REGULAR ARTICLE

Proteomic analysis of the wing imaginal discs of *Drosophila melanogaster*

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We have combined high-resolution two-dimensional (2-D) gel electrophoresis and mass spectrometry with the aim of identifying proteins represented in the 2-D gel database of the wing imaginal discs of *Drosophila melanogaster*. First, we obtained a high-resolution 2-D gel pattern of [³⁵S]methionine + [³⁵S]cysteine-labeled polypeptides of Schneider cells, a permanent cell line of *Drosophila* embryonic origin, and compared it with the standard pattern of polypeptides of the wing imaginal disc. These studies reveal qualitative and quantitative differences between the two samples, but have more than 600 polypeptides in common. Second, we carried out preparative 2-D polyacrylamide gel electrophoresis using Schneider cells mixed with radioactively labeled wing imaginal discs in order to isolate some of the shared polypeptides and characterize them by matrix-assisted laser desorption/ionization-time of flight MALDI-TOF analysis. Using this strategy we identified 100 shared proteins represented in the database, and in each case confirmed their identity by MALDI-TOF/TOF analysis.

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1 Introduction

The generation of form in biological systems remains a challenging problem. Since the pioneering studies of Thomas H. Morgan and his coworkers begun in 1908, *Drosophila melanogaster*, has constituted one of the most powerful developmental model systems. The most important of its advantages are: ease of culturing, short generation time, small genome (about 1.6×10^8 base pairs of DNA per haploid genome, now fully sequenced), low chromosome number ($n = 4$), presence of polytene chromosomes, and 90 years of accumulated genetic knowledge.

The structures on the surface of the adult *Drosophila* fly (such as wings, legs and antennae) are ideal for investigating the processes underlying morphogenesis. These structures are not formed from differentiated larval cells but rather from

small groups of proliferating but relatively undifferentiated cells called imaginal discs [1]. These provide a favorable system for analyzing the mechanisms controlling developmental cell proliferation and the genetic control of pattern, because of the separation in time between cell proliferation and differentiation, and the facility with which controlling genes can be identified and characterized. The 19 imaginal discs (9 pairs and 1 fused genital discs) are set aside very early in embryogenesis, and each is committed to a particular developmental pathway (e.g., left wing or right wing, left eye or right eye, etc.). The imaginal discs remain in a relatively undifferentiated state near the surface of the larvae until changing hormonal levels during pupation cause them to differentiate and undergo morphogenesis [2]. Detailed fate maps have been established for the different imaginal discs [3].

Imaginal discs have a simple histological structure consisting mainly of a single layer of cells forming a sac, connected to the larval epidermis by a stalk. The cells of the imaginal discs divide continuously during larval development. For example, the wing imaginal discs develop from a few cells until, at maturity, they contain about 50 000 cells [4]. At metamorphosis, the discs evaginate, expand, and replace

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the larval epidermis, which undergoes programmed death. Thus the control of cell multiplication can be studied in the absence of complications due to simultaneous overt differentiation such as occurs in most vertebrate tissues.

We use 2-DE to analyze aspects of the development, morphogenesis and genetic variation of the wing imaginal disc of *Drosophila* [5]. Improvements in separation, as well as in labeling technique, have made it possible to resolve more than a thousand [^{35}S]methionine + [^{35}S]cysteine-labeled polypeptides from a single imaginal disc. We have constructed a quantitative protein database used as reference to detect changes in gene expression related to tissue type [6], stage of development [7], or genetic lesion [8]. However, the key to interpreting the data obtained by such analysis is the ability to identify (and characterize) the proteins of interest.

Since the amount of protein derived from wing imaginal discs is very limited, we have turned to the permanent Schneider cell line that was derived from *Drosophila* embryos. The goals of the experiments reported here were twofold: first to compare the pattern of proteins synthesized in wing imaginal discs and in Schneider cells; second, to explore the possibility of using proteins from the Schneider cells, purified *via* a limited number of preparative 2-D gels, to identify the corresponding proteins in wing imaginal discs. For this purpose we have started a systematic MALDI-TOF analysis that has permitted us to identify many proteins, some already known, others novel. We present the analysis of one hundred such proteins in this study.

2 Materials and methods

2.1 Fly strains and cell culture

Laboratory stocks of wild-type *D. melanogaster* (strain Vallecas Spain) were used.

We used the established cell line designated Schneider, of *D. melanogaster*. The cells were grown in bottles (25 cm²) in 20 mL of M3 medium supplemented with 5% foetal bovine serum. For labeling, they were incubated for 120 min in 300 μL of methionine- and cysteine-free medium with 300 μCi [^{35}S]methionine + [^{35}S]cysteine (SJQ 0079; Amersham, Little Chalfont, UK). At the end of the labeling period, the medium was removed and the cells were resuspended in 100 μL of lysis buffer and stored at -70°C .

2.2 Sample preparation

Imaginal discs were dissected from mature larvae (about 0–4 h before puparium formation) using a fibre optic light source to prevent heating of the tissue. Dissections were carried out in buffered Ringer's solution (10 mM Trizma base; 95 mM NaCl; 3 mM CaCl_2 ; 3 mM KCl, adjusted to pH 7.0) freshly made up and filtered through a 0.22 μm filter. As a rule we used 10 imaginal discs in each labeling experiment. The dissected discs were placed in 100 μL of buffered Ring-

er's solution in a well of a Microtest II tissue culture plate (Falcon No 3042; Becton Dickinson, France) and incubated for 60 min in 80 μL of Ringer's solution containing 80 μCi of [^{35}S]methionