AF401562) ribosomal protein L9 [Ictalurus punctatus]	209	68	3.00E-53					
00368_Ci_oc	1	CAC14236.1	(AL445678) hypothetical protein L7845.04 [Leishmania major]	33.2	29	2.5					
00370_Ci_oc	1	AAF01742.1	AF182400_1 (AF182400) J-binding protein [Crithidia fasciculata]	32.1	43	5.7					
00372_Ci_oc	1	T19032	hypothetical protein C07A4.3 - Caenorhabditis elegans >gi|3874056|emb|CAB01716.1| (Z78536) contains similarity to Pfam domain: PF00188 (SCP-like extracellular protein), Score=42.3, E-value=3.5e-11, N=1 [Caenorhabditis elegans]	36.7	36	0.22					
00375_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.83	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2.4
00378_Ci_oc	1	XP_001324.2	| calponin 3 [Homo sapiens]	40.2	77	0.019					
00380_Ci_oc	1	No Match					NP_245088.1	RbsR [Pasteurella multocida] gb|AAK02235.1| (AE006049) RbsR [Pasteurella multocida]	29.7	40	5.7

00385_Ci_oc	1	NP_038636.1	| nascent polypeptide-associated complex alpha polypeptide [Mus musculus] >gi|7513740|pir||T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse >gi|1666689|gb|AAB18732.1| (U48363) alpha-NAC, muscle-specific form gp220 [Mus musculus] >gi|1666692|gb|AAB18734.1| (U48364) alpha-NAC, muscle-specific form gp220 [Mus musculus]	58.6	51	6.00E-08	NP_038636.1	nascent polypeptide-associated complex alpha polypeptide [Mus musculus] pir||T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse gb|AAB18732.1| (U48363) alpha-NAC, muscle-specific form gp220 [Mus musculus] gb|AAB18734.1| (U48364) alpha-NAC, muscle-specific form gp220 [Mus musculus]	64.8	44	8.00E-10
00389_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	3.3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	36.7	93	0.22
00393_Ci_oc	1	AAF06326.1	AF190647_1 (AF190647) SerH3 immobilization antigen [Tetrahymena thermophila]	36.4	26	0.29					
00394_Ci_oc	1	No Match									
00398_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2.1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.71
00399_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.1	2123261AN	chemosensory receptor [Caenorhabditis elegans]	30.9	25	8.4
00401_Ci_oc	2	AAG13295.1	AF266175_1 (AF266175) 60S ribosomal protein L24 [Gillichthys mirabilis]	163	55	1.00E-39	AAG13295.1	AF266175_1 (AF266175) 60S ribosomal protein L24 [Gillichthys mirabilis]	159	71	3.00E-38
00402_Ci_oc	1	O35587	TM21_MESAU TRANSMEMBRANE PROTEIN TMP21 PRECURSOR (21 KDA TRANSMEMBRANE TRAFFICKING PROTEIN) (INTEGRAL MEMBRANE PROTEIN P23) >gi|2388893|emb|CAA04796.1| (AJ001513) integral membrane protein BHKp23 [Mesocricetus auratus]	66.7	88	2.00E-10					
00404_Ci_oc	1	AAG00784.2	AF128510_2 (AF128510) NADH dehydrogenase subunit 2 [Laudakia stellio]	35.2	45	0.65					
00411_Ci_oc	1	XP_017626.1	| ribosomal protein S12 [Homo sapiens] >gi|14277700|ref|NP_001007.2| ribosomal protein S12; 40S ribosomal protein S12 [Homo sapiens] >gi|1173191|sp|P46405|RS12_PIG 40S RIBOSOMAL PROTEIN S12 >gi|1085435|pir||JC4159 ribosomal protein S12 - pig >gi|872315|emb|CAA55946.1| (X79417) 40S ribosomal protein S12 [Sus scrofa] >gi|10800444|emb|CAC12946.1| (AL137783) dJ1181K21.1 (Ribosomal protein S12) [Homo sapiens] >gi|12805235|gb|AAH02079.1|AAH02079 (BC002079) Similar to ribosomal protein S12 [Mus musculus] >gi|12833134|dbj|BAB22404.1| (AK002848) putative [Mus musculus] >gi|12842004|dbj|BAB25433.1| (AK008057) putative [Mus musculus]	194	72	5.00E-49	XP_017626.1	ribosomal protein S12 [Homo sapiens] ref|NP_001007.2| ribosomal protein S12; 40S ribosomal protein S12 [Homo sapiens] sp|P46405|RS12_PIG 40S RIBOSOMAL PROTEIN S12 pir||JC4159 ribosomal protein S12 - pig emb|CAA55946.1| (X79417) 40S ribosomal protein S12 [Sus scrofa] emb|CAC12946.1| (AL137783) dJ1181K21.1 (Ribosomal protein S12) [Homo sapiens] gb|AAH02079.1|AAH02079 (BC002079) Similar to ribosomal protein S12 [Mus musculus] dbj|BAB22404.1| (AK002848) putative [Mus musculus] dbj|BAB25433.1| (AK008057) putative [Mus musculus]	191	79	5.00E-48
00414_Ci_oc	1	BAA36973.1	(AB015438) alpha 1 type I collagen [Cynops pyrrhogaster]	52.7	64	3.00E-06					
00415_Ci_oc	1	No Match									
00423_Ci_oc	1	No Match					NP_212368.1	conserved hypothetical integral membrane protein [Borrelia burgdorferi] pir||B70129 conserved hypothetical integral membrane protein BB0234 - Lyme disease spirochete gb|AAC66615.1| (AE001133) conserved hypothetical integral membrane protein [Borrelia burgdorferi]	32.8	30	0.58
00424_Ci_oc	1	AAK13589.1	(AF139989) rRNA intron-encoded homing endonuclease [Oryza sativa]	53.9	65	8.00E-07	AAK13589.1	(AF139989) rRNA intron-encoded homing endonuclease [Oryza sativa]	52.3	65	3.00E-06
00425_Ci_oc	1	No Match									
00427_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9
00429_Ci_oc	1	No Match					No Match				
00431_Ci_oc	1	NP_396265.1	| AGR_pAT_475p [Agrobacterium tumefaciens] >gi|15162115|gb|AAK90706.1| (AE007902) AGR_pAT_475p [Agrobacterium tumefaciens]	44.1	52	3.00E-04	NP_396265.1	AGR_pAT_475p [Agrobacterium tumefaciens] gb|AAK90706.1| (AE007902) AGR_pAT_475p [Agrobacterium tumefaciens]	55	58	1.00E-07
00432_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2
00433_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.3	T16673	hypothetical protein R03H10.6 - Caenorhabditis elegans gb|AAG00002.1| (U29382) Hypothetical protein R03H10.6 [Caenorhabditis elegans]	30.5	37	9
00437_Ci_oc	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.63	BAB67823.1	(AB067517) KIAA1930 protein [Homo sapiens]	34	30	0.42
00442_Ci_oc	1	AAL09385.1	AF305878_1 (AF305878) TonB-linked outer membrane protein [Bacteroides caccae]	29.7	40	5.7					
00451_Ci_oc	1	No Match									
00454_Ci_oc	1	NP_113962.1	| rab acceptor 1 (prenylated) [Rattus norvegicus] >gi|2564205|gb|AAB81721.1| (AF025506) prenylated rab acceptor 1 [Rattus norvegicus]	78	32	8.00E-14					
00455_Ci_oc	2	No Match									
00459_Ci_oc	2	CAB88388.1	(AJ252184) L12 ribosomal protein [Hydra vulgaris]	109	68	3.00E-23	CAB88388.1	(AJ252184) L12 ribosomal protein [Hydra vulgaris]	109	68	3.00E-23
00461_Ci_oc	1	NP_039010.1	| ORF FPV047 Semaphorin vaccinia A39R homolog [Fowlpox virus] >gi|7271545|gb|AAF44391.1|AF198100_38 (AF198100) ORF FPV047 Semaphorin vaccinia A39R homolog [Fowlpox virus]	30.9	48	5.9	CAC18197.1	(AL451015) probable spliceosome-associated protein SAP-49 [Neurospora crassa]	32.5	48	3.3
00463_Ci_oc	1	AAK95211.1	AF402837_1 (AF402837) 40S ribosomal protein S27-2 [Ictalurus punctatus]	128	93	5.00E-29	AAK95210.1	AF402836_1 (AF402836) 40S ribosomal protein S27-1 [Ictalurus punctatus]	136	76	3.00E-31
00464_Ci_oc	1	NP_064932.1	| AMV150 [Amsacta moorei entomopoxvirus] >gi|9944673|gb|AAG02856.1|AF250284_150 (AF250284) AMV150 [Amsacta moorei entomopoxvirus]	31.3	29	9.7					
00465_Ci_oc	1	O74756	CHS2_SCHPO CHITIN SYNTHASE 2 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 2) >gi|7490227|pir||T39664 chitin synthase 2 - fission yeast (Schizosaccharomyces pombe) >gi|3738175|emb|CAA21311.1| (AL031856) chitin synthase 2 [Schizosaccharomyces pombe]	33.2	51	0.84	No Match				
00467_Ci_oc	1	No Match					AAK07471.1	AF327745_1 (AF327745) long chain fatty acyl CoA synthetase [Gobionotothen gibberifrons]	56.6	55	2.00E-07
00468_Ci_oc	1	AAA62273.1	(U01849) ORF2 [Trypanosoma brucei]	32.5	36	4.3					

00471_Ci_oc	1	P53446	ALF2_LAMJA FRUCTOSE-BISPHOSPHATE ALDOLASE, NON-MUSCLE TYPE >gi|1362663|pir||JC4189 fructose-bisphosphate aldolase (EC 4.1.2.13), non-muscle-type - Pacific lamprey >gi|974730|dbj|BAA07607.1| (D38619) aldolase [Lethenteron japonicum]	32.1	30	5.7					
00472_Ci_oc	1	AAF49893.1	(AE003540) CG10753 gene product [Drosophila melanogaster]	146	84	1.00E-34					
00473_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2					
00474_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.1					
00475_Ci_oc	1	AAH09408.1	AAH09408 (BC009408) CTP synthase [Homo sapiens]	78.8	61	5.00E-14					
00476_Ci_oc	3	XP_016419.1	| hypothetical protein XP_016419 [Homo sapiens] >gi|15301237|ref|XP_053383.1| hypothetical protein XP_053383 [Homo sapiens]	101	55	8.00E-21					
00477_Ci_oc	1	AAF54180.1	(AE003677) CG2747 gene product [alt 2] [Drosophila melanogaster] >gi|10726373|gb|AAG22133.1| (AE003677) CG2747 gene product [alt 1] [Drosophila melanogaster]	64	43	1.00E-09	AAF54180.1	(AE003677) CG2747 gene product [alt 2] [Drosophila melanogaster] gb|AAG22133.1| (AE003677) CG2747 gene product [alt 1] [Drosophila melanogaster]	64	39	1.00E-09
00478_Ci_oc	1	NP_188574.1	| putative late embryogenesis abundant protein [Arabidopsis thaliana]	41.8	33	0.007					
00481_Ci_oc	1	F81516	hypothetical protein CP0987 [imported] - Chlamydophila pneumoniae (strain AR39)	45.7	61	9.00E-05	F81516	hypothetical protein CP0987 [imported] - Chlamydophila pneumoniae (strain AR39)	45.7	61	1.00E-04
00482_Ci_oc	1	XP_055351.1	| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide [Homo sapiens] >gi|16165607|ref|XP_055352.1| hypothetical protein XP_055352 [Homo sapiens] >gi|16165610|ref|XP_055350.1| hypothetical protein XP_055350 [Homo sapiens] >gi|16165614|ref|XP_055349.1| hypothetical protein XP_055349 [Homo sapiens]	40.6	69	0.015					
00487_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9
00489_Ci_oc	1	NP_057229.1	| PTD008 protein [Homo sapiens] >gi|13650547|ref|XP_015674.1| PTD008 protein [Homo sapiens] >gi|14759601|ref|XP_032650.1| PTD008 protein [Homo sapiens] >gi|12585211|sp|Q9Y284|CGE0_HUMAN PROTEIN CGI-140 (PROTEIN PTD008) >gi|4929749|gb|AAD34135.1|AF151898_1 (AF151898) CGI-140 protein [Homo sapiens] >gi|5531837|gb|AAD44493.1| (AF078861) PTD008 [Homo sapiens] >gi|12001952|gb|AAG43119.1|AF059620_1 (AF059620) My006 protein [Homo sapiens] >gi|12846649|dbj|BAB27250.1| (AK010893) putative [Mus musculus]	102	72	4.00E-21					
00490_Ci_oc	1	NP_055075.1	| HLA class II region expressed gene KE2; KE2 protein [Homo sapiens] >gi|11417510|ref|XP_004112.1| HLA class II region expressed gene KE2 [Homo sapiens] >gi|6016432|sp|O15212|PFD6_HUMAN PREFOLDIN SUBUNIT 6 (PROTEIN KE2) >gi|2648022|emb|CAB09993.1| (Z97184) cICF0811.5.1 (HLA class II region expressed gene KE2, isoform 1) [Homo sapiens]	73.4	57	2.00E-12					
00491_Ci_oc	1	AAK52799.2	AF363029_1 (AF363029) 60S ribosomal protein L37A [Branchiostoma belcheri]	125	70	3.00E-28	AAK52799.2	AF363029_1 (AF363029) 60S ribosomal protein L37A [Branchiostoma belcheri]	125	69	3.00E-28
00561_Ci_oc	3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2	NP_191097.1	zinc finger protein OBP3 [Arabidopsis thaliana] pir||T47676 zinc finger protein OBP3 - Arabidopsis thaliana emb|CAB75895.1| (AL132975) zinc finger protein OBP3 [Arabidopsis thaliana]	31.7	27	4.8
00493_Ci_oc	2	T24047	hypothetical protein R08B4.3 - Caenorhabditis elegans >gi|3878965|emb|CAA92002.1| (Z68008) cDNA EST yk339a7.3 comes from this gene~cDNA EST yk339a7.5 comes from this gene [Caenorhabditis elegans]	80	35	2.00E-14					
00495_Ci_oc	4	AAG60623.1	AF294917_1 (AF294917) ribosomal protein S6 [Aplysia californica]	109	52	3.00E-23					
00496_Ci_oc	1	XP_039115.1	| hypothetical protein XP_039115 [Homo sapiens]	31.7	44	7.4					
00497_Ci_oc	2	No Match									
00499_Ci_oc	1	AAF86874.1	AF201938_1 (AF201938) DC3 [Homo sapiens] >gi|12654205|gb|AAH00921.1|AAH00921 (BC000921) Similar to HSPC133 protein [Homo sapiens]	77.3	62	2.00E-21					
00500_Ci_oc	1	NP_244578.1	| BH3711~unknown conserved protein in others [Bacillus halodurans] >gi|10176335|dbj|BAB07430.1| (AP001519) BH3711~unknown conserved protein in others [Bacillus halodurans]	32.5	33	4.3					
00502_Ci_oc	1	NP_143110.1	| sugar-binding transport system permease protein [Pyrococcus horikoshii] >gi|3915506|sp|O58968|YC15_PYRHO HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN PH1215 >gi|7442715|pir||A71065 probable sugar-binding transport system permease protein - Pyrococcus horikoshii >gi|3257632|dbj|BAA30315.1| (AP000005) 292aa long hypothetical sugar-binding transport system permease protein [Pyrococcus horikoshii]	32.1	30	5.7					
00503_Ci_oc	1	NP_073529.1	| 144R protein [Yaba-like disease virus] >gi|12056303|emb|CAC21382.1| (AJ293568) 144R protein [Yaba-like disease virus]	31.3	27	9.7					
00504_Ci_oc	1	No Match									

00509_Ci_oc	1	P91303	VATG_CAEEL PROBABLE VACUOLAR ATP SYNTHASE SUBUNIT G (V-ATPASE G SUBUNIT) (VACUOLAR PROTON PUMP G SUBUNIT) (V-ATPASE 13 KDA SUBUNIT) >gi|7503578|pir||T25764 hypothetical protein F46F11.5 - Caenorhabditis elegans >gi|13384453|gb|AAK21386.1| (U88173) Hypothetical protein F46F11.5 [Caenorhabditis elegans]	73	42	3.00E-12					
00511_Ci_oc	1	XP_043342.1	| hypothetical protein XP_043342 [Homo sapiens] >gi|14723111|ref|XP_043340.1| hypothetical protein XP_043340 [Homo sapiens] >gi|16157502|ref|XP_056245.1| hypothetical protein XP_056245 [Homo sapiens]	43.4	57	0.002					
00514_Ci_oc	1	No Match					AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.71
00517_Ci_oc	1	No Match									
00519_Ci_oc	1	XP_009574.3	| nucleolar protein (KKE/D repeat) [Homo sapiens] >gi|13436284|gb|AAH04937.1|AAH04937 (BC004937) Unknown (protein for MGC:10779) [Homo sapiens]	34.8	40	0.85					
00520_Ci_oc	1	NP_060518.1	| hypothetical protein FLJ10292 [Homo sapiens] >gi|14765544|ref|XP_046628.1| hypothetical protein FLJ10292 [Homo sapiens] >gi|14765552|ref|XP_046627.1| hypothetical protein FLJ10292 [Homo sapiens] >gi|7022229|dbj|BAA91522.1| (AK001154) unnamed protein product [Homo sapiens] >gi|9294743|gb|AAF86648.1|AF165518_1 (AF165518) MAGOH isoform [Homo sapiens] >gi|10434283|dbj|BAB14202.1| (AK022720) unnamed protein product [Homo sapiens] >gi|15012020|gb|AAH10905.1|AAH10905 (BC010905) Similar to hypothetical protein FLJ10292 [Homo sapiens]	222	82	3.00E-57					
00523_Ci_oc	1	S49097	penicillin-binding protein 2 - Neisseria meningitidis >gi|509159|emb|CAA42186.1| (X59627) penicillin-binding protein 2 [Neisseria meningitidis]	70.6	46	5.00E-12	S49097	penicillin-binding protein 2 - Neisseria meningitidis emb|CAA42186.1| (X59627) penicillin-binding protein 2 [Neisseria meningitidis]	70.6	46	5.00E-12
00526_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.68					
00811_Ci_oc	3	NP_080296.1	| RIKEN cDNA 2700049I22 gene [Mus musculus] >gi|12832389|dbj|BAB22086.1| (AK002419) putative [Mus musculus] >gi|12842474|dbj|BAB25616.1| (AK008344) putative [Mus musculus] >gi|12846190|dbj|BAB27066.1| (AK010618) putative [Mus musculus] >gi|12849123|dbj|BAB28217.1| (AK012402) putative [Mus musculus] >gi|15214576|gb|AAH12413.1|AAH12413 (BC012413) RIKEN cDNA 2700049I22 gene [Mus musculus]	76.9	62	2.00E-13	NP_080296.1	RIKEN cDNA 2700049I22 gene [Mus musculus] dbj|BAB22086.1| (AK002419) putative [Mus musculus] dbj|BAB25616.1| (AK008344) putative [Mus musculus] dbj|BAB27066.1| (AK010618) putative [Mus musculus] dbj|BAB28217.1| (AK012402) putative [Mus musculus] gb|AAH12413.1|AAH12413 (BC012413) RIKEN cDNA 2700049I22 gene [Mus musculus]	76.9	61	2.00E-13
00530_Ci_oc	1	T12607	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Anotea flavida chloroplast (fragment) >gi|1654236|gb|AAB17741.1| (U55322) Anotea flavida NADH dehydrogenase	32.1	36	5.7					
00534_Ci_oc	3	NP_080151.1	| RNA binding motif protein [Mus musculus] >gi|12845066|dbj|BAB26605.1| (AK009953) putative [Mus musculus]	74.5	65	9.00E-13	NP_080151.1	RNA binding motif protein [Mus musculus] dbj|BAB26605.1| (AK009953) putative [Mus musculus]	100	70	2.00E-20
00536_Ci_oc	1	NP_000987.2	| ribosomal protein L35a; 60S ribosomal protein L35a [Homo sapiens] >gi|12654423|gb|AAH01037.1|AAH01037 (BC001037) ribosomal protein L35a [Homo sapiens] >gi|15012089|gb|AAH10949.1|AAH10949 (BC010949) Unknown (protein for MGC:13603) [Homo sapiens]	173	76	1.00E-42	NP_067087.1	ribosomal protein L35a [Rattus norvegicus] ref|NP_067313.2| ribosomal protein L35a [Mus musculus] sp|P04646|R35A_RAT 60S RIBOSOMAL PROTEIN L35A pir||R5RT5A ribosomal protein L35a, cytosolic - rat emb|CAA27193.1| (X03475) ribosomal protein L35a (aa 1-110) [Rattus norvegicus] dbj|BAB27124.1| (AK010692) putative [Mus musculus] emb|CAA76215.2| (Y16430) ribosomal protein L35a [Mus musculus]	187	76	1.00E-46
00537_Ci_oc	1	T16084	hypothetical protein F16H11.1 - Caenorhabditis elegans >gi|1280135|gb|AAA98007.1| (U55376) Hypothetical protein F16H11.1 [Caenorhabditis elegans]	35.2	26	0.65					
00538_Ci_oc	1	Q36507	CYB_PICPJ CYTOCHROME B >gi|296846|emb|CAA47155.1| (X66593) apocytochrome B [Pichia pijperi]	32.8	30	2.7					
00539_Ci_oc	1	NP_068697.1	| thymus expressed acidic protein [Mus musculus] >gi|6706786|emb|CAB66138.1| (AJ131776) hypothetical thymus-expressed acidic protein [Mus musculus] >gi|14581661|gb|AAK60420.1| (AY034612) stress-induced protein SIP27 [Mus musculus]	47.3	58	1.00E-04	CAB92720.1	(AL109824) dJ1181N3.1 (similar to collagen) [Homo sapiens]	49.2	35	4.00E-05
00540_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.7	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2.1
00544_Ci_oc	1	AAF58640.1	(AE003825) inv gene product [Drosophila melanogaster]	31.7	34	5.3	AAF58640.1	(AE003825) inv gene product [Drosophila melanogaster]	32.8	34	2.3
00545_Ci_oc	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.6	No Match				
00547_Ci_oc	3	NP_032801.1	| platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit [Mus musculus] >gi|3024348|sp|Q61206|PA1B_MOUSE PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (PAF ACETYLHYDROLASE 30 KDA SUBUNIT) (PAF-AH 30 KDA SUBUNIT) (PAF-AH BETA SUBUNIT) (PAFAH BETA SUBUNIT) >gi|1373363|gb|AAC52997.1| (U57747) platelet-activating factor acetylhydrolase isoform Ib beta subunit [Mus musculus]	75.3	35	5.00E-13					
00556_Ci_oc	1	P37236	FREQ_DROME FREQUENIN (D-FRQ) >gi|404035|gb|AAA28539.1| (L08064) frequenin [Drosophila melanogaster] >gi|10728317|gb|AAG22356.1| (AE003508) CG5744 gene product [Drosophila melanogaster]	52.3	73	5.00E-06					
00558_Ci_oc	1	P91478	YOK3_CAEEL HYPOTHETICAL 41.7 KD PROTEIN T20F5.3 IN CHROMOSOME I >gi|7508070|pir||T29207 hypothetical protein T20F5.3 - Caenorhabditis elegans >gi|1703616|gb|AAB37664.1| (U80442) Hypothetical protein T20F5.3 [Caenorhabditis elegans]	33.2	33	2.5					

00565_Ci_oc	1	BAA03515.1	(D14689) KIAA0023 [Homo sapiens]	30.5	40	6.9	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	30.1	51	9.2
00567_Ci_oc	3	NP_001002.1	| ribosomal protein S7; 40S ribosomal protein S7 [Homo sapiens] >gi|6755376|ref|NP_035430.1| ribosomal protein S7 [Mus musculus] >gi|134000|sp|P23821|RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 (S8) >gi|279641|pir||R3RT7 ribosomal protein S7, cytosolic [validated] - rat >gi|2119071|pir||JC4388 ribosomal protein S7, cytosolic - human >gi|297172|emb|CAA37457.1| (X53377) ribosomal protein S7 [Rattus rattus] >gi|551251|emb|CAA81022.1| (Z25749) ribosomal protein S7 [Homo sapiens] >gi|2811284|gb|AAB97861.1| (AF043285) ribosomal protein S7 [Mus musculus] >gi|12804027|gb|AAH02866.1|AAH02866 (BC002866) ribosomal protein S7 [Homo sapiens] >gi|12805115|gb|AAH02014.1|AAH02014 (BC002014) ribosomal protein S7 [Mus musculus] >gi|227241|prf||1617114A ribosomal protein S7 [Rattus norvegicus]	180	72	9.00E-45					
00571_Ci_oc	1	BAA89236.1	(AB024511) TMV response-related gene product [Nicotiana tabacum]	32.5	38	4.3					
00572_Ci_oc	1	NP_396378.1	| AGR_pAT_651p [Agrobacterium tumefaciens] >gi|15162250|gb|AAK90819.1| (AE007913) AGR_pAT_651p [Agrobacterium tumefaciens]	187	59	9.00E-47	NP_396378.1	AGR_pAT_651p [Agrobacterium tumefaciens] gb|AAK90819.1| (AE007913) AGR_pAT_651p [Agrobacterium tumefaciens]	137	61	1.00E-31
00574_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	30.5	91	3.4	S29552	trypsin (EC 3.4.21.4) - Anabaena sp. (strain PCC 7120) (fragment) emb|CAA45036.1| (X63439) trypsin [Anabaena sp.]	29.3	26	7.7
00575_Ci_oc	1	BAA89696.1	(AB030945) ran GTP-binding protein [Xenopus laevis]	139	73	2.00E-32					
00578_Ci_oc	1	BAB55707.1	(AP003075) hypothetical protein [Oryza sativa]	35.6	39	0.5					
00579_Ci_oc	1	NP_127290.1	| hypothetical protein [Pyrococcus abyssi] >gi|7518026|pir||B75010 hypothetical protein PAB1063 - Pyrococcus abyssi (strain Orsay) >gi|5459034|emb|CAB50520.1| (AJ248288) hypothetical protein [Pyrococcus abyssi]	32.1	30	5.7					
00580_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.5	No Match				
00582_Ci_oc	1	CAC38784.1	(AJ278329) putative FK506-binding protein [Suberites domuncula]	120	82	1.00E-26					
00590_Ci_oc	2	A53221	acidic ribosomal protein P1 - hydromedusa (Polyorchis penicillatus) >gi|227678|prf||1709160A acidic ribosomal protein A1 [Polyorchis penicillatus]	102	51	4.00E-21	A53221	acidic ribosomal protein P1 - hydromedusa (Polyorchis penicillatus) prf||1709160A acidic ribosomal protein A1 [Polyorchis penicillatus]	102	49	4.00E-21
00591_Ci_oc	1	No Match									
00592_Ci_oc	1	P00430	COXO_BOVIN CYTOCHROME C OXIDASE POLYPEPTIDE VIIC PRECURSOR (VIIIA) >gi|66286|pir||OSBO8A cytochrome-c oxidase (EC 1.9.3.1) chain VIIc precursor [validated] - bovine >gi|1947041|gb|AAC48719.1| (U58655) cytochrome c oxidase subunit VIIc [Bos taurus] >gi|6015488|emb|CAB57793.1| (X15725) cytochrome c oxidase, subunit VIIc [Bos taurus]	37.5	37	0.13	T21413	hypothetical protein F26E4.6 - Caenorhabditis elegans emb|CAB02999.1| (Z81070) similar to cytochrome C oxidase~cDNA EST EMBL:T01623 comes from this gene~cDNA EST EMBL:T02214 comes from this gene~cDNA EST EMBL:T00813 comes from this gene~cDNA EST EMBL:T00814 comes from this gene~cDNA EST EMBL:T00069 comes from this gene~c>	31.7	36	7.3
00697_Ci_oc	3	Q26481	RL5_STYCL 60S RIBOSOMAL PROTEIN L5 >gi|1374957|gb|AAC05598.1| (L78668) ribosomal protein L5 [Styela clava]	169	67	5.00E-43					
00598_Ci_oc	1	T15987	hypothetical protein F09E10.3 - Caenorhabditis elegans >gi|1118145|gb|AAB52488.1| (U41749) Hypothetical protein F09E10.3 [Caenorhabditis elegans]	51.2	46	3.00E-08	T15987	hypothetical protein F09E10.3 - Caenorhabditis elegans gb|AAB52488.1| (U41749) Hypothetical protein F09E10.3 [Caenorhabditis elegans]	64.8	34	7.00E-10
00599_Ci_oc	1	No Match					No Match				
00604_Ci_oc	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.4	AAK92210.1	(AY043208) ribonucleoside-diphosphate reductase subunit B [Bacteroides fragilis]	32.1	32	4.2
00605_Ci_oc	1	T21967	hypothetical protein F38E11.4 - Caenorhabditis elegans >gi|3876924|emb|CAA92773.1| (Z68342) contains similarity to Pfam domain: PF00024 (PAN domain), Score=293.1, E-value=1.1e-84, N=4 [Caenorhabditis elegans]	30.9	27	7.1					
00611_Ci_oc	1	T00118	hrSH2 protein - sea squirt (Halocynthia roretzi) >gi|2879933|dbj|BAA24828.1| (AB010891) HrSH2 [Halocynthia roretzi]	30.9	43	4.4	AAD28745.1	AF126176_1 (AF126176) inositolphosphorylceramide synthase; IPC1p [Candida glabrata]	31.7	21	7.4
00613_Ci_oc	1	CAB04947.2	(Z82078) predicted using Genefinder~contains similarity to Pfam domain: PF00005 (ABC transporter), Score=210.9, E-value=6.1e-60, N=1~cDNA EST yk4g6.5 comes from this gene~cDNA EST yk10f3.5 comes from this gene~cDNA EST yk135g3.5 comes from this gene~cD>	32.5	27	4.3					
00616_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.67	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	29.7	90	5.8
00617_Ci_oc	1	AAF79446.1	AC025808_28 (AC025808) F18O14.20 [Arabidopsis thaliana] >gi|15810125|gb|AAL07206.1| (AY056127) unknown protein [Arabidopsis thaliana]	38.7	31	0.057					
00618_Ci_oc	1	BAA99561.1	(AB036814) alpha-tubulin [Chlorella vulgaris]	77.3	100	8.00E-14	T16307	hypothetical protein F40F4.5 - Caenorhabditis elegans gb|AAA81432.1| (U40420) Hypothetical protein F40F4.5 [Caenorhabditis elegans]	77.3	100	8.00E-14
00620_Ci_oc	1	S72692	probable membrane protein Q0320 - yeast (Saccharomyces cerevisiae) mitochondrion	31.7	32	7.4					
00622_Ci_oc	1	AAD40193.1	(AF085358) HSPC029 [Homo sapiens]	128	43	5.00E-29					
00625_Ci_oc	1	CAA15646.1	(AL009171) 62D9.i [Drosophila melanogaster]	35.6	30	0.49	AAF69726.1	AC068783_2 (AC068783) L108.2 [Leishmania major]	35.2	32	0.65
00627_Ci_oc	1	NP_253569.1	| hypothetical protein [Pseudomonas aeruginosa] >gi|11350314|pir||D83036 hypothetical protein PA4882 [imported] - Pseudomonas aeruginosa (strain PAO1) >gi|9951156|gb|AAG08267.1|AE004901_9 (AE004901) hypothetical protein [Pseudomonas aeruginosa]	51.2	51	1.00E-05					
00628_Ci_oc	1	AAK95131.1	(AF401559) ribosomal protein L7 [Ictalurus punctatus]	267	78	8.00E-71	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9

