

Annotated expressed sequence tags and xenobiotic detoxification in the aphid *Myzus persicae* (Sulzer)

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Abstract Aphids (Hemiptera: Aphididae) are phytophagous insects that are important agricultural pests. The enormous negative economic impacts caused by aphids worldwide are well known, and are mostly due to their high multiplication rate and the transmission of phytopathogenic viruses. Aphid management strategies mainly involve chemical treatments which are pollutants and are increasingly inefficient, since aphids have developed multiple insecticide-resistant mechanisms. Among the most economically important species is the green peach aphid *Myzus persicae* Sulzer (Aphididae: Macrosiphini), which is able to colonize a wide range of host plants belonging to many different families, and transmits numerous plant viruses. Because of its large prevalence, *M. persicae* has been the target of massive insecticide treatments; consequently, it has evolved several insecticide-resistant mechanisms. In this work, a collection of expressed genes from *M. persicae* is presented in order to identify putative genes involved in xenobiotic detoxification. After cDNA cloning and sequencing, 959 expressed sequence tags (EST) were annotated. Most sequences matched known genes corresponded to metabolism proteins (26%), ribosomal proteins (23%) and structural proteins (8%). Among them, several sequences corresponded to proteins putatively involved in sensing, degradation or detoxification of plant xenobiotic products.

Key words aphid, detoxification, EST, genomics, insect-plant relationships, *Myzus persicae*
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Introduction

Aphids are major crop pests worldwide. There are three main reasons for their economic importance. First, due to their clonal reproduction and telescoping generations, aphids can rapidly build up large populations and reach economic-impact thresholds. Second, many aphids act as vectors of plant viruses that may induce huge yield losses.

Third, aphids have developed in recent times multiple detoxification mechanisms in response to massive insecticide treatments and plant resistance genes released into new varieties. Aphids have indeed evolved resistance mechanisms against most insecticides and are regularly reported to overcome resistant crops. The green peach aphid, *Myzus persicae*, is a cosmopolitan and polyphagous species. Because of its ability to adapt on many plants, to transmit plant viruses in more than 30 plant families (Hill, 1983) and to develop resistance to all major insecticide classes (Devonshire *et al.*, 1998), *M. persicae* is considered as one of the most important insect pest worldwide. Insecticide resistance has been intensively studied these last three decades and at least four mechanisms have been

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identified, all of them being found in field populations of *M. persicae*: (i) the overproduction of detoxifying esterases, either E4 or FE4, conferring resistance to organophosphates (OP) and pyrethroids; (ii) the modification of the acetylcholinesterase (AChE), the target of OPs and carbamates, providing resistance against dimethyl carbamate insecticides (Moores & Devonshire, 2000); (iii) the *kdr* mutation of the voltage-gated sodium channel (Martinez-Torres *et al.*, 1999), which is the target of pyrethroids; and (iv) the *rdl* mutation of the GABA receptor (Anthony *et al.*, 1998), which is the target of cyclodiene insecticides. By contrast, mechanisms involved in the detoxification of plant defenses in aphids are poorly known. Cytochrome P450-dependant monooxygenases (MOs) and glutathione S-transferases (GSTs) have been reported as important mechanisms involved in detoxification of xenobiotic compounds from diverse origins (Feyereisen, 1999; Scott, 1999; Hemingway, 2000; Enayati *et al.*, 2005). In several aphid species the activities of these detoxifying enzymes have been associated with host-plant allelochemicals (Leszczynski & Dixon, 1992; Leszczynski *et al.*, 1994; Figueroa *et al.*, 1999; Loayza-Muro *et al.*, 2000; Francis *et al.*, 2001; Mukanganyama *et al.*, 2003) and insecticides (Owusu & Horiike, 1996; Rufingier *et al.*, 1999; Wu & Miyata, 2005), with GSTs being particularly important in the detoxification of glucosinolates for *M. persicae* feeding on cruciferous host-plants (Francis *et al.*, 2005).

Transcriptomic approaches constitute a powerful tool to identify new genes and gene functions, and have been successfully applied to many organisms. It is only recently that comprehensive genomic analyses have been performed on aphids (Hunter *et al.*, 2003; Tagu *et al.*, 2004). Since June 2003, the International Aphid Genomics Consortium (IAGC) has decided to develop and share tools and data for the different disciplines of genomics (e.g. transcriptomics, genetic maps, bioinformatics) in order to stimulate fundamental research on mechanisms involved in plant damage caused by aphids (<http://www.princeton.edu/~dstern/AphidResLinks.htm>). The main efforts over the last three years have focused on a single species, the pea aphid *Acyrtosiphon pisum* (Harris), for which a large collection of expressed sequence tags (ESTs) has been obtained (Sabater-Muñoz *et al.*, 2006) and the genome sequence is already available as traces at the National Center for Biotechnology Information (NCBI). While this species is well adapted for laboratory studies (e.g., large body size, rapid development), it is not a major crop pest. For this reason the IAGC decided as a second step, to develop genomic tools applied to agronomically relevant aphid pest species such as *M. persicae*. This study describes a set of expressed genes in *M. persicae* genes, with an emphasis on

proteins putatively involved in detoxification processes related to host plant use and insecticide resistance mechanisms.

Materials and Methods

Myzus persicae clone mp1 (Terradot *et al.*, 1999) was collected in a potato field at Roscoff (Bretagne, western France) in 1966 and was maintained in conditions of continuous parthenogenetic reproduction under long photoperiods (L:D, 16:8) and warm temperatures (20°C). Five hundred wingless adult parthenogenetic females were collected, immediately frozen in liquid nitrogen, and kept at -80°C until use. Total RNA was extracted using the RNeasy Plant Mini Kit (Qiagen, Hilden, Germany) in the RTL extraction buffer, following the manufacturer's instructions. Poly-A RNAs were purified from 600 mg of total RNA by using the PolyAtract mRNA Isolation System III kit from Promega (Madison, WI, USA). Complementary DNA synthesis and cloning were performed with the Creator™ Smart™ cDNA Library Construction Kit (BD Biosciences Clontech, Palo Alto, CA, USA) as described in Tagu *et al.* (2004). Ligation products were electroporated in electrocompetent *Escherichia coli* TOP10 cells (Invitrogen, Paisley, UK). Bacterial colonies ($n = 1\ 920$) were inoculated into 96-well plates containing selective LB medium and 10% (v/v) glycerol, and grown overnight in standing culture at 37°C, and stored at -80°C. Backup plates were also produced. Polymerase chain reaction (PCR) of cDNA inserts was performed as described by Tagu *et al.* (2004) from defrosted bacterial glycerol stock as a template. Excess primers and nucleotides were removed by filtration on Sephadex (SigmaSpin Post-Reaction Clean-Up Plates Kit, Sigma, St Louis, Missouri, USA). The resulting purified PCR products were then rearranged in 96-well plates and used as templates (30–50 ng) for a sequencing reaction (Tagu *et al.*, 2004) at the sequencing facilities of OUEST-Genopole® (Roscoff, France). The name given to each EST corresponds to the name of the cDNA library (MpW for *Myzus persicae*, Whole-body), followed by the Roman number of the microplate, the letter of the row in the microplate and the Arabic number of the column in the microplate (e.g. II-G10). Sequences ($n = 959$) have been deposited to dbEST database under the accession numbers DW361650–DW362608. Sequence processing was performed by using the Staden package (<http://staden.sourceforge.net/>) to clean vector and adaptor sequences and poly-A tails using default parameters. Sequences were then assembled (Gap4 from the Staden Package) to form contigs. We performed different Blast analyses on contig sequences including BlastX, tBlastX

and BlastN, but only BlastX gave the more reliable data. Hence, the contigs were annotated using BlastX (Altschul *et al.*, 1997) against UniProt (Bairoch *et al.*, 2005): only significant matches with an E-value $< 1.0 \times 10^{-5}$ was considered to identify known genes or open reading frames. Additionally, a BlastN annotation was also performed to identify putative non-coding RNA (e.g. rRNA) or non insect DNA (e.g. bacteria) sequences.

Results

EST and contigs production

The *M. persicae* cDNA library was constructed from poly-A RNA extracted for whole individuals produced under parthenogenetic reproduction. About 100 000 bacterial colonies were obtained, and 1 920 bacteria were individually kept as glycerol stocks. Amplified inserts with small size (< 600 bp including 478 bp of vector) were eliminated before sequencing. A total of 1 042 5'-end sequences of the selected cDNAs were obtained. Neither yeast nor *E. coli* contaminants were found. Virtually all aphids harbor the bacteria *Buchnera aphidicola*, their primary endosymbiont, which contains an A/T rich genome (Shigenobu *et al.*, 2000) that may act as a template for the oligo(dT) priming during first strand cDNA synthesis (Tagu *et al.*, 2004). Here, no *Buchnera* contaminant sequences were detected. After all these filtration steps, the final set of *M. persicae* ESTs consisted of 959 sequences.