00638_Ci_oc	1	XP_030891.1	| hypothetical protein FLJ14668 [Homo sapiens] >gi|15929034|gb|AAH14975.1|AAH14975 (BC014975) hypothetical protein FLJ14668 [Homo sapiens]	83.5	37	2.00E-15	XP_030891.1	hypothetical protein FLJ14668 [Homo sapiens] gb|AAH14975.1|AAH14975 (BC014975) hypothetical protein FLJ14668 [Homo sapiens]	95.6	37	4.00E-19
00641_Ci_oc	1	XP_005645.4	| similar to surfeit 2; Surfeit-2 (H. sapiens) [Homo sapiens] >gi|15680137|gb|AAH14411.1|AAH14411 (BC014411) Unknown (protein for MGC:19914) [Homo sapiens]	55.8	39	4.00E-07					
00643_Ci_oc	1	CAB53105.1	(AJ245645) cell division inhibitor MinD [Prototheca wickerhamii]	33.2	39	2.5					
00648_Ci_oc	1	Q9Y794	ORC4_SCHPO ORIGIN RECOGNITION COMPLEX SUBUNIT 4 >gi|11359205|pir||T50400 origin recognition complex subunit 4-related protein orp4p [imported] - fission yeast (Schizosaccharomyces pombe) >gi|4512109|gb|AAD21618.1| (AF125185) origin recognition complex subunit 4-related protein Orp4p [Schizosaccharomyces pombe] >gi|6723967|emb|CAB66441.1| (AL136535) origin recognition complex subunit 4-related protein orp4p [Schizosaccharomyces pombe]	32.8	33	2.2					
00649_Ci_oc	1	No Match					No Match				
00652_Ci_oc	1	NP_268480.1	| putative preprotein translocase [Streptococcus pyogenes] >gi|13621388|gb|AAK33202.1| (AE006478) putative preprotein translocase [Streptococcus pyogenes M1 GAS]	33.2	40	2.5	AAF57324.1	(AE003785) CG8426 gene product [Drosophila melanogaster]	32.8	26	3.3
00655_Ci_oc	1	NP_080911.1	| RIKEN cDNA 5730536A07 gene [Mus musculus] >gi|12832857|dbj|BAB22285.1| (AK002690) putative [Mus musculus] >gi|13543144|gb|AAH05745.1|AAH05745 (BC005745) RIKEN cDNA 5730536A07 gene [Mus musculus]	51.5	75	8.00E-06					
00656_Ci_oc	1	No Match					AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	34.4	92	1.1
00665_Ci_oc	1	NP_250127.1	| probable RND efflux transporter [Pseudomonas aeruginosa] >gi|11351804|pir||B83466 probable RND efflux transporter PA1436 [imported] - Pseudomonas aeruginosa (strain PAO1) >gi|9947386|gb|AAG04825.1|AE004573_4 (AE004573) probable RND efflux transporter [Pseudomonas aeruginosa]	54.3	42	3.00E-07	NP_250127.1	probable RND efflux transporter [Pseudomonas aeruginosa] pir||B83466 probable RND efflux transporter PA1436 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04825.1|AE004573_4 (AE004573) probable RND efflux transporter [Pseudomonas aeruginosa]	54.3	42	3.00E-07
00666_Ci_oc	1	Q92122	KPYK_XENLA PYRUVATE KINASE, MUSCLE ISOZYME (CYTOSOLIC THYROID HORMONE BINDING PROTEIN) (CTHBP) >gi|1085221|pir||S51374 pyruvate kinase (EC 2.7.1.40), muscle - clawed frog >gi|433355|gb|AAA63581.1| (U03878) cytosolic thyroid hormone binding protein/pyruvate kinase type M2 [Xenopus laevis]	75.3	71	5.00E-13					
00667_Ci_oc	1	P26808	POL_MLVFP POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; RIBONUCLEASE H] >gi|479807|pir||S35475 pol polyprotein - Friend murine leukemia virus (strain PVC-211) >gi|331900|gb|AAA46477.1| (M93134) pol protein [Friend murine leukemia virus]	32.5	42	4.3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	3.3
00686_Ci_oc	3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.69	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2
00673_Ci_oc	1	BAB27236.1	(AK010872) putative [Mus musculus]	37.9	46	0.099					
00674_Ci_oc	1	XP_010365.1	| hypothetical protein XP_010365 [Homo sapiens] >gi|15310494|ref|XP_053949.1| hypothetical protein XP_053949 [Homo sapiens] >gi|2808420|emb|CAB10730.1| (Z97632) dJ196E23.2 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) [Homo sapiens] >gi|14602772|gb|AAH09896.1|AAH09896 (BC009896) Unknown (protein for MGC:2033) [Homo sapiens]	130	60	1.00E-29					
00676_Ci_oc	1	NP_113651.1	| steroid dehydrogenase-like [Homo sapiens] >gi|14775534|ref|XP_049299.1| steroid dehydrogenase-like [Homo sapiens] >gi|13183088|gb|AAK15047.1|AF237684_1 (AF237684) steroid dehydrogenase-like protein [Homo sapiens]	76.1	42	3.00E-13					
00678_Ci_oc	1	I30010	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Leishmania tarentolae mitochondrion	31.3	26	9.7					
00687_Ci_oc	1	AAG10398.2	AF190741_1 (AF190741) long-chain fatty acid CoA ligase [Callithrix jacchus]	101	50	1.00E-20					
00711_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1
00712_Ci_oc	1	NP_229996.1	| iron-sulfur cluster-binding protein [Vibrio cholerae] >gi|11355612|pir||F82333 iron-sulfur cluster-binding protein VC0342 [imported] - Vibrio cholerae (group O1 strain N16961) >gi|9654758|gb|AAF93515.1| (AE004123) iron-sulfur cluster-binding protein [Vibrio cholerae]	171	61	4.00E-42	NP_229996.1	iron-sulfur cluster-binding protein [Vibrio cholerae] pir||F82333 iron-sulfur cluster-binding protein VC0342 [imported] - Vibrio cholerae (group O1 strain N16961) gb|AAF93515.1| (AE004123) iron-sulfur cluster-binding protein [Vibrio cholerae]	173	62	2.00E-42
00714_Ci_oc	3	NP_405904.1	| pyridoxamine kinase [Yersinia pestis] >gi|15980364|emb|CAC91173.1| (AJ414152) pyridoxamine kinase [Yersinia pestis]	32.8	30	3.1	AAB54244.1	(AF003385) R08F11.2 gene product [Caenorhabditis elegans]	41	29	0.011
00716_Ci_oc	1	BAB22088.1	(AK002421) putative [Mus musculus] >gi|12861970|dbj|BAB32314.1| (AK021173) putative [Mus musculus] >gi|13559394|dbj|BAB40856.1| (AB049651) mitochondrial ribosomal protein L33 (L33mt) [Mus musculus]	44.9	55	8.00E-04	BAB22088.1	(AK002421) putative [Mus musculus] dbj|BAB32314.1| (AK021173) putative [Mus musculus] dbj|BAB40856.1| (AB049651) mitochondrial ribosomal protein L33 (L33mt) [Mus musculus]	44.9	55	8.00E-04
00718_Ci_oc	2	O42249	GBLP_ORENI GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (RECEPTOR OF ACTIVATED PROTEIN KINASE C) (RACK) >gi|2558966|gb|AAB81618.1| (AF025331) receptor for activated protein kinase C [Oreochromis niloticus]	259	79	2.00E-68					

00719_Ci_oc	1	T21021	hypothetical protein F16D3.2 - Caenorhabditis elegans >gi|3876030|emb|CAB01499.1| (Z78062) weak similarity with E. coli helicase (Swiss Prot accession number P30015)~cDNA EST yk16e6.3 comes from this gene~cDNA EST EMBL:T00276 comes from this gene~cDNA EST EMBL:T00335 comes from this gene~cDNA EST yk225a11.3 comes from this gene~cDNA>	31.3	34	9.7					
00727_Ci_oc	2	CAB40968.1	(AJ238272) 40S ribosomal protein S24 [Oryzias latipes]	121	63	8.00E-27	O42387	RS24_FUGRU 40S RIBOSOMAL PROTEIN S24 emb|CAA04728.1| (AJ001398) ribosomal protein S24 [Takifugu rubripes]	132	64	2.00E-30
00731_Ci_oc	1	BAB22063.1	(AK002389) putative [Mus musculus] >gi|12833655|dbj|BAB22613.1| (AK003160) putative [Mus musculus] >gi|12837875|dbj|BAB23983.1| (AK005374) putative [Mus musculus] >gi|12841884|dbj|BAB25388.1| (AK007982) putative [Mus musculus]	67.1	41	1.00E-10	BAB22063.1	(AK002389) putative [Mus musculus] dbj|BAB22613.1| (AK003160) putative [Mus musculus] dbj|BAB23983.1| (AK005374) putative [Mus musculus] dbj|BAB25388.1| (AK007982) putative [Mus musculus]	67.1	41	1.00E-10
00735_Ci_oc	2	No Match									
00737_Ci_oc	1	T20183	hypothetical protein C53B4.8 - Caenorhabditis elegans >gi|3875174|emb|CAA92458.1| (Z68215) cDNA EST yk212e11.5 comes from this gene~cDNA EST yk212e11.3 comes from this gene [Caenorhabditis elegans] >gi|3875181|emb|CAA94231.1| (Z70270) cDNA EST yk212e11.5 comes from this gene~cDNA EST yk212e11.3 comes from this gene [Caenorhabditis elegans]	32.5	36	2	AAF58640.1	(AE003825) inv gene product [Drosophila melanogaster]	32.8	34	2.4
00739_Ci_oc	1	NP_112248.1	| adenylate kinase 2 [Rattus norvegicus] >gi|266401|sp|P29410|KAD2_RAT ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL (ATP-AMP TRANSPHOSPHORYLASE) >gi|484520|pir||JQ1944 adenylate kinase (EC 2.7.4.3) 2, mitochondrial - rat >gi|220796|dbj|BAA02378.1| (D13061) adenylate kinase 2 [Rattus norvegicus]	145	66	4.00E-34					
00744_Ci_oc	1	CAA69386.1	(Y08204) olfactory receptor [Xenopus laevis]	34.4	44	1.1					
00745_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.1	AAC83803.1	(AF096997) glycosyltransferase homolog Lob2A [Haemophilus somnus]	32.8	38	2
00747_Ci_oc	1	CAC04186.1	(AL121989) dJ604K5.1 (15 kDa selenoprotein) [Homo sapiens]	80	60	2.00E-14					
00753_Ci_oc	2	F71617	SERA antigen/papain-like proteinase with active Cys PFB0325c - malaria parasite (Plasmodium falciparum) >gi|3845154|gb|AAC71854.1| (AE001387) SERA antigen/papain-like protease with active Cys [Plasmodium falciparum]	32.1	32	5.7					
00755_Ci_oc	1	CAB48391.1	(AJ243736) peroxiredoxin [Globodera rostochiensis]	195	75	6.00E-56	BAA90476.1	(AB022045) thioredoxin peroxidase [Ascaris suum]	210	74	9.00E-54
00757_Ci_oc	1	NP_039852.1	| BORF1 late reading frame, 2 NXT/S homologous to VZV RF20 [Human herpesvirus 4] >gi|139172|sp|P03187|VP19_EBV PROBABLE CAPSID ASSEMBLY AND DNA MATURATION PROTEIN (CAPSID PROTEIN VP19C) >gi|73930|pir||QQBE9 BORF1 protein - human herpesvirus 4 (strain B95-8) >gi|1334854|emb|CAA24840.1| (V01555) BORF1 late reading frame, 2 NXT/S homologous to VZV RF20 [Human herpesvirus 4] >gi|225105|prf||1208408A gene BORF1 [Human herpesvirus 4]	31.7	35	2.6	NP_215164.1	hypothetical protein Rv0650 [Mycobacterium tuberculosis H37Rv] ref|NP_335090.1| glucokinase, putative [Mycobacterium tuberculosis CDC1551] pir||G70614 hypothetical protein Rv0650 - Mycobacterium tuberculosis (strain H37RV) emb|CAB07107.1| (Z92772) hypothetical protein Rv0650 [Mycobacterium tuberculosis H37Rv] gb|AAK44904.1| (AE006962) glucokinase, putative [Mycobacterium tuberculosis CDC1551]	35.2	27	0.23
00761_Ci_oc	1	NP_110643.1	| Adenine specific DNA methylase (Mod-related) [Thermoplasma volcanium] >gi|14324340|dbj|BAB59268.1| (AP000991) modification methylase [Thermoplasma volcanium]	90.1	39	2.00E-17					
00762_Ci_oc	1	No Match									
00763_Ci_oc	1	No Match									
00765_Ci_oc	1	NP_250573.1	| probable transporter [Pseudomonas aeruginosa] >gi|11352290|pir||C83410 probable transporter PA1882 [imported] - Pseudomonas aeruginosa (strain PAO1) >gi|9947873|gb|AAG05271.1|AE004614_5 (AE004614) probable transporter [Pseudomonas aeruginosa]	100	54	1.00E-20					
00768_Ci_oc	1	XP_045055.1	| hypothetical protein XP_045055 [Homo sapiens] >gi|14775596|ref|XP_045054.1| hypothetical protein XP_045054 [Homo sapiens]	142	88	1.00E-33	XP_045055.1	hypothetical protein XP_045055 [Homo sapiens] ref|XP_045054.1| hypothetical protein XP_045054 [Homo sapiens]	142	88	1.00E-33
00770_Ci_oc	1	AAA87047.1	(U45958) pistil extensin-like protein [Nicotiana alata]	33.2	47	2.5					
00772_Ci_oc	1	NP_073283.1	| NADH dehydrogenase subunit 5 [Myxine glutinosa] >gi|15214152|sp|Q9G2W8|NU5M_MYXGL NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 >gi|12055923|emb|CAC20659.1| (AJ404477) NADH dehydrogenase subunit 5 [Myxine glutinosa]	34	37	1.5					
00774_Ci_oc	1	XP_047609.1	| hypothetical protein XP_047609 [Homo sapiens]	34	46	0.94					
00779_Ci_oc	2	BAB03536.1	(AB020521) AmnE [Pseudomonas sp.]	41	47	0.002	BAB03536.1	(AB020521) AmnE [Pseudomonas sp.]	44.1	51	3.00E-04
00780_Ci_oc	1	NP_080699.1	| RIKEN cDNA 2410018C20 gene [Mus musculus] >gi|12846058|dbj|BAB27014.1| (AK010538) putative [Mus musculus] >gi|12851419|dbj|BAB29034.1| (AK013882) putative [Mus musculus]	159	66	3.00E-38					
00784_Ci_oc	1	AAD47078.1	AF164347_1 (AF164347) developmental protein DG1113 [Dictyostelium discoideum]	34	29	1	AAD47078.1	AF164347_1 (AF164347) developmental protein DG1113 [Dictyostelium discoideum]	35.2	28	0.45
00786_Ci_oc	1	AAB02139.1	(M37831) cytochrome c oxidase subunit IV [Mus musculus] >gi|1372989|gb|AAB02140.1| (M37829) cytochrome c oxidase subunit IV [Mus musculus]	63.2	40	2.00E-09					
00787_Ci_oc	1	AAC38258.1	(AF004848) zinc-protease transporter [Pseudomonas fluorescens]	31.3	44	1.8					
00791_Ci_oc	1	XP_030162.2	| hypothetical protein XP_030162 [Homo sapiens]	35.2	19	0.65					
00798_Ci_oc	1	P49207	RL34_HUMAN 60S RIBOSOMAL PROTEIN L34 >gi|2119149|pir||I68524 ribosomal protein L34 - human >gi|1008856|gb|AAC41916.1| (L38941) ribosomal protein L34 [Homo sapiens]	153	68	1.00E-36	P49207	RL34_HUMAN 60S RIBOSOMAL PROTEIN L34 pir||I68524 ribosomal protein L34 - human gb|AAC41916.1| (L38941) ribosomal protein L34 [Homo sapiens]	153	66	1.00E-36

00799_Ci_oc	1	T40627	probable ribonucleoprotein SPBC660.15 - fission yeast (Schizosaccharomyces pombe) >gi|4049514|emb|CAA22535.1| (AL034563) RNA-binding protein [Schizosaccharomyces pombe]	32.1	30	5.7	E72642	hypothetical protein APE0573 - Aeropyrum pernix (strain K1) dbj|BAA79541.1| (AP000060) 264aa long hypothetical protein [Aeropyrum pernix]	34	32	1.5
00800_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	3.7
00802_Ci_oc	1	NP_036045.1	| Wnt inhibitory factor 1 [Mus musculus] >gi|12230783|sp|Q9WUA1|WIF1_MOUSE WNT INHIBITORY FACTOR 1 PRECURSOR (WIF-1) >gi|4585372|gb|AAD25403.1|AF122923_1 (AF122923) Wnt inhibitory factor-1 [Mus musculus] >gi|15342002|gb|AAH13268.1|AAH13268 (BC013268) Similar to Wnt inhibitory factor 1 [Mus musculus]	38.3	36	0.075	NP_036045.1	Wnt inhibitory factor 1 [Mus musculus] sp|Q9WUA1|WIF1_MOUSE WNT INHIBITORY FACTOR 1 PRECURSOR (WIF-1) gb|AAD25403.1|AF122923_1 (AF122923) Wnt inhibitory factor-1 [Mus musculus] gb|AAH13268.1|AAH13268 (BC013268) Similar to Wnt inhibitory factor 1 [Mus musculus]	38.3	30	0.075
00804_Ci_oc	1	AAK59472.1	(AY034967) unknown protein [Arabidopsis thaliana]	31.3	26	9.7					
00808_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.7	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.7
00810_Ci_oc	3	No Match					AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	37.5	100	0.13
00814_Ci_oc	1	AAF22134.1	AF127180_1 (AF127180) nephrocystin [Mus musculus]	37.1	26	0.17					
00815_Ci_oc	1	BAA74505.1	(AB008095) ribosomal protein L41 [Candida maltosa]	164	79	2.00E-42	BAA74505.1	(AB008095) ribosomal protein L41 [Candida maltosa]	188	79	4.00E-47
00820_Ci_oc	1	T23114	hypothetical protein H24D24.1 - Caenorhabditis elegans >gi|3878067|emb|CAA18357.1| (AL022274) H24D24.1 [Caenorhabditis elegans]	32.5	27	4.3					
00821_Ci_oc	1	CAB67657.2	(AL132966) splicing factor-like protein [Arabidopsis thaliana]	39.1	42	0.044					
00823_Ci_oc	1	BAB22112.1	(AK002454) putative [Mus musculus]	100	64	1.00E-20					
00825_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	35.6	47	0.25	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	35.6	45	0.25
00826_Ci_oc	1	No Match									
00832_Ci_oc	1	AAB71275.2	(AF026209) Hypothetical protein C05E4.6 [Caenorhabditis elegans]	32.5	37	4.3					
00838_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.69
00839_Ci_oc	1	No Match									
00842_Ci_oc	1	CAC70135.1	(AL161712) Y66D12A.14 [Caenorhabditis elegans]	32.5	30	4.3					
00843_Ci_oc	2	NP_110135.1	| cytadherence accessory protein HMW1 [Mycoplasma pneumoniae] >gi|2498457|sp|Q50365|HMW1_MYCPN CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCESSORY PROTEIN 1) >gi|2146089|pir||S73720 cytadherence accessory protein HMW1 - Mycoplasma pneumoniae (strain ATCC 29342) >gi|639790|gb|AAA61697.1| (L38997) HMW1 [Mycoplasma pneumoniae] >gi|1674076|gb|AAB96042.1| (AE000038) cytadherence accessory protein HMW1 [Mycoplasma pneumoniae]	31.7	30	7.4	NP_110135.1	cytadherence accessory protein HMW1 [Mycoplasma pneumoniae] sp|Q50365|HMW1_MYCPN CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 1 (CYTADHERENCE ACCESSORY PROTEIN 1) pir||S73720 cytadherence accessory protein HMW1 - Mycoplasma pneumoniae (strain ATCC 29342) gb|AAA61697.1| (L38997) HMW1 [Mycoplasma pneumoniae] gb|AAB96042.1| (AE000038) cytadherence accessory protein HMW1 [Mycoplasma pneumoniae]	31.7	28	7.4
00845_Ci_oc	1	AAK92186.1	AF400214_1 (AF400214) ribosomal protein S17 [Spodoptera frugiperda]	81.1	82	9.00E-15					
00847_Ci_oc	1	NP_223499.1	| THIAMINE PHOSPHATE PYROPHOSPHORYLASE [Helicobacter pylori J99] >gi|7388318|sp|Q9ZL01|THIE_HELPJ PROBABLE THIAMINE-PHOSPHATE PYROPHOSPHORYLASE (TMP PYROPHOSPHORYLASE) (TMP-PPASE) (THIAMINE-PHOSPHATE SYNTHASE) >gi|7434088|pir||G71889 thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) - Helicobacter pylori (strain J99) >gi|4155348|gb|AAD06361.1| (AE001508) THIAMINE PHOSPHATE PYROPHOSPHORYLASE [Helicobacter pylori J99]	32.5	30	4.3					
00848_Ci_oc	1	CAC18540.1	(AJ292366) putative U6-snRNA-associated protein [Echinococcus multilocularis]	36.4	80	0.005	NP_009011.1	Sm protein F [Homo sapiens] ref|XP_032335.1| Sm protein F [Homo sapiens] sp|Q9Y4Y8|LSM6_HUMAN U6 SNRNA-ASSOCIATED SM-LIKE PROTEIN LSM6 emb|CAB45869.1| (AJ238098) Lsm6 protein [Homo sapiens] gb|AAD56230.1|AF182292_1 (AF182292) U6 snRNA-associated Sm-like protein LSm6 [Homo sapiens] dbj|BAB31555.1| (AK019126) putative [Mus musculus]	144	90	1.00E-33
00850_Ci_oc	1	BAA90520.1	(AB037679) 14-3-3 protein [Ciona intestinalis]	254	98	6.00E-67					
00851_Ci_oc	1	AAH04803.1	AAH04803 (BC004803) Similar to hypothetical protein [Mus musculus]	46.9	43	1.00E-04	AAH04803.1	AAH04803 (BC004803) Similar to hypothetical protein [Mus musculus]	46.9	43	1.00E-04
00853_Ci_oc	2	NP_223038.1	| putative [Helicobacter pylori J99] >gi|7464681|pir||G71945 hypothetical protein jhp0319 - Helicobacter pylori (strain J99) >gi|4154856|gb|AAD05909.1| (AE001468) putative [Helicobacter pylori J99]	32.1	24	5.7					
00854_Ci_oc	3	NP_006799.1	| protein translocation complex beta; protein transport protein SEC61 beta subunit [Homo sapiens] >gi|15297966|ref|XP_052762.1| protein translocation complex beta [Homo sapiens] >gi|585961|sp|P38391|S61B_HUMAN PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT >gi|631370|pir||S42410 protein translocation complex Sec61 beta chain, endoplasmic reticulum - human >gi|631516|pir||S42409 protein translocation complex Sec61 beta chain, endoplasmic reticulum - dog >gi|459746|gb|AAA19639.1| (L25052) protein translocation complex beta subunit [Canis familiaris] >gi|459834|gb|AAA19706.1| (L25085) Sec61-complex beta-subunit [Homo sapiens] >gi|12314173|emb|CAC08000.1| (AL137067) bA13B9.2 (novel protein similar to the beta subunit of transport protein SEC61) [Homo sapiens] >gi|12804623|gb|AAH01734.1|AAH01734 (BC001734) protein translocation complex beta [Homo sapiens] >gi|740571|prf||2005371A Sec61 protein:SUBUNIT=beta [Canis familiaris]	87.4	58	1.00E-16					
00858_Ci_oc	1	CAC37126.2	(AL359683) hypothetical predicted protein P1046.21, unknown function [Leishmania major]	32.5	50	4.3					

00859_Ci_oc	1	NP_079762.1	| RIKEN cDNA 1700006C06 gene [Mus musculus] >gi|12832529|dbj|BAB22147.1| (AK002499) putative [Mus musculus] >gi|12838354|dbj|BAB24174.1| (AK005662) putative [Mus musculus]	96.7	54	2.00E-19					
00860_Ci_oc	1	NP_103497.1	| unknown protein [Mesorhizobium loti] >gi|14022674|dbj|BAB49283.1| (AP002998) unknown protein [Mesorhizobium loti]	53.1	34	3.00E-06					
00863_Ci_oc	1	No Match									
00864_Ci_oc	1	NP_080297.1	| RIKEN cDNA 2700064H14 gene [Mus musculus] >gi|16160570|ref|XP_057654.1| similar to RIKEN cDNA 2700064H14 gene (M. musculus) [Homo sapiens] >gi|12838736|dbj|BAB24312.1| (AK005908) putative [Mus musculus] >gi|12849259|dbj|BAB28271.1| (AK012484) putative [Mus musculus] >gi|15277926|gb|AAH12948.1|AAH12948 (BC012948) Similar to RIKEN cDNA 2700064H14 gene [Homo sapiens]	111	53	7.00E-24					
00866_Ci_oc	2	AAF05608.1	AF190857_1 (AF190857) Ccl [Klebsiella pneumoniae]	33.6	34	1.9					
00874_Ci_oc	1	No Match									
00877_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.69					
00879_Ci_oc	1	P49310	GRP1_SINAL GLYCINE-RICH RNA-BINDING PROTEIN GRP1A >gi|7439999|pir||T10463 glycine-rich protein 1a - white mustard >gi|496233|gb|AAA59212.1| (L31374) homology with RNA-binding proteins in meristematic tissue [Sinapis alba]	34.8	47	0.85					
00885_Ci_oc	1	AAF34491.1	(AF181004) cytochrome oxidase subunit I [Nanna inermis]	167	53	9.00E-41					
00889_Ci_oc	1	P54611	VATE_DROME VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) (VACUOLAR PROTON PUMP E SUBUNIT) (V-ATPASE 28 KDA SUBUNIT) >gi|1033188|gb|AAB09738.1| (U38198) V-ATPase subunit E [Drosophila melanogaster] >gi|1055352|gb|AAB09739.1| (U38951) vacuolar ATPase subunit E [Drosophila melanogaster] >gi|5052526|gb|AAD38593.1|AF145618_1 (AF145618) BcDNA.GH03683 [Drosophila melanogaster] >gi|7296718|gb|AAF51997.1| (AE003602) Vha26 gene product [alt 1] [Drosophila melanogaster] >gi|7296719|gb|AAF51998.1| (AE003602) Vha26 gene product [alt 2] [Drosophila melanogaster]	126	49	2.00E-28					
00893_Ci_oc	1	NP_001003.1	| ribosomal protein S8; 40S ribosomal protein S8 [Homo sapiens] >gi|6677813|ref|NP_033124.1| ribosomal protein S8 [Mus musculus] >gi|13928986|ref|NP_113894.1| ribosomal protein S8 [Rattus norvegicus] >gi|14742856|ref|XP_046554.1| ribosomal protein S8 [Homo sapiens] >gi|134009|sp|P09058|RS8_HUMAN 40S RIBOSOMAL PROTEIN S8 >gi|70907|pir||R3RT8 ribosomal protein S8, cytosolic [validated] - rat >gi|107619|pir||S25022 ribosomal protein S8, cytosolic - human >gi|625511|pir||S42110 ribosomal protein S8 - mouse >gi|36150|emb|CAA47670.1| (X67247) ribosomal protein S8 [Homo sapiens] >gi|57139|emb|CAA29732.1| (X06423) ribosomal protein S8 (AA 1-208) [Rattus norvegicus] >gi|313298|emb|CAA52050.1| (X73829) ribosomal protein S8 [Mus musculus] >gi|12843566|dbj|BAB26032.1| (AK009023) putative [Mus musculus] >gi|12846246|dbj|BAB27090.1| (AK010650) putative [Mus musculus] >gi|12846913|dbj|BAB27359.1| (AK011048) putative [Mus musculus] >gi|12846930|dbj|BAB27366.1| (AK011058) putative [Mus musculus] >gi|12847901|dbj|BAB27754.1| (AK011642) putative [Mus musculus] >gi|12849175|dbj|BAB28236.1|	210	72	1.00E-53	NP_001003.1	ribosomal protein S8; 40S ribosomal protein S8 [Homo sapiens] ref|NP_033124.1| ribosomal protein S8 [Mus musculus] ref|NP_113894.1| ribosomal protein S8 [Rattus norvegicus] ref|XP_046554.1| ribosomal protein S8 [Homo sapiens] sp|P09058|RS8_HUMAN 40S RIBOSOMAL PROTEIN S8 pir||R3RT8 ribosomal protein S8, cytosolic [validated] - rat pir||S25022 ribosomal protein S8, cytosolic - human pir||S42110 ribosomal protein S8 - mouse emb|CAA47670.1| (X67247) ribosomal protein S8 [Homo sapiens] emb|CAA29732.1| (X06423) ribosomal protein S8 (AA 1-208) [Rattus norvegicus] emb|CAA52050.1| (X73829) ribosomal protein S8 [Mus musculus] dbj|BAB26032.1| (AK009023) putative [Mus musculus] dbj|BAB27090.1| (AK010650) putative [Mus musculus] dbj|BAB27359.1| (AK011048) putative [Mus musculus] dbj|BAB27366.1| (AK011058) putative [Mus musculus] dbj|BAB27754.1| (AK011642) putative [Mus musculus] dbj|BAB28236.1| (AK012435) putative [Mus musculus] dbj|BAB28394.1| (AK012665) putative [Mus musculus]	192	72	4.00E-48
00897_Ci_oc	2	NP_001000.2	| ribosomal protein S5; 40S ribosomal protein S5 [Homo sapiens] >gi|14755545|ref|XP_034265.1| ribosomal protein S5 [Homo sapiens] >gi|16162725|ref|XP_058096.1| hypothetical protein XP_058096 [Homo sapiens] >gi|15929961|gb|AAH15405.1|AAH15405 (BC015405) ribosomal protein S5 [Homo sapiens]	279	93	2.00E-74					
00906_Ci_oc	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.7					
00907_Ci_oc	1	S14974	extensin class I (clone uG-18) - tomato (fragment) >gi|1345537|emb|CAA39215.1| (X55685) extensin (class I) [Lycopersicon esculentum]	32.1	41	3.1					
00916_Ci_oc	2	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	64	73	1.00E-09					
00918_Ci_oc	1	CAA55385.1	(X78801) ovomacroglobulin, ovostatin [Gallus gallus]	31.7	34	7.4	No Match				
00920_Ci_oc	1	No Match									
00921_Ci_oc	1	AAB06703.1	(U40703) sporozoite surface protein p67 [Theileria parva]	34	28	1.5					
00924_Ci_oc	1	BAA86200.1	(AB033282) nucleolin like protein CiRGG1 [Ciona intestinalis]	62.8	62	2.00E-09	BAA86200.1	(AB033282) nucleolin like protein CiRGG1 [Ciona intestinalis]	62.8	60	3.00E-09
00925_Ci_oc	1	No Match									
00927_Ci_oc	1	NP_078770.1	| orf8 [lymphocystis disease virus 1]	32.1	42	5.7					
00930_Ci_oc	1	CAB88106.2	(AL117334) dJ687F11.2 (novel protein (contains part of translation of cDNA DKFZp434N061, Em:AL110249)) [Homo sapiens]	32.8	58	3.3					
00933_Ci_oc	1	BAA11765.1	(D83069) ADT/ATP translocase [Halocynthia roretzi]	68.3	62	7.00E-11					
00935_Ci_oc	1	No Match									
00936_Ci_oc	1	AAK97625.1	AF395204_1 (AF395204) kynurenine aminotransferase [Aedes aegypti]	32.8	51	3.1	AAK97625.1	AF395204_1 (AF395204) kynurenine aminotransferase [Aedes aegypti]	32.8	50	3.2
00938_Ci_oc	2	XP_009716.4	| chaperonin containing TCP1, subunit 8 (theta) [Homo sapiens]	59.3	68	4.00E-08					
00939_Ci_oc	1	AAH15387.1	AAH15387 (BC015387) Similar to RIKEN cDNA 1110001O19 gene [Homo sapiens]	43	25	0.003	AAH15387.1	AAH15387 (BC015387) Similar to RIKEN cDNA 1110001O19 gene [Homo sapiens]	47.6	25	1.00E-04

00940_Ci_oc	1	XP_049002.1	| zinc family member 5 protein [Homo sapiens] >gi|14916471|ref|NP_149123.1| zinc family member 5 protein [Homo sapiens] >gi|14165182|gb|AAK55418.1|AF378304_1 (AF378304) zinc family member 5 protein [Homo sapiens]	34	30	0.95	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	4.9
00954_Ci_oc	1	No Match									
00955_Ci_oc	1	AAF28958.1	AF161398_1 (AF161398) HSPC280 [Homo sapiens]	43.4	79	0.002					
00956_Ci_oc	1	CAB71856.1	(AL[illegible]) hypothetical protein [illegible] [Streptomyces coelicolor A3(2)]	32.5	45	4					
00958_Ci_oc	1	No Match									
00959_Ci_oc	1	No Match									
00960_Ci_oc	1	P13008	RS26_DROME 40S RIBOSOMAL PROTEIN S26 (DS31) >gi|71054|pir||R3FF26 ribosomal protein S26 - fruit fly (Drosophila melanogaster) >gi|8494|emb|CAA32463.1| (X14247) ribosomal protein S31 [Drosophila melanogaster] >gi|4469169|emb|CAB38441.1| (X13625) ribosomal protein S31; putative [Drosophila melanogaster] >gi|7298445|gb|AAF53666.1| (AE003659) RpS26 gene product [Drosophila melanogaster]	41.8	32	0.007	P27085	RS26_OCTVU 40S RIBOSOMAL PROTEIN S26 emb|CAB57819.1| (X17303) ribosomal protein S26 [Octopus vulgaris]	111	66	5.00E-24
00961_Ci_oc	1	NP_000971.1	| ribosomal protein L18a; 60S ribosomal protein L18a [Homo sapiens] >gi|14766238|ref|XP_038593.1| ribosomal protein L18a [Homo sapiens] >gi|730538|sp|Q02543|RL1X_HUMAN 60S RIBOSOMAL PROTEIN L18A >gi|401845|gb|AAC18781.1| (L05093) ribosomal protein L18a [Homo sapiens] >gi|3702270|gb|AAC62828.1| (AC005796) ribosomal protein L18a [Homo sapiens] >gi|13960144|gb|AAH07512.1|AAH07512 (BC007512) ribosomal protein L18a [Homo sapiens]	207	66	1.00E-52	P11249	RL1X_RAT 60S RIBOSOMAL PROTEIN L18A pir||JC4231 ribosomal protein L18a - rat pir||R5RT18 ribosomal protein L18a, cytosolic [validated] - rat emb|CAA32385.1| (X14181) ribosomal protein L18a (AA 1-175) [Rattus rattus] dbj|BAB27304.1| (AK010983) putative [Mus musculus]	164	66	6.00E-40
00962_Ci_oc	1	AAF64457.1	(AF240374) ribosomal protein L18 [Oreochromis niloticus] >gi|7595806|gb|AAF64458.1|AF240375_1 (AF240375) ribosomal protein L18 [Oreochromis niloticus] >gi|7595809|gb|AAF64459.1|AF240376_1 (AF240376) ribosomal protein L18 [Oreochromis mossambicus]	226	71	1.00E-58	AAF64457.1	(AF240374) ribosomal protein L18 [Oreochromis niloticus] gb|AAF64458.1|AF240375_1 (AF240375) ribosomal protein L18 [Oreochromis niloticus] gb|AAF64459.1|AF240376_1 (AF240376) ribosomal protein L18 [Oreochromis mossambicus]	177	72	8.00E-44
00964_Ci_oc	1	AAF78205.1	AF228877_1 (AF228877) unknown [Strongylocentrotus purpuratus]	33.6	38	1.9					
00008_Ci_oc	1	No Match									
00013_Ci_oc	1	No Match									
00025_Ci_oc	1	AAF47912.1	(AE003481) CG13722 gene product [Drosophila melanogaster]	29.7	39	5.8	AAD50044.1	AC007980_9 (AC007980) cytosolic tRNA-Ala synthetase [Arabidopsis thaliana]	30.1	44	9.6
00027_Ci_oc	1	No Match									
00039_Ci_oc	1	B44418	surface antigen - Trypanosoma brucei	41	43	0.004	S67946	protein-tyrosine kinase (EC 2.7.1.112) - Geodia cydonium	30.9	30	6.9
00042_Ci_oc	1	No Match					S54360	reverse transcriptase - Trypanosoma cruzi (fragment) emb|CAB41693.1| (X83098) reverse transcriptase [Trypanosoma cruzi]	34	28	0.96
00079_Ci_oc	1	AAF55209.1	(AE003709) CG6045 gene product [Drosophila melanogaster]	31.3	46	9.7					
00084_Ci_oc	1	AAD05194.1	(AC005587) similar to meningioma-expressed antigen 6 (MEA6); similar to U94780 (PID:g2231999) [Homo sapiens] >gi|9368992|emb|CAB99213.1| (AL135904) dJ1005H11.2 (WUGSC:H_DJ0988G15.3 PROTEIN) [Homo sapiens]	31.7	36	7.4					
00090_Ci_oc	1	No Match					CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	31.3	65	4.3
00097_Ci_oc	1	No Match									
00119_Ci_oc	1	BAB55174.1	(AK027523) unnamed protein product [Homo sapiens]	145	84	3.00E-34					
00194_Ci_oc	1	AAA45797.1	(M17921) latency associated transcript (LAT) ORF-2 [human herpesvirus 1]	33.2	38	2.5					
00203_Ci_oc	1	No Match									
00210_Ci_oc	1	No Match									
00213_Ci_oc	1	NP_003449.1	| bassoon (presynaptic cytomatrix protein), neuronal double zinc finger protein; zinc finger protein 231 [Homo sapiens] >gi|3982598|gb|AAC83555.1| (AF052224) neuronal double zinc finger protein [Homo sapiens]	36	43	0.38					
00219_Ci_oc	1	NP_067375.1	| proteoglycan 3 (megakaryocyte stimulating factor, articular superficial zone protein) [Mus musculus] >gi|7209719|dbj|BAA92310.1| (AB034730) This gene is isolated by means of differential display method using ttw, an excellent mouse model for ectopic ossification.~similar to megakaryocyte stimulating factor precursor and cartilage superficial zone protein [Mus musculus]	40.2	26	0.019					
00225_Ci_oc	1	XP_008695.4	| CTD (carboxy-terminal domina, RNA polymerase II, polypeptide A) phosphatase, subunit 1 [Homo sapiens]	35.2	38	0.65					
00230_Ci_oc	1	No Match					No Match				
00231_Ci_oc	1	P03181	YHL1_EBV HYPOTHETICAL BHLF1 PROTEIN >gi|73912|pir||QQBE3 BHLF1 protein - human herpesvirus 4 (strain B95-8)	39.5	35	0.033					
00254_Ci_oc	1	AAD37000.1	AF093102_2 (AF093102) structural polyprotein [Venezuelan equine encephalitis virus]	36	38	0.38	NP_061359.1	3-monooxgenase/tryptophan 5-monooxgenase activation protein, gamma polypeptide [Mus musculus] gb|AAC14345.1| (AF058799) 14-3-3 protein gamma [Mus musculus]	34.4	76	0.004
00272_Ci_oc	1	No Match					AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	1.9
00345_Ci_oc	1	No Match									
00367_Ci_oc	1	No Match									
00374_Ci_oc	1	No Match									
00379_Ci_oc	1	T39828	hypothetical protein SPBC19F8.05 - fission yeast (Schizosaccharomyces pombe) >gi|3150138|emb|CAA19125.1| (AL023594) hypothetical protein [Schizosaccharomyces pombe]	32.8	27	3					

00381_Ci_oc	1	NP_106111.1	| transcriptional regulator [Mesorhizobium loti] >gi|14025296|dbj|BAB51897.1| (AP003006) transcriptional regulator [Mesorhizobium loti]	64	29	1.00E-09	NP_106111.1	transcriptional regulator [Mesorhizobium loti] dbj|BAB51897.1| (AP003006) transcriptional regulator [Mesorhizobium loti]	65.2	29	6.00E-10
00386_Ci_oc	1	No Match									
00392_Ci_oc	1	T15833	hypothetical protein C54A12.4 - Caenorhabditis elegans >gi|861254|gb|AAA68305.1| (U28733) similar to RAS-related proteins [Caenorhabditis elegans]	40.6	35	0.015					
00408_Ci_oc	1	No Match					AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	7.3
00416_Ci_oc	1	No Match									
00422_Ci_oc	1	AAF13347.1	AF122023_1 (AF122023) unknown [Eufolliculina uhligi]	29.3	47	7.3					
00430_Ci_oc	1	NP_174727.1	| mutator-like transposase, putative [Arabidopsis thaliana]	32.5	30	2	NP_174727.1	mutator-like transposase, putative [Arabidopsis thaliana]	33.2	28	1.3
00447_Ci_oc	1	No Match									
00450_Ci_oc	1	No Match									
00452_Ci_oc	1	No Match									
00521_Ci_oc	1	NP_196996.1	| putative protein [Arabidopsis thaliana] >gi|11357726|pir||T51437 hypothetical protein F2G14_40 - Arabidopsis thaliana >gi|9755659|emb|CAC01811.1| (AL391146) putative protein [Arabidopsis thaliana] >gi|13926280|gb|AAK49610.1|AF372894_1 (AF372894) AT5g14920/F2G14_40 [Arabidopsis thaliana] >gi|15010790|gb|AAK74054.1| (AY045696) AT5g14920/F2G14_40 [Arabidopsis thaliana] >gi|15810065|gb|AAL06958.1| (AY055791) AT5g14920/F2G14_40 [Arabidopsis thaliana]	33.6	39	1.9					
00551_Ci_oc	1	NP_191483.1	| putative protein [Arabidopsis thaliana] >gi|11357636|pir||T48992 hypothetical protein F25L23.100 - Arabidopsis thaliana >gi|7801674|emb|CAB91594.1| (AL356014) putative protein [Arabidopsis thaliana]	31.7	47	7.4					
00559_Ci_oc	1	No Match									
00595_Ci_oc	1	No Match									
00596_Ci_oc	1	NP_003932.1	| Wiskott-Aldrich syndrome gene-like protein; neural Wiskott-Aldrich syndrome protein; Wiskott-Aldrich syndrome gene-like [Homo sapiens] >gi|13431960|sp|O00401|WASL_HUMAN NEURAL WISKOTT-ALDRICH SYNDROME PROTEIN (N-WASP) >gi|2116984|dbj|BAA20128.1| (D88460) N-WASP [Homo sapiens]	32.5	52	0.49					
00602_Ci_oc	1	XP_052058.1	| hypothetical protein XP_052058 [Homo sapiens] >gi|16158076|ref|XP_055716.1| hypothetical protein XP_055716 [Homo sapiens]	29.7	46	5.3					
00606_Ci_oc	1	No Match				T15987	hypothetical protein F09E10.3 - Caenorhabditis elegans gb|AAB52488.1| (U41749) Hypothetical protein F09E10.3 [Caenorhabditis elegans]	64.8	34	7.00E-10
00607_Ci_oc	1	No Match					AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	91	2
00614_Ci_oc	1	NP_048276.1	| ORF MSV205 tryptophan repeat gene family protein [Melanoplus sanguinipes entomopoxvirus] >gi|11362387|pir||T28366 ORF MSV205 tryptophan repeat gene family protein - Melanoplus sanguinipes entomopoxvirus >gi|4049796|gb|AAC97756.1| (AF063866) ORF MSV205 tryptophan repeat gene family protein [Melanoplus sanguinipes entomopoxvirus]	32.5	31	4.3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	91	5
00621_Ci_oc	1	XP_002446.2	| hypothetical protein XP_002446 [Homo sapiens] >gi|14731368|ref|XP_027939.1| DKFZP564A2416 protein [Homo sapiens]	31.3	29	1.9	BAB21479.1	(AB048261) integrin alpha Hr1 precursor [Halocynthia roretzi]	76.9	32	2.00E-13
00634_Ci_oc	1	NP_174132.1	| serine carboxypeptidase II, putative [Arabidopsis thaliana] >gi|12322985|gb|AAG51475.1|AC069471_6 (AC069471) serine carboxypeptidase II, putative [Arabidopsis thaliana]	34	25	1.5					
00670_Ci_oc	1	NP_056418.1	| DKFZP586M1019 protein [Homo sapiens] >gi|13654971|ref|XP_009037.2| DKFZP586M1019 protein [Homo sapiens] >gi|7512925|pir||T08760 hypothetical protein DKFZp586M1019.1 - human >gi|4886469|emb|CAB43385.1| (AL050284) hypothetical protein [Homo sapiens] >gi|12803883|gb|AAH02787.1|AAH02787 (BC002787) DKFZP586M1019 protein [Homo sapiens] >gi|14602475|gb|AAH09743.1|AAH09743 (BC009743) DKFZP586M1019 protein [Homo sapiens]	34	28	1.5					
00690_Ci_oc	1	No Match									
00694_Ci_oc	1	CAA30394.1	(X07516) proline-rich protein (51 is 2nd base in codon) [Homo sapiens]	33.6	27	1.9					
00705_Ci_oc	1	P18503	CAS4_EPHMU SHORT-CHAIN COLLAGEN C4 >gi|112570|pir||S11449 collagen short chain - freshwater sponge (Ephydatia muelleri) (fragment) >gi|9298|emb|CAA36831.1| (X52598) short chain collagen (partial) (366 AA) [Ephydatia muelleri]	34.8	53	0.97					
00706_Ci_oc	1	BAB03062.1	(AP001306) contains similarity to cell wall-plasma membrane linker protein~gene_id:MKA23.5 [Arabidopsis thaliana]	36.4	29	0.29					
00708_Ci_oc	1	No Match									
00710_Ci_oc	1	No Match									
00717_Ci_oc	1	No Match									
00728_Ci_oc	1	No Match									

00730_Ci_oc	1	NP_191160.1	| putative protein [Arabidopsis thaliana] >gi|11288861|pir||T49213 hypothetical protein F27K19.190 - Arabidopsis thaliana >gi|7573496|emb|CAB87855.1| (AL163832) putative protein [Arabidopsis thaliana] >gi|15810457|gb|AAL07116.1| (AY056267) unknown protein [Arabidopsis thaliana]	34	35	1.5					
00743_Ci_oc	1	No Match					AAG08964.1	AF156177_1 (AF156177) beta-thymosin [Sycon raphanus]	69.1	77	2.00E-11
00766_Ci_oc	1	NP_116401.1	| T48 [Tupaia herpesvirus] >gi|14210733|gb|AAK57096.1| (AF281817) T48 [Tupaia herpesvirus]	39.1	36	0.014					
00781_Ci_oc	1	No Match									
00793_Ci_oc	1	No Match					T29288	hypothetical protein C34D4.15 - Caenorhabditis elegans gb|AAB00702.1| (U58755) Hypothetical protein C34D4.15 [Caenorhabditis elegans]	41.8	32	0.007
00856_Ci_oc	1	No Match									
00876_Ci_oc	1	No Match									
00882_Ci_oc	1	No Match									
00898_Ci_oc	1	AAF60407.1	(AC024746) Hypothetical protein Y110A2AL.12 [Caenorhabditis elegans]	30.9	40	2.6					
00912_Ci_oc	1	No Match									
00926_Ci_oc	1	No Match									

Table C-2: List of EST clones of Ascidian otolith cell

			analyses based on 3' ESTs					analyses based on 5' ESTs			
clone ID	frequenc	accession No.	homologous sequence which showed the highest E-value	score	identity (%)	E-value	accession No.	homologous sequence which showed the highest E-value	score	identity (%)	E-value
00001_Ci_ot	1	AAF76861.1	(AF232708) chloride ion current inducer protein I(Cln) [Homo sapiens]	35.2	37	0.35	AAF76861.1	(AF232708) chloride ion current inducer protein I(Cln) [Homo sapiens]	37.5	34	0.05
00002_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.1					
00004_Ci_ot	1	NP_420095.1	serine protease [Caulobacter crescentus] >gi13422617gbAAK23263.1 (AE005803) serine protease [Caulobacter crescentus]	184	57	8.00E-46	NP_420095.1	serine protease [Caulobacter crescentus] gb|AAK23263.1| (AE005803) serine protease [Caulobacter crescentus]	183	57	1.00E-45
00005_Ci_ot	5	CAC28101.2	(AJ307410) COX3 protein [Yarrowia lipolytica]	32.8	38	3.3	CAC28101.2	(AJ307410) COX3 protein [Yarrowia lipolytica]	32.8	38	3.3
00006_Ci_ot	1	NP_180214.1	unknown protein [Arabidopsis thaliana] >gi7487879pirT00979 hypothetical protein T9J22.13 - Arabidopsis thaliana >gi2739371gbAAC14495.1 (AC002505) unknown protein [Arabidopsis thaliana]	35.2	32	0.65	NP_050064.1	NADH dehydrogenase subunit 6 [Pedinomonas minor] pir||T11321 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - Pedinomonas minor mitochondrion gb|AAD19673.1| (AF116775) NADH dehydrogenase subunit 6 [Pedinomonas minor]	34.4	31	1.1
00305_Ci_ot	18	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.8	No Match				
00008_Ci_ot	1	NP_418274.1	putative enzyme [Escherichia coli K12] >gi7466527pirG65187 hypothetical protein b3830 - Escherichia coli (strain K-12) >gi2367305gbAAC76833.1 (AE000458) putative enzyme [Escherichia coli K12]	32.1	41	1.5	AAK29175.1	(AY028808) AV2 protein [cotton leaf curl virus] gb|AAK64240.1|AF363011_1 (AF363011) movement/pre-coat protein [cotton leaf curl virus]	32.1	31	1.1
00009_Ci_ot	43	No Match					T18454	hypothetical protein C0550w - malaria parasite (Plasmodium falciparum) emb|CAA15596.1| (AL008970) hypothetical protein, PFC0550w [Plasmodium falciparum]	34	40	0.28
00010_Ci_ot	1	AAH04070.1	AAH04070 (BC004070) Unknown (protein for MGC:8213) [Mus musculus] >gi13924522gbAAK49039.1AF251503_1 (AF251503) putative nuclear matrix protein SNEV [Mus musculus]	110	65	1.00E-23	AAH04070.1	AAH04070 (BC004070) Unknown (protein for MGC:8213) [Mus musculus] gb|AAK49039.1|AF251503_1 (AF251503) putative nuclear matrix protein SNEV [Mus musculus]	184	72	6.00E-46
00011_Ci_ot	1	BAB46881.1	(AB060868) hypothetical protein [Macaca fascicularis]	75.3	32	5.00E-13	CAB43000.1	(AJ238043) tellurite resistance [Escherichia coli]	32.8	28	3.3
00012_Ci_ot	1	NP_149843.1	380R [Chilo iridescent virus] >gi15042460gbAAK82240.1AF303741_381 (AF303741) 380R [Chilo iridescent virus]	31.3	45	9.7	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	44.9	66	8.00E-04
00013_Ci_ot	2	NP_038181.1	SecY-independent transporter protein [Chrysodidymus synuroideus] >gi7110475gbAAF36947.1AF222718_21 (AF222718) SecY-independent transporter protein [Chrysodidymus synuroideus]	31.3	31	9.7	AAF60756.1	(AC006804) Hypothetical protein Y53G8B.3 [Caenorhabditis elegans]	34.8	30	0.54
00016_Ci_ot	1	CAC40660.1	(AJ242781) inositol 1,4,5-trisphosphate 3-kinase, isoform B [Rattus norvegicus]	201	58	4.00E-51	AAF59320.1	(AE003843) CG11360 gene product [Drosophila melanogaster]	34.8	31	0.85
00021_Ci_ot	1	AAF67108.1	AF224059_1 (AF224059) putative variable cytadhesin protein [Mycoplasma gallisepticum]	36.4	37	0.16	NP_055721.1	KIAA1072 protein [Homo sapiens] dbj|BAA83024.1| (AB028995) KIAA1072 protein [Homo sapiens]	32.1	38	2.7
00031_Ci_ot	1	No Match									
00032_Ci_ot	1	NP_180071.1	similar to extragenic suppressor of bimD6 mutation {Emericella nidulans} [Arabidopsis thaliana] >gi4559353gbAAD23014.1AC006585_9 (AC006585) putative SUDD-like protein [Arabidopsis thaliana]	35.2	31	0.65	AAF23835.1	AC007234_7 (AC007234) F1E22.19 [Arabidopsis thaliana]	34.8	46	0.78
00038_Ci_ot	1	NP_000978.1	ribosomal protein L26 [Homo sapiens] >gi6677777refNP_033106.1 ribosomal protein L26 [Mus musculus] >gi400990spQ02877RL26_HUMAN 60S RIBOSOMAL PROTEIN L26 >gi423068pirS33713 ribosomal protein L26, cytosolic - human >gi1071990pirS48864 ribosomal protein L26 - mouse >gi36115embCAA49189.1 (X69392) ribosomal protein L26 [Homo sapiens] >gi565624embCAA56716.1 (X80699) L26 [Mus musculus]	183	62	1.00E-45	XP_011224.2	ribosomal protein L26 homolog [Homo sapiens]	176	63	1.00E-43
00042_Ci_ot	1	AAF47152.1	(AE003462) CG3195 gene product [Drosophila melanogaster]	153	66	1.00E-36	CAB88388.1	(AJ252184) L12 ribosomal protein [Hydra vulgaris]	242	78	2.00E-63
00044_Ci_ot	1	AAD16010.1	(AF080569) DnaJ-like 2 protein [Homo sapiens]	29.7	44	5.7	No Match				
00050_Ci_ot	1	No Match					CAA44719.1	(X62947) 55 kd protein [Homo sapiens]	34.4	29	1.1
00051_Ci_ot	2	O42249	GBLP_ORENI GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (RECEPTOR OF ACTIVATED PROTEIN KINASE C) (RACK) >gi2558966gbAAB81618.1 (AF025331) receptor for activated protein kinase C [Oreochromis niloticus]	256	78	1.00E-67	I49700	G protein beta subuit like - mouse dbj|BAA06185.1| (D29802) G protein beta subuit like [Mus musculus]	217	78	7.00E-56
00055_Ci_ot	1	T39144	very hypothetical protein SPAC8C9.07 - fission yeast (Schizosaccharomyces pombe) >gi2408090embCAB16295.1 (Z99168) very hypothetical protein [Schizosaccharomyces pombe]	31.7	50	7.4	BAB20439.1	(AB036064) transglutaminase [Asterina pectinifera]	73.4	32	2.00E-12
00057_Ci_ot	1	JQ0948	A5 antigen precursor - African clawed frog >gi222963dbjBAA01260.1 (D10467) A5-protein [Xenopus laevis]	37.1	26	0.17	AAK68224.1	U21324_7 (U21324) Hypothetical protein C35D10.15 [Caenorhabditis elegans]	33.2	44	2.5
00058_Ci_ot	1	NP_198121.1	putative protein [Arabidopsis thaliana]	31.3	54	3.7	CAA10856.2	(AJ222584) maturase-like protein [Euglena viridis]	32.5	33	4.3
00060_Ci_ot	1	No Match					No Match				
00066_Ci_ot	1	NP_077003.1	hypothetical protein MGC2574 [Homo sapiens] >gi13647420refXP_015544.1 hypothetical protein MGC2574 [Homo sapiens] >gi14784784refXP_043499.1 hypothetical protein MGC2574 [Homo sapiens] >gi10438660dbjBAB15304.1 (AK025974) unnamed protein product [Homo sapiens] >gi12655057gbAAH01378.1AAH01378 (BC001378) Unknown (protein for MGC:2574) [Homo sapiens]	80	46	2.00E-14	NP_077003.1	hypothetical protein MGC2574 [Homo sapiens] ref|XP_015544.1| hypothetical protein MGC2574 [Homo sapiens] ref|XP_043499.1| hypothetical protein MGC2574 [Homo sapiens] dbj|BAB15304.1| (AK025974) unnamed protein product [Homo sapiens] gb|AAH01378.1|AAH01378 (BC001378) Unknown (protein for MGC:2574) [Homo sapiens]	81.1	45	9.00E-15
00068_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	1.9	E72688	hypothetical protein APE0925 - Aeropyrum pernix (strain K1) dbj|BAA79909.1| (AP000060) 202aa long hypothetical protein [Aeropyrum pernix]	31.3	33	2
00071_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.8	No Match				
00072_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.5	No Match				