Clusters and contigs were produced from these 959 *M. persicae* sequences. A total of 532 contigs were identified. Ten corresponding to rRNA sequences were eliminated and 12 corresponding to mitochondrial encoded proteins were identified (Appendix 1).

Functional annotation

On the basis of sequence similarity (using BlastX) to proteins with known function in public databases, a putative cellular role was assigned to 63% of the *M. persicae* contigs (Appendix 1). The remaining 37% fell into the "hypothetical" (2%) or "no hit" (35%) categories (Fig. 1). This proportion was similar to that observed for other aphid EST projects such as *T. citricida* (Hunter *et al.*, 2003), *Rhopalosiphum padi* (Tagu *et al.*, 2004) or *Acyrtosiphon pisum* (Sabater-Muñoz *et al.*, 2006). The largest proportion of functionally assigned sequences fell into three functional categories: metabolism (26%), ribosomal proteins (23%), and structure (8%). The distribution was very similar to ESTs from *R. padi* (Tagu *et al.*, 2004) obtained from the same type of material (whole body of wingless

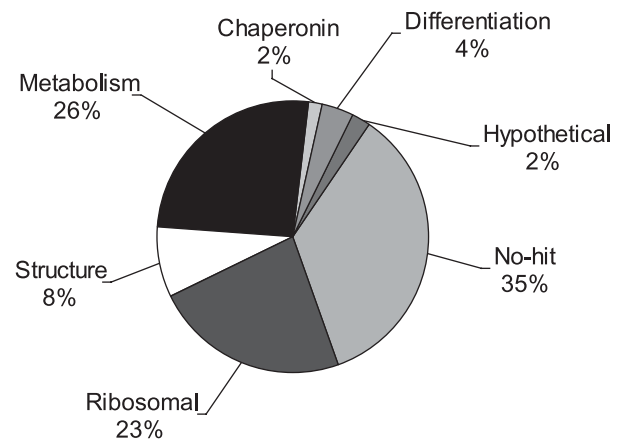


Fig. 1 Distribution by functional categories of 532 contig sequences characterized in this study, after a sequence similarity analysis using BlastX against proteins with known function in public databases.

parthenogenetic individuals). This indicated that such a small collection of ESTs mainly revealed the most expressed genes (e.g. ribosomal proteins) as well as the house-keeping function expressed in the whole-body (e.g. cell structure).

Discussion

Sequence homologies and origin

Many different contigs of *M. persicae* were orthologous to the same sequence from UniProt (Appendix 1). This was mainly observed for the 'Ribosomal protein' class (20 contigs were concerned) but also for 'Structural proteins' and 'Metabolism' (12 contigs). This observation was also true for the pea aphid *A. pisum* (Sabater-Muñoz *et al.*, 2006) and might reflect either a duplication of some aphid genes compared to other insect orders or allelic variation for a same gene. However, more precise studies are necessary to distinguish between true paralogues and some errors which could have occurred during EST assembly.

Xenobiotic detoxification

In the case of *M. persicae*, some of the genes identified in that EST collection may be useful for further studies on detoxification of plant allelochemicals and insecticides. A GST (Table 1) belonging to the sigma class of these enzymes which are widely distributed in insects and other animals (Enayati *et al.*, 2005) has been identified. The group of GST plays an important role in the protection against oxidative stress (Singh *et al.*, 2001; Enayati *et al.*,

2005). Furthermore, Francis *et al.* (2005) have recently isolated and characterized a homodimeric GST from *M. persicae* apparently involved in glucosinolate detoxification from cruciferous host-plants. Similarly, enhanced activity of GSTs has been associated with xenobiotic detoxification in *Sitobion avenae* and other cereal aphids reared on wheat cultivars, showing high levels of hydroxamic acids (Leszczynski & Dixon, 1992; Leszczynski *et al.*, 1994; Loayza-Muro *et al.*, 2000). Finally, this group of enzymes has also been related to insecticide resistance in *Aphis gossypii* (Owusu & Horiike, 1996), *Nasonovia ribisnigri* (Rufingier *et al.*, 1999) and *Lipaphis erysimi* (Wu & Miyata, 2005).

At least five different contigs involved in electron transfer or antioxidant activities have been identified for *M. persicae* (Table 1). Among them a cytochrome P450

monooxygenase contig from the CYP4 family has been detected. The *Cyp4* gene family has been associated with insecticide resistance in *Helicoverpa armigera* (Pittendrigh *et al.*, 1997), *Diabrotica virgifera* (Scharf *et al.*, 2001) and *Anopheles gambiae* (Ranson *et al.*, 2002). In aphids, a single report from Loayza-Muro *et al.* (2000) found an increased activity of monooxygenases, MOs, in *S. avenae* reared on wheat cultivars showing high levels of hydroxamic acids. However, it is well known that MOs are fundamental for host-plant allelochemical and insecticide detoxification mechanisms in various insect groups (Feyereisen, 1999; Scott, 1999; Scott & Wen, 2001).

Other contigs with putative functional importance for aphid host-plant interaction, including chemosensory proteins (Table 1), are related to sensing and tasting of plant compounds (Wanner *et al.*, 2005), which have been

Table 1 *Myzus persicae* contig sequence putatively involved in plant product detoxification and insecticide resistance.

Contig name	Protein	Function	Species	Reference
12-08_D03_II-H12_004	Chemosensory protein	Rapid rejection of toxic plant compounds	<i>Manduca sexta</i>	Glendinning (1996)
12-15_A12_XIX-C09_002	Juvenile hormone binding protein	Juvenile hormone transport. Target-site for insensitivity mechanism	<i>Drosophila melanogaster</i>	Shemshedini & Wilson (1990)
12-08_J03_III-A09_010	Cathepsin B-N	Processing of exogenous ingested polypeptides	<i>Aphis gossypii</i>	Deraison <i>et al.</i> (2004); Moon <i>et al.</i> (2004)
12-16_H09_VI-E10_004	Hsc70	Protein folding, translocation across membranes, lysosomal and ubiquitin-dependant degradation of cellular proteins	<i>Chironomus tentans</i>	Yoshimi <i>et al.</i> (2002)
12-15_F08_XX-F02_012	Heat shock protein	Assists the structure formation of proteins <i>in vivo</i>	<i>Callosobruchus maculatus</i>	
12-08_L09_III-E08_011	Glutathione S-transferase (GST)	Conjugation of electrophilic molecules (xenobiotic) with reduced glutathione (GSH)	<i>Aulacorthum solani</i> <i>Acyrtosiphon pisum</i>	Francis <i>et al.</i> (2001)
12-14_H07_XVI-E09_015	Cytochrome b (b5)	Electron carrier to cytochrome P450	<i>Anopheles gambiae</i>	Nikou <i>et al.</i> (2003)
12-09_L18_VII-F11_011	Cytochrome c oxidase subunit I	Belongs to complex of the mitochondrial respiratory chain electron transfer to molecular oxygen	<i>Blattella germanica</i> (L.)	Pridgeon & Liu (2003)
12-11_E15_IX-C12_006	Cytochrome P450	Binds molecular oxygen and receives electrons from NADPH	<i>Anopheles minimus</i>	Bergé <i>et al.</i> (1998); Rongnoparut <i>et al.</i> (2003)
12-08_B04_VI-E09_002	Thioredoxin 2	Antioxidative function and substrate for thioredoxin peroxidase	<i>Drosophila melanogaster</i>	Bauer <i>et al.</i> (2002)
12-14_H07_XVI-E09_015	Ubiquinol-cytochrome c reductase (Complex III)	Catalyzes the ubiquinol oxidation and cytochrome c reduction by a mechanism known as the Q cycle	<i>Calliphoraerythrocephala</i> <i>hala</i> <i>Bemisia tabaci</i>	Jewess <i>et al.</i> (2002); García-Vallve (2004)

recently identified and are involved in aphid host-plant interaction (Jacobs *et al.*, 2005). Cathepsin B (Table 1) could be related to cathepsin proteolytic activity in the digestive system of *A. pisum*, *A. gossypii* and *M. persicae* (Cristofolletti *et al.*, 2003; Rahbé *et al.*, 2003; Deraison *et al.*, 2004). Cysteine proteinase inhibitors present in artificial diets or transgenic plants were shown to reduce the activity of cathepsins of *M. persicae* and consequently to reduce its performance (Rahbé *et al.*, 2003). A contig related to juvenile hormone-binding proteins (Table 1), involved in resistance to juvenoid insecticides was also detected (Shemshedini & Wilson, 1990). Juvenile hormones have a key role in the control of aphid metamorphosis and polyphenism, and therefore juvenoid insecticides have strong effects on aphid development (Hardie *et al.*, 1996). Finally, contigs associated with the inactivation by protein folding through chaperonins were also identified (Table 1). Such proteins are involved in the ubiquitinylation necessary for targeting proteins to be degraded by proteasome and the expression of heat-shock proteins (Hsc70) related to abiotic stress from insecticides (Yoshimi *et al.*, 2002).