00073_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	1.9	No Match				
00074_Ci_ot	1	CAA71263.1	(Y10212) transglutiminase [Ciona intestinalis]	119	81	2.00E-26	CAA71263.1	(Y10212) transglutiminase [Ciona intestinalis]	173	98	1.00E-42
00078_Ci_ot	2	CAC41647.1	(AJ315576) putative acetamidase [Ustilago maydis]	31.7	40	3.4	AAD47860.1	AF171685_1 (AF171685) envelope glycoprotein [Porcine reproductive and respiratory syndrome virus]	31.3	50	3.2
00083_Ci_ot	1	Q09703	YA2C_SCHPO HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME I PRECURSOR >gi2130381pirS58156 hypothetical protein SPAC2F7.12 - fission yeast (Schizosaccharomyces pombe) >gi7491059pirT38560 hypothetical protein SPAC2F7.12 - fission yeast (Schizosaccharomyces pombe)	32.8	38	3.3	AAF49243.1	(AE003519) CG13379 gene product [Drosophila melanogaster]	87	44	2.00E-16
00084_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.6	BAB29332.1	(AK014408) putative [Mus musculus]	30.5	39	8.2
00699_Ci_ot	6	P55379	Y4BL_RHISN PUTATIVE TRANSPOSASE Y4BL/Y4KJ/Y4TB >gi11352867pirT47075 hypothetical protein Y4kJ [imported] - Rhizobium sp. (NGR234) plasmid pNGR234a >gi2182320gbAAB91627.1 (AE000066) Y4bL [Rhizobium sp. NGR234] >gi2182486gbAAB91741.1 (AE000081) Y4kJ [Rhizobium sp. NGR234] >gi2182632gbAAB91856.1 (AE000097) Y4tB [Rhizobium sp. NGR234]	34	39	1.4	AAG60368.1	AF214940_1 (AF214940) conotoxin scaffold III/IV precursor [Conus tessulatus]	31.3	52	9.7
00086_Ci_ot	1	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	37.5	62	0.13	No Match				
00748_Ci_ot	7	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9	No Match				
00091_Ci_ot	2	NP_075622.1	ribosomal protein S19 [Mus musculus] >gi133857spP17074RS19_RAT 40S RIBOSOMAL PROTEIN S19 >gi71019pirR3RT19 ribosomal protein S19, cytosolic [validated] - rat >gi57716embCAA36003.1 (X51707) ribosomal protein S19 (AA 1-145) [Rattus rattus] >gi7648818gbAAF65683.1AF216207_1 (AF216207) ribosomal protein S19 [Mus musculus] >gi12850925dbjBAB28898.1 (AK013524) putative [Mus musculus] >gi12858583dbjBAB31370.1 (AK018725) putative [Mus musculus]	210	69	9.00E-54	AAK95202.1	AF402828_1 (AF402828) 40S ribosomal protein S19 [Ictalurus punctatus]	54.3	63	3.00E-07
00092_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	5	No Match				
00093_Ci_ot	2	AAF61072.1	AF220553_1 (AF220553) 40S ribosomal protein S15A [Paralichthys olivaceus]	214	86	7.00E-55	AAF61072.1	AF220553_1 (AF220553) 40S ribosomal protein S15A [Paralichthys olivaceus]	240	86	9.00E-63
00096_Ci_ot	1	No Match					No Match				
00097_Ci_ot	1	BAB28163.1	(AK012326) putative [Mus musculus]	32.5	36	3.4	XP_004268.2	syntaxin 11 [Homo sapiens] sp|O75558|STXB_HUMAN SYNTAXIN 11 gb|AAC24004.1| (AF071504) syntaxin 11 [Homo sapiens]	37.1	21	0.11
00098_Ci_ot	1	XP_051716.1	hypothetical protein XP_051716 [Homo sapiens]	86.2	71	8.00E-17	XP_051716.1	hypothetical protein XP_051716 [Homo sapiens]	151	83	7.00E-36
00099_Ci_ot	1	NP_104249.1	permease of ABC sugar transporter [Mesorhizobium loti] >gi14023429dbjBAB50035.1 (AP003001) permease of ABC sugar transporter [Mesorhizobium loti]	32.1	41	5.7	AAF06355.1	AF102579_1 (AF102579) 5'-phosphoribosylaminoimidazole carboxylase-5'-phosphoribosyl-4-(N-succinocarboxamide)- 5-aminoimidazole synthetase [Drosophila melanogaster] gb|AAF06356.1|AF102580_1 (AF102580) 5'-phosphoribosylaminoimidazole carboxylase-5'-phosphoribosyl-4-(N-succinocarboxamide)- 5-aminoimidazole synthetase [Drosophila melanogaster]	94.4	50	1.00E-18
00604_Ci_ot	4	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.6					
00103_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	1.9	No Match				
00104_Ci_ot	1	No Match					AAF59114.2	(AE003838) CG8706 gene product [Drosophila melanogaster]	51.2	45	1.00E-05
00106_Ci_ot	2	No Match					No Match				
00107_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.9	AAD51003.1	AF170925_1 (AF170925) photosystem II chlorophyll-binding protein CP-47 [Mastigocladus laminosus]	31.7	31	3.4
00108_Ci_ot	3	P31027	RL44_KLULA 60S RIBOSOMAL PROTEIN L44 (L41) >gi424005pirS32478 ribosomal protein L36a.e - yeast (Kluyveromyces marxianus var. lactis) >gi173301gbAAA35262.1 (M94988) ribosomal protein [Kluyveromyces lactis]	127	75	3.00E-40	CAA10856.2	(AJ222584) maturase-like protein [Euglena viridis]	32.8	33	3.3
00112_Ci_ot	1	No Match					CAB41711.2	(Z98547) hypothetical protein, PFC0430w [Plasmodium falciparum]	39.1	38	0.044
00297_Ci_ot	2	CAA10856.2	(AJ222584) maturase-like protein [Euglena viridis]	32.8	35	1.5	CAA10856.2	(AJ222584) maturase-like protein [Euglena viridis]	32.8	33	0.98
00366_Ci_ot	2	D71614	hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum) >gi3845190gbAAC71881.1 (AE001396) hypothetical protein [Plasmodium falciparum]	66	50	3.00E-10	D71614	hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum) gb|AAC71881.1| (AE001396) hypothetical protein [Plasmodium falciparum]	66.7	50	2.00E-10
00115_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	35.6	50	0.26	No Match				
00116_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	30.5	91	3.5					
00117_Ci_ot	3	A61144	probable flagellar protein (clone FCH-F8-4) - Trypanosoma cruzi (fragment)	36.7	83	0.084	A61144	probable flagellar protein (clone FCH-F8-4) - Trypanosoma cruzi (fragment)	36.7	83	0.054
00119_Ci_ot	1	AAD52909.1	AF142738_1 (AF142738) maturase-like protein [Melilotus alba]	32.8	27	3.3	AAD52909.1	AF142738_1 (AF142738) maturase-like protein [Melilotus alba]	32.8	26	3.2
00120_Ci_ot	1	No Match					NP_173784.1	unknown protein [Arabidopsis thaliana] gb|AAC98027.1| (AC005990) Contains repeated region with similarity to gb|U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb|Z34165 and gb|Z18788 come from this gene	36.4	25	0.29
00121_Ci_ot	1	No Match					AAK26121.1	AC084406_4 (AC084406) hypothetical protein [Oryza sativa]	35.2	34	0.65
00122_Ci_ot	1	P23403	RS20_XENLA 40S RIBOSOMAL PROTEIN S20 (S22) >gi85846pirA37974 ribosomal protein S20, cytosolic - African clawed frog >gi214758gbAAA49953.1 (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]	193	81	1.00E-48	P23403	RS20_XENLA 40S RIBOSOMAL PROTEIN S20 (S22) pir||A37974 ribosomal protein S20, cytosolic - African clawed frog gb|AAA49953.1| (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]	198	82	4.00E-50
00124_Ci_ot	1	AAK95151.1	AF401579_1 (AF401579) ribosomal protein L24 [Ictalurus punctatus]	171	70	6.00E-42	AAG13295.1	AF266175_1 (AF266175) 60S ribosomal protein L24 [Gillichthys mirabilis]	163	74	9.00E-40

00125_Ci_ot	1	No Match					AAF47305.1	(AE003465) RpL19 gene product [Drosophila melanogaster]	122	61	9.00E-32
00126_Ci_ot	2	AAK37484.1	(AF322122) teosinte branched1 protein [Coix lacryma-jobi]	32.8	37	3.3	AAC17029.2	(AF067219) Hypothetical protein R12E2.8 [Caenorhabditis elegans]	54.7	30	9.00E-07
00127_Ci_ot	3	XP_054253.2	hypothetical protein XP_054253 [Homo sapiens]	32.8	54	3.3	AAK39523.1	(AF355190) RNA-binding motif protein 3 [Rattus norvegicus]	31.7	53	2.3
00130_Ci_ot	1	T37929	probable major facilitator protein - fission yeast (Schizosaccharomyces pombe)	31.3	28	9.7	No Match				
00132_Ci_ot	10	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.5	AAF70118.1	AF262948_1 (AF262948) cysteine-leucine rich protein [Leishmania tarentolae]	29.3	40	7.5
00133_Ci_ot	1	NP_421615.1	TonB-dependent receptor, putative [Caulobacter crescentus] >gi13424425gbAAK24783.1 (AE005947) TonB-dependent receptor, putative [Caulobacter crescentus]	33.6	37	0.38					
00134_Ci_ot	1	NP_127297.1	hypothetical protein [Pyrococcus abyssi] >gi7450091pirA75011 hypothetical protein PAB1284 - Pyrococcus abyssi (strain Orsay) >gi5459041embCAB50527.1 (AJ248288) hypothetical protein [Pyrococcus abyssi]	32.8	36	3.3	No Match				
00135_Ci_ot	1	NP_010977.2	Homology to rat L34; Rpl34ap [Saccharomyces cerevisiae] >gi6174938spP87262R34A_YEAST 60S RIBOSOMAL PROTEIN L34-A >gi1084587pirS53549 ribosomal protein L34.e.A, cytosolic - yeast (Saccharomyces cerevisiae) >gi2194156gbAAB64609.1 (U18813) Yer056c-ap [Saccharomyces cerevisiae]	98.3	44	5.00E-20	NP_010977.2	Homology to rat L34; Rpl34ap [Saccharomyces cerevisiae] sp|P87262|R34A_YEAST 60S RIBOSOMAL PROTEIN L34-A pir||S53549 ribosomal protein L34.e.A, cytosolic - yeast (Saccharomyces cerevisiae) gb|AAB64609.1| (U18813) Yer056c-ap [Saccharomyces cerevisiae]	116	52	1.00E-25
00136_Ci_ot	1	No Match					P49154	RS2_URECA 40S RIBOSOMAL PROTEIN S2 gb|AAA74095.1| (U30454) ribosomal protein S2 [Urechis caupo]	51.5	43	8.00E-06
00137_Ci_ot	1	No Match					AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	33.6	86	1.9
00138_Ci_ot	1	BAB68391.1	(AB058682) opsin [Ciona intestinalis]	38.3	86	7.00E-06	BAB68391.1	(AB058682) opsin [Ciona intestinalis]	37.5	38	0.13
00139_Ci_ot	1	P15627	COAT_SOCMV COAT PROTEIN >gi76789pirJS0374 hypothetical 51.6K protein - soybean chlorotic mottle virus	33.2	41	1.1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	41.4	43	0.009
00140_Ci_ot	1	No Match					AAF48473.1	(AE003499) CG9213 gene product [Drosophila melanogaster]	29.7	29	7.7
00142_Ci_ot	1	No Match					P16076	MF25_XENLA MYOGENIC FACTOR 25 pir||C34783 myogenesis protein MyoDb - African clawed frog gb|AAA49902.1| (M31118) MyoD1 homologous protein; putative [Xenopus laevis]	32.1	43	5.7
00145_Ci_ot	1	No Match					No Match				
00146_Ci_ot	1	No Match					No Match				
00147_Ci_ot	1	BAB60730.1	(AB062937) hypothetical protein [Macaca fascicularis]	69.1	56	9.00E-18	No Match				
00149_Ci_ot	1	AAC15517.1	(AF020348) CROL BETA [Drosophila melanogaster]	112	35	4.00E-24	BAB63446.1	(AB047636) gonadotropin inducible ovarian transcription factor 1 [Rattus norvegicus]	76.1	32	3.00E-13
00151_Ci_ot	1	AAF75775.1	(AF265682) rearranged immunoglobulin heavy chain variable region [Mus musculus]	36	35	0.38	T16251	hypothetical protein F35A5.1 - Caenorhabditis elegans gb|AAB52641.1| (U46675) F35A5.1 gene product [Caenorhabditis elegans]	34.4	29	1.1
00152_Ci_ot	1	AAL09706.1	AF420431_1 (AF420431) ribosomal protein L11 [Branchiostoma belcheri]	190	76	9.00E-48	AAL09706.1	AF420431_1 (AF420431) ribosomal protein L11 [Branchiostoma belcheri]	191	75	4.00E-48
00153_Ci_ot	1	O13892	YE38_SCHPO HYPOTHETICAL PROTEIN C20G4.08 IN CHROMOSOME I >gi7522315pirT38122 hypothetical protein SPAC20G4.08 - fission yeast (Schizosaccharomyces pombe) (fragment) >gi2330763embCAB11257.1 (Z98600) hypothetical protein [Schizosaccharomyces pombe]	32.1	50	3.3	No Match				
00154_Ci_ot	1	S71547	peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat	74.9	53	3.00E-13	S71547	peptidylprolyl isomerase (EC 5.2.1.8) B, 20.3K - rat	73.7	60	3.00E-13
00155_Ci_ot	1	XP_018054.2	hypothetical protein XP_018054 [Homo sapiens]	60.5	87	3.00E-09	AAH05678.1	AAH05678 (BC005678) Similar to ribosomal protein S8 [Homo sapiens]	55.8	86	8.00E-08
00156_Ci_ot	1	S23737	proline-rich protein precursor - kidney bean >gi21046embCAA42942.1 (X60391) proline-rich protein [Phaseolus vulgaris]	31.7	34	7.4					
00159_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2	No Match				
00160_Ci_ot	1	NP_041946.1	PSII(CP47) polypeptide [Euglena gracilis] >gi3334477spP14813PSBB_EUGGR PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi418920pirS34551 photosystem II chlorophyll a-binding protein psbB - Euglena gracilis chloroplast >gi415789embCAA50133.1 (X70810) PSII(CP47) polypeptide [Euglena gracilis]	29.3	44	8.8	No Match				
00161_Ci_ot	1	NP_071439.1	PP3111 protein [Homo sapiens] >gi10732650gbAAG22491.1AF202637_1 (AF202637) PP3111 [Homo sapiens]	32.8	30	0.98	No Match				
00163_Ci_ot	1	BAB40166.1	(AP002910) hypothetical protein~similar to Oryza sativa chromosome 1, P0463F06.26	36.4	33	0.18	No Match				
00165_Ci_ot	1	BAB69370.1	(AB070954) non-ribosomal peptide synthetase [Streptomyces avermitilis]	31.3	39	1.9	BAA34233.1	(AB013720) SRK23Bol [Brassica oleracea]	31.3	43	9.7
00166_Ci_ot	2	NP_075861.1	RIKEN cDNA 0610025G13 gene [Mus musculus] >gi9650960dbjBAB03500.1 (AB037665) ribosomal protein L38 [Mus musculus] >gi12832807dbjBAB22266.1 (AK002659) putative [Mus musculus] >gi12845598dbjBAB26814.1 (AK010277) putative [Mus musculus] >gi12846024dbjBAB27000.1 (AK010518) putative [Mus musculus] >gi12849103dbjBAB28208.1 (AK012391) putative [Mus musculus]	37.5	80	5.00E-07	P55027	TYR1_AMBME 5,6-DIHYDROXYINDOLE-2-CARBOXYLIC ACID OXIDASE PRECURSOR (DHICA OXIDASE) (TYROSINASE-RELATED PROTEIN 1) (TRP-1) (TRP1) gb|AAC17168.1| (AF064803) tyrosinase-related-protein-1 [Ambystoma mexicanum]	31.7	28	7.4

00169_Ci_ot	1	No Match					NP_033118.1	ribosomal protein S17 [Mus musculus] sp|P06584|RS17_CRIGR 40S RIBOSOMAL PROTEIN S17 gb|AAA37018.1| (M13933) ribosomal protein S17 [Cricetulus griseus] dbj|BAA04943.1| (D25213) ribosomal protein S17 [Mus musculus] emb|CAB46825.1| (AJ388523) Ribosomal protein [Canis familiaris] gb|AAH02044.1|AAH02044 (BC002044) ribosomal protein S17 [Mus musculus] dbj|BAB25394.1| (AK007992) putative [Mus musculus] dbj|BAB27087.1| (AK010647) putative [Mus musculus]	126	87	1.00E-37
00676_Ci_ot	9	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.1	NP_196884.1	putative protein [Arabidopsis thaliana] dbj|BAB11108.1| (AB005230) gene_id:MAC12.25~pir||S77419~similar to unknown protein [Arabidopsis thaliana] gb|AAL08242.1| (AY056386) AT5g13800/MAC12_25 [Arabidopsis thaliana]	31.7	33	3.7
00412_Ci_ot	12	S31196	hypothetical protein - potato	33.2	57	2.3	No Match				
00174_Ci_ot	1	NP_107000.1	putative N-acetyl-mannosamine transferase [Mesorhizobium loti] >gi14026188dbjBAB52786.1 (AP003009) putative N-acetyl-mannosamine transferase [Mesorhizobium loti]	30.1	50	5.3	No Match				
00175_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.68	NP_039292.1	ORF2136 [Marchantia polymorpha] sp|P09975|YCF2_MARPO HYPOTHETICAL 259 KDA PROTEIN (ORF 2136) pir||A05037 hypothetical protein 2136 - liverwort (Marchantia polymorpha) chloroplast emb|CAA28078.1| (X04465) ORF2136 [Marchantia polymorpha]	29.3	46	8.1
00176_Ci_ot	3	R5HU23	ribosomal protein L23 - human	211	78	7.00E-54	R5HU23	ribosomal protein L23 - human	217	80	1.00E-55
00177_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.66	No Match				
00179_Ci_ot	1	No Match					NP_287478.1	orf, hypothetical protein [Escherichia coli O157:H7 EDL933] ref|NP_309762.1| hypothetical protein [Escherichia coli O157:H7] gb|AAG56090.1|AE005340_7 (AE005340) orf, hypothetical protein [Escherichia coli O157:H7 EDL933] dbj|BAB35158.1| (AP002556) hypothetical protein [Escherichia coli O157:H7]	32.1	38	5.7
00181_Ci_ot	1	BAB27585.1	(AK011387) putative [Mus musculus]	113	51	2.00E-24	BAB55205.1	(AK027569) unnamed protein product [Homo sapiens]	44.1	44	0.001
00182_Ci_ot	1	No Match					No Match				
00184_Ci_ot	1	P49667	RL21_PYUST 60S RIBOSOMAL PROTEIN L21 >gi10061embCAA78893.1 (Z16079) ribosomal protein [Pyura stolonifera] >gi160811gbAAA29803.1 (L03714) ribosomal protein L21 [Pyura stolonifera]	67.9	72	3.00E-18	AAK92159.1	AF400187_1 (AF400187) ribosomal protein L21 [Spodoptera frugiperda]	116	69	1.00E-35
00186_Ci_ot	1	NP_125813.1	DNA POLYMERASE II LARGE SUBUNIT [Pyrococcus abyssi] >gi13431496spQ9V2F4DP2L_PYRAB DNA POLYMERASE II LARGE SUBUNIT (POL II) [CONTAINS: PAB POLC INTEIN] >gi7514786pirE75199 DNA-directed DNA polymerase (EC 2.7.7.7) II large chain PAB2404 - Pyrococcus abyssi (strain Orsay) >gi5457553embCAB49044.1 (AJ248283) DNA POLYMERASE II LARGE SUBUNIT (EC 2.7.7.7) [Pyrococcus abyssi]	34.4	35	1.1	No Match				
00187_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.67	No Match				
00751_Ci_ot	2	NP_218340.1	mmpL8 [Mycobacterium tuberculosis H37Rv] >gi15843447refNP_338484.1 membrane protein, MmpL family [Mycobacterium tuberculosis CDC1551] >gi6225690spO07800MML8_MYCTU PUTATIVE MEMBRANE PROTEIN MMPL8 >gi7478406pirC70522 probable mmpL8 protein - Mycobacterium tuberculosis (strain H37RV) >gi3261809embCAB10022.1 (Z97188) mmpL8 [Mycobacterium tuberculosis H37Rv] >gi13883817gbAAK48298.1 (AE007186) membrane protein, MmpL family [Mycobacterium tuberculosis CDC1551]	36	40	0.22	NP_218340.1	mmpL8 [Mycobacterium tuberculosis H37Rv] ref|NP_338484.1| membrane protein, MmpL family [Mycobacterium tuberculosis CDC1551] sp|O07800|MML8_MYCTU PUTATIVE MEMBRANE PROTEIN MMPL8 pir||C70522 probable mmpL8 protein - Mycobacterium tuberculosis (strain H37RV) emb|CAB10022.1| (Z97188) mmpL8 [Mycobacterium tuberculosis H37Rv] gb|AAK48298.1| (AE007186) membrane protein, MmpL family [Mycobacterium tuberculosis CDC1551]	37.1	40	0.076
00189_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.7					
00191_Ci_ot	1	No Match					BAB23794.1	(AK005070) putative [Mus musculus]	43.4	44	0.002
00192_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.1	S09145	ND5 intron 4 protein - Podospora anserina mitochondrion	30.5	28	8.4
00193_Ci_ot	1	No Match					T31841	hypothetical protein T05B4.3 - Caenorhabditis elegans gb|AAC69054.1| (AF016445) Hypothetical protein T05B4.3 [Caenorhabditis elegans]	29.3	54	7.4
00194_Ci_ot	1	NP_078650.1	orf103 [lymphocystis disease virus 1]	32.8	31	3.3	NP_107691.1	chloromuconate cycloisomerase [Mesorhizobium loti] dbj|BAB53477.1| (AP003011) chloromuconate cycloisomerase [Mesorhizobium loti]	32.8	40	3.3
00195_Ci_ot	1	No Match					S51497	peptidylprolyl isomerase (EC 5.2.1.8) A - cyclosporin fungus prf||2113249A cyclophilin [Tolypocladium inflatum]	64.4	69	3.00E-21
00197_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	3.2	AAB88272.1	(U79732) rps4 [Plasmodium berghei]	31.3	25	8.1
00198_Ci_ot	1	BAB27423.1	(AK011132) putative [Mus musculus] >gi12847063dbjBAB27424.1 (AK011133) putative [Mus musculus]	288	84	4.00E-77	BAB27423.1	(AK011132) putative [Mus musculus] dbj|BAB27424.1| (AK011133) putative [Mus musculus]	281	85	4.00E-75
00199_Ci_ot	1	NP_311650.1	putative anti-terminator regulatory protein [Escherichia coli O157:H7] >gi13363094dbjBAB37046.1 (AP002562) putative anti-terminator regulatory protein [Escherichia coli O157:H7]	30.1	56	4.7					
00201_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2.1					
00203_Ci_ot	1	T31435	DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - Vairimorpha necatrix >gi4001824gbAAD12604.1 (AF060234) largest subunit of RNA polymerase II; RPO21 [Vairimorpha necatrix]	32.5	28	4.3	BAB26911.1	(AK010400) putative [Mus musculus]	32.1	41	5.7

00204_Ci_ot	1	NP_057701.1	hypothetical protein [Homo sapiens] >gi13385932refNP_080711.1 RIKEN cDNA 1810045K17 gene [Mus musculus] >gi13628550refXP_007160.3 hypothetical protein [Homo sapiens] >gi7582276gbAAF64258.1AF208844_1 (AF208844) BM-002 [Homo sapiens] >gi12841557dbjBAB25255.1 (AK007788) putative [Mus musculus] >gi12842366dbjBAB25572.1 (AK008280) putative [Mus musculus] >gi13528783gbAAH05193.1AAH05193 (BC005193) hypothetical protein [Homo sapiens]	151	87	6.00E-36	NP_057701.1	hypothetical protein [Homo sapiens] ref|NP_080711.1| RIKEN cDNA 1810045K17 gene [Mus musculus] ref|XP_007160.3| hypothetical protein [Homo sapiens] gb|AAF64258.1|AF208844_1 (AF208844) BM-002 [Homo sapiens] dbj|BAB25255.1| (AK007788) putative [Mus musculus] dbj|BAB25572.1| (AK008280) putative [Mus musculus] gb|AAH05193.1|AAH05193 (BC005193) hypothetical protein [Homo sapiens]	148	86	6.00E-35
00207_Ci_ot	1	AAG08964.1	AF156177_1 (AF156177) beta-thymosin [Sycon raphanus]	62.5	70	2.00E-09	AAG08964.1	AF156177_1 (AF156177) beta-thymosin [Sycon raphanus]	69.1	77	1.00E-11
00472_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.69					
00209_Ci_ot	1	NP_370937.1	hypothetical protein [Staphylococcus aureus subsp. aureus Mu50] >gi14246181dbjBAB56575.1 (AP003359) hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]	30.1	45	9.6	B71612	hypothetical protein PFB0555c - malaria parasite (Plasmodium falciparum) gb|AAC71900.1| (AE001402) hypothetical protein [Plasmodium falciparum]	30.1	38	7.5
00211_Ci_ot	1	AAK95131.1	(AF401559) ribosomal protein L7 [Ictalurus punctatus]	108	61	2.00E-23	AAK95131.1	(AF401559) ribosomal protein L7 [Ictalurus punctatus]	88.2	58	2.00E-17
00213_Ci_ot	1	P49028	MGN_DROME MAGO NASHI PROTEIN >gi476103gbAAC13746.1 (U03559) mago nashi protein [Drosophila melanogaster] >gi7291246gbAAF46677.1 (AE003453) mago gene product [Drosophila melanogaster]	93.6	70	2.00E-18	NP_060518.1	hypothetical protein FLJ10292 [Homo sapiens] ref|XP_046628.1| hypothetical protein FLJ10292 [Homo sapiens] ref|XP_046627.1| hypothetical protein FLJ10292 [Homo sapiens] dbj|BAA91522.1| (AK001154) unnamed protein product [Homo sapiens] gb|AAF86648.1|AF165518_1 (AF165518) MAGOH isoform [Homo sapiens] dbj|BAB14202.1| (AK022720) unnamed protein product [Homo sapiens] gb|AAH10905.1|AAH10905 (BC010905) Similar to hypothetical protein FLJ10292 [Homo sapiens]	268	85	3.00E-71
00214_Ci_ot	1	Q9USK8	MOK1_SCHPO CELL WALL ALPHA-1,3-GLUCAN SYNTHASE MOK1 >gi11358999pirT43435 alpha-glucan synthase (EC 2.4.1.-) mok1 - fission yeast (Schizosaccharomyces pombe) >gi3808058dbjBAA34054.1 (AB019183) alpha-glucan synthase Mok1 [Schizosaccharomyces pombe]	32.5	37	4.3	NP_068650.1	NADH dehydrogenase subunit 4 [Triatoma dimidiata] gb|AAG31615.1|AF301594_8 (AF301594) NADH dehydrogenase subunit 4 [Triatoma dimidiata]	32.5	30	4.3
00215_Ci_ot	1	P19859	IVBC_NAJNA VENOM CHYMOTRYPSIN INHIBITOR >gi104369pirS12957 venom animal Kunitz-type chymotrypsin inhibitor - Indian cobra >gi227331prf1702215A chymotrypsin inhibitor [Naja naja]	30.5	42	7.3	P19859	IVBC_NAJNA VENOM CHYMOTRYPSIN INHIBITOR pir||S12957 venom animal Kunitz-type chymotrypsin inhibitor - Indian cobra prf||1702215A chymotrypsin inhibitor [Naja naja]	30.5	42	7.3
00217_Ci_ot	2	AAA03341.1	(U02032) ribosomal protein L23a [Homo sapiens]	222	81	2.00E-57	AAA35681.1	(L13799) homology to rat ribosomal protein L23 [Homo sapiens]	223	81	1.00E-57
00218_Ci_ot	1	CAB95306.1	(AL359781) hypothetical protein L3302.03 [Leishmania major]	31.3	35	9.7	NP_113524.1	hypothetical protein [Guillardia theta] emb|CAC27093.1| (AJ010592) hypothetical protein [Guillardia theta]	36.7	23	0.22
00221_Ci_ot	1	BAB25753.1	(AK008574) putative [Mus musculus]	78	40	8.00E-14	CAC42299.1	(Z78420) cDNA EST EMBL:AU111704 comes from this gene~cDNA EST EMBL:AU115543 comes from this gene [Caenorhabditis elegans]	69.9	42	2.00E-11
00224_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.2	AAF53545.1	(AE003652) CG13261 gene product [Drosophila melanogaster]	30.5	28	8.7
00225_Ci_ot	1	NP_006300.1	leucine rich repeat (in FLII) interacting protein 2 [Homo sapiens] >gi11435159refXP_003203.1 leucine rich repeat (in FLII) interacting protein 2 [Homo sapiens] >gi5257201gbAAD41257.1AF115509_1 (AF115509) LRR FLI-I interacting protein 2 [Homo sapiens]	64.4	75	1.00E-09	NP_060194.1	leucine rich repeat (in FLII) interacting protein 2 [Homo sapiens] ref|XP_003204.1| leucine rich repeat (in FLII) interacting protein 2 [Homo sapiens] dbj|BAA91035.1| (AK000255) unnamed protein product [Homo sapiens]	66.7	77	2.00E-10
00226_Ci_ot	1	No Match					No Match				
00229_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.8	No Match				
00231_Ci_ot	1	NP_281785.1	hypothetical protein Cj0602c [Campylobacter jejuni] >gi11346663pirA81408 hypothetical protein Cj0602c [imported] - Campylobacter jejuni (strain NCTC 11168) >gi6968069embCAB75238.1 (AL139075) hypothetical protein Cj0602c [Campylobacter jejuni]	30.1	42	7.7	CAC22701.1	(AL389894) hypothetical protein L2969.06 [Leishmania major]	30.1	32	7.9
00232_Ci_ot	1	No Match									
00233_Ci_ot	1	No Match									
00235_Ci_ot	2	A38096	perlecan precursor - human >gi184427gbAAA52700.1 (M85289) heparan sulfate proteoglycan [Homo sapiens]	37.5	31	0.13	NP_036045.1	Wnt inhibitory factor 1 [Mus musculus] sp|Q9WUA1|WIF1_MOUSE WNT INHIBITORY FACTOR 1 PRECURSOR (WIF-1) gb|AAD25403.1|AF122923_1 (AF122923) Wnt inhibitory factor-1 [Mus musculus] gb|AAH13268.1|AAH13268 (BC013268) Similar to Wnt inhibitory factor 1 [Mus musculus]	38.3	30	0.075
00236_Ci_ot	3	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	41.4	73	0.009	NP_071278.1	Formate hydrogenlyase subunit 6/NADH:ubiquinone oxidoreductase 23 kD subunit (chain I) [Archaeoglobus fulgidus]	32.1	30	5.7
00237_Ci_ot	2	Q10453	H33_CAEEL HISTONE H3.3 >gi7439813pirT16361 hypothetical protein F45E1.6 - Caenorhabditis elegans >gi860702gbAAB04902.1 (U28732) Hypothetical protein F45E1.6 [Caenorhabditis elegans]	152	95	4.00E-36	NP_002098.1	H3 histone, family 3A [Homo sapiens] ref|NP_005315.1| H3 histone, family 3B (H3.3B) [Homo sapiens] ref|NP_032236.1| H3 histone, family 3A [Mus musculus] ref|NP_032237.1| H3 histone, family 3B [Mus musculus] ref|XP_017864.1| H3 histone, family 3A [Homo sapiens] ref|XP_018430.1| hypothetical protein XP_018430 [Homo sapiens] ref|XP_037280.1| hypothetical protein XP_037280 [Homo sapiens] ref|XP_036113.1| H3 histone, family 3B (H3.3B) [Homo sapiens] ref|XP_036111.1| hypothetical protein XP_036111 [Homo sapiens] sp|P06351|H33_HUMAN HISTONE H3.3 (H3.A) (H3.B) (H3.3Q) pir||S10168 histone H3.3A - rabbit pir||S04186 histone H3.3 - mouse pir||S34185 histone H3 - rat pir||A45941 histone H3 - Atlantic surf clam pir||HSHU33 histone H3.3 - human pir||S61220 histone H3.3 - fruit fly (Drosophila melanogaster) pir||S61215 histone H3.3 - fruit fly (Drosophila melanogaster) pir||S20109 histone H3.3Q - fruit fly (Drosophila melanogaster) pir||I50245 histone H3.3B - chicken pir||S61218 histone H3.3 - fruit fly (Drosophila hydei) pir||S61214 histone H3.3 - fruit fly (Drosophila hydei) emb|CAA36179.1|	265	99	4.00E-70