Conclusions

The present data represent a first step toward the identification and annotation of transcript complements in *M. persicae*. The next step will be the use of these ESTs for cDNA array-based technologies and comparative hybridizations in order to identify aphid genes involved in host plant acceptance, feeding and metabolization of host plant defense chemicals and insecticides.

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Appendix 1 *Myzus persicae* contig sequence similarities. An: accession number.

Contig name	Protein homologue	Species	UniProt An	E-value
Ribosomal proteins (n = 124)				
12-08_O12_V-F01_016	40S ribosomal protein S2 (Strings of pearls protein)	<i>Drosophila melanogaster</i>	P31009	2.0E-68
12-15_G03_XVII-G06_013	40S ribosomal protein S2	<i>Urechis caupo</i>	P49154	1.0E-49
12-08_F07_III-D02_006	40S ribosomal protein S20 (S22)	<i>Xenopus laevis</i>	P23403	4.0E-40
12-08_A07_I-E01_002	40S ribosomal protein S21	<i>Sus scrofa</i>	P63221	6.0E-29
12-11_D07_X-F01_004	40S ribosomal protein S25	<i>Drosophila melanogaster</i>	P48588	3.0E-27
12-11_B11_XI-A05_002	40S ribosomal protein S28	<i>Drosophila melanogaster</i>	Q9W334	2.0E-20
12-11_D15_XI-D01_004	40S ribosomal protein S28	<i>Drosophila melanogaster</i>	Q9W334	2.0E-20
12-11_L07_X-G04_012	40S ribosomal protein S28	<i>Drosophila melanogaster</i>	Q9W334	2.0E-20
12-16_C10_XX-G08_006	40S ribosomal protein S28	<i>Drosophila melanogaster</i>	Q9W334	2.0E-19
12-15_G02_XVII-E10_014	40S ribosomal protein S6	<i>Spodoptera frugiperda</i>	Q95V32	6.0E-82
12-15_G04_XVII-H10_014	40S ribosomal protein S8	<i>Apis mellifera</i>	O76756	9.0E-49
12-15_E08_XX-E12_010	60S acidic ribosomal protein P1 (RP21C) (Acidic ribosomal protein RPA2)	<i>Drosophila melanogaster</i>	P08570	8.0E-22
12-08_O10_V-D12_015	60S ribosomal protein L10 (QM protein homolog)	<i>Bombyx mandarina</i>	O96647	1.0E-114
12-10_D02_XIII-E01_003	60S ribosomal protein L12 (Fragment)	<i>Sus scrofa</i>	Q6QAS5	6.0E-64
12-10_H21_IV-E01_007	60S ribosomal protein L13A	<i>Spodoptera frugiperda</i>	Q962U0	4.0E-52
12-11_M08_XII-D05_014	60S ribosomal protein L13A	<i>Spodoptera frugiperda</i>	Q962U0	6.0E-21
12-09_A21_II-E04_001	60S ribosomal protein L15 (YL10)	<i>Chironomus tentans</i>	P30736	1.0E-40
12-14_E10_XVII-A01_010	60S ribosomal protein L15	<i>Drosophila melanogaster</i>	O17445	2.00E-49
12-09_N14_VII-D12_013	60S ribosomal protein L18a	<i>Drosophila melanogaster</i>	P41093	1.0E-59
12-15_B03_XVII-F05_003	60S ribosomal protein L18a	<i>Drosophila melanogaster</i>	P41093	6.0E-64
12-14_H10_XVII-A04_016	60S ribosomal protein L27A or L22 (Fragment)	<i>Platichthys flesus</i>	Q98TL6	2.0E-42
12-09_F10_VII-A12_005	60S ribosomal protein L31	<i>Spodoptera frugiperda</i>	Q7KF90	4.0E-47
12-09_P15_IV-B01_016	60S ribosomal protein L31	<i>Spodoptera frugiperda</i>	Q7KF90	3.0E-47
12-10_P22_VIII-A08_015	60S ribosomal protein L31	<i>Spodoptera frugiperda</i>	Q7KF90	1.0E-46
12-15_A10_XVIII-H08_002	60S ribosomal protein L31	<i>Spodoptera frugiperda</i>	Q7KF90	4.0E-47
12-15_D11_XIX-B09_007	60S ribosomal protein L31	<i>Spodoptera frugiperda</i>	Q7KF90	3.0E-46
12-11_O15_IX-D11_016	60S ribosomal protein L32	<i>Spodoptera frugiperda</i>	Q962T1	1.0E-56
12-08_H03_III-A07_008	60S ribosomal protein L35	<i>Caenorhabditis elegans</i>	P34662	9.0E-19
12-09_B18_VII-F06_001	60S ribosomal protein L40	<i>Aedes albopictus</i>	Q5MIQ5	1.0E-67
12-10_B04_XIII-E12_002	60S ribosomal protein L44	<i>Aedes triseriatus</i>	Q9NB33	4.0E-21
12-16_B09_XX-F07_003	60S ribosomal protein L44	<i>Aedes triseriatus</i>	Q9NB33	3.0E-43
12-14_A11_XVII-A05_001	60S ribosomal protein L44	<i>Aedes triseriatus</i>	Q9NB33	1.0E-42
12-14_A12_XVII-C01_002	60S ribosomal protein L44	<i>Aedes triseriatus</i>	Q9NB33	7.0E-44
12-14_G05_XVI-B09_013	60S ribosomal protein L44	<i>Aedes triseriatus</i>	Q9NB33	7.0E-44
12-15_G09_XVIII-G08_013	60S ribosomal protein L5	<i>Helianthus annuus</i>	O65353	1.0E-57
12-11_K11_IX-A11_012	60S ribosomal protein L5	<i>Helianthus annuus</i>	O65353	3.0E-71
12-15_A04_XVII-G12_002	60S ribosomal protein L5	<i>Helianthus annuus</i>	O65353	3.0E-71
12-10_L04_XIII-G02_012	60S ribosomal protein L7a (Surfeit locus protein 3)	<i>Takifugu rubripes</i>	O57592	1.0E-41
12-10_N21_IV-E10_013	Acidic p0 ribosomal protein	<i>Dascillus cervinus</i>	Q6EV09	4.0E-67
12-15_D09_XVIII-G05_007	Hoip-prov protein (RpL7)	<i>Xenopus laevis</i>	Q7ZWY8	1.0E-43
12-11_D09_X-H01_003	MRPS35 protein (Fragment)	<i>Homo sapiens</i>	Q6P4C6	2.00E-23

(to be continued)