00238_Ci_ot	4	AAF64457.1	(AF240374) ribosomal protein L18 [Oreochromis niloticus] >gi7595806gbAAF64458.1AF240375_1 (AF240375) ribosomal protein L18 [Oreochromis niloticus] >gi7595809gbAAF64459.1AF240376_1 (AF240376) ribosomal protein L18 [Oreochromis mossambicus]	224	72	9.00E-58	AAF64457.1	(AF240374) ribosomal protein L18 [Oreochromis niloticus] gb|AAF64458.1|AF240375_1 (AF240375) ribosomal protein L18 [Oreochromis niloticus] gb|AAF64459.1|AF240376_1 (AF240376) ribosomal protein L18 [Oreochromis mossambicus]	243	72	2.00E-63
00239_Ci_ot	1	AAF99890.1	(U88314) Hypothetical protein C46H11.11 [Caenorhabditis elegans]	32.8	41	1.8	A38560	nitrate transport protein crnA - Emericella nidulans	32.5	43	2.4
00242_Ci_ot	1	No Match									
00243_Ci_ot	1	No Match					No Match				
00251_Ci_ot	1	CAB56294.1	(AJ249397) putative protein translation factor [Phleum pratense]	42.6	60	0.003	P51971	SUI1_CHICK PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG	33.6	51	1
00252_Ci_ot	1	AAD31170.1	(AF116572) ribonuclease [Drosophila melanogaster] >gi7304132gbAAF59169.1 (AE003839) drosha gene product [Drosophila melanogaster]	31.7	34	7.4	No Match				
00309_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.1	NP_105292.1	hypothetical protein, contains weak similarity to NADH dehydrogenase I [Mesorhizobium loti] dbj|BAB51078.1| (AP003004) hypothetical protein [Mesorhizobium loti]	29.3	33	7.1
00254_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.9					
00255_Ci_ot	1	NP_002571.1	pancreatitis-associated protein [Homo sapiens] >gi14725496refXP_046239.1 pancreatitis-associated protein [Homo sapiens] >gi16160135refXP_056778.1 hypothetical protein XP_056778 [Homo sapiens] >gi16160139refXP_056779.1 hypothetical protein XP_056779 [Homo sapiens] >gi464341spQ06141PAP1_HUMAN PANCREATITIS-ASSOCIATED PROTEIN 1 PRECURSOR >gi1082679pirA49616 pancreatitis-associated protein precursor - human >gi262369gbAAB24642.1 (S51768) PAP-H [Homo sapiens] >gi285971dbjBAA02728.1 (D13510) PAP homologous protein [Homo sapiens] >gi312807embCAA48605.1 (X68641) preprotein [Homo sapiens] >gi482909gbAAA60020.1 (L15533) pancreatitis-associated protein [Homo sapiens] >gi444785prf1908220A pancreatitis-associated protein [Homo sapiens]	34	40	0.93	CAC22679.1	(AL389894) AMP deaminase [Leishmania major]	33.6	35	1.1
00257_Ci_ot	1	NP_111587.1	Predicted membrane protein [Thermoplasma volcanium] >gi14325332dbjBAB60236.1 (AP000995) unknown product [Thermoplasma volcanium]	35.2	28	0.65	No Match				
00259_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.66	XP_047191.1	similar to ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY (H. sapiens) [Homo sapiens]	31.3	45	2.1
00261_Ci_ot	1	NP_326556.1	MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) [Mycoplasma pulmonis] >gi14090140embCAC13898.1 (AL445565) MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) [Mycoplasma pulmonis]	31.3	36	9.7	BAB60909.1	(AP003213) contains ESTs AU101313(E10180),AU161063(C53367),C19264(E10180), AU063176(C53367),C19811(E10967)~unknown protein [Oryza sativa]	69.9	30	2.00E-11
00262_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	37.1	41	0.087					
00264_Ci_ot	2	NP_034899.1	matrilin 1, cartilage matrix protein 1 [Mus musculus] >gi1705570spP51942CAMA_MOUSE CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1) >gi2137188pirS66522 cartilage matrix protein precursor - mouse >gi1163179gbAAB06521.1 (U35035) cartilage matrix protein precursor [Mus musculus]	52.3	44	5.00E-06	NP_356583.1	AGR_L_1590p [Agrobacterium tumefaciens] gb|AAK89368.1| (AE008278) AGR_L_1590p [Agrobacterium tumefaciens]	33.2	27	2.5
00265_Ci_ot	1	P54295	YENR_YEREN TRANSCRIPTIONAL ACTIVATOR PROTEIN YENR >gi7467315pirS70176 yenR protein - Yersinia enterocolitica >gi773400embCAA53694.1 (X76082) yenR [Yersinia enterocolitica]	31.3	50	5.8	BAA20779.1	(AB002319) KIAA0321 [Homo sapiens]	30.1	30	7.3
00266_Ci_ot	1	NP_176679.1	hypothetical protein [Arabidopsis thaliana]	31.3	28	9.7	NP_002725.1	protein kinase, cAMP-dependent, regulatory, type I, alpha; tissue-specific extinguisher 1 [Homo sapiens] ref|XP_008409.3| protein kinase, cAMP-dependent, regulatory, type I, alpha [Homo sapiens] ref|XP_045784.2| hypothetical protein XP_045784 [Homo sapiens] sp|P10644|KAP0_HUMAN CAMP-DEPENDENT PROTEIN KINASE TYPE I-ALPHA REGULATORY CHAIN (TISSUE-SPECIFIC EXTINGUISHER-1) (TSE1) pir||OKHU1R protein kinase (EC 2.7.1.37), cAMP-dependent, type I-alpha regulatory chain - human gb|AAB50921.1| (M33336) cAMP-dependent protein kinase type I-alpha subunit [Homo sapiens] gb|AAB50922.1| (M18468) cAMP-dependent protein kinase regulatory subunit type 1 [Homo sapiens]	32.5	33	4.3
00267_Ci_ot	1	T28709	hypothetical protein T21D12.3 - Caenorhabditis elegans >gi2315829gbAAC48091.1 (AF016687) Hypothetical protein T21D12.3 [Caenorhabditis elegans]	33.2	50	2.5	S12206	hypothetical protein 2 (rRNA external transcribed spacer) - mouse	46.1	57	3.00E-04
00268_Ci_ot	1	No Match					No Match				
00269_Ci_ot	1	AAB16848.1	(U70731) putative poly(A)-binding protein FabM [Emericella nidulans]	30.5	37	4.1	No Match				
00270_Ci_ot	2	AAD42259.1	AF109920_1 (AF109920) alpha-amidating enzyme precursor 2 [Lymnaea stagnalis]	30.5	41	3.4					
00271_Ci_ot	1	XP_038228.1	hypothetical protein XP_038228 [Homo sapiens]	36	36	0.075	XP_054158.1	hypothetical protein XP_054158 [Homo sapiens] gb|AAH11928.1|AAH11928 (BC011928) hypothetical protein FLJ12517 [Homo sapiens]	34.4	35	0.24
00272_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.64					

00754_Ci_ot	1	NP_197057.1	| biotin carboxyl carrier protein precursor-like protein [Arabidopsis thaliana] >gi|11357199|pir||T51531 biotin carboxyl carrier protein homolog T20K14.140 [imported] - Arabidopsis thaliana >gi|9755808|emb|CAC01752.1| (AL391143) biotin carboxyl carrier protein precursor-like protein [Arabidopsis thaliana]	33.6	33	1.7	No Match				
00757_Ci_ot	1	AAF14302.1	AF190581_3 (AF190581) HSP70h [Beet yellows virus]	29.7	32	7.7	No Match				
00760_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.75	NP_174432.1	hypothetical protein [Arabidopsis thaliana] gb|AAG51261.1|AC027135_2 (AC027135) hypothetical protein [Arabidopsis thaliana]	29	27	9.7
00763_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.71					
00764_Ci_ot	1	Q24572	CAF1_DROME CHROMATIN ASSEMBLY FACTOR 1 P55 SUBUNIT (CAF-1 P55 SUBUNIT) (DCAF-1) (NUCLEOSOME REMODELING FACTOR 55 KDA SUBUNIT) (NURF-55) >gi|1407828|gb|AAB37257.1| (U62388) chromatin assembly factor 1 p55 subunit [Drosophila melanogaster] >gi|7299974|gb|AAF55146.1| (AE003708) Caf1 gene product [Drosophila melanogaster]	103	74	2.00E-21	AAF87775.1	AF279275_1 (AF279275) Rbap46 polypeptide [Gallus gallus]	329	92	2.00E-89
00766_Ci_ot	1	No Match					No Match				
00768_Ci_ot	1	AAF49111.1	(AE003515) CG15881 gene product [Drosophila melanogaster]	75.7	35	4.00E-13	AAF49111.1	(AE003515) CG15881 gene product [Drosophila melanogaster]	96	39	3.00E-19
00769_Ci_ot	1	S68207	G protein-coupled receptor 6C.1 - human >gi|1015421|gb|AAA79061.1| (U35399) G protein-coupled receptor [Homo sapiens] >gi|1585167|prf||2124311B G protein-coupled receptor [Homo sapiens]	33.2	37	1.5	CAB57948.1	(AJ237599) iroquois homologue 2 [Gallus gallus]	32.1	34	1.9
00019_Ci_ot	1	No Match									
00020_Ci_ot	1	No Match					AAA64228.1	(L32024) hemagglutinin [Influenza A virus]	34.4	32	0.75
00026_Ci_ot	1	XP_029533.1	| hypothetical protein XP_029533 [Homo sapiens]	30.1	50	4.4					
00027_Ci_ot	1	CAC01992.2	(AL390114) probable hypothetical 42.7 Kd protein [Leishmania major]	33.2	40	2.5	NP_196392.1	putative protein [Arabidopsis thaliana] dbj|BAB11454.1| (AB010070) gb|AAD23008.1~gene_id:MBK20.21~similar to unknown protein [Arabidopsis thaliana]	42.2	51	0.002
00028_Ci_ot	1	No Match					No Match				
00029_Ci_ot	1	No Match					No Match				
00030_Ci_ot	1	No Match					NP_113329.1	hypothetical protein [Guillardia theta] gb|AAK39886.1|AF165818_94 (AF165818) hypothetical protein [Guillardia theta]	32.1	38	5.7
00034_Ci_ot	1	No Match					No Match				
00035_Ci_ot	1	No Match					NP_312998.1	hypothetical protein [Escherichia coli O157:H7] dbj|BAB38394.1| (AP002567) hypothetical protein [Escherichia coli O157:H7]	31.7	57	3.1
00039_Ci_ot	1	AAF56353.1	(AE003749) CG7016 gene product [Drosophila melanogaster]	33.2	47	2.5	XP_005866.1	multiple inositol polyphosphate phosphatase 2 [Homo sapiens] gb|AAD09751.1| (AF084943) multiple inositol polyphosphate phosphatase [Homo sapiens]	115	42	3.00E-25
00040_Ci_ot	1	AAF76184.1	(AF269231) 5-HT1A [Oryctolagus cuniculus]	31.7	31	2	No Match				
00043_Ci_ot	1	No Match					AAF57630.1	(AE003798) CG15097 gene product [Drosophila melanogaster]	31.7	39	4.5
00045_Ci_ot	1	JG0183	myosin Myok - Dictyostellium	36.4	37	0.12	NP_006750.2	UDP-glucose pyrophosphorylase 2; UTP-glucose-1-phosphate uridyltransferase; UDP-glucose diphosphorylase; UGPase 2 [Homo sapiens] sp|Q16851|UDP2_HUMAN UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE 2 (UDP-GLUCOSE PYROPHOSPHORYLASE 2) (UDPGP 2) (UGPASE 2) pir||S62599 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9), skeletal muscle [validated] - human	58.2	39	8.00E-08
00046_Ci_ot	1	AAA36502.1	(K02576) salivary proline-rich protein 1 [Homo sapiens]	33.6	40	0.61					
00048_Ci_ot	1	BAA23266.1	(AB000735) hypothetical protein [Nocardioides sp.]	32.1	36	1.1	AAB68434.1	(U10555) Qcr10p: 8.5 kDa subunit of the quinol cytochrome oxidoreductase complex [Saccharomyces cerevisiae]	32.8	26	1.6
00052_Ci_ot	1	XP_029379.1	| similar to ribosomal protein L7 (H. sapiens) [Homo sapiens]	30.5	35	4.5	No Match				
00061_Ci_ot	1	CAC43328.1	(AJ291743) putative beta7 proteasome subunit [Nicotiana tabacum]	29	52	9.9	AAC67388.1	(AF062594) nucleosome assembly protein [Rattus norvegicus]	35.6	53	0.48
00064_Ci_ot	1	No Match					No Match				
00128_Ci_ot	1	NP_108388.1	| hypothetical protein [Mesorhizobium loti] >gi|14027580|dbj|BAB53849.1| (AP003013) hypothetical protein [Mesorhizobium loti]	33.2	32	2.2					
00129_Ci_ot	1	S16292	nitrate reductase (NADPH) (EC 1.6.6.3) - Neurospora crassa	33.2	29	2.5					
00131_Ci_ot	1	P39191	ALU4_HUMAN ALU SUBFAMILY SB2 SEQUENCE CONTAMINATION WARNING ENTRY	32.1	62	2.00E-04	NP_171928.1	unknown protein [Arabidopsis thaliana] gb|AAB70444.1| (AC000104) EST gb|H76414 comes from this gene. [Arabidopsis thaliana]	32.1	34	5.7
00144_Ci_ot	1	No Match					No Match				
00148_Ci_ot	1	No Match					AAL09706.1	AF420431_1 (AF420431) ribosomal protein L11 [Branchiostoma belcheri]	76.1	52	3.00E-13
00150_Ci_ot	1	T50210	probable ABC transporter [imported] - fission yeast (Schizosaccharomyces pombe) >gi|6723887|emb|CAB66463.1| (AL136538) putative ABC transporter [Schizosaccharomyces pombe]	33.6	48	1.4	No Match				
00162_Ci_ot	1	BAB27210.1	(AK010829) putative [Mus musculus] >gi|12855484|dbj|BAB30352.1| (AK016638) putative [Mus musculus]	34	25	1	Q59173	CDSA_BRUAB PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) (CDP-DG SYNTHETASE) gb|AAA96785.1| (U51683) CdsA [Brucella melitensis biovar Abortus]	30.1	51	4.7
00168_Ci_ot	1	AAC05838.1	(AF052516) hemolysin erythrocyte lysis protein 2 [Prevotella intermedia]	29.3	48	9.1					

00725_Ci_ot	1	CAA43964.1	(X61972) macropain subunit iota [Homo sapiens]	158	63	6.00E-38	NP_058979.1	proteasome (prosome, macropain) subunit, alpha type 6 [Rattus norvegicus] ref|XP_046642.1| proteasome (prosome, macropain) subunit, alpha type, 6 [Homo sapiens] sp|P34062|PSA6_HUMAN PROTEASOME SUBUNIT ALPHA TYPE 6 (PROTEASOME IOTA CHAIN) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KDA PROSOMAL PROTEIN) (PROS-27) (P27K) pir||JX0230 multicatalytic endopeptidase complex (EC 3.4.99.46) iota chain - rat pir||S30274 multicatalytic endopeptidase complex (EC 3.4.99.46) iota chain - human emb|CAA42052.1| (X59417) prosomal P27K protein [Homo sapiens] dbj|BAA01587.1| (D10755) proteasome subunit R-IOTA [Rattus sp.] gb|AAH02979.1|AAH02979 (BC002979) proteasome (prosome, *macropain) subunit, alpha type 6 [Homo sapiens] prf||1912298A prosomal* RNA-binding protein p27K [Homo sapiens]	240	82	1.00E-62
00727_Ci_ot	1	NP_077276.1	| hypothetical protein MGC2217 [Homo sapiens] >gi|12803445|gb|AAH02546.1|AAH02546 (BC002546) Unknown (protein for MGC:2217) [Homo sapiens]	72.6	37	3.00E-12	NP_077276.1	hypothetical protein MGC2217 [Homo sapiens] gb|AAH02546.1|AAH02546 (BC002546) Unknown (protein for MGC:2217) [Homo sapiens]	66.7	34	1.00E-10
00729_Ci_ot	1	AAK95196.1	AF402822_1 (AF402822) 40S ribosomal protein S14 [Ictalurus punctatus]	48.8	96	1.00E-05	P48855	RS14_PROCL 40S RIBOSOMAL PROTEIN S14 dbj|BAA03461.1| (D14609) ribosomal protein [Procambarus clarkii]	57.8	90	2.00E-08
00731_Ci_ot	1	AAF55685.1	(AE003727) CG16718 gene product [Drosophila melanogaster]	33.6	41	1.9	NP_033774.1	aryl-hydrocarbon receptor repressor [Mus musculus] dbj|BAA37132.1| (AB015140) AhR repressor [Mus musculus]	34.4	33	1.1
00732_Ci_ot	1	T15264	hypothetical protein F59E12.9 - Caenorhabditis elegans >gi|2088843|gb|AAB54259.1| (AF003386) Hypothetical protein F59E12.9 [Caenorhabditis elegans]	36	45	0.18	No Match				
00735_Ci_ot	1	NP_010918.1	| catalyzes the interconversion of fructose-6-P and mannose-6-P; Pmi40p [Saccharomyces cerevisiae] >gi|729984|sp|P29952|MANA_YEAST MANNOSE-6-PHOSPHATE ISOMERASE (PHOSPHOMANNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) >gi|1078096|pir||S50461 mannose-6-phosphate isomerase (EC 5.3.1.8) - yeast (Saccharomyces cerevisiae) >gi|603595|gb|AAB64536.1| (U18778) Pmi40p: mannose-6-phosphate isomerase [Saccharomyces cerevisiae]	112	46	3.00E-24	T40155	mannose-6-phosphate isomerase - fission yeast (Schizosaccharomyces pombe) emb|CAA17896.1| (AL022103) mannose-6-phosphate isomerase [Schizosaccharomyces pombe]	109	42	2.00E-23
00736_Ci_ot	1	CAA07642.1	(AJ007747) hypothetical protein BbLPS1.03 [Bordetella bronchiseptica]	29.3	75	7.6	No Match				
00740_Ci_ot	1	NP_112645.1	| mitochondrial voltage dependent anion channel 3 [Rattus norvegicus] >gi|15214186|sp|Q9R1Z0|POR3_RAT VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3 (VDAC-3) (RVDAC3) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN 3) >gi|10119782|dbj|BAB13475.1| (AB039664) mitochondrial voltage dependent anion channel [Rattus norvegicus]	41.4	54	2.00E-08	AAF65254.1	AF221690_1 (AF221690) voltage-dependent anion channel [Squalus acanthias]	170	62	1.00E-41
00741_Ci_ot	1	AAF65254.1	AF221690_1 (AF221690) voltage-dependent anion channel [Squalus acanthias]	125	57	5.00E-28	AAF65254.1	AF221690_1 (AF221690) voltage-dependent anion channel [Squalus acanthias]	158	65	1.00E-43
00743_Ci_ot	1	AAG02250.1	(AY005807) ferritin heavy chain-like protein [Dermatophagoides pteronyssinus]	96.7	54	2.00E-19	P08267	FRIH_CHICK FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT) *pir||A26886 ferritin heavy chain - chicken gb|AAA48768.1|* (M16343) ferritin H subunit [Gallus gallus] emb|CAA75004.1| (Y14698) ferritin H chain [Gallus gallus]	112	55	4.00E-24
00745_Ci_ot	1	No Match					NP_060759.1	hypothetical protein FLJ10979 [Homo sapiens] ref|XP_008540.5| hypothetical protein FLJ10979 [Homo sapiens] dbj|BAA91935.1| (AK001841) unnamed protein product [Homo sapiens]	145	51	4.00E-34
00747_Ci_ot	1	NP_006799.1	| protein translocation complex beta; protein transport protein SEC61 beta subunit [Homo sapiens] >gi|15297966|ref|XP_052762.1| protein translocation complex beta [Homo sapiens] >gi|585961|sp|P38391|S61B_HUMAN PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT >gi|631370|pir||S42410 protein translocation complex Sec61 beta chain, endoplasmic reticulum - human >gi|631516|pir||S42409 protein translocation complex Sec61 beta chain, *endoplasmic reticulum - dog* >gi|459746|gb|AAA19639.1| (L25052) protein translocation complex beta subunit [Canis familiaris] >gi|459834|gb|AAA19706.1| (L25085) Sec61-complex beta-subunit [Homo sapiens] >gi|12314173|emb|CAC08000.1| (AL137067) bA13B9.2 (*novel* protein similar to the beta subunit of transport protein SEC61) [Homo sapiens] >gi|12804623|gb|AAH01734.1|AAH01734 (BC001734) protein translocation complex beta [Homo sapiens] >gi|740571|prf||2005371A Sec61 protein:SUBUNIT=beta [Canis familiaris]	59.7	52	3.00E-08	CAB56698.1	(AJ249754) sec61beta protein [Drosophila melanogaster] gb|AAF58229.1| (AE003814) Sec61beta gene product [Drosophila melanogaster]	68.7	48	5.00E-11
00749_Ci_ot	1	AAH10458.1	AAH10458 (BC010458) N-myc downstream-regulated gene 2 [Homo sapiens]	36	47	0.38	Q9ULP0	BDM1_HUMAN BRAIN DEVELOPMENT-RELATED MOLECULE 1 dbj|BAA86494.1| (AB033006) KIAA1180 protein [Homo sapiens]	49.2	48	4.00E-05
00750_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	33.6	41	0.9	No Match				
00753_Ci_ot	1	AAB94760.1	(AF039202) Hsp70/Hsp90 organizing protein; hop [Cricetulus griseus]	108	51	4.00E-23	XP_011988.4	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo sapiens]	144	53	1.00E-33

00667_Ci_ot	1	No Match					T07933	polyadenylate-binding protein RB47 precursor, chloroplast - Chlamydomonas reinhardtii gb|AAC39368.1| (AF043297) poly(A) binding protein RB47 [Chlamydomonas reinhardtii]	31.7	33	7.4
00668_Ci_ot	1	No Match									
00669_Ci_ot	1	T28770	hypothetical protein W03D2.1 - Caenorhabditis elegans	36	39	0.13	No Match				
00670_Ci_ot	2	No Match					AAC40774.1	(AF037218) unknown [Human herpesvirus 7]	32.1	28	5.7
00671_Ci_ot	1	AAF78063.1	AF266749_1 (AF266749) ribsomal protein S29 [Culex pipiens quinquefasciatus]	101	75	7.00E-21	AAF78063.1	AF266749_1 (AF266749) ribsomal protein S29 [Culex pipiens quinquefasciatus]	101	75	5.00E-21
00672_Ci_ot	1	T19252	hypothetical protein C14A4.10 - Caenorhabditis elegans >gi|3874237|emb|CAA90114.1| (Z49909) similar to FUN81 protein [Caenorhabditis elegans]	31.7	51	0.083	NP_005636.1	TATA box binding protein (TBP)-associated factor, RNA polymerase II, K, 18kD [Homo sapiens] ref|XP_042780.1| TATA box binding protein (TBP)-associated factor, RNA polymerase II, K, 18kD [Homo sapiens] sp|Q15543|T2DB_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 18 KDA SUBUNIT (TAFII-18) (TAFII18) pir||S54782 PolII transcription factor TFIID chain hTAFII18 - human emb|CAA58827.1| (X84003) PolII transcription factor TFIID [Homo sapiens] dbj|BAB24972.1| (AK007339) putative [Mus musculus]	59.3	40	1.00E-15
00673_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.72					
00675_Ci_ot	1	AAK95156.1	AF401584_1 (AF401584) ribosomal protein L29 [Ictalurus punctatus]	98.7	80	3.00E-20	AAK95156.1	AF401584_1 (AF401584) ribosomal protein L29 [Ictalurus punctatus]	98.7	80	2.00E-20
00678_Ci_ot	1	Q33568	CYB_TRYBO CYTOCHROME B >gi|1085645|pir||S52054 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Trypanoplasma borreli mitochondrion >gi|563142|gb|AAA73455.1| (U11684) apocytochrome b [Trypanoplasma borreli] >gi|576733|gb|AAA65017.1| (U14182) apocytochrome b [Trypanoplasma borreli]	32.1	34	5.7	NP_206966.1	hypothetical protein [Helicobacter pylori 26695] pir||G64540 hypothetical protein HP0167 - Helicobacter pylori (strain 26695) gb|AAD07240.1| (AE000537) H. pylori predicted coding region HP0167 [Helicobacter pylori 26695]	32.5	22	4.3
00681_Ci_ot	1	No Match					T34946	probable isoleucyl-tRNA synthetase - Streptomyces coelicolor emb|CAB51985.1| (AL109663) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]	31.7	50	5.2
00686_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.66	AAG43184.1	AF107545_1 (AF107545) disease resistance-like protein [Brassica napus]	29.7	45	6
00687_Ci_ot	1	AAF54990.1	(AE003701) CG9286 gene product [Drosophila melanogaster]	35.2	65	8.00E-05	NP_054766.1	HSPC023 protein [Homo sapiens] ref|XP_008979.1| HSPC023 protein [Homo sapiens] gb|AAD44484.1| (AF078852) HSPC023 [Homo sapiens] gb|AAH15465.1|AAH15465 (BC015465) Similar to HSPC023 protein [Homo sapiens]	42.2	44	0.005
00689_Ci_ot	1	AAH13550.1	AAH13550 (BC013550) Similar to PCAF associated factor 65 beta [Mus musculus]	119	44	2.00E-26	NP_055224.1	PCAF associated factor 65 beta [Homo sapiens] gb|AAC39906.1| (AF069736) PCAF associated factor 65 beta [Homo sapiens]	50.4	29	2.00E-05
00690_Ci_ot	1	No Match									
00697_Ci_ot	1	No Match					No Match				
00700_Ci_ot	1	BAB32661.1	(AB055884) 60S ribosomal protein L35 [Sus scrofa]	83.1	49	2.00E-15	BAB32661.1	(AB055884) 60S ribosomal protein L35 [Sus scrofa]	158	68	5.00E-38
00701_Ci_ot	1	No Match									
00706_Ci_ot	1	NP_102659.1	| unknown protein [Mesorhizobium loti] >gi|14021834|dbj|BAB48445.1| (AP002996) unknown protein [Mesorhizobium loti]	33.6	38	1.4	NP_102659.1	unknown protein [Mesorhizobium loti] dbj|BAB48445.1| (AP002996) unknown protein [Mesorhizobium loti]	33.6	38	1.1
00707_Ci_ot	1	T14375	S-receptor kinase (EC 2.7.1.-) 1 - turnip >gi|2662048|dbj|BAA23676.1| (AB000970) receptor kinase 1 [Brassica rapa]	31.7	50	7.4	No Match				
00708_Ci_ot	1	AAG49547.1	AF261103_3 (AF261103) translation initiation factor IF2 [Myxococcus xanthus]	34.4	28	1.1	AAK98657.1	AC090873_13 (AC090873) Hypothetical protein [Oryza sativa]	35.2	36	0.65
00709_Ci_ot	1	BAB27483.1	(AK011234) putative [Mus musculus]	150	52	1.00E-35	BAB27483.1	(AK011234) putative [Mus musculus]	153	53	2.00E-36
00711_Ci_ot	2	AAF54020.1	(AE003671) CG10101 gene product [Drosophila melanogaster]	32.5	28	4.3	CAA73168.1	(Y12591) translation initiation factor eIF4A II [Xenopus laevis]	156	74	4.00E-42
00713_Ci_ot	1	NP_056299.1	| GCIP-interacting protein p29; DKFZP564O2082 protein; GCIP-interacting protein p29 [Homo sapiens] >gi|14727624|ref|XP_044761.1| GCIP-interacting protein p29 [Homo sapiens] >gi|7512787|pir||T12485 hypothetical protein DKFZp564O2082.1 - human >gi|4468310|emb|CAB37991.1| (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens] >gi|5262632|emb|CAB45754.1| (AL080166) hypothetical protein [Homo sapiens] >gi|11967379|gb|AAG42073.1|AF273089_1 (AF273089) P29 [Homo sapiens] >gi|14790043|gb|AAH10862.1|AAH10862 (BC010862) Similar to GCIP-interacting protein p29 [Homo sapiens]	65.2	68	6.00E-10	AAK53393.1	AF366369_1 (AF366369) GCIP-interacting protein p29 [Rattus norvegicus]	136	43	3.00E-31
00715_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2.1					
00716_Ci_ot	1	O46503	S1C1_RABIT SULFOTRANSFERASE 1C1 (RABSULT1C2) >gi|2828826|gb|AAC00410.1| (AF026304) sulfotransferase [Oryctolagus cuniculus]	51.5	34	1.00E-07					
00717_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.63	No Match				
00722_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.1	No Match				

00635_Ci_ot	1	S04573	Ig kappa chain precursor V region (MRL-histone 7L) - mouse (fragment) >gi|52032|emb|CAA32773.1| (X14620) MRL-histone 7 L IgG3(kappa) precursor [Mus musculus]	33.2	68	2.5	AAD34535.1	(AF136490) gag protein [Murine leukemia virus]	32.1	32	5.7
00636_Ci_ot	1	AAA45797.1	(M17921) latency associated transcript (LAT) ORF-2 [human herpesvirus 1]	36.7	36	0.22	No Match				
00703_Ci_ot	2	XP_038444.1	| hypothetical protein XP_038444 [Homo sapiens]	43.4	90	7.00E-04	NP_033610.1	zuotin related factor 2 [Mus musculus] pir||A57591 Id-associated protein 1 - mouse dbj|BAA09854.1| (D63784) MIDA1 [Mus musculus]	43.4	90	4.00E-04
00638_Ci_ot	1	AAB26882.1	TIE-2=receptor-like tyrosine kinase [rats, brain, Peptide, 1083 aa]	33.6	27	1.9	NP_199468.1	unknown protein [Arabidopsis thaliana] dbj|BAA97527.1| (AB028605) gene_id:F10E10.3~unknown protein [Arabidopsis thaliana]	32.5	40	4.3
00639_Ci_ot	1	S72690	probable membrane protein Q0270 - yeast (Saccharomyces cerevisiae) mitochondrion	40.2	35	0.019	NP_172682.1	hypothetical protein [Arabidopsis thaliana]	32.1	31	5.7
00640_Ci_ot	1	No Match					CAB97423.1	(AL389898) putative serine/threonine protein kinase [Streptomyces coelicolor A3(2)]	33.2	43	2.5
00642_Ci_ot	2	CAB86166.1	(AJ286331) gp160 [Human immunodeficiency virus type 1]	30.9	31	7.4	AAF52728.2	(AE003623) CG17789 gene product [Drosophila melanogaster]	32.8	29	0.66
00643_Ci_ot	1	NP_113191.1	| 40S ribosomal protein S14 [Guillardia theta] >gi|13794381|gb|AAK39758.1|AF083031_115 (AF083031) 40S ribosomal protein S14 [Guillardia theta]	30.1	50	7.3	No Match				
00645_Ci_ot	1	BAB26841.1	(AK010308) putative [Mus musculus]	148	61	5.00E-35	BAB27516.1	(AK011284) putative [Mus musculus] gb|AAK57536.1| (AY034383) dynein light chain-2 [Rattus norvegicus] gb|AAH10744.1|AAH10744 (BC010744) Similar to RIKEN cDNA 6720463E02 gene [Homo sapiens] gb|AAH11289.1|AAH11289 (BC011289) RIKEN cDNA 6720463E02 gene [Mus musculus] gb|AAK38749.1| (AY029255) dynein light chain 2 [Mus musculus]	120	92	1.00E-40
00646_Ci_ot	1	No Match					AAF99431.1	(AY005800) cytochrome c [Rhodovulum sulfidophilum]	31.7	22	7.4
00647_Ci_ot	1	No Match					A53221	acidic ribosomal protein P1 - hydromedusa (Polyorchis penicillatus) prf||1709160A acidic ribosomal protein A1 [Polyorchis penicillatus]	78.8	55	5.00E-14
00648_Ci_ot	1	XP_010183.3	| protein phosphatase, EF hand calcium-binding domain 1 [Homo sapiens] >gi|14758607|ref|XP_040201.1| hypothetical protein XP_040201 [Homo sapiens] >gi|14758614|ref|XP_040202.1| hypothetical protein XP_040202 [Homo sapiens] >gi|12643541|sp|O14829|PPE1_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE WITH EF-HANDS-1 (PPEF-1) (PROTEIN PHOSPHATASE WITH EF CALCIUM-BINDING DOMAIN) (PPEF) (SERINE/THREONINE PROTEIN PHOSPHATASE 7) (PP7) >gi|2586411|gb|AAB82795.1| (AF023455) protein phosphatase with EF-hands-1 [Homo sapiens] >gi|2967685|gb|AAC05825.1| (AF027977) serine/threonine protein phosphatase 7 catalytic subunit [Homo sapiens]	30.9	24	6.6	No Match				
00649_Ci_ot	1	NP_422183.1	| oxidoreductase, FAD-binding [Caulobacter crescentus] >gi|13425097|gb|AAK25351.1| (AE005999) oxidoreductase, FAD-binding [Caulobacter crescentus]	71.8	62	3.00E-12	NP_422183.1	oxidoreductase, FAD-binding [Caulobacter crescentus] gb|AAK25351.1| (AE005999) oxidoreductase, FAD-binding [Caulobacter crescentus]	73.4	64	7.00E-13
00652_Ci_ot	1	CAB01920.1	(Z79640) COS2.1 [Ciona intestinalis]	37.5	55	0.13	XP_050271.1	hypothetical protein XP_050271 [Homo sapiens]	44.5	24	0.001
00653_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	29.7	91	5.4	NP_177084.1	polyneuridine aldehyde esterase, putative [Arabidopsis thaliana] gb|AAF27064.1|AC008262_13 (AC008262) F4N2.19 [Arabidopsis thaliana]	30.1	53	4.4
00654_Ci_ot	1	AAH14649.1	AAH14649 (BC014649) Similar to cerebroside (3'-phosphoadenylylsulfate:galactosylceramide 3') sulfotransferase [Homo sapiens]	36.7	45	0.22	No Match				
00655_Ci_ot	1	NP_172668.1	| putative extensin [Arabidopsis thaliana] >gi|3157926|gb|AAC17609.1| (AC002131) Strong similarity to extensin-like protein gb|Z34465 from Zea mays. [Arabidopsis thaliana] >gi|13809918|gb|AAK07681.1| (AY026364) leucine-rich repeat/extensin 1 [Arabidopsis thaliana]	32.5	29	0.84	No Match				
00656_Ci_ot	2	NP_014525.1	| multicopy supressor of snf1 and sta10 mutations; Msn1p [Saccharomyces cerevisiae] >gi|2507068|sp|P22148|MSN1_YEAST MSN1 PROTEIN (MULTICOPY SUPPRESSOR OF SNF1 PROTEIN 1) >gi|1078130|pir||S51881 MSN1 protein - yeast (Saccharomyces cerevisiae) >gi|663236|emb|CAA88144.1| (Z48149) multicopy of SNF1 protein 1 [Saccharomyces cerevisiae] >gi|1419989|emb|CAA99135.1| (Z74858) ORF YOL116w [Saccharomyces cerevisiae]	34.4	32	0.48	No Match				
00657_Ci_ot	1	1615125A	vitellogenin [Oreochromis mossambicus]	31.3	40	8.1	No Match				
00660_Ci_ot	1	XP_029932.1	| hypothetical C2H2 zinc finger protein FLJ22504 [Homo sapiens]	32.8	46	3.3	NP_079593.1	RIKEN cDNA 0610008M19 gene [Mus musculus] dbj|BAB22654.1| (AK003225) putative [Mus musculus] dbj|BAB26421.1| (AK009657) putative [Mus musculus]	66.3	34	3.00E-10
00661_Ci_ot	1	AAC31539.1	(AF076600) CpyA [Dictyostelium discoideum]	32.1	31	5.7	No Match				
00662_Ci_ot	1	No Match					No Match				
00663_Ci_ot	1	NP_113312.1	| hypothetical protein [Guillardia theta] >gi|13794494|gb|AAK39869.1|AF165818_77 (AF165818) hypothetical protein [Guillardia theta]	32.5	38	4.3	NP_032155.1	glutamate cysteine ligase (gamma-glutamylcysteine synthetase), regulatory [Mus musculus] gb|AAB96893.1| (U95053) glutamate-cysteine ligase regulatory subunit [Mus musculus] gb|AAG15424.1| (AF149060) glutamate-cysteine ligase regulatory subunit [Mus musculus]	53.5	32	2.00E-06
00666_Ci_ot	1	CAB62384.1	(AJ242012) beta-bungarotoxin A7 chain [Bungarus multicinctus]	79.2	38	4.00E-14	No Match				

00581_Ci_ot	1	NP_294202.1	| penicillin-binding protein 1 [Deinococcus radiodurans] >gi|7473266|pir||B75514 penicillin-binding protein 1 - Deinococcus radiodurans (strain R1) >gi|6458167|gb|AAF10059.1|AE001907_5 (AE001907) penicillin-binding protein 1 [Deinococcus radiodurans]	32.8	36	1.8	AAK95194.1	AF402820_1 (AF402820) 40S ribosomal protein S12 [Ictalurus punctatus]	58.6	59	2.00E-08
00582_Ci_ot	1	No Match					NP_110746.1	ATPase involved in DNA repair [Thermoplasma volcanium] dbj|BAB59370.1| (AP000991) purine NTPase [Thermoplasma volcanium]	33.6	35	1.9
00584_Ci_ot	1	NP_176206.1	| hypothetical protein [Arabidopsis thaliana] >gi|4249377|gb|AAD14474.1|AAD14474 (AC005966) Similar to gi|2829865 F3I6.4 from Arabidopsis thaliana BAC gb|AC002396	58.6	37	6.00E-08	T24254	hypothetical protein R74.4 - Caenorhabditis elegans emb|CAA85274.1| (Z36238) contains similarity to Pfam domain: PF00226 (DnaJ domain), Score=131.2, E-value=6e-36, N=1~cDNA EST yk164e12.5 comes from this gene~cDNA EST yk164e12.3 comes from this gene [Caenorhabditis elegans]	65.6	44	5.00E-10
00587_Ci_ot	1	NP_036011.1	| rhodopsin kinase; G-Protein receptor kinase 1 [Mus musculus] >gi|13633680|sp|Q9WVL4|RK_MOUSE RHODOPSIN KINASE (RK) >gi|5114043|gb|AAD40189.1|AF085240_1 (AF085240) rhodopsin kinase [Mus musculus]	65.2	50	6.00E-10	NP_062370.1	G protein-coupled receptor kinase 2, groucho gene related (Drosophila); G protein-coupled receptor kinase 4 [Mus musculus] gb|AAC09266.1| (AF040745) G protein-coupled receptor kinase 4; GRK4 [Mus musculus]	57.4	35	1.00E-07
00634_Ci_ot	2	CAB51908.1	(AJ000992) GDT1 protein [Dictyostelium discoideum]	32.1	48	5.3	No Match				
00591_Ci_ot	1	No Match									
00592_Ci_ot	1	AAF53877.1	(AE003665) CG10757 gene product [Drosophila melanogaster]	43	36	0.001	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	77.6	66	4.00E-15
00593_Ci_ot	1	NP_180911.1	| putative serine carboxypeptidase II [Arabidopsis thaliana] >gi|2459435|gb|AAB80670.1| (AC002332) putative serine carboxypeptidase II [Arabidopsis thaliana]	33.2	37	2.5					
00594_Ci_ot	1	No Match					NP_036420.1	TRAM-like protein; KIAA0057 gene product; TRAM-like protein [Homo sapiens] ref|XP_004094.1| TRAM-like protein [Homo sapiens] dbj|BAA06540.1| (D31762) similar to human TRAMP protein. [Homo sapiens] emb|CAB71119.1| (AL049611) dJ180E22.2 (KIAA0057) [Homo sapiens]	31.7	54	2.4
00597_Ci_ot	1	AAG23737.1	AF207990_1 (AF207990) fer-1 like protein 3 [Homo sapiens]	30.5	48	8.5					
00598_Ci_ot	1	No Match									
00600_Ci_ot	1	NP_105619.1	| dehydrogenase subunit I [Mesorhizobium loti] >gi|14024803|dbj|BAB51405.1| (AP003005) dehydrogenase subunit I [Mesorhizobium loti]	34.8	28	0.85	NP_181574.1	unknown protein [Arabidopsis thaliana]	32.8	38	3.3
00603_Ci_ot	1	No Match									
00605_Ci_ot	1	BAA22067.1	(D89990) myosin heavy chain [Cyprinus carpio]	32.5	33	4.3	NP_199894.1	small zinc finger-like protein [Arabidopsis thaliana] sp|Q9XGY4|IM08_ARATH MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM8 gb|AAD39990.1|AF150083_1 (AF150083) small zinc finger-like protein [Arabidopsis thaliana] dbj|BAB08904.1| (AB025617) small zinc finger-like protein [Arabidopsis thaliana]	56.6	35	2.00E-07
00606_Ci_ot	1	No Match									
00607_Ci_ot	1	T28625	variant-specific surface protein 3 - malaria parasite (Plasmodium falciparum) >gi|886377|gb|AAA75397.1| (L40609) variant-specific surface protein [Plasmodium falciparum]	32.5	31	4.3	AAF53802.1	(AE003663) Top2 gene product [Drosophila melanogaster]	34	39	1.5
00609_Ci_ot	1	NP_221036.1	| EXODEOXYRIBONUCLEASE LARGE SUBUNIT (xseA) [Rickettsia prowazekii] >gi|14194742|sp|Q9ZCP8|EX7L_RICPR PROBABLE EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT (EXONUCLEASE VII LARGE SUBUNIT) >gi|7435202|pir||F71673 exodeoxyribonuclease large chain (xseA) RP675 - Rickettsia prowazekii >gi|3861212|emb|CAA15112.1| (AJ235272) EXODEOXYRIBONUCLEASE LARGE SUBUNIT (xseA) [Rickettsia prowazekii]	31.7	33	7.4	No Match				
00610_Ci_ot	1	No Match					AAA56734.1	(U13866) non-functional lacZ alpha peptide [unidentified cloning vector]	32.5	30	4.3
00616_Ci_ot	1	AAD29866.1	(AF093830) alpha-1,2-fucosyltransferase [Helicobacter pylori]	33.6	56	1.9	No Match				
00618_Ci_ot	1	T39773	hypothetical protein SPBC18H10.09 - fission yeast (Schizosaccharomyces pombe) >gi|3006186|emb|CAA18406.1| (AL022304) hypothetical protein [Schizosaccharomyces pombe]	31.3	33	9.7	NP_173506.1	predicted protein [Arabidopsis thaliana] gb|AAF80624.1|AC069251_17 (AC069251) F2D10.34 [Arabidopsis thaliana] gb|AAK76523.1| (AY045849) putative ring-H2 finger protein [Arabidopsis thaliana]	33.6	35	1.9
00620_Ci_ot	1	No Match									
00621_Ci_ot	1	AAB50686.1	(S80905) Con1 [Homo sapiens]	36.7	38	0.049					
00623_Ci_ot	1	NP_326506.1	| DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII) [Mycoplasma pulmonis] >gi|14424449|sp|P47729|DPO3_MYCPU DNA POLYMERASE III POLC-TYPE (POLIII) >gi|14090090|emb|CAC13848.1| (AL445565) DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII) [Mycoplasma pulmonis]	34	43	1.5	No Match				
00625_Ci_ot	1	BAB29301.1	(AK014366) putative [Mus musculus]	34.4	33	0.75	NP_177894.1	unknown protein [Arabidopsis thaliana] gb|AAG51633.1|AC012193_15 (AC012193) unknown protein; 14107-15252 [Arabidopsis thaliana]	43.8	37	0.002
00631_Ci_ot	1	No Match									
00633_Ci_ot	1	NP_228676.1	| hypothetical protein [Thermotoga maritima] >gi|7460108|pir||F72322 hypothetical protein TM0867 - Thermotoga maritima (strain MSB8) >gi|4981402|gb|AAD35949.1|AE001753_5 (AE001753) hypothetical protein [Thermotoga maritima]	31.7	37	5.8					

00583_Ci_ot	2	P47833	RL30_CHICK 60S RIBOSOMAL PROTEIN L30 >gi|422700|pir||S34608 ribosomal protein L30, cytosolic - chicken >gi|402507|dbj|BAA03394.1| (D14521) ribosomal protein L30 [Gallus gallus] >gi|10442706|gb|AAG17442.1|AF297033_1 (AF297033) ribosomal protein L30 [Ophiophagus hannah]	190	85	8.00E-48	P47833	RL30_CHICK 60S RIBOSOMAL PROTEIN L30 pir||S34608 ribosomal protein L30, cytosolic - chicken dbj|BAA03394.1| (D14521) ribosomal protein L30 [Gallus gallus] gb|AAG17442.1|AF297033_1 (AF297033) ribosomal protein L30 [Ophiophagus hannah]	193	86	1.00E-48
00441_Ci_ot	4	AAB19650.1	retinaldehyde-binding protein, CRALBP [cattle, Peptide, 316 aa]	80.8	47	1.00E-14	NP_065624.1	retinaldehyde-binding protein 1 [Mus musculus] sp|Q9Z275|CRAL_MOUSE CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP) gb|AAC99427.1| (AF084642) cellular retinaldehyde-binding protein; CRALBP [Mus musculus] dbj|BAB29216.1| (AK014227) putative [Mus musculus]	100	35	2.00E-20
00447_Ci_ot	2	P19889	RLA0_DROME 60S ACIDIC RIBOSOMAL PROTEIN P0 (DEOXYRIBONUCLEASE (APURINIC OR APYRIMIDINIC)) (APURINIC-APYRIMIDINIC ENDONUCLEASE) >gi|71140|pir||R5FFP0 acidic ribosomal protein P0 - fruit fly (Drosophila melanogaster) >gi|576817|gb|AAA53372.1| (M25772) DNA repair protein [Drosophila melanogaster] >gi|7296522|gb|AAF51807.1| (AE003596) RpP0 gene product [Drosophila melanogaster]	58.9	61	7.00E-11	P47826	RLA0_CHICK 60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) pir||I50151 acidic ribosomal phosphoprotein - chicken gb|AAC38020.1| (L28704) acidic ribosomal phosphoprotein [Gallus gallus]	217	75	7.00E-56
00449_Ci_ot	1	No Match					No Match				
00452_Ci_ot	1	CAA07235.1	(AJ006770) extensin [Cicer arietinum]	32.1	30	5.7					
00453_Ci_ot	1	NP_247456.1	| conserved hypothetical protein [Methanococcus jannaschii] >gi|2495998|sp|Q57904|Y480_METJA HYPOTHETICAL PROTEIN MJ0480 >gi|2128335|pir||H64359 hypothetical protein MJ0480 - Methanococcus jannaschii >gi|1591183|gb|AAB98471.1| (U67498) conserved hypothetical protein [Methanococcus jannaschii]	36	38	0.38	P31009	RS2_DROME 40S RIBOSOMAL PROTEIN S2 (STRINGS OF PEARLS PROTEIN) pir||S50325 ribosomal protein S2 - fruit fly (Drosophila melanogaster) gb|AAC34198.1| (U01334) ribosomal protein S2 [Drosophila melanogaster] gb|AAA87053.1| (U01335) ribosomal protein S2 [Drosophila melanogaster] gb|AAF52822.1| (AE003626) sop gene product [Drosophila melanogaster]	195	81	3.00E-49
00455_Ci_ot	1	AAH05398.1	AAH05398 (BC005398) Unknown (protein for MGC:12537) [Homo sapiens]	51.2	54	5.00E-10	AAH05398.1	AAH05398 (BC005398) Unknown (protein for MGC:12537) [Homo sapiens]	80.4	59	1.00E-14
00457_Ci_ot	1	BAA96009.1	(AB040918) KIAA1485 protein [Homo sapiens]	33.6	35	1.9	BAA96009.1	(AB040918) KIAA1485 protein [Homo sapiens]	32.5	28	4
00458_Ci_ot	1	CAB37612.1	(AL035395) /prediction=(method:"genscan", version:"1.0", score:"20.04")~/prediction=(method:"genefinder", version:"084")~/match=(desc:"GH06477.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH06477 5prime simi> >gi|7290391|gb|AAF45849.1| (AE003426) CG18508 gene product [Drosophila melanogaster]	41.4	41	0.008	CAB37612.1	(AL035395) /prediction=(method:"genscan", version:"1.0", score:"20.04")~/prediction=(method:"genefinder", version:"084")~/match=(desc:"GH06477.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH06477 5prime simi> gb|AAF45849.1| (AE003426) CG18508 gene product [Drosophila melanogaster]	47.6	38	9.00E-05
00460_Ci_ot	1	NP_282475.1	| putative sugar-phosphate nucleotide transferase [Campylobacter jejuni] >gi|11347153|pir||F81276 probable sugar-phosphate nucleotide transferase Cj1329 [imported] - Campylobacter jejuni (strain NCTC 11168) >gi|6968763|emb|CAB73756.1| (AL139078) putative sugar-phosphate nucleotide transferase [Campylobacter jejuni]	31.3	45	9.7	AAH08622.1	AAH08622 (BC008622) Similar to PTD010 protein [Mus musculus] gb|AAL07803.1|AF412297_1 (AF412297) growth hormone-inducible membrane protein [Mus musculus]	98.3	47	7.00E-20
00461_Ci_ot	1	AAH07560.1	AAH07560 (BC007560) LIM and SH3 protein 1 [Homo sapiens]	74.5	52	8.00E-13	AAH12460.1	AAH12460 (BC012460) Similar to LIM and SH3 protein 1 [Homo sapiens]	76.9	52	1.00E-13
00465_Ci_ot	1	No Match					NP_065262.1	solute carrier family 16 (monocarboxylic acid transporters), member 8; proton-coupled monocarboxylate transporter 3 gene; proton-coupled monocarboxylate transporter 3 [Mus musculus] sp|O35308|MOT3_MOUSE MONOCARBOXYLATE TRANSPORTER 3 (MCT 3) (PROTON-COUPLED MONOCARBOXYLATE TRANSPORTER 3) gb|AAF45042.1|AF178956_1 (AF178956) proton-coupled monocarboxylate transporter 3 [Mus musculus] gb|AAB70582.2| (AF019111) monocarboxylate transporter 3 [Mus musculus]	33.2	32	2.5
00466_Ci_ot	1	No Match					NP_249982.1	hypothetical protein [Pseudomonas aeruginosa] pir||C83485 hypothetical protein PA1291 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG04680.1|AE004558_9 (AE004558) hypothetical protein [Pseudomonas aeruginosa]	31.7	31	6
00467_Ci_ot	1	NP_049582.1	| orf328 [Tetrahymena pyriformis] >gi|5306143|gb|AAD41927.1|AF160864_15 (AF160864) orf328 [Tetrahymena pyriformis]	31.3	30	5.8	No Match				
00473_Ci_ot	1	XP_015428.1	| hypothetical protein XP_015428 [Homo sapiens]	72.6	75	4.00E-12	XP_015428.1	hypothetical protein XP_015428 [Homo sapiens]	96.3	64	3.00E-19
00476_Ci_ot	1	XP_016378.1	| hypothetical protein XP_016378 [Homo sapiens]	32.8	43	3.3					
00478_Ci_ot	1	AAK95163.1	AF401591_1 (AF401591) ribosomal protein L36 [Ictalurus punctatus]	94.4	71	5.00E-19	BAB21249.1	(AB046396) ribosomal protein L36 [Gallus gallus]	110	77	5.00E-24
00480_Ci_ot	1	AAF58563.1	(AE003823) CG8860 gene product [Drosophila melanogaster]	92.1	67	5.00E-18	AAF58563.1	(AE003823) CG8860 gene product [Drosophila melanogaster]	92.1	66	5.00E-18
00481_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2					
00483_Ci_ot	1	Q9WVA1	IM8A_RAT MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM8 A (DEAFNESS DYSTONIA PROTEIN 1 HOMOLOG) >gi|5107153|gb|AAD39989.1|AF150082_1 (AF150082) small zinc finger-like protein [Rattus norvegicus]	51.2	39	1.00E-05	NP_199894.1	small zinc finger-like protein [Arabidopsis thaliana] sp|Q9XGY4|IM08_ARATH MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM8 gb|AAD39990.1|AF150083_1 (AF150083) small zinc finger-like protein [Arabidopsis thaliana] dbj|BAB08904.1| (AB025617) small zinc finger-like protein [Arabidopsis thaliana]	55	32	7.00E-07
00484_Ci_ot	1	BAA74829.1	(AB020762) Pax19 [Ciona intestinalis]	57.8	83	1.00E-07	BAA74829.1	(AB020762) Pax19 [Ciona intestinalis]	94	89	3.00E-39

00381_Ci_ot	1	NP_014927.1	| Hypothetical ORF; Yor284wp [Saccharomyces cerevisiae] >gi|2132113|pir||S67186 hypothetical protein YOR284w - yeast (Saccharomyces cerevisiae) >gi|1279708|emb|CAA61788.1| (X89633) hypothetical protein [Saccharomyces cerevisiae] >gi|1420632|emb|CAA99511.1| (Z75192) ORF YOR284w [Saccharomyces cerevisiae]	37.5	31	0.13	NP_014927.1	Hypothetical ORF; Yor284wp [Saccharomyces cerevisiae] pir||S67186 hypothetical protein YOR284w - yeast (Saccharomyces cerevisiae) emb|CAA61788.1| (X89633) hypothetical protein [Saccharomyces cerevisiae] emb|CAA99511.1| (Z75192) ORF YOR284w [Saccharomyces cerevisiae]	37.5	28	0.12
00383_Ci_ot	1	NP_179499.1	| hypothetical protein [Arabidopsis thaliana] >gi|7487277|pir||T00529 hypothetical protein T20K24.10 - Arabidopsis thaliana >gi|3176711|gb|AAD12027.1| (AC002392) hypothetical protein [Arabidopsis thaliana]	31.3	56	1.9	Q9U3Z7	NHPX_DROME NHP2-LIKE PROTEIN (*HOI-POLLOI PROTEIN*) gb|AAF20209.1|AF208396_1 (AF208396) Hoi-polloi [Drosophila melanogaster] gb|AAF52798.2| (AE003625) hoip gene product [Drosophila melanogaster]	54.7	70	2.00E-07
00387_Ci_ot	1	No Match					No Match				
00389_Ci_ot	2	AAF49846.1	(AE003539) RpS4 gene product [alt 2] [Drosophila melanogaster] >gi|7294505|gb|AAF49847.1| (AE003539) RpS4 gene product [alt 1] [Drosophila melanogaster]	166	75	2.00E-40	AAF49846.1	(AE003539) RpS4 gene product [alt 2] [Drosophila melanogaster] gb|AAF49847.1| (AE003539) RpS4 gene product [alt 1] [Drosophila melanogaster]	166	75	1.00E-40
00391_Ci_ot	1	AAF49893.1	(AE003540) CG10753 gene product [Drosophila melanogaster]	138	80	7.00E-32	AAF49893.1	(AE003540) CG10753 gene product [Drosophila melanogaster]	158	84	6.00E-38
00392_Ci_ot	1	No Match					No Match				
00393_Ci_ot	1	No Match					No Match				
00396_Ci_ot	1	T24047	hypothetical protein R08B4.3 - Caenorhabditis elegans >gi|3878965|emb|CAA92002.1| (Z68008) cDNA EST yk339a7.3 comes from this gene~cDNA EST yk339a7.5 comes from this gene [Caenorhabditis elegans]	32.1	30	0.003	T24047	hypothetical protein R08B4.3 - Caenorhabditis elegans emb|CAA92002.1| (Z68008) cDNA EST yk339a7.3 comes from this gene~cDNA EST yk339a7.5 comes from this gene [Caenorhabditis elegans]	52.3	31	5.00E-06
00397_Ci_ot	1	P41115	RS11_XENLA 40S RIBOSOMAL PROTEIN S11 >gi|1079315|pir||JC2499 ribosomal protein S11 - African clawed frog >gi|551286|emb|CAA55387.1| (X78805) ribosomal protein S11 [Xenopus laevis]	220	75	3.00E-59	P41115	RS11_XENLA 40S RIBOSOMAL PROTEIN S11 *pir||JC2499 ribosomal* protein S11 - African clawed frog emb|CAA55387.1| (X78805) ribosomal protein S11 [Xenopus laevis]	247	75	1.00E-64
00401_Ci_ot	1	NP_113254.1	| hypothetical protein [Guillardia theta] >gi|13794439|gb|AAK39814.1|AF165818_22 (AF165818) hypothetical protein [Guillardia theta]	31.7	34	4.5	No Match				
00403_Ci_ot	2	XP_044326.2	| similar to ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY (H. sapiens) [Homo sapiens]	76.5	75	5.00E-14	XP_050264.1	similar to ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY (H. sapiens) [Homo sapiens]	78.8	71	1.00E-14
00405_Ci_ot	1	AAK30648.1	(AF115639) maturase K [Sedum modestum]	32.5	56	4.3	BAB22918.1	(AK003655) putative [Mus musculus]	53.9	66	2.00E-06
00406_Ci_ot	1	NP_176058.1	| hypothetical protein [Arabidopsis thaliana] >gi|9954748|gb|AAG09099.1|AC009323_10 (AC009323) Unknown protein [Arabidopsis thaliana]	36.4	42	0.29	O17570	RL38_CAEEL 60S RIBOSOMAL PROTEIN L38 pir||T18996 hypothetical protein C06B8.8 - *Caenorhabditis elegans* emb|CAB03853.1| (Z81463) predicted using Genefinder~Weak similarity to N-terminus of acetylcholine receptor proteins, contains similarity to Pfam domain: PF01781 (Ribosomal L38e protein family), Score=163.5, E-value=1.1e-45, N=1~cDNA EST yk166f5.3 comes from this gene>	63.6	54	1.00E-09
00414_Ci_ot	1	AAB46894.2	(S83169) core protein [Hepatitis C virus]	36.4	44	0.23	AAF50674.1	(AE003563) Trn gene product [Drosophila melanogaster]	32.1	46	5.7
00416_Ci_ot	1	AAL06581.1	AF411943_2 (AF411943) transposase OrfB [Helicobacter pylori]	31.3	58	9.7	No Match				
00417_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.86	AAF52494.1	(AE003616) CG13784 gene product [Drosophila melanogaster]	30.9	48	2.5
00419_Ci_ot	1	No Match					AAF48428.1	(AE003498) CG9091 gene product [Drosophila melanogaster]	100	55	1.00E-20
00426_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	2.1					
00427_Ci_ot	1	AAF66673.1	AF143953_1 (AF143953) ORF30 [Spodoptera litura nucleopolyhedrovirus]	31.7	34	5.8	CAB06308.1	(Z83978) S [Avian infectious bronchitis virus]	31.7	46	4.6
00433_Ci_ot	1	AAK95133.1	AF401561_1 (AF401561) ribosomal protein L8 [Ictalurus punctatus]	148	61	7.00E-48	NP_000964.1	ribosomal protein L8; 60S ribosomal protein L8 [Homo sapiens] ref|NP_036183.1| ribosomal protein L8 [Mus musculus] ref|XP_035336.1| similar to ribosomal protein L8 (H. sapiens) [Homo sapiens] ref|XP_035337.1| similar to ribosomal protein L8 (H. sapiens) [Homo sapiens] ref|XP_054560.1| similar to ribosomal protein L8 (H. sapiens) [Homo sapiens] ref|XP_054567.1| hypothetical protein XP_054567 [Homo sapiens] ref|NP_150644.1| ribosomal protein L8; 60S ribosomal protein L8 [Homo sapiens] sp|P25120|RL8_HUMAN 60S RIBOSOMAL PROTEIN L8 pir||R5RTL8 ribosomal protein L8, cytosolic [validated] - rat pir||JN0923 ribosomal protein L8, cytosolic - human emb|CAA44071.1| (X62145) ribosomal protein L8 [Rattus rattus] emb|CAA82248.1| (Z28407) *ribosomal* protein L8 [Homo sapiens] gb|AAC35587.1| (U67771) ribosomal protein L8 [Mus musculus] gb|AAH00077.1|AAH00077 (BC000077) ribosomal protein L8 [Homo sapiens] gb|AAH07935.1|AAH07935 (BC007935) ribosomal protein L8 [Homo sapiens]	257	75	9.00E-68
00434_Ci_ot	1	S52053	cytochrome-c oxidase (EC 1.9.3.1) chain I - Trypanoplasma borreli mitochondrion >gi|563140|gb|AAA73454.1| (U11683) cytochrome c oxidase subunit 1 [Trypanoplasma borreli]	32.5	35	4.3	XP_012797.2	adaptor-related protein complex 2, sigma 1 subunit, isoform AP17 [Homo sapiens] ref|XP_028263.1| adaptor-related protein complex 2, sigma 1 subunit [Homo sapiens] sp|Q00380|A2S1_MOUSE CLATHRIN COAT ASSEMBLY PROTEIN AP17 (CLATHRIN COAT ASSOCIATED PROTEIN AP17) (PLASMA MEMBRANE ADAPTOR AP-2 17 KDA PROTEIN) (HA2 17 KDA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN 2 SMALL CHAIN) pir||B40535 *clathrin-associated protein 17 - rat gb|AAA40742.1|* (M37194) clathrin-associated protein 17 [Rattus norvegicus] gb|AAH06337.1|AAH06337 (BC006337) Unknown (protein for MGC:12798) [Homo sapiens]	281	95	5.00E-75
00435_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.3	No Match				