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Contig name	Protein homologue	Species	UniProt An	E-value
12-11_N12_XIV-E02_014	QM protein	<i>Plutella xylostella</i>	Q6F451	9.0E-91
12-12_P24_XV-D08_016	Ribosomal protein L10A	<i>Bombyx mori</i>	Q5UAS9	2.0E-25
12-08_L08_VI-H11_012	Ribosomal protein L11	<i>Bombyx mori</i>	Q5UAS8	2.0E-84
12-14_D07_XVI-D08_007	Ribosomal protein L11	<i>Bombyx mori</i>	Q5UAS8	7.0E-63
12-10_L02_XIII-E06_011	Ribosomal protein L13	<i>Bombyx mori</i>	Q5UAS6	6.0E-15
12-11_I10_XII-E04_009	Ribosomal protein L14	<i>Bombyx mori</i>	Q5UAS4	5.0E-38
12-10_H01_X-B07_007	Ribosomal protein L17	<i>Bombyx mori</i>	Q5UAS2	6.0E-58
12-11_C13_IX-B03_003	Ribosomal protein L17	<i>Bombyx mori</i>	Q5UAS2	5.0E-68
12-15_F01_XVII-D08_011	Ribosomal protein L17	<i>Bombyx mori</i>	Q5UAS2	1.0E-74
12-15_F07_XVIII-E06_011	Ribosomal protein L17/23	<i>Spodoptera frugiperda</i>	Q962Y9	8.0E-73
12-07_E03_I-C02_006	Ribosomal protein L18 (Fragment)	<i>Branchiostoma lanceolatum</i>	Q86LX2	1.0E-57
12-08_G05_I-D06_007	Ribosomal protein L19	<i>Bombyx mori</i>	Q5UAR9	7.0E-59
12-12_K24_XIII-D06_012	Ribosomal protein L20	<i>Spodoptera frugiperda</i>	Q95UN2	3.0E-30
12-11_M10_XII-E07_013	Ribosomal protein L21	<i>Helicoverpa zea</i>	Q5UC14	6.0E-42
12-09_M16_V-H05_014	Ribosomal protein L24	<i>Bombyx mori</i>	Q5UAR4	1.0E-38
12-09_P10_VII-B09_015	Ribosomal protein L26	<i>Plutella xylostella</i>	Q6F448	2.0E-47
12-10_B02_XIII-D10_001	Ribosomal protein L26	<i>Ictalurus punctatus</i>	Q90YU2	4.0E-35
12-14_D04_XVI-A03_008	Ribosomal protein L27	<i>Spodoptera frugiperda</i>	Q962T3	1.0E-54
12-10_P04_XIII-G05_016	Ribosomal protein L28	<i>Plutella xylostella</i>	Q6F474	4.0E-38
12-10_M22_VI-C08_013	Ribosomal protein L29	<i>Bombyx mori</i>	Q5UAQ9	3.0E-15
12-09_E23_II-F09_006	Ribosomal protein L30	<i>Agropecten irradians</i>	Q8ITC5	3.0E-43
12-11_B09_X-G11_001	Ribosomal protein L34	<i>Spodoptera frugiperda</i>	Q8WQ16	1.0E-41
12-10_K02_XII-A07_011	Ribosomal protein L35A	<i>Bombyx mori</i>	Q5UAQ3	2.0E-41
12-16_F09_XX-G01_011	Ribosomal protein L36A	<i>Spodoptera frugiperda</i>	Q962S8	4.0E-39
12-09_M14_V-G02_013	Ribosomal protein L37	<i>Bombyx mori</i>	Q5UAQ0	5.0E-38
12-12_I23_X-A08_010	Ribosomal protein L37	<i>Bombyx mori</i>	Q5UAQ0	1.0E-32
12-08_P07_III-D09_016	Ribosomal protein L37A	<i>Spodoptera frugiperda</i>	Q962S6	1.0E-31
12-11_J11_XI-A10_010	Ribosomal protein L37A	<i>Spodoptera frugiperda</i>	Q962S6	2.0E-27
12-12_D23_XI-H03_004	Ribosomal protein L37A	<i>Spodoptera frugiperda</i>	Q962S6	2.0E-29
12-15_E07_XX-E01_009	Ribosomal protein L37A	<i>Spodoptera frugiperda</i>	Q962S6	5.0E-29
12-11_A08_XII-C10_002	Ribosomal protein L38	<i>Plutella xylostella</i>	Q6F450	1.0E-29
12-14_G10_XVII-A03_014	Ribosomal protein L38	<i>Plutella xylostella</i>	Q6F450	1.0E-29
12-11_H10_XIV-B03_007	Ribosomal protein L39	<i>Bombyx mori</i>	Q5UAP7	1.0E-15
12-15_F07_XX-E02_011	Ribosomal protein L39	<i>Bombyx mori</i>	Q5UAP7	2.0E-13
12-15_G08_XX-F03_014	Ribosomal protein L39	<i>Bombyx mori</i>	Q5UAP7	3.0E-15
12-12_O18_XIII-A11_015	Ribosomal protein L44	<i>Plutella xylostella</i>	Q6F481	6.0E-34
12-11_L06_XIII-H06_011	Ribosomal protein L7	<i>Bombyx mori</i>	Q5UAT4	3.0E-51
12-15_C08_XX-E08_006	Ribosomal protein L8	<i>Bombyx mori</i>	Q5UAT2	5.0E-83
12-10_N01_X-B11_013	Ribosomal protein L9	<i>Bombyx mori</i>	Q5UAT1	1.0E-76
12-11_M07_VIII-G06_014	Ribosomal protein P2	<i>Bombyx mori</i>	Q5UAT9	5.0E-12
12-15_C06_XX-C11_006	Ribosomal protein P2	<i>Bombyx mori</i>	Q5UAT9	1.0E-13
12-11_E08_XII-C12_006	Ribosomal protein P2-like (Fragment)	<i>Culicoides sonorensis</i>	Q5QBF5	7.0E-17
12-12_E20_XIII-B02_006	Ribosomal protein S11 (Ribosomal protein S11-2)	<i>Bombyx mori</i>	Q66SW3	1.0E-66
12-11_A15_IX-C08_002	Ribosomal protein S12	<i>Bombyx mori</i>	Q5UAN1	1.0E-36
12-12_K20_XIII-B05_012	Ribosomal protein S16	<i>Bombyx mori</i>	Q5UAM6	1.0E-63
12-09_J16_VII-E09_010	Ribosomal protein S18	<i>Plutella xylostella</i>	Q6F458	2.0E-47
12-15_G08_XVIII-F11_014	Ribosomal protein S18	<i>Plutella xylostella</i>	Q6F458	3.0E-66

(to be continued)

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Contig name	Protein homologue	Species	UniProt An	E-value
12-08_N05_III-C05_013	Ribosomal protein S24	<i>Plutella xylostella</i>	Q6F461	2.0E-39
12-10_L22_VIII-A04_011	Ribosomal protein S27	<i>Aedes albopictus</i>	Q5MIR3	2.0E-38
12-11_B06_XIII-G06_001	Ribosomal protein S27	<i>Aedes albopictus</i>	Q5MIR3	4.0E-28
12-14_G04_XVI-A06_014	Ribosomal protein S27	<i>Aedes albopictus</i>	Q5MIR3	1.0E-39
12-12_M18_XIII-A09_013	Ribosomal protein S27a	<i>Aedes albopictus</i>	Q5MIS5	3.0E-32
12-09_I16_V-H01_010	Ribosomal protein S29	<i>Plutella xylostella</i>	Q6F473	3.0E-25
12-08_G10_V-D04_007	Ribosomal protein S30	<i>Bombyx mori</i>	Q5UAL2	2.0E-32
12-15_C02_XVII-E02_006	Ribosomal protein S3a (Fragment)	<i>Crassostrea gigas</i>	Q70MP2	5.0E-18
12-11_F08_XIV-A03_006	Ribosomal protein S4	<i>Spodoptera frugiperda</i>	Q95V34	2.0E-94
12-16_D10_XX-G10_008	Ribosomal protein S5	<i>Spodoptera frugiperda</i>	Q95V33	2.0E-53
12-10_F02_XIII-E03_005	Ribosomal protein SA	<i>Bombyx mori</i>	Q5UAP4	5.0E-96
12-11_K10_XII-E05_011	Ribosomal protein, large P2	<i>Ixodes pacificus</i>	Q6B8B1	2.0E-12
12-15_D12_XIX-D03_008	Ribosomal RNA assembly protein mis3	<i>Schizosaccharomyces pombe</i>	O74777	4.0E-11
12-08_B05_III-B07_001	S13e ribosomal protein	<i>Timarcha balearica</i>	Q6EUZ0	6.0E-62
12-10_E02_XII-A02_005	S14e ribosomal protein	<i>Dascillus cervinus</i>	Q6EUY9	6.0E-57
12-09_I18_VI-A03_009	S15Ae ribosomal protein	<i>Timarcha balearica</i>	Q6EUY7	2.0E-57
12-09_K19_II-D11_012	S15Ae ribosomal protein	<i>Timarcha balearica</i>	Q6EUY7	6.0E-62
12-12_I24_XIII-D05_010	S17e ribosomal protein	<i>Carabus granulatus</i>	Q6EUY6	2.0E-38
12-14_C09_XVI-G06_005	S17e ribosomal protein	<i>Carabus granulatus</i>	Q6EUY6	6.0E-57
12-14_F01_XV-E04_011	S19e ribosomal protein	<i>Dascillus cervinus</i>	Q6EUY0	2.0E-51
12-15_E05_XVIII-A10_009	S19e ribosomal protein	<i>Dascillus cervinus</i>	Q6EUY0	1.0E-46
12-10_H24_VIII-B01_008	S23e ribosomal protein	<i>Carabus granulatus</i>	Q6EUX7	1.0E-70
12-11_D05_X-D04_003	S23e ribosomal protein	<i>Carabus granulatus</i>	Q6EUX7	1.0E-75
12-11_H09_X-H07_007	S23e ribosomal protein	<i>Carabus granulatus</i>	Q6EUX7	9.0E-44
12-12_C21_IX-H03_003	S23e ribosomal protein	<i>Carabus granulatus</i>	Q6EUX7	9.0E-72
12-15_H01_XVII-D11_015	S25e ribosomal protein	<i>Timarcha balearica</i>	Q6EUX5	1.0E-28
12-11_O10_XII-E12_015	S26e ribosomal protein	<i>Dascillus cervinus</i>	Q6EUX3	5.0E-51
12-14_E03_XV-H01_009	S26e ribosomal protein	<i>Dascillus cervinus</i>	Q6EUX3	5.0E-52
12-15_D05_XVIII-A07_007	S26e ribosomal protein	<i>Dascillus cervinus</i>	Q6EUX3	5.0E-51
12-08_P03_III-B04_016	S3Ae ribosomal protein	<i>Timarcha balearica</i>	Q6EV04	1.0E-102
12-10_P24_VIII-B10_016	S3e ribosomal protein	<i>Carabus granulatus</i>	Q6EV05	6.0E-66
12-08_A04_IV-G12_002	S7e ribosomal protein	<i>Timarcha balearica</i>	Q6EV00	2.0E-64
12-14_G01_XV-E11_013	S7e ribosomal protein	<i>Timarcha balearica</i>	Q6EV00	3.0E-64
12-10_C02_XII-A01_003	S8e ribosomal protein	<i>Dascillus cervinus</i>	Q6EUZ9	1.0E-63
12-15_F02_XVII-E09_012	S9e ribosomal protein	<i>Meladema coriacea</i>	Q6EUZ7	2.0E-73
12-08_O06_V-B06_015	Ubiquitin/ribosomal protein S27Ae fusion protein	<i>Papilio dardanus</i>	Q6EV22	1.0E-48
Structure (n = 41)				
12-11_I11_IX-A09_010	2 coiled coil domains of eukaryotic origin (31.3 kD)-like protein	<i>Oryza sativa</i>	Q6K5F3	1.00E-06
12-15_C03_XIX-G07_005	2 coiled coil domains of eukaryotic origin (31.3 kD)-like protein	<i>Oryza sativa</i>	Q6K5F4	7.00E-07
12-10_B03_X-C01_002	Actin (Fragment)	<i>Sitobion avenae</i>	Q6PTC2	1.0E-16
12-15_E11_XIX-B10_009	Actin (Fragment)	<i>Sitobion avenae</i>	Q6PTC1	2.0E-53
12-08_C10_V-C10_003	Actin (Fragment)	<i>Reticulitermes flavipes</i>	Q64I75	1.00E-81
12-15_A11_XIX-B01_001	Actin 1 (Fragment)	<i>Culicoides sonorensis</i>	Q8WRE6	4.0E-87
12-16_A10_XX-G06_002	Actin, muscle	<i>Strongylocentrotus purpuratus</i>	P12431	2.0E-64
12-15_D04_XX-A05_008	Actin	<i>Timarcha balearica</i>	Q5RLJ4	1.00E-138

(to be continued)

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Contig name	Protein homologue	Species	UniProt An	E-value
12-10_L23_IV-F06_012	Alpha 2-tubulin	<i>Sitobion avenae</i>	Q6QA77	4.0E-25
12-12_E19_IX-F05_006	Alpha 2-tubulin	<i>Sitobion avenae</i>	Q6QA77	2.0E-19
12-10_B01_X-B03_001	Beta-2 tubulin	<i>Sitobion avenae</i>	Q6S3D4	1.0E-47
12-10_E03_VIII-D11_006	Beta-tubulin	<i>Bombyx mori</i>	Q8T8B2	2.0E-76
12-14_H01_XV-E12_015	Cuticular protein	<i>Myzus persicae</i>	Q95V16	2.0E-26
12-12_D18_XIV-H07_003	Endocuticle structural glycoprotein (ABD-4A)	<i>Locusta migratoria</i>	P21799	2.0E-19
12-15_F09_XVIII-G07_011	Endocuticle structural glycoprotein SgAbd-8	<i>Schistocerca gregaria</i>	Q7M4F2	2.0E-07
12-12_E24_XIII-D03_006	H3 histone, family 3B	<i>Mus musculus</i>	Q8VDJ2	2.00E-17
12-11_L05_X-D11_011	H3 histone	<i>Mus musculus</i>	Q9D0H3	3.0E-16
12-12_J23_XI-H08_010	Heterochromatin protein 1 (HP1) (Nonhistone chromosomal protein C1A9 antigen)	<i>Drosophila melanogaster</i>	P05205	2.0E-17
12-15_E02_XIX-F07_010	Histone H2A variant (Fragment)	<i>Strongylocentrotus purpuratus</i>	P08991	6.0E-49
12-16_C09_XX-F10_005	Histone H3.3B	<i>Chinchilla lanigera</i>	Q6QN07	3.00E-64
12-11_C08_XII-C11_004	Mitotic apparatus protein p62	<i>Lytechinus pictus</i>	P91753	5.0E-13
12-15_G12_XIX-D08_014	Mitotic apparatus protein p62	<i>Lytechinus pictus</i>	P91753	9.0E-15
12-12_E18_XII-H11_005	Muscle LIM protein 1	<i>Drosophila melanogaster</i>	P53777	5.0E-26
12-08_K12_V-E10_012	Muscle myosin heavy chain (Fragment)	<i>Drosophila melanogaster</i>	Q7JN62	1.0E-61
12-08_A12_V-E01_002	Muscular protein 20 (Fragment)	<i>Dascillus cervinus</i>	Q5ZQH9	3.0E-50
12-10_G03_VIII-D12_008	Muscular protein 20 (Fragment)	<i>Dascillus cervinus</i>	Q5ZQI6	2.00E-21
12-16_H10_XX-H07_016	Myosin 2 light chain (Myosin 1 light chain)	<i>Lonomia obliqua</i>	Q5MG18	4.0E-48
12-12_M14_XII-G06_013	Myosin 2 light chain (Myosin 1 light chain)	<i>Lonomia obliqua</i>	Q5MG18	3.0E-33
12-11_B10_XIV-A12_001	Myosin 2 light chain (Myosin 1 light chain)	<i>Lonomia obliqua</i>	Q5MG18	7.0E-18
12-11_F07_X-F02_006	Myosin 2 light chain (Myosin 1 light chain)	<i>Lonomia obliqua</i>	Q5MG18	1.0E-47
12-12_F21_XI-G05_005	Myosin 2 light chain (Myosin 1 light chain)	<i>Lonomia obliqua</i>	Q5MG18	3.0E-39
12-10_F03_X-C04_006	Myosin 2 light chain (Myosin 1 light chain)	<i>Lonomia obliqua</i>	Q5MG18	3.0E-46
12-15_H04_XX-A12_016	Myosin regulatory light chain 2 (MLC-2)	<i>Drosophila melanogaster</i>	P18432	2.0E-33
12-09_O16_V-H06_016	Paramyosin, long form	<i>Drosophila melanogaster</i>	P35415	2.0E-44
12-15_F10_XIX-A06_012	Ser/Arg-related nuclear matrix protein	<i>Homo sapiens</i>	O60585	1.00E-38
12-10_E04_XII-B03_006	Tropomyosin	<i>Myzus persicae</i>	Q64F38	2.0E-62
12-12_A20_XIII-A12_002	Troponin C 47D (Fragment)	<i>Drosophila virilis</i>	Q6WEW9	5.0E-29
12-11_E07_VIII-F05_006	Troponin I 1	<i>Lonomia obliqua</i>	Q5MG13	8.0E-11
12-15_B07_XVIII-D09_003	Troponin T isoform 1	<i>Apis mellifera</i>	Q3B711	2.0E-10
12-10_F21_IV-D09_005	Troponin T isoform 1	<i>Apis mellifera</i>	Q3B711	3.0E-11
Metabolism (n = 125)				
12-15_E03_XVII-F12_009	1-acyl-sn-glycerol-3-phosphate acyltransferase delta (EC 2.3.1.51)	<i>Homo sapiens</i>	Q9NRZ5	3.0E-14
12-15_A08_XX-E05_002	20S proteasome beta5 subunit	<i>Drosophila melanogaster</i>	Q9NHX7	6.00E-28
12-11_J13_XI-C04_009	3-oxoacyl-(Acyl-carrier protein) reductase (EC 1.1.1.100)	<i>Leptospira interrogans</i>	Q8F0K8	2.0E-05