00344_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.9	NP_186897.1	unknown protein [Arabidopsis thaliana] gb|AAF32455.1| (AC021640) unknown protein [Arabidopsis thaliana] gb|AAK59844.1| (AY037243) AT3g02480/F16B3_11 [Arabidopsis thaliana]	32.8	73	1.4
00345_Ci_ot	1	A39321	mucin - rat (fragment) >gi|205546|gb|AAA41642.1| (M76740) mucin [Rattus norvegicus]	33.2	40	2.5	P98068	SPAN_STRPU SPAN PROTEIN PRECURSOR gb|AAA30072.1| (M84144) SpAN protein [Strongylocentrotus purpuratus]	43	34	0.003
00680_Ci_ot	4	NP_354858.1	| AGR_C_3445p [Agrobacterium tumefaciens] >gi|15156995|gb|AAK87643.1| (AE008107) AGR_C_3445p [Agrobacterium tumefaciens]	31.3	65	9.7	NP_067000.1	U6 snRNA-associated Sm-like protein [Homo sapiens] ref|XP_042364.1| U6 snRNA-associated Sm-like protein [Homo sapiens] sp|Q9Y333|LSM2_HUMAN U6 SNRNA-ASSOCIATED SM-LIKE PROTEIN LSM2 (G7B PROTEIN) gb|AAB72037.1| (U85207) snRNP core Sm protein homolog Sm-X5 [Mus musculus] gb|AAD21818.1| (AF134726) snRNP [Homo sapiens] emb|CAB52190.1| (AJ245416) G7b protein [Homo sapiens] gb|AAD56226.1|AF182288_1 (AF182288) U6 snRNA-associated Sm-like protein LSm2 [Homo sapiens] gb|AAG33023.1| (AF196468) SMX5-like protein [Homo sapiens] gb|AAG49438.1|AF136977_1 (AF136977) snRNP core SM-like protein SM-x5 [Homo sapiens] gb|AAH09192.1|AAH09192 (BC009192) U6 snRNA-associated Sm-like protein [Homo sapiens] dbj|BAB63302.1| (AP000503) small nuclear ribonuclear protein D homolog [Homo sapiens] gb|AAH14288.1|AAH14288 (BC014288) Similar to U6 snRNA-associated Sm-like protein [Mus musculus] gb|AAL14450.1|AF397035_3 (AF397035) small ribonuclear protein G7b [Mus musculus] gb|AAL14458.1|AF397036_3 (AF397036) small ribonuclear protein G7b [Mus musculus]	162	98	1.00E-41
00348_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.81	No Match				
00349_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	1.8	No Match				
00350_Ci_ot	1	XP_001789.4	| hematopoietic PBX-interacting protein [Homo sapiens]	32.8	41	0.1	A72635	hypothetical protein APE1536 - Aeropyrum pernix (strain K1) dbj|BAA80535.1| (AP000061) 252aa long hypothetical protein [Aeropyrum pernix]	33.2	37	2.5
00351_Ci_ot	1	AAF00520.1	AF185958_1 (AF185958) polyprotein [Pleione virus Y]	31.7	50	7.4	NP_055816.2	SMART/HDAC1 associated repressor protein; Msx2 interacting nuclear target (MINT) homolog [Homo sapiens] gb|AAK52750.1|AF356524_1 (AF356524) *nuclear receptor transcription cofactor* [Homo sapiens]	31.7	31	7.4
00353_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	41.4	35	0.009	NP_080803.1	RIKEN cDNA 2510006C20 gene [Mus musculus] dbj|BAB25147.1| (AK007629) putative [Mus musculus] dbj|BAB27264.1| (AK010914) putative [Mus musculus]	61.3	59	2.00E-09
00354_Ci_ot	2	NP_326469.1	| unknown; predicted coding region [Mycoplasma pulmonis] >gi|14090053|emb|CAC13811.1| (AL445565) unknown; predicted coding region [Mycoplasma pulmonis]	31.3	33	9.7	NP_077152.1	RIKEN cDNA 2810405I11 gene [Mus musculus] gb|AAH02229.1|AAH02229 (BC002229) Similar to CHMP1.5 protein [Mus musculus]	187	65	1.00E-46
00356_Ci_ot	1	XP_009189.3	| eukaryotic translation elongation factor 2 [Homo sapiens]	188	69	4.00E-47	Q90705	EF2_CHICK ELONGATION FACTOR 2 (EF-2) gb|AAA87587.1| (U46663) *elongation factor 2 [Gallus gallus]*	265	73	2.00E-70
00357_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.98	NP_276305.1	conserved protein [Methanothermobacter thermautotrophicus] pir||H69023 conserved hypothetical protein MTH1177 - Methanobacterium thermoautotrophicum (strain Delta H) gb|AAB85666.1| (AE000886) conserved protein [Methanothermobacter thermautotrophicus]	30.9	48	2.5
00358_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	31.3	100	1.9	T32090	hypothetical protein K09F6.2 - Caenorhabditis elegans gb|AAB66193.1| (AF016683) K09F6.2 gene product [Caenorhabditis elegans]	29.3	42	7.8
00359_Ci_ot	2	NP_038260.1	COX1_15121| cytochrome c oxidase subunit I [Echinococcus multilocularis] >gi|6139002|dbj|BAA84935.2| (AB018440) cytochrome oxidase subunit 1 [Echinococcus multilocularis]	35.2	24	0.65	NP_038260.1	COX1_15121 cytochrome c oxidase subunit I [Echinococcus multilocularis] dbj|BAA84935.2| (AB018440) *cytochrome oxidase subunit 1* [Echinococcus multilocularis]	35.2	24	0.55
00705_Ci_ot	2	BAB20445.1	(AB037927) DNA polymerase [Hepatitis B virus]	34.8	37	0.85	No Match				
00361_Ci_ot	1	No Match					NP_404881.1	*putative tryptophan-specific transport protein [Yersinia pestis]* emb|CAC90116.1| (AJ414147) putative tryptophan-specific transport protein [Yersinia pestis]	33.2	38	0.51
00362_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.7	S28284	hypothetical protein B0464.7 - Caenorhabditis elegans	32.5	40	3
00364_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.71					
00365_Ci_ot	1	AAK84507.1	AC024696_3 (AC024696) Hypothetical protein F07B7.11 [Caenorhabditis elegans] >gi|15145317|gb|AAK84513.1|AC024696_9 (AC024696) Hypothetical protein F07B7.4 [Caenorhabditis elegans]	161	68	9.00E-39	AAK84507.1	AC024696_3 (AC024696) Hypothetical protein F07B7.11 [Caenorhabditis elegans] gb|AAK84513.1|AC024696_9 (AC024696) Hypothetical protein F07B7.4 [Caenorhabditis elegans]	162	66	2.00E-39
00368_Ci_ot	1	O57592	RL7A_FUGRU 60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) >gi|2826820|emb|CAA75444.1| (Y15171) ribosomal protein L7a [Takifugu rubripes]	199	73	1.00E-53	O57592	RL7A_FUGRU 60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) emb|CAA75444.1| (Y15171) ribosomal protein L7a [Takifugu rubripes]	180	66	2.00E-44
00369_Ci_ot	1	BAB28279.1	(AK012494) putative [Mus musculus]	31.3	38	9.7	No Match				
00370_Ci_ot	1	No Match					No Match				
00371_Ci_ot	1	BAB28260.1	(AK012465) putative [Mus musculus]	71.8	70	1.00E-12	BAB28260.1	(AK012465) putative [Mus musculus]	71.4	76	2.00E-12
00372_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.64	No Match				
00376_Ci_ot	1	No Match					No Match				
00378_Ci_ot	1	AAC34392.1	(AF056116) PAS1 [*Takifugu rubripes*]	128	57	6.00E-29	NP_394249.1	chromosome segregation protein related ptotein [Thermoplasma acidophilum] *emb|CAC11918.1| (AL445065) chromosome segregation* protein related ptotein [Thermoplasma acidophilum]	34.8	30	0.85

00317_Ci_ot	1	1FF9	A Chain A, Apo Saccharopine Reductase >gi|12084624|pdb|1E5Q|A Chain A, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine >gi|12084625|pdb|1E5Q|B Chain B, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine >gi|12084626|pdb|1E5Q|C Chain C, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine >gi|12084627|pdb|1E5Q|D Chain D, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine >gi|12084628|pdb|1E5Q|E Chain E, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine >gi|12084629|pdb|1E5Q|F Chain F, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine >gi|12084630|pdb|1E5Q|G Chain G, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine >gi|12084631|pdb|1E5Q|H Chain H, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine >gi|12084778|pdb|1E5L|A Chain A, Apo Saccharopine Reductase From	103	55	2.00E-21	1FF9	A Chain A, Apo Saccharopine Reductase pdb|1E5Q|A Chain A, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine pdb|1E5Q|B Chain B, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine pdb|1E5Q|C Chain C, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine pdb|1E5Q|D Chain D, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine pdb|1E5Q|E Chain E, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine pdb|1E5Q|F Chain F, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine pdb|1E5Q|G Chain G, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine pdb|1E5Q|H Chain H, Ternary Complex Of Saccharopine Reductase From Magnaporthe Grisea, Nadph And Saccharopine pdb|1E5L|A Chain A, Apo Saccharopine Reductase From Magnaporthe Grisea pdb|1E5L|B Chain B, Apo Saccharopine Reductase From Magnaporthe Grisea	102	55	3.00E-21
00318_Ci_ot	1	0912260A	histone H2B [Strongylocentrotus purpuratus]	94.8	53	7.00E-19	0912260A	histone H2B [Strongylocentrotus purpuratus]	95.2	53	5.00E-19
00319_Ci_ot	1	P14544	COX1_LEITA CYTOCHROME C OXIDASE POLYPEPTIDE I >gi|83977|pir||D30010 cytochrome-c oxidase (EC 1.9.3.1) chain I - Leishmania tarentolae mitochondrion	31.7	28	7.4	No Match				
00320_Ci_ot	1	No Match					No Match				
00321_Ci_ot	1	Q9XT28	ATX1_SHEEP COPPER TRANSPORT PROTEIN ATOX1 (METAL TRANSPORT PROTEIN ATX1) (COPPER CHAPERONE SAH) >gi|5052347|gb|AAD38514.1|AF134813_1 (AF134813) copper chaperone [Ovis aries]	58.9	47	5.00E-08					
00325_Ci_ot	1	T50176	probable peptide synthetase [imported] - fission yeast (Schizosaccharomyces pombe) >gi|6912019|emb|CAB72227.1| (AL138854) putative peptide synthetase; with 3 Phosphopantetheine attachment sites [Schizosaccharomyces pombe]	33.2	37	2.4	T50176	probable peptide synthetase [imported] - fission yeast (Schizosaccharomyces pombe) emb|CAB72227.1| (AL138854) putative peptide synthetase; with 3 Phosphopantetheine attachment sites [Schizosaccharomyces pombe]	33.2	32	2
00326_Ci_ot	1	XP_055834.1	hypothetical protein XP_055834 [Homo sapiens]	33.6	38	1.3	NP_105556.1	unknown protein [Mesorhizobium loti] dbj|BAB51342.1| (AP003004) unknown protein [Mesorhizobium loti]	36.7	42	0.22
00327_Ci_ot	3	NP_001016.1	ribosomal protein S23; 40S ribosomal protein S23; homolog of yeast ribosomal protein S28 [Homo sapiens] >gi|11417289|ref|XP_004020.1| ribosomal protein S23 [Homo sapiens] >gi|13195604|ref|NP_077137.1| RIKEN cDNA 2410044J15 gene [Mus musculus] >gi|16160499|ref|XP_056322.1| hypothetical protein XP_056322 [Homo sapiens] >gi|730647|sp|P39028|RS23_HUMAN 40S RIBOSOMAL PROTEIN S23 >gi|543449|pir||S41955 ribosomal protein S23, cytosolic [validated] - rat >gi|631360|pir||S42105 ribosomal protein S23, cytosolic - human >gi|414349|dbj|BAA03400.1| (D14530) ribosomal protein [Homo sapiens] >gi|453281|emb|CAA54584.1| (X77398) ribosomal protein S23 [Rattus norvegicus] >gi|12805351|gb|AAH02145.1|AAH02145 (BC002145) ribosomal protein S23 [Mus musculus] >gi|12832654|dbj|BAB22198.1| (AK002573) putative [Mus musculus] >gi|12846150|dbj|BAB27050.1| (AK010594) putative [Mus musculus] >gi|12846172|dbj|BAB27058.1| (AK010608) putative [Mus musculus] >gi|12849180|dbj|BAB28238.1| (AK012438) putative [Mus musculus] >gi|12851192|dbj|BAB28969.1| (AK013720) putative [Mus musculus]	260	88	1.00E-68	NP_001016.1	ribosomal protein S23; 40S ribosomal protein S23; homolog of yeast ribosomal protein S28 [Homo sapiens] ref|XP_004020.1| ribosomal protein S23 [Homo sapiens] ref|NP_077137.1| RIKEN cDNA 2410044J15 gene [Mus musculus] ref|XP_056322.1| hypothetical protein XP_056322 [Homo sapiens] sp|P39028|RS23_HUMAN 40S RIBOSOMAL PROTEIN S23 pir||S41955 ribosomal protein S23, cytosolic [validated] - rat pir||S42105 ribosomal protein S23, cytosolic - human dbj|BAA03400.1| (D14530) ribosomal protein [Homo sapiens] emb|CAA54584.1| (X77398) ribosomal protein S23 [Rattus norvegicus] gb|AAH02145.1|AAH02145 (BC002145) ribosomal protein S23 [Mus musculus] dbj|BAB22198.1| (AK002573) putative [Mus musculus] dbj|BAB27050.1| (AK010594) putative [Mus musculus] dbj|BAB27058.1| (AK010608) putative [Mus musculus] dbj|BAB28238.1| (AK012438) putative [Mus musculus] dbj|BAB28969.1| (AK013720) putative [Mus musculus]	266	89	2.00E-70
00328_Ci_ot	2	D71606	hypothetical protein PFB0800c - malaria parasite (Plasmodium falciparum) >gi|3845280|gb|AAC71949.1| (AE001418) hypothetical protein [Plasmodium falciparum]	38.7	31	0.049	D71606	hypothetical protein PFB0800c - malaria parasite (Plasmodium falciparum) gb|AAC71949.1| (AE001418) hypothetical protein [Plasmodium falciparum]	38.7	29	0.04
00329_Ci_ot	1	AAG13464.1	AC026758_1 (AC026758) hypothetical protein [Oryza sativa]	32.8	36	3.3	No Match				
00330_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.7	T01265	starch synthase DULL1 - maize gb|AAC14014.1| (AF023159) starch synthase DULL1 [Zea mays]	32.5	34	2.9
00331_Ci_ot	1	No Match					AAD38903.1	AF128806_1 (AF128806) cap binding protein eIF-4E [Oryzias latipes]	59.3	64	4.00E-08
00334_Ci_ot	1	XP_032639.1	| similar to karyopherin beta 2b, transportin (H. sapiens) [Homo sapiens]	81.5	67	7.00E-20	XP_032639.1	similar to karyopherin beta 2b, transportin (H. sapiens) [Homo sapiens]	77.6	75	6.00E-19
00335_Ci_ot	1	AAB70096.1	(U48418) Mrs7p [Saccharomyces cerevisiae]	30.1	44	4.2	S72290	ribosomal protein S19 - Plasmodium falciparum plastid emb|CAA64580.1| (X95276) rps19 [Plasmodium falciparum]	33.6	50	1.9
00337_Ci_ot	1	No Match					No Match				
00339_Ci_ot	2	XP_017626.1	| ribosomal protein S12 [Homo sapiens]	196	74	1.00E-49	No Match				
00340_Ci_ot	1	No Match					No Match				
00341_Ci_ot	1	AAH05782.1	AAH05782 (BC005782) Unknown (protein for MGC:12025) [Mus *musculus*]	36	33	0.22	NP_395441.1	NADH dehydrogenase subunit 2 [Chimaera monstrosa] emb|CAC84200.1| (AJ310140) NADH subunit 2 [Chimaera monstrosa]	32.1	30	1.7
00342_Ci_ot	1	BAB55174.1	(AK027523) unnamed protein product [Homo sapiens]	150	82	1.00E-35	BAB55174.1	(AK027523) unnamed protein product [Homo sapiens]	171	79	8.00E-42
00343_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide.[Cloning vector pTriplEx]	32.8	100	2.9	T41690	conserved hypothetical protein SPCP1E11.11 - fission yeast (Schizosaccharomyces pombe) emb|CAB54870.1| (AL117183) conserved hypothetical protein [Schizosaccharomyces pombe]	34.4	37	0.81

00273_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	34.4	58	0.56	No Match				
00274_Ci_ot	1	Q9UDW1	UCRX_HUMAN UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.2 KDA PROTEIN (CYTOCHROME C1, NONHEME 7 KDA PROTEIN) (COMPLEX III SUBUNIT X) (7.2 KDA CYTOCHROME C1-ASSOCIATED PROTEIN SUBUNIT) >gi6094657gbAAF03513.1AC004882_5 (AC004882) similar to cytochrome Bc1 J chain; similar to 1BGY (PID:g4139401) [Homo sapiens] >gi6841460gbAAF29083.1AF161468_1 (AF161468) HSPC119 [Homo sapiens] >gi12081913dbjBAB20672.1 (AB028598) ubiquinol-cytochrome C reductase complex 7.2 kDa protein homologue [Homo sapiens] >gi13529296gbAAH05402.1AAH05402 (BC005402) Unknown (protein for MGC:12543) [Homo sapiens]	43	46	0.003	XP_032235.2	KIAA0284 protein [Homo sapiens]	31.7	34	7.4
00276_Ci_ot	1	CAC48844.1	(AL603643) putative cellulase H precursor protein [Sinorhizobium meliloti]	33.2	33	2.5					
00277_Ci_ot	2	NP_112159.1	hypothetical protein FLJ21617; erythroid differentiation-related factor 1 [Homo sapiens] >gi14738329refXP_045827.1 hypothetical protein FLJ21617 [Homo sapiens] >gi10437752dbjBAB15100.1 (AK025270) unnamed protein product [Homo sapiens]	65.2	75	1.00E-10	P39193	ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY	66.7	85	4.00E-11
00278_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.6	NP_180450.1	putative RING zinc finger ankyrin protein [Arabidopsis thaliana] gb|AAC79588.1| (AC005727) putative C3HC4-type RING zinc finger/ankyrin protein [Arabidopsis thaliana] gb|AAK49587.1|AF370581_1 (AF370581) putative RING zinc finger ankyrin protein [Arabidopsis thaliana]	34	46	1.5
00279_Ci_ot	1	AAB16848.1	(U70731) putative poly(A)-binding protein FabM [Emericella nidulans]	30.1	41	5.3	No Match				
00281_Ci_ot	3	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	0.64	No Match				
00282_Ci_ot	1	CAA33190.1	(X15081) MURF2 protein (AA 1-348) [Crithidia fasciculata]	32.8	34	3.3	AAB60878.1	(AF001965) 2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase [Pseudomonas sp. MA-1]	32.8	37	3.3
00283_Ci_ot	1	No Match									
00284_Ci_ot	2	NP_077420.1	DNA helicase-primase complex component [Cercopithecine herpesvirus 7] >gi11036606gbAAG27235.1AF275348_56 (AF275348) DNA helicase-primase complex component [Cercopithecine herpesvirus 7]	38.7	35	0.057					
00286_Ci_ot	2	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	3	No Match				
00288_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.6	No Match				
00289_Ci_ot	4	BAA89429.1	(AB036756) B-actin [Pagrus major]	116	100	2.00E-25	AAC28356.1	(AF076516) cytoskeletal actin 1 [Molgula oculata] gb|AAC28357.1| (AF076517) cytoskeletal actin 1 [Molgula occulta]	291	100	6.00E-78
00293_Ci_ot	1	CAB39024.2	(AL034559) hypothetical protein, PFC0875w [Plasmodium falciparum]	35.2	30	0.65	T33703	hypothetical protein F49F1.12 - Caenorhabditis elegans gb|AAF99960.1| (AF100656) Hypothetical protein F49F1.12 [Caenorhabditis elegans]	36	37	0.37
00296_Ci_ot	1	T31070	notch homolog - sea urchin (Lytechinus variegatus) >gi2570351gbAAB82088.1 (AF000634) notch homolog [Lytechinus variegatus]	34.4	55	1.1	BAB47147.1	(AB050669) complement component C6 [Branchiostoma belcheri]	52.7	45	3.00E-06
00300_Ci_ot	1	P23403	RS20_XENLA 40S RIBOSOMAL PROTEIN S20 (S22) >gi85846pirA37974 ribosomal protein S20, cytosolic - African clawed frog >gi214758gbAAA49953.1 (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]	93.6	51	2.00E-18	P23403	RS20_XENLA 40S RIBOSOMAL PROTEIN S20 (S22) pir||A37974 ribosomal protein S20, cytosolic - African clawed frog gb|AAA49953.1| (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]	204	84	6.00E-52
00302_Ci_ot	1	No Match					No Match				
00307_Ci_ot	1	AAF79805.1	AC020646_28 (AC020646) T32E20.17 [Arabidopsis thaliana]	31.7	33	7.4	No Match				
00308_Ci_ot	1	AAF57849.1	(AE003803) CG4853 gene product [Drosophila melanogaster]	31.7	40	7.4	AAF57849.1	(AE003803) CG4853 gene product [Drosophila melanogaster]	31.7	38	7.4
00313_Ci_ot	1	AAA84370.1	(U39779) beta-galactosidase alpha polypeptide [Cloning vector pTriplEx]	32.8	100	2.6					
00315_Ci_ot	1	AAF49296.1	(AE003522) CG5567 gene product [Drosophila melanogaster]	58.6	40	6.00E-08	BAB26698.1	(AK010094) putative [Mus musculus]	93.2	42	2.00E-18
00316_Ci_ot	1	NP_014993.1	putative proline-specific permease; Put4p [Saccharomyces cerevisiae] >gi1709941spP15380PUT4_YEAST PROLINE-SPECIFIC PERMEASE >gi2133062pirS67257 proline transport protein - yeast (Saccharomyces cerevisiae) >gi1199850embCAA65035.1 (X95720) 10 transmembrane spans amino acid permease; O6345 [Saccharomyces cerevisiae] >gi1420758embCAA99676.1 (Z75256) ORF YOR348c [Saccharomyces cerevisiae]	29.7	43	5.7	NP_015082.1	Homolog of the mammalian IQGAP1 and 2 genes; probable regulator of cellular morphogenesis, inducing actin-ring formation in association with cytokinesis; Iqg1p [Saccharomyces cerevisiae] pir||S61023 hypothetical protein YPL242c - yeast (Saccharomyces cerevisiae) emb|CAA91603.1| (Z67751) putative protein [Saccharomyces cerevisiae] emb|CAA97963.1| (Z73598) ORF YPL242c [Saccharomyces cerevisiae] gb|AAB70827.1| (AF019644) Iqg1p [Saccharomyces cerevisiae]	29.7	35	5.7

00178_Ci_ot	1	1DI4	A Chain A, Role Of Amino Acid Residues At Turns In The Conformational Stability And Folding Of Human Lysozyme	30.9	25	7.2	D71614	hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum) gb|AAC71881.1| (AE001396) hypothetical protein [Plasmodium falciparum]	63.6	48	8.00E-10
00205_Ci_ot	1	No Match					NP_173299.1	3-phosphoserine phosphatase [Arabidopsis thaliana] gb|AAF98410.1|AC026238_2 (AC026238) 3-phosphoserine phosphatase [Arabidopsis thaliana]	146	46	1.00E-34
00230_Ci_ot	1	T27620	hypothetical protein ZC504.3 - Caenorhabditis elegans >gi|3881454|emb|CAA90342.1| (Z50029) cell division cycle 2-like protein, contains similarity to Pfam domain: PF00069 (Eukaryotic protein kinase domain), Score=276.6, E-value=1e-79, N=1~cDNA EST yk74g7.3 comes from this gene~cDNA EST yk74g7.5 comes from this gene~cDNA EST yk488a4.>	38.7	36	0.05	XP_006578.2	protein phosphatase 1, regulatory (inhibitor) subunit 12A [Homo sapiens]	43.4	35	0.001
00240_Ci_ot	1	NP_001002.1	| ribosomal protein S7; 40S ribosomal protein S7 [Homo sapiens] >gi|6755376|ref|NP_035430.1| ribosomal protein S7 [Mus musculus] >gi|134000|sp|P23821|RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 (S8) >gi|279641|pir||R3RT7 ribosomal protein S7, cytosolic [validated] - rat >gi|2119071|pir||JC4388 ribosomal protein S7, cytosolic - human >gi|297172|emb|CAA37457.1| (X53377) ribosomal protein S7 [Rattus rattus] >gi|551251|emb|CAA81022.1| (Z25749) ribosomal protein S7 [Homo sapiens] >gi|2811284|gb|AAB97861.1| (AF043285) ribosomal protein S7 [Mus musculus] >gi|12804027|gb|AAH02866.1|AAH02866 (BC002866) ribosomal protein S7 [Homo sapiens] >gi|12805115|gb|AAH02014.1|AAH02014 (BC002014) ribosomal protein S7 [Mus musculus] >gi|227241|prf||1617114A ribosomal protein S7 [Rattus norvegicus]	171	60	5.00E-42	NP_001002.1	ribosomal protein S7; 40S ribosomal protein S7 [Homo sapiens] ref|NP_035430.1| ribosomal protein S7 [Mus musculus] sp|P23821|RS7_HUMAN 40S RIBOSOMAL PROTEIN S7 (S8) pir||R3RT7 ribosomal protein S7, cytosolic [validated] - rat pir||JC4388 ribosomal protein S7, cytosolic - human emb|CAA37457.1| (X53377) ribosomal protein S7 [Rattus rattus] emb|CAA81022.1| (Z25749) ribosomal protein S7 [Homo sapiens] gb|AAB97861.1| (AF043285) ribosomal protein S7 [Mus musculus] gb|AAH02866.1|AAH02866 (BC002866) ribosomal protein S7 [Homo sapiens] gb|AAH02014.1|AAH02014 (BC002014) ribosomal protein S7 [Mus musculus] prf||1617114A ribosomal protein S7 [Rattus norvegicus]	206	69	2.00E-52
00241_Ci_ot	1	AAD17806.1	(AF092936) proopiomelanocortin B [Acipenser transmontanus]	31.7	38	2.6	CAC22701.1	(AL389894) hypothetical protein L2969.06 [Leishmania major]	30.1	32	7.9
00250_Ci_ot	1	No Match					XP_028354.2	DNA replication factor [Homo sapiens] ref|XP_028352.2| DNA replication factor [Homo sapiens]	33.2	34	2.5
00263_Ci_ot	1	XP_029942.1	| KIAA0877 protein [Homo sapiens]	34.4	34	0.23	BAA93042.1	(AB040452) beta-galactosidase [Shuttle vector pRES19]	35.2	43	0.65
00290_Ci_ot	1	No Match					No Match				
00333_Ci_ot	1	AAA45877.1	(M17322) DNA-binding protein (BMRF1) [Human herpesvirus 4]	29.7	33	5.9	No Match				
00336_Ci_ot	1	O94111	DYL1_EMENI DYNEIN LIGHT CHAIN, CYTOPLASMIC (8 KDA CYTOPLASMIC DYNEIN LIGHT CHAIN) >gi|4099025|gb|AAD00525.1| (U81827) 8 kDa cytoplasmic dynein light chain [Emericella nidulans]	73.4	80	1.00E-19	BAB27516.1	(AK011284) putative [Mus musculus] gb|AAK57536.1| (AY034383) dynein light chain-2 [Rattus norvegicus] gb|AAH10744.1|AAH10744 (BC010744) Similar to RIKEN cDNA 6720463E02 gene [Homo sapiens] gb|AAH11289.1|AAH11289 (BC011289) RIKEN cDNA 6720463E02 gene [Mus musculus] gb|AAK38749.1| (AY029255) dynein light chain 2 [Mus musculus]	184	95	6.00E-46
00367_Ci_ot	1	No Match					No Match				
00384_Ci_ot	1	A42808	Ig light chain-binding protein precursor - Peptostreptococcus magnus	33.2	34	2.5	BAA93716.1	(AB033119) long Meq [Gallid herpesvirus 2]	35.2	33	0.65
00411_Ci_ot	1	NP_196392.1	| putative protein [Arabidopsis thaliana] >gi|9759597|dbj|BAB11454.1| (AB010070) gb|AAD23008.1~gene_id:MBK20.21~similar to unknown protein [Arabidopsis thaliana]	43.4	37	0.002					
00422_Ci_ot	1	T26134	hypothetical protein W04A4.5 - Caenorhabditis elegans	31.7	36	7.4	NP_009445.1	Protein Kinase C; Pkc1p [Saccharomyces cerevisiae] sp|P24583|KPC1_YEAST PROTEIN KINASE C-LIKE 1 (PKC 1) pir||S45390 protein kinase C (EC 2.7.1.-) PKC1 - yeast (Saccharomyces cerevisiae) emb|CAA55990.1| (X79489) D-1151 protein; protein kinase C [Saccharomyces cerevisiae] emb|CAA84932.1| (Z35866) ORF YBL105c [Saccharomyces cerevisiae]	29	55	9.5
00423_Ci_ot	1	No Match					No Match				
00424_Ci_ot	1	B33848	secretory protein 2 - midge (Chironomus tentans) (fragment)	37.5	38	0.12	BAB26669.1	(AK010053) putative [Mus musculus]	59.7	45	1.00E-13
00431_Ci_ot	1	NP_103642.1	| hypothetical protein [Mesorhizobium loti] >gi|14022820|dbj|BAB49428.1| (AP002999) hypothetical protein [Mesorhizobium loti]	29.7	50	5.6	No Match				
00439_Ci_ot	1	AAF53069.1	(AE003631) CG4713 gene product [Drosophila melanogaster]	36.4	36	0.29	NP_065624.1	retinaldehyde-binding protein 1 [Mus musculus] sp|Q9Z275|CRAL_MOUSE CELLULAR RETINALDEHYDE-BINDING PROTEIN (CRALBP) gb|AAC99427.1| (AF084642) cellular retinaldehyde-binding protein; CRALBP [Mus musculus] dbj|BAB29216.1| (AK014227) putative [Mus musculus]	79.2	33	4.00E-14
00445_Ci_ot	1	No Match					AAF51643.2	(AE003592) CG11451 gene product [Drosophila melanogaster]	31.7	29	7.4
00446_Ci_ot	1	Q66578	POLG_EC22H GENOME POLYPROTEIN [CONTAINS: COAT PROTEIN VP0 (P1AB); COAT PROTEIN VP3 (P1C); COAT PROTEIN VP1 (P1D); CORE PROTEIN P2A; CORE PROTEIN P2B; CORE PROTEIN P2C; CORE PROTEIN P3A; GENOME-LINKED PROTEIN VPG (P3B); PICORNAIN 3C (PROTEASE 3C) (P3C); RNA-DIRECT> >gi|423985|pir||A46182 polyprotein - echovirus 22 >gi|256079|gb|AAB23363.1| (S45208) polyprotein [Human parechovirus 1] >gi|323689|gb|AAA72291.1| (L02971) [Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds.], gene product [Human parechovirus 1]	32.1	40	5.7	NP_079868.1	RIKEN cDNA 2410039E09 gene [Mus musculus] sp|P17078|RL35_RAT 60S RIBOSOMAL PROTEIN L35 pir||R5RT35 ribosomal protein L35, cytosolic [validated] - rat emb|CAA36001.1| (X51705) ribosomal protein L35 (AA 1-123) [Rattus rattus] dbj|BAB27082.1| (AK010639) putative [Mus musculus] dbj|BAB28169.1| (AK012335) putative [Mus musculus]	37.1	32	0.15
00448_Ci_ot	1	AAH03241.1	AAH03241 (BC003241) Unknown (protein for MGC:6373) [Mus musculus]	29.7	39	7.5	NP_199647.1	putative protein [Arabidopsis thaliana] dbj|BAA98193.1| (AP000372) gb|AAF02158.1~gene_id:K23F3.8~similar to unknown protein [Arabidopsis thaliana]	34.8	38	0.85