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Contig name	Protein homologue	Species	UniProt An	E-value
12-09_D20_VII-G07_004	46 kDa FK506-binding nuclear protein (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (Rotamase)	<i>Spodoptera frugiperda</i>	Q26486	2.0E-11
12-09_H16_VII-E07_008	Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase)	<i>Drosophila melanogaster</i>	Q94519	3.0E-26
12-09_L20_VII-H01_012	Acyl-CoA-binding protein (ACBP) (EP)	<i>Chaetophractus villosus</i>	P82934	3.0E-15
12-16_A11_XX-H10_001	ADP/ATP translocase	<i>Apis mellifera</i>	Q6VQ13	2.0E-57
12-14_E02_XV-F07_010	Aldo-keto reductase (EC 1.1.1.2)	<i>Gallus gallus</i>	Q90W83	9.00E-28
12-10_H04_XIII-F08_008	Aminopeptidase N precursor (EC 3.4.11.2) (Microsomal aminopeptidase) (APN2)	<i>Manduca sexta</i>	P91885	3.0E-06
12-09_C21_II-E07_003	APG3L protein	<i>Homo sapiens</i>	Q6PKC5	4.00E-10
12-11_O09_IX-A03_015	ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.14) (Protein bellwether)	<i>Drosophila melanogaster</i>	P35381	3.0E-06
12-09_J10_VII-B06_009	ATP synthase B chain, mitochondrial precursor (EC 3.6.3.14) (FO-ATP synthase subunit B)	<i>Drosophila melanogaster</i>	Q94516	2.00E-19
12-12_A16_XII-G08_002	ATP synthase beta (Fragment)	<i>Drosophila simulans</i>	Q6W4K6	2.0E-40
12-12_J22_XV-B10_009	ATP synthase epsilon chain, mitochondrial (EC 3.6.3.14)	<i>Ipomoea batatas</i>	Q06450	1.00E-08
12-08_E07_I-E03_006	ATP synthase f chain, mitochondrial (EC 3.6.3.14)	<i>Homo sapiens</i>	P56134	3.00E-09
12-08_E05_I-D05_005	ATP synthase lipid-binding protein, mitochondrial precursor (EC 3.6.3.14) (ATPase protein 9)	<i>Manduca sexta</i>	Q9U505	1.0E-33
12-15_F05_XVIII-B02_011	ATP-dependent RNA helicase P62	<i>Drosophila melanogaster</i>	P19109	4.0E-46
12-09_F13_III-G10_005	BcDNA.GM05329	<i>Drosophila melanogaster</i>	Q9U9Q7	7.0E-47
12-09_D15_IV-A01_004	Calmodulin	<i>Strongylocentrotus intermedius</i>	Q76LB7	8.0E-66
12-14_H11_XVII-B11_015	Calnexin	<i>Xenopus tropicalis</i>	Q6DK68	4.0E-39
12-09_D19_IV-C09_004	Carboxypeptidase N catalytic chain precursor (EC 3.4.17.3)	<i>Homo sapiens</i>	P15169	2.0E-17
12-12_E17_IX-E05_005	Casein kinase II, alpha chain (EC 2.7.1.37) (CK II alpha subunit)	<i>Spodoptera frugiperda</i>	O76484	3.0E-25
12-08_J03_III-A09_010	Cathepsin B-N	<i>Myzus persicae</i>	Q64G01	3.0E-91
12-11_B08_XIII-H12_002	Cathepsin B-N	<i>Myzus persicae</i>	Q64G01	8.0E-52
12-08_O08_V-C07_016	Cathepsin B-N	<i>Myzus persicae</i>	Q64G01	3.0E-53
12-08_L01_II-H07_011	CCAAT/enhancer binding protein gamma (C/EBP gamma) (IG/EBP-1) (GPE1-BP)	<i>Mus musculus</i>	P53568	3.0E-06
12-12_H14_XIV-E10_007	CG15551-PB, isoform B	<i>Drosophila melanogaster</i>	Q86B69	3.00E-05
12-09_K15_II-B10_012	Complexin	<i>Drosophila melanogaster</i>	Q9NBA0	2.00E-05
12-12_C17_IX-E03_003	Complexin	<i>Drosophila melanogaster</i>	Q9NBA0	2.00E-05
12-14_C12_XVII-C03_006	Cyclophilin G precursor	<i>Tachypleus tridentatus</i>	O44073	1.0E-06
12-12_A14_XII-F10_001	Cytochrome c oxidase polypeptide Vb (Fragment)	<i>Drosophila simulans</i>	Q7YZE8	2.00E-21

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Contig name	Protein homologue	Species	UniProt An	E-value
12-12_A17_IX-E01_001	Cytochrome c oxidase polypeptide VIb (Fragment)	<i>Drosophila mauritiana</i>	Q7YZE2	3.00E-16
12-14_F03_XV-H03_011	Cytochrome c oxidase subunit Va (EC 1.9.3.1)	<i>Dascillus cervinus</i>	Q95V82	3.0E-38
12-11_M12_XII-F08_014	Cytochrome c oxidase subunit VIa	<i>Homo sapiens</i>	Q9UEG9	4.0E-13
12-09_I13_II-A05_009	Cytochrome c oxidase subunit VIa	<i>Homo sapiens</i>	Q9UEG9	1.00E-10
12-12_H21_XI-G06_007	Cytochrome c oxidase subunit VIc	<i>Thunnus obesus</i>	Q71SZ9	6.0E-16
12-15_C07_XX-D10_005	Cytochrome c	<i>Sarcophaga peregrina</i>	P12831	8.0E-44
12-11_E15_IX-C12_006	Cytochrome P450 (Fragment)	<i>Myzus persicae</i>	Q9BLQ0	4.0E-16
12-12_B14_XIV-E05_001	Cytochrome P450 CYP4	<i>Antheraea yamamai</i>	Q5NT77	2.00E-31
12-12_N21_XI-G09_013	Dehydrogenase/reductase SDR family member 7 precursor	<i>Homo sapiens</i>	Q9Y394	4.00E-21
12-10_C03_VIII-D06_004	DmRNase-66B protein	<i>Drosophila melanogaster</i>	Q24485	2.0E-31
12-08_L11_III-G01_012	DNA-directed RNA polymerases I, II, and III 7.0 kDa polypeptide (EC 2.7.7.6) (ABC10-alpha)	<i>Mus musculus</i>	Q63871	4.00E-16
12-15_G01_XIX-E11_013	DNAJ-1	<i>Culicoides sonorensis</i>	Q86DT4	4.0E-40
12-10_K04_XII-B06_012	DNAJC8 protein (OTTHUMP00000045047) (DnaJ (Hsp40) homolog, subfamily C, member 8)	<i>Homo sapiens</i>	Q8N4Z5	5.00E-28
12-09_N20_VII-H04_014	Elongation factor 4A	<i>Culicoides sonorensis</i>	Q5QBK8	1.0E-43
12-08_J01_II-H05_009	Elongation initiation factor 5C (CG2922-PA) (Cg2922-pb) (LD21309p)	<i>Drosophila melanogaster</i>	Q9VNE2	2.0E-12
12-12_B24_XV-C08_002	Enolase (Fragment)	<i>Drosophila subobscura</i>	O44101	7.0E-29
12-14_D01_XV-D12_007	Eukaryotic translation initiation factor 1A	<i>Drosophila melanogaster</i>	Q9NJB4	1.0E-48
12-15_C11_XIX-B06_005	Eukaryotic translation initiation factor 1A	<i>Drosophila melanogaster</i>	Q9NJB4	5.0E-45
12-16_G09_XX-G03_013	Eukaryotic translation initiation factor 3 p66 subunit	<i>Drosophila melanogaster</i>	Q9NHP3	4.00E-47
12-08_I06_V-B02_009	Eukaryotic translation initiation factor 3, subunit 5 (Epsilon)	<i>Mus musculus</i>	Q6IRT4	6.0E-10
12-11_I09_VIII-H08_009	Exosome complex exonuclease RRP41 (EC 3.1.13.-) (Ribosomal RNA processing protein 41)	<i>Mus musculus</i>	Q92119	2.00E-05
12-12_P21_XI-G11_015	Fed tick salivary protein 1	<i>Ixodes scapularis</i>	Q5S1X9	2.00E-06
12-08_A10_V-C08_001	Ferritin precursor	<i>Manduca sexta</i>	Q9N2P3	3.0E-36
12-14_F12_XVII-C10_012	FKBP1B protein	<i>Xenopus laevis</i>	Q5XG46	1.00E-45
12-15_F03_XIX-G11_011	FKBP1B protein	<i>Xenopus laevis</i>	Q5XG46	1.00E-45
12-14_H09_XVI-H01_015	Fructose 1,6-bisphosphate aldolase	<i>Antheraea yamamai</i>	Q75PQ3	9.00E-42
12-12_C14_XII-F11_003	Galactokinase 2	<i>Xenopus tropicalis</i>	Q6DJ33	1.0E-22
12-08_L09_III-E08_011	Glutathione S-transferase	<i>Gryllotalpa orientalis</i>	Q6RUR4	6.0E-41
12-15_B02_XIX-F04_004	Glyceraldehyde 3-phosphate dehydrogenase	<i>Sitobion avenae</i>	Q6PPI3	4.0E-70
12-12_H20_XV-A09_008	Glyceraldehyde-3-phosphate dehydrogenase	<i>Plutella xylostella</i>	Q8MPI0	6.0E-75

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Contig name	Protein homologue	Species	UniProt An	E-value
12-10_P01_X-B12_015	Glycylpeptide N-tetradecanoyl-transferase (EC 2.3.1.97) (Peptide N- myristoyltransferase)	<i>Drosophila melanogaster</i>	O61613	1.0E-69
12-15_H05_XX-C08_015	Lectin 4 C type lectin	<i>Lonomia obliqua</i>	Q5MGD7	7.00E-08
12-14_H02_XV-F11_016	Low molecular mass ubiquinone-binding protein	<i>Rattus norvegicus</i>	Q7TQ16	4.00E-13
12-09_N19_IV-D02_014	Lysophospholipase II	<i>Xenopus tropicalis</i>	Q6DJB2	1.00E-44
12-12_H24_XV-C12_008	Lysozyme i-1	<i>Anopheles gambiae</i>	Q6GU90	8.00E-14
12-11_C07_VIII-F04_004	Malate dehydrogenase 1a, NAD (Soluble)	<i>Danio rerio</i>	Q7T3D9	8.00E-62
12-09_M15_II-B12_014	Mitochondrial ATP synthase e chain	<i>Aedes albopictus</i>	Q5MIP8	3.0E-07
12-11_C05_VIII-E07_003	Mitochondrial ATP synthase e chain	<i>Aedes albopictus</i>	Q5MIP8	7.0E-08
12-12_E22_XIII-C05_005	Mitochondrial ATP synthase e chain	<i>Aedes albopictus</i>	Q5MIP8	2.0E-07
12-08_C05_I-D01_003	Mitochondrial import inner membrane translocase subunit TIM10	<i>Rattus norvegicus</i>	P62074	3.00E-15
12-14_A03_XV-G06_001	N- acetyltransferase containing protein	<i>Mus musculus</i>	Q8CES0	4.0E-14
12-14_A04_XV-H07_002	NADH-ubiquinone oxidoreductase 18 kDa subunit, mitochondrial precursor (EC 1.6.5.3)	<i>Mus musculus</i>	Q9CXZ1	6.00E-23
12-14_F04_XVI-A05_012	NADH-ubiquinone oxidoreductase B12 subunit (EC 1.6.5.3)	<i>Homo sapiens</i>	O43676	8.00E-05
12-15_C07_XVIII-D10_005	NADH-ubiquinone oxidoreductase PDSW subunit (EC 1.6.5.3)	<i>Homo sapiens</i>	O96000	8.00E-12
12-14_B12_XVII-C02_004	NADH-ubiquinone oxidoreductase SGDH subunit, mitochondrial precursor (EC 1.6.5.3)	<i>Homo sapiens</i>	O43674	1.00E-19
12-09_F12_VII-C02_006	Novel protein similar to human isovaleryl Coenzyme A dehydrogenase (IVD)	<i>Danio rerio</i>	Q8AW60	9.0E-20
12-09_B15_III-H11_002	Nuclear cap binding protein subunit 2	<i>Danio rerio</i>	Q8JGR6	5.00E-51
12-11_N08_XIV-A08_014	Nuclear transport factor 2	<i>Aedes aegypti</i>	Q6Q9G0	5.0E-51
12-08_M07_I-E10_014	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin)	<i>Drosophila melanogaster</i>	P25007	2.0E-80
12-09_J14_VII-D07_009	Peroxiredoxin V protein	<i>Branchiostoma belcheri</i>	Q8T5Q7	7.0E-41
12-12_L17_XI-E07_011	Peroxiredoxin-like protein	<i>Aedes aegypti</i>	Q5UG08	3.00E-18
12-15_C04_XIX-H12_006	Phosphoglycerate dehydrogenase (Fragment)	<i>Culicoides sonorensis</i>	Q5QBI6	6.0E-31
12-12_J24_XV-D02_010	Phospholipid hydroperoxide glutathione peroxidase	<i>Gallus gallus</i>	Q8QG67	1.0E-34
12-08_M02_IV-G10_013	Polymerase (RNA) II (DNA directed) polypeptide C	<i>Mus musculus</i>	Q99M46	6.00E-55
12-12_K22_XIII-C08_011	Prdx3 protein	<i>Rattus norvegicus</i>	Q6P9W3	7.0E-33
12-09_I19_II-D08_010	Proteasome (Prosome, macropain) 26S subunit, ATPase 2	<i>Rattus norvegicus</i>	Q6P7R9	4.0E-72
12-10_K24_VI-D08_012	Proteasome subunit beta type 3 (EC 3.4.25.1) (20S proteasome subunit beta-3)	<i>Drosophila melanogaster</i>	Q9XYN7	9.0E-44

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Contig name	Protein homologue	Species	UniProt An	E-value
12-08_G12_V-E05_008	Protein disulphide isomerase isoform (D-ERp60)	<i>Drosophila melanogaster</i>	Q9TWZ1	2.0E-21
12-12_E23_X-A06_006	Protein disulphide isomerase isoform (D-ERp60)	<i>Drosophila melanogaster</i>	Q9TWZ1	9.00E-59
12-12_N17_XI-E09_013	Protein transport protein SEC61 gamma subunit	<i>Gryllotalpa orientalis</i>	Q7Z1B8	6.0E-15
12-08_G06_V-A12_007	Ptpn2-prov protein	<i>Xenopus laevis</i>	Q6DD82	7.0E-05
12-09_E17_II-C07_005	Putative oxalate:formate antiporter	<i>Bacteroides fragilis</i>	Q64XE1	3.00E-05
12-12_G23_X-A07_008	Sec61beta-prov protein	<i>Xenopus laevis</i>	Q8AVT7	6.00E-21
12-10_D01_X-B04_003	SGT1 protein homolog	<i>Mus musculus</i>	Q9CS74	6.00E-14
12-07_C01_I-A02_003	Signal recognition particle 19 kDa protein (SRP19)	<i>Homo sapiens</i>	P09132	1.0E-29
12-10_J24_VIII-B02_010	Similar to eukaryotic translation initiation factor 3, subunit 1 alpha, 35kDa	<i>Danio rerio</i>	Q7SXU0	8.0E-06
12-12_M21_IX-H11_013	Steroid alpha reductase family protein 1	<i>Caenorhabditis elegans</i>	Q9N5Y2	2.00E-51
12-09_A15_II-B03_002	Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.5)	<i>Mus musculus</i>	Q9Z2I9	6.0E-19
12-09_M23_II-G01_014	Survival motor neuron protein	<i>Canis familiaris</i>	O02771	3.0E-05
12-15_G02_XIX-G02_014	Tat-binding protein-1	<i>Drosophila melanogaster</i>	Q9XZC3	3.00E-11
12-15_E03_XIX-G09_009	Tceb2-prov protein	<i>Xenopus laevis</i>	Q6PHL7	2.0E-25
12-14_H03_XV-H06_015	Tetratricopeptide repeat protein 11 (TPR repeat protein 11) (CGI-135)	<i>Homo sapiens</i>	Q9Y3D6	1.0E-17
12-14_F08_XVI-F07_012	Thiamine transporter 1 (THTR-1) (ThTr1) (Thiamine carrier 1) (TC1)	<i>Homo sapiens</i>	O60779	2.00E-22
12-08_B04_VI-E09_002	Thioredoxin 2	<i>Drosophila yakuba</i>	Q6XHI1	1.0E-21
12-15_A01_XVII-D03_001	Transcription initiation factor TFIID subunit 11 (TAFII30 beta)	<i>Drosophila melanogaster</i>	P49906	1.0E-40
12-09_O18_VI-A07_015	Translation factor SUI1-like protein	<i>Aedes aegypti</i>	Q5QC99	5.0E-42
12-12_O14_XII-G07_015	Translationally controlled tumor protein	<i>Plutella xylostella</i>	Q60FS1	4.0E-33
12-11_F11_XI-A08_006	Ubfm1 protein	<i>Danio rerio</i>	Q803Y4	9.00E-08
12-11_I12_XII-F05_010	Ubiquinol-cytochrome C reductase complex 6.4 kDa protein (EC 1.10.2.2) (Complex III)	<i>Mus musculus</i>	Q9CPX8	2.0E-07
12-15_E10_XIX-A05_010	Ubiquinol-cytochrome C reductase complex 6.4 kDa protein (EC 1.10.2.2) (Complex III)	<i>Mus musculus</i>	Q9CPX8	3.0E-07
12-15_B10_XVIII-H11_004	Ubiquinol-cytochrome C reductase complex protein	<i>Spodoptera litura</i>	Q8I918	3.0E-10
12-16_E10_XX-H03_010	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor (EC 1.10.2.2)	<i>Saimiri sciureus</i>	Q69BJ7	1.0E-65
12-09_D14_VII-D03_003	Ubiquitin 1 (Ubiquitin/fusion protein)	<i>Physarum polycephalum</i>	Q966Q8	7.0E-19
12-14_G12_XVII-C12_014	Ubiquitin-conjugating enzyme 9-2 (Ubiquitin-conjugating enzyme E2I2) (Ube2i2 protein)	<i>Danio rerio</i>	Q9DDJ0	8.0E-05