00485_Ci_ot	1	No Match					AAK95131.1	(AF401559) ribosomal protein L7 [Ictalurus punctatus]	197	70	8.00E-50
00486_Ci_ot	1	BAA11580.1	(D82816) product is unknown [Gallus gallus]	34.4	26	1.1	NP_354601.1	AGR_C_2959p [Agrobacterium tumefaciens] gb|AAK87386.1| (AE008082) AGR_C_2959p [Agrobacterium tumefaciens]	95.6	56	1.00E-19
00487_Ci_ot	1	No Match					BAB67790.1	(AB067484) KIAA1897 protein [Homo sapiens]	33.6	29	1.9
00490_Ci_ot	1	AAA86693.1	(U17961) p62 [Mus musculus]	32.8	39	3.3	No Match				
00491_Ci_ot	1	BAB47152.1	(AB027502) vascular endothelial cell specific protein 16 [Rattus norvegicus]	32.5	51	4.3	No Match				
00492_Ci_ot	1	NP_040477.1	| unidentified open reading frame; putative [Xanthomonas phage Cf1c] >gi|281265|pir||S26824 hypothetical protein - phage Cf1c >gi|166170|gb|AAA32201.1| (M57538) unidentified open reading frame; putative [Xanthomonas phage Cf1c]	36	37	0.38					
00493_Ci_ot	1	No Match					No Match				
00494_Ci_ot	1	No Match					BAB64303.1	(AB030838) beta-conglycinin alpha prime subunit [Glycine max]	41.4	29	0.008
00495_Ci_ot	1	AAF57886.1	(AE003804) CG17288 gene product [Drosophila melanogaster]	32.8	32	3.3	T20112	hypothetical protein C50F4.5 - Caenorhabditis elegans emb|CAA94740.1| (Z70750) Histone H2B, contains similarity to Pfam domain: PF00125 (Core histone H2A/H2B/H3/H4), Score=191.2; E-value=5.4e-54, N=1 [Caenorhabditis elegans]	157	66	9.00E-38
00497_Ci_ot	1	P79331	ATS2_BOVIN ADAM-TS 2 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 2) (ADAMTS-2) (ADAM-TS2) (PROCOLLAGEN I/II AMINO-PROPEPTIDE PROCESSING ENZYME) (PROCOLLAGEN I N-PROTEINASE) (PC I-NP) (PROCOLLAGEN N-ENDOPEPTIDASE) (PNPI) >gi|7513524|pir||T18517 procollagen N-endopeptidase (EC 3.4.24.14) I - bovine >gi|1865716|emb|CAA65253.1| (X96389) procollagen I N-proteinase [Bos taurus]	31.7	33	7.4	AAL09328.1	AF302806_1 (AF302806) steroleosin [Sesamum indicum] gb|AAL13315.1|AF421889_1 (AF421889) steroleosin [Sesamum indicum]	47.6	29	1.00E-04
00498_Ci_ot	1	No Match					D71606	hypothetical protein PFB0800c - *malaria parasite* (Plasmodium falciparum) gb|AAC71949.1| (AE001418) hypothetical protein [Plasmodium falciparum]	33.6	28	1.5
00499_Ci_ot	1	NP_371197.1	| hypothetical protein [Staphylococcus *aureus subsp. aureus* Mu50] >gi|15926350|ref|NP_373883.1| hypothetical protein, similar to sugar efflux transpoter [Staphylococcus aureus subsp. aureus N315] >gi|13700564|dbj|BAB41861.1| (AP003131) ORFID:SA0628~hypothetical protein, similar to sugar efflux transpoter [Staphylococcus aureus subsp. aureus N315] >gi|14246442|dbj|BAB56835.1| (AP003360) hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]	31.7	46	7.4	NP_280613.1	Vng1900c [Halobacterium sp. NRC-1] sp|Q9HNX7|PPNK_HALN1 PROBABLE INORGANIC POLYPHOSPHATE/ATP-NAD KINASE (POLY(P)/ATP NAD KINASE) gb|AAG20093.1| (AE005089) Vng1900c [Halobacterium sp. NRC-1]	33.6	37	1.9
00500_Ci_ot	1	EDBEIF	immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser)	32.8	44	3.3					
00501_Ci_ot	1	No Match					No Match				
00503_Ci_ot	1	NP_280760.1	| thermosome subunit beta; CctB [Halobacterium sp. NRC-1] >gi|10581511|gb|AAG20240.1| (AE005099) thermosome subunit beta; CctB [Halobacterium sp. NRC-1]	31.7	27	7.4	NP_004825.1	mitogen-activated protein kinase kinase kinase kinase 4; HPK/GCK-like kinase [Homo sapiens] gb|AAD16137.1| (AF096300) HPK/GCK-like kinase HGK [Homo sapiens]	202	80	2.00E-51
00504_Ci_ot	1	NP_189514.1	| hypothetical protein [Arabidopsis thaliana] >gi|11994779|dbj|BAB03169.1| (AP002057) gene_id:T19N8.1~pir||B71428~similar to unknown protein [Arabidopsis thaliana]	32.1	31	5.7	No Match				
00505_Ci_ot	1	AAK12638.1	AF317653_1 (AF317653) *G protein-coupled receptor* [Homo sapiens]	38.3	37	0.075	P47961	RS4_CRIGR 40S RIBOSOMAL PROTEIN S4 dbj|BAA05485.1| (D26473) Ribosomal Protein [Cricetulus griseus]	223	76	1.00E-57
00508_Ci_ot	1	No Match					AAF47305.1	(AE003465) RpL19 gene product [Drosophila melanogaster]	51.5	46	3.00E-06
00509_Ci_ot	1	NP_062854.1	| ORF8 [*Physarum polycephalum*] >gi|9712207|dbj|BAB08088.1| (AB027295) ORF8 [Physarum polycephalum]	32.8	28	3.3	CAC04184.1	(AL353771) dJ677H15.2 (*splicing factor, arginine/serine-rich* 11) [Homo sapiens]	40.6	24	0.014
00510_Ci_ot	1	NP_193373.1	| hypothetical protein [Arabidopsis thaliana] >gi|7485179|pir||G71430 hypothetical protein - Arabidopsis thaliana >gi|2244997|emb|CAB10417.1| (Z97341) hypothetical protein [Arabidopsis thaliana] >gi|7268389|emb|CAB78682.1| (AL161543) hypothetical protein [Arabidopsis thaliana]	31.3	34	9.7	T23469	hypothetical protein K08E7.3 - Caenorhabditis elegans emb|CAB01225.1| (Z77666) predicted using Genefinder~contains similarity to Pfam domain: PF00610 (Domain found in Dishevelled, Egl-10, and Pleckstrin), Score=88.1, E-value=5.8e-23, N=1~cDNA EST EMBL:T02284 comes from this gene~cDNA EST yk21a11.5 comes from this gene~cD>	38.7	28	0.058
00512_Ci_ot	1	AAB03346.1	(U62317) hypothetical protein 384D8_7 [Homo sapiens]	31.3	35	9.7					
00514_Ci_ot	1	No Match					No Match				
00516_Ci_ot	1	No Match					AAF48000.2	(AE003485) CG11122 gene product [Drosophila melanogaster]	41.4	34	0.009
00517_Ci_ot	1	No Match					AAF34413.1	AF172282_2 (AF172282) hypothetical protein [Oryza sativa]	32.1	34	4.7
00518_Ci_ot	1	AAD56727.1	(AF124729) acinusS' [Mus musculus]	32.1	34	5.7	BAA32303.1	(AB007927) KIAA0458 protein [Homo sapiens]	43.4	29	0.002
00519_Ci_ot	1	BAB23506.1	(AK004723) putative [Mus musculus]	34.4	39	1.1	No Match				
00523_Ci_ot	1	CAA08811.1	(AJ009756) 1,2-beta-fructan 1F-fructosyltransferase [Helianthus tuberosus]	32.8	32	3.3	NP_033302.1	simple repeat sequence-containing transcript [Mus musculus] sp|Q06666|T2_MOUSE OCTAPEPTIDE-REPEAT PROTEIN T2 pir||S71512 hypothetical protein T2 - mouse emb|CAA48048.1| (X67863) T2 [Mus musculus]	37.9	29	0.091
00524_Ci_ot	1	T28980	hypothetical protein T28A11.15 - Caenorhabditis elegans >gi|1699122|gb|AAC48119.1| (U80027) Hypothetical protein T28A11.15 [Caenorhabditis elegans]	33.6	48	1.9	NP_418862.1	translation initiation factor IF-2 [Caulobacter crescentus] gb|AAK22030.1| (AE005678) translation initiation factor IF-2 [Caulobacter crescentus]	38.3	31	0.068
00526_Ci_ot	1	S37581	probable acyltransferase - Mycobacterium leprae	35.6	38	0.5	BAB62745.1	(AB055428) membrane-bound alkaline phosphatase [Bombyx mori]	33.6	43	1.9
00527_Ci_ot	1	NP_357531.1	| AGR_L_3482p [Agrobacterium tumefaciens] >gi|15160347|gb|AAK90316.1| (AE008376) AGR_L_3482p [Agrobacterium tumefaciens]	32.1	39	5.7					

00528_Ci_ot	1	No Match					P08798	PSV_DICDI PRESPORE VESICLE PROTEIN PRECURSOR (PSV) pir||S28358 prespore vesicle protein - slime mold (Dictyostelium discoideum) emb|CAA40438.1| (X57149) prespore vesicle protein [Dictyostelium discoideum]	42.2	25	0.005
00530_Ci_ot	1	BAA00447.1	(D00570) open reading frame (251 AA) [Mus musculus]	32.1	35	5.7					
00531_Ci_ot	1	No Match									
00532_Ci_ot	1	No Match					No Match				
00533_Ci_ot	1	AAF54668.1	(AE003692) CG17309 gene product [Drosophila melanogaster]	36.7	43	0.22	No Match				
00534_Ci_ot	1	No Match					T28734	hypothetical protein F26G5.9 - Caenorhabditis elegans gb|AAC48041.1| (AF022974) Hypothetical protein F26G5.9 [Caenorhabditis elegans] gb|AAD47816.1|AF164625_1 (AF164625) tandem-array-modifier protein [Caenorhabditis elegans]	33.6	35	1.9
00535_Ci_ot	1	NP_148061.1	| hypothetical protein [Aeropyrum pernix] >gi|7516627|pir||A72542 hypothetical protein APE1622 - Aeropyrum pernix (strain K1) >gi|5105309|dbj|BAA80622.1| (AP000062) 370aa long hypothetical protein [Aeropyrum pernix]	32.8	32	3.3	NP_147204.1	membrane-associated ATPase beta chain [Aeropyrum pernix] sp|Q9YF36|VATB_AERPE V-TYPE ATP SYNTHASE BETA CHAIN (V-TYPE ATPASE SUBUNIT B) pir||D72733 probable membrane-associated ATPase beta chain APE0404 - Aeropyrum pernix (strain K1) dbj|BAA79360.1| (AP000059) 466aa long hypothetical membrane-associated ATPase beta chain [Aeropyrum pernix]	34.4	29	1.1
00536_Ci_ot	1	CAA08799.1	(AJ009721) capsid protein [Feline calicivirus]	32.5	48	4.3	AAK64503.1	AC074202_5 (AC074202) L4946.5 [Leishmania major]	32.5	29	4.3
00538_Ci_ot	1	NP_105093.1	| hypothetical protein, contains similarity to NADH oxidase [Mesorhizobium loti] >gi|14024275|dbj|BAB50879.1| (AP003003) hypothetical protein [Mesorhizobium loti]	32.8	58	3.3	No Match				
00540_Ci_ot	1	No Match					No Match				
00542_Ci_ot	1	No Match					NP_188532.1	hypothetical protein [Arabidopsis thaliana]	40.6	27	0.013
00543_Ci_ot	1	AAG13529.1	AC023240_2 (AC023240) putative secretory protein [Oryza sativa]	32.5	31	4.3	BAA20797.2	(AB002337) KIAA0339 protein [Homo sapiens]	34	37	1.3
00544_Ci_ot	1	NP_341594.1	| ATP-dependent helicase [Sulfolobus solfataricus] >gi|13813146|gb|AAK40384.1| (AE006643) ATP-dependent helicase [Sulfolobus solfataricus]	32.8	39	3.3					
00545_Ci_ot	1	AAA66558.1	(M21943) immediate-early phosphoprotein [Saimiriine herpesvirus 2]	32.5	47	4.3					
00546_Ci_ot	1	No Match									
00548_Ci_ot	1	No Match					XP_045498.1	KIAA1810 protein [Homo sapiens]	33.2	43	2.5
00549_Ci_ot	1	NP_196142.1	| unknown protein [Arabidopsis thaliana] >gi|10176735|dbj|BAB09966.1| (AB010692) gene_id:K18I23.3~unknown protein [Arabidopsis thaliana]	32.8	34	3.3	No Match				
00550_Ci_ot	1	NP_015446.1	| THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3.; Thi22p [Saccharomyces cerevisiae] >gi|2132289|pir||S69014 hypothetical protein YPR121w - yeast (Saccharomyces cerevisiae) >gi|1066472|gb|AAB68062.1| (U40828) Weak similarity to hypothetical protein 3 (A. thaliana, PIR accession number S23315) [Saccharomyces cerevisiae]	31.3	29	9.7	NP_035946.1	Ras-GTPase-activating protein (GAP<120>) SH3-domain-binding protein 2 [Mus musculus] gb|AAC53553.1| (U65313) ras-GTPase-activating protein SH3-domain binding protein [Mus musculus]	32.5	34	4.3
00551_Ci_ot	1	No Match					S33165	cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - basidiomycete (Phanerochaete chrysosporium) pir||S44716 cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - basidiomycete (Phanerochaete chrysosporium) emb|CAA80252.1| (Z22527) cellulase [Phanerochaete chrysosporium]	33.6	31	1.9
00552_Ci_ot	1	NP_233030.1	| conserved hypothetical protein [Vibrio cholerae] >gi|11354803|pir||G82433 conserved hypothetical protein VCA0641 [imported] - Vibrio cholerae (group O1 strain N16961) >gi|9658056|gb|AAF96542.1| (AE004394) conserved hypothetical protein [Vibrio cholerae]	32.8	47	3.3					
00553_Ci_ot	1	S39237	gene C3 protein - tomato yellow leaf curl virus >gi|433854|emb|CAA82239.1| (Z28390) C3 [tomato yellow leaf curl virus]	33.6	39	1.9	P10164	PRP2_RAT ACIDIC PROLINE-RICH PROTEIN PRP25 PRECURSOR pir||B29149 proline-rich protein - rat (fragment) gb|AAA41948.1| (M11901) proline-rich salivary protein [Rattus norvegicus]	46.5	38	3.00E-04
00554_Ci_ot	1	XP_002501.4	| peptidyl-prolyl isomerase G (cyclophilin G) [Homo sapiens] >gi|14724730|ref|XP_027423.1| hypothetical protein XP_027423 [Homo sapiens]	32.8	32	3.3	NP_072096.1	hypothetical protein AF053356-CDS2; hypothetical protein AF053356_CDS2 [Homo sapiens] ref|XP_017026.2| hypothetical protein AF053356-CDS2 [Homo sapiens] gb|AAC78792.1| (AF053356) ORF2 [Homo sapiens]	34.4	37	1.1
00555_Ci_ot	1	No Match					AAF03888.1	AF187068_1 (AF187068) proboscipedia ortholog [Tribolium castaneum]	31.7	40	2.7
00556_Ci_ot	1	No Match					NP_056965.1	RIG-like 7-1; Dickkopf gene 3 [Homo sapiens] gb|AAB92664.1| (AF034208) RIG-like 7-1 [Homo sapiens]	30.9	31	5
00558_Ci_ot	1	D34768	ORF4 protein - Orf virus (strain NZ2) >gi|332566|gb|AAA46790.1| (M30023) ORF4 [Orf virus]	36.7	43	0.22	P34695	TF3A_RANPI TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA) pir||JC1441 transcription factor IIIA - northern leopard frog gb|AAA49534.1| (M85211) transcription factor IIIA [Rana pipiens] emb|CAA41260.1| (X58369) transcription factor IIIA [Rana pipiens]	29.7	35	6
00559_Ci_ot	1	No Match					No Match				
00560_Ci_ot	1	No Match					T12698	extensin - common sunflower gb|AAA33375.1| (M76546) hydroxyproline-rich protein [Helianthus annuus] prf||1908433A Hyp-rich glycoprotein [Helianthus annuus]	33.6	39	2

00561_Ci_ot	1	No Match					NP_006697.1	transcription factor CA150 [Homo sapiens] pir||T08599 probable transcription factor CA150 - human gb|AAB80727.1| (AF017789) putative transcription factor CA150 [Homo sapiens]	32.5	38	2.7
00563_Ci_ot	1	NP_113253.1	| 60S ribosomal protein L23 [Guillardia theta] >gi|13794438|gb|AAK39813.1|AF165818_21 (AF165818) 60S ribosomal protein L23 [Guillardia theta]	31.7	40	7.4	No Match				
00564_Ci_ot	1	NP_189287.1	| hypothetical protein [Arabidopsis thaliana] >gi|9293934|dbj|BAB01837.1| (AB028611) CHP-rich zinc finger protein-like [Arabidopsis thaliana]	33.6	32	1.9	T21503	hypothetical protein F28D9.1 - Caenorhabditis elegans emb|CAB04214.2| (Z81518) contains similarity to Pfam domain: PF01480 (PWI domain), Score=151.2, E-value=5.7e-42, N=1~cDNA EST yk113g9.3 comes from this gene~cDNA EST yk113g9.5 comes from this gene~cDNA EST yk166b11.3 comes from this gene~cDNA EST yk166b11.5 comes from>	41.4	32	0.009
00565_Ci_ot	1	No Match					No Match				
00566_Ci_ot	1	No Match									
00567_Ci_ot	1	NP_216670.1	| ftsW [Mycobacterium tuberculosis H37Rv] >gi|15841646|ref|NP_336683.1| cell division protein FtsW [Mycobacterium tuberculosis CDC1551] >gi|2493593|sp|O06223|FTWH_MYCTU HYPOTHETICAL 56.3 KDA FTSW-LIKE PROTEIN RV2154C >gi|7477917|pir||F70579 probable cell division protein FtsW - Mycobacterium tuberculosis (strain H37RV) >gi|2104324|emb|CAB08673.1| (Z95388) ftsW [Mycobacterium tuberculosis H37Rv] >gi|13881898|gb|AAK46497.1| (AE007068) cell division protein FtsW [Mycobacterium tuberculosis CDC1551]	34	29	1.5	No Match				
00568_Ci_ot	1	No Match					AAD11782.1	(AF091239) c-13 antigen [Plasmodium falciparum]	30.1	30	6.7
00569_Ci_ot	1	No Match					XP_005389.4	testis-specific protein kinase 1 [Homo sapiens]	39.9	34	0.02
00570_Ci_ot	1	CAB55617.1	(AL117384) hypothetical protein L5883.06 [Leishmania major]	33.2	36	2.5	No Match				
00571_Ci_ot	1	BAB21544.1	(AB022782) hydroxyproline-rich glycoprotein [Arabidopsis thaliana]	32.5	30	4.3	S71753	repellent protein 1 precursor - smut fungus (Ustilago maydis) gb|AAC49419.1| (U56826) repellent protein [Ustilago maydis]	34.8	33	0.85
00572_Ci_ot	1	No Match					BAB69705.1	(AB072736) hypothetical protein [Macaca fascicularis]	32.1	47	5.7
00573_Ci_ot	1	No Match									
00574_Ci_ot	1	No Match									
00576_Ci_ot	1	NP_187512.1	| hypothetical protein [Arabidopsis thaliana] >gi|5923665|gb|AAD56316.1|AC009326_3 (AC009326) hypothetical protein [Arabidopsis thaliana] >gi|6403487|gb|AAF07827.1|AC010871_3 (AC010871) hypothetical protein [Arabidopsis thaliana]	37.1	28	0.17	AAF45638.1	(AE003421) sta gene product [Drosophila melanogaster]	66	58	4.00E-10
00577_Ci_ot	1	No Match					XP_051716.1	hypothetical protein XP_051716 [Homo sapiens]	132	75	2.00E-30
00578_Ci_ot	1	No Match					T39040	hypothetical protein SPAC6F6.06c - fission yeast (Schizosaccharomyces pombe) emb|CAB11730.1| (Z98981) possibly involved in cell polarity; by similarity to yeast rax2 [Schizosaccharomyces pombe]	31.3	31	9.7
00579_Ci_ot	1	No Match					NP_003583.1	cullin 1 [Homo sapiens] sp|Q13616|CUL1_HUMAN CULLIN HOMOLOG 1 (CUL-1) gb|AAC50544.1| (U58087) Hs-CUL-1 [Homo sapiens]	83.5	75	2.00E-15
00580_Ci_ot	1	No Match					S01717	Balbiani ring protein 1-gamma (clone pCp20) - midge (Chironomus pallidivittatus) (fragment) emb|CAA29737.1| (X06431) gamma protein constant region [Chironomus pallidivittatus]	33.6	42	1.9
00599_Ci_ot	1	NP_014394.1	| an ORF of unknown function located in a centromeric region duplicated between chromosomes III and XIV; Hrb1p [Saccharomyces cerevisiae] >gi|730962|sp|P38922|HRB1_YEAST HRB1 PROTEIN (TOM34 PROTEIN) >gi|630174|pir||S45459 TOM34 protein - yeast (Saccharomyces cerevisiae) >gi|495308|gb|AAA64803.1| (U02536) Tom34p [Saccharomyces cerevisiae] >gi|496714|emb|CAA54378.1| (X77114) N2009 [Saccharomyces cerevisiae] >gi|1301818|emb|CAA95863.1| (Z71280) ORF YNL004w [Saccharomyces cerevisiae]	36	30	0.38	BAB07977.1	(AP002524) hypothetical protein~similar to Drosophila melanogaster chromosome 3L, CG10171 gene product [Oryza sativa] dbj|BAB63468.1| (AP002903) hypothetical protein~similar to Drosophila melanogaster chromosome 3L, CG10171 gene product [Oryza sativa]	35.2	44	0.65
00601_Ci_ot	1	No Match									
00608_Ci_ot	1	CAA88026.1	(Z47983) PstC-2.tub [Mycobacterium tuberculosis]	32.8	44	3.3	BAA06441.1	(D30766) Feline herpesvirus type 1 immediate early protein [Feline herpesvirus 1]	34.4	33	1.1
00615_Ci_ot	1	AAF14717.1	AF197725_1 (AF197725) maturase [Triglochin maritimum]	32.5	31	2.5	No Match				
00617_Ci_ot	1	NP_031760.1	| procollagen, type IV, alpha 3 [Mus musculus] >gi|5739385|gb|AAD50449.1|AF169387_1 (AF169387) alpha 3 collagen IV [Mus musculus]	30.5	47	3.4	No Match				
00626_Ci_ot	1	T25220	hypothetical protein T24B8.4 - Caenorhabditis elegans >gi3880148embCAA92756.1 (Z68338) predicted using Genefinder~contains similarity to Pfam domain: PF02205 (Wiskott Aldrich syndrome homology region 2), Score=43.6, E-value=1.5e-09, N=2~cDNA EST yk96d7.5 comes from this gene~cDNA EST yk96d7.3 comes from this gene~cDNA EST yk76d1>	39.1	44	0.042	AAG43829.1	AF212370_1 (AF212370) spinster type V [Drosophila melanogaster]	34.4	43	0.61
00627_Ci_ot	1	T45053	hypothetical protein Y39B6B.aa [imported] - Caenorhabditis elegans >gi6434467embCAB60932.1 (AL132896) predicted using Genefinder; preliminary prediction [Caenorhabditis elegans] >gi15209347embCAC51071.1 (AL132948) predicted using Genefinder~preliminary prediction [Caenorhabditis elegans]	33.2	26	2.5	NP_360661.1	organic solvent tolerance protein homolog [Rickettsia conorii] gb|AAL03562.1| (AE008654) organic solvent tolerance protein homolog [Rickettsia conorii]	32.5	41	4.3

00628_Ci_ot	1	B21124	Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster) (fragment)	31.7	32	7.4					
00630_Ci_ot	1	AAD48017.1	AF165529_1 (AF165529) chlorophyll a/b binding protein [Rumex palustris]	34.4	30	1.1	O01639	E75_CHOFU ECDYSONE-INDUCIBLE PROTEIN E75 gb|AAB52717.1| (U63930) hormone receptor 75 [Choristoneura fumiferana]	34	44	1.5
00650_Ci_ot	1	S69205	stripe a/b protein - fruit fly (Drosophila melanogaster) >gi1147789gbAAB02355.1 (U42403) stripe a protein [Drosophila melanogaster]	30.5	40	3.3					
00726_Ci_ot	1	No Match					XP_037229.1	hypothetical protein FLJ11467 [Homo sapiens]	39.5	55	0.007
00737_Ci_ot	1	NP_251777.1	hypothetical protein [Pseudomonas aeruginosa] >gi11349799pirC83259 hypothetical protein PA3087 [imported] - Pseudomonas aeruginosa (strain PAO1) >gi9949196gbAAG06475.1AE004733_2 (AE004733) hypothetical protein [Pseudomonas aeruginosa]	41.4	44	0.003	NP_251777.1	hypothetical protein [Pseudomonas aeruginosa] pir||C83259 hypothetical protein PA3087 [imported] - Pseudomonas aeruginosa (strain PAO1) gb|AAG06475.1|AE004733_2 (AE004733) hypothetical protein [Pseudomonas aeruginosa]	54.3	58	3.00E-07
00756_Ci_ot	1	NP_004116.1	guanine nucleotide binding protein 10 [Homo sapiens] >gi11429220refXP_005556.1 guanine nucleotide binding protein 10 [Homo sapiens] >gi1730222spP50151GBGA_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-10 SUBUNIT >gi2119454pirI39158 GTP-binding regulatory protein gamma-10 chain - human >gi995919gbAAC50205.1 (U31383) G protein gamma-10 subunit [Homo sapiens] >gi12313894embCAC22155.1 (AL135787) bA16L21.3 (guanine nucleotide binding protein 10) [Homo sapiens] >gi14714507gbAAH10384.1AAH10384 (BC010384) guanine nucleotide binding protein 10 [Homo sapiens] >gi15929554gbAAH15206.1AAH15206 (BC015206) Similar to guanine nucleotide binding protein 10 [Homo sapiens]	46.5	37	2.00E-04	NP_150283.1	G-protein gamma 8 subunit [Homo sapiens] sp|Q9UK08|GBG8_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-8 SUBUNIT (GAMMA-9) gb|AAF04569.1|AF188179_1 (AF188179) G-protein gamma 8 subunit [Homo sapiens]	43	39	0.002
00772_Ci_ot	1	XP_036527.1	serine/arginine repetitive matrix 2 [Homo sapiens]	46.5	24	2.00E-04	T28625	variant-specific surface protein 3 - malaria parasite (Plasmodium falciparum) gb|AAA75397.1| (L40609) variant-specific surface protein [Plasmodium falciparum]	31.7	28	7.4