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Contig name	Protein homologue	Species	UniProt An	E-value
12-14_F11_XVII-B06_011	Ubiquitin-conjugating enzyme E2 M (EC 6.3.2.19) (Ubiquitin-protein ligase M)	<i>Mus musculus</i>	P61082	7.0E-05
12-15_D06_XX-D01_008	Ubiquitin-conjugating enzyme E2-17 kDa (EC 6.3.2.19) (Ubiquitin-protein ligase)	<i>Drosophila melanogaster</i>	P25867	2.00E-51
12-09_G17_II-C09_007	Ubiquitin-like protein 5	<i>Mus musculus</i>	Q9EPV8	9.0E-34
12-09_O17_II-D02_015	Ubiquitin-like protein SMT3B precursor (Sentrin 2) (Ubiquitin-related protein SUMO-3)	<i>Mus musculus</i>	P61957	1.00E-27
12-12_B21_XI-G01_001	Vacuolar ATP synthase catalytic subunit A, osteoclast isoform (EC 3.6.3.14)	<i>Homo sapiens</i>	P38607	1.0E-33
12-09_L16_VII-F01_012	Vacuolar ATP synthase subunit F (EC 3.6.3.14)	<i>Manduca sexta</i>	P31478	4.0E-46
12-08_C09_I-F02_003	Vacuolar ATP synthase subunit S1 precursor (EC 3.6.3.14)	<i>Bos taurus</i>	P40682	6.00E-10
12-12_K18_XIII-A07_011	Vacuolar ATPase M9	<i>Aedes albopictus</i>	Q5MIS8	8.0E-26
12-11_G05_VIII-E09_007	Vascular endothelial cell specific protein 11 (Septin 2)	<i>Rattus norvegicus</i>	Q91Y81	1.00E-61
12-08_G07_I-E05_008	Ywhab-prov protein	<i>Xenopus laevis</i>	Q8AVQ3	9.00E-34
Chaperonin (n = 9)				
12-14_A06_XVI-B11_002	BAG2 protein	<i>Homo sapiens</i>	Q6FID0	2.0E-14
12-15_F04_XX-A07_012	Chaperonin containing TCP1, subunit 2 (Beta)	<i>Rattus norvegicus</i>	Q5XIM9	1.0E-06
12-10_M04_XII-B07_014	Chaperonin containing TCP1, subunit 3 (Gamma)	<i>Danio rerio</i>	Q7T2P2	3.0E-73
12-16_H09_XX-G05_015	Heat shock 70 kDa protein cognate 4 (Hsc 70-4)	<i>Manduca sexta</i>	Q9U639	2.0E-59
12-08_D04_VI-E10_004	Heat shock protein 4 heat shock cognate 70 protein	<i>Lonomia obliqua</i>	Q5MGD5	3.0E-69
12-15_F08_XX-F02_012	Heat shock protein HSP 90-beta (HSP 84)	<i>Rattus norvegicus</i>	P34058	5.0E-61
12-08_L02_VI-E06_011	Hsp90	<i>Opisththalmus carinatus</i>	Q5WQZ6	3.0E-61
12-14_C04_XVI-A02_006	Hsp90-related protein TRAP1	<i>Drosophila melanogaster</i>	Q7KNF3	1.00E-28
12-10_J22_VIII-A02_009	PPIL4 protein (Fragment)	<i>Homo sapiens</i>	Q6P392	8.00E-21
Differentiation (n = 21)				
12-09_H15_IV-A07_008	Abnormal wing disc-like protein	<i>Choristoneura parallela</i>	Q8MUR5	2.0E-59
12-12_G20_XIII-B03_008	Angiotensin like 1	<i>Homo sapiens</i>	Q8IY63	2.0E-14
12-09_E14_V-F07_005	APC-binding protein EB2	<i>Mus musculus</i>	Q6PER3	3.00E-10
12-12_K23_X-A09_012	Cdc5l-prov protein	<i>Xenopus tropicalis</i>	Q66JL3	8.00E-40
12-08_L07_III-D06_012	CGI-25 protein (ENOS interacting protein)	<i>Homo sapiens</i>	Q9Y314	9.00E-27
12-08_D03_II-H12_004	Chemosensory protein	<i>Leucophaea maderae</i>	Q8MTC3	9.00E-24
12-10_K03_VIII-E02_012	Cyclin L2	<i>Homo sapiens</i>	Q5T2N6	6.00E-30
12-12_I16_XII-H01_010	Epidermal Langerhans cell protein LCP1	<i>Homo sapiens</i>	O94842	2.00E-07
12-08_H02_VI-E04_007	Follicular variant translocation protein 1 precursor (FVT-1)	<i>Homo sapiens</i>	Q06136	2.0E-08
12-11_H07_X-F10_008	Imaginal disc growth factor	<i>Pieris rapae</i>	Q6IWP3	3.0E-10
12-08_O02_IV-G11_015	Inhibitor of growth protein 4	<i>Mus musculus</i>	Q8C0D7	4.00E-13

(to be continued)

(Continued)

Contig name	Protein homologue	Species	UniProt An	E-value
12-15_A12_XIX-C09_002	Juvenile hormone binding protein	<i>Heliothis virescens</i>	Q25175	7.00E-05
12-09_L19_IV-D01_012	Macrophage migration inhibitory factor	<i>Ixodes pacificus</i>	Q9GUA9	6.0E-26
12-08_P04_VI-F06_016	Miple	<i>Drosophila melanogaster</i>	Q9Y0V9	5.00E-16
12-10_N03_X-C11_014	Nucleolar GTP-binding protein 1 (Chronic renal failure gene protein) (GTP-binding protein)	<i>Mus musculus</i>	Q99ME9	1.0E-35
12-12_H16_XIV-G04_008	Programmed cell death protein 6 (Probable calcium-binding protein ALG- 2) (PMP41)	<i>Mus musculus</i>	P12815	3.0E-05
12-09_L14_VII-D08_011	Proliferation-associated 2G4-like	<i>Danio rerio</i>	Q6PHD8	6.00E-31
12-10_G22_VI-C02_007	Receptor for activated protein kinase C homolog	<i>Plutella xylostella</i>	Q60FS2	7.0E-57
12-15_A09_XVIII-G01_001	UBA/UBX 33.3 kDa protein	<i>Homo sapiens</i>	Q04323	1.00E-19
12-08_N09_III-E09_013	Zcchc8-prov protein	<i>Xenopus laevis</i>	Q6DD45	6.0E-06
12-14_A05_XVI-B01_001	Zinc finger protein 622 (Zinc finger-like protein 9)	<i>Homo sapiens</i>	Q969S3	2.00E-41
Hypothetical proteins (n = 12)				
12-12_G16_XII-G12_008	CG1397-PA (LD10746p)	<i>Drosophila melanogaster</i>	Q9VZ21	3.0E-31
12-08_P08_VII-A07_016	CG18624-PA, isoform A	<i>Drosophila melanogaster</i>	Q9W3N7	4.0E-05
12-09_B13_III-G05_001	CG30101-PA (LD27203p)	<i>Drosophila melanogaster</i>	Q9V808	7.0E-07
12-11_O05_VIII-F02_015	CG30415-PA, isoform A	<i>Drosophila melanogaster</i>	Q8MLR9	2.0E-10
12-09_A17_II-C05_001	CG7099-PA	<i>Drosophila melanogaster</i>	Q9VJY7	1.0E-05
12-11_N11_XI-A12_014	ENSANGP00000013411	<i>Anopheles gambiae</i>	Q7PM90	3.0E-20
12-15_C09_XVIII-G03_005	ENSANGP00000015228 (Fragment)	<i>Anopheles gambiae</i>	Q7PPG0	5.0E-06
12-10_E01_VIII-C02_005	Ethanol induced protein	<i>Mus musculus</i>	Q8CEW7	2.0E-13
12-12_J20_XV-A11_010	Hypothetical protein MGC5987	<i>Homo sapiens</i>	Q86V88	1.0E-08
12-15_E08_XVIII-F05_010	Hypothetical protein zgc:73376	<i>Danio rerio</i>	Q6PBJ5	6.0E-08
12-09_F20_VII-G09_006	Uncharacterized conserved membrane protein	<i>Idiomarina loihiensis</i>	Q5QW14	4.00E-13
12-14_F02_XV-F09_012	RE11282p (Fragment)	<i>Drosophila melanogaster</i>	Q8IGW9	2.0E-09
Mitochondrion encoded (n = 12)				
12-14_B08_XVI-F01_004	ATP synthase A chain subunit 6	<i>Myzus persicae</i>	Q9B6J3	8.0E-25
12-09_M21_II-F02_013	Cytochrome b (Fragment)	<i>Schizaphis graminum</i>	Q8LWP5	8.0E-35
12-09_N18_VII-G02_013	Cytochrome b (Fragment)	<i>Schizaphis graminum</i>	Q6JCP3	2.0E-19
12-09_I23_II-F11_010	Cytochrome b	<i>Schizaphis graminum</i>	Q699M8	1.0E-64
12-14_H07_XVI-E09_015	Cytochrome b	<i>Schizaphis graminum</i>	Q699M8	8.0E-36
12-15_D08_XX-E09_008	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)	<i>Schizaphis graminum</i>	Q699N8	1.0E-35
12-15_F11_XIX-B11_011	Cytochrome c oxidase polypeptide III (EC 1.9.3.1)	<i>Schizaphis graminum</i>	Q699N4	2.0E-09
12-09_L18_VII-F11_011	Cytochrome c oxidase subunit I (Fragment)	<i>Schizaphis graminum</i>	Q94XN1	2.0E-51
12-14_D06_XVI-C04_008	Cytochrome oxidase subunit I (Fragment)	<i>Sitobion avenae</i>	Q9MLD5	3.0E-61
12-09_B20_VII-G05_002	Cytochrome oxidase subunit I	<i>Diuraphis noxia</i>	Q85QQ1	6.0E-48
12-15_H02_XIX-G04_016	NADH dehydrogenase subunit 4	<i>Schizaphis graminum</i>	Q699N1	5.0E-08
12-08_J07_III-D05_010	NADH-ubiquinone oxidoreductase chain 3 (EC 1.6.5.3)	<i>Schizaphis graminum</i>	Q699N3	5.0E-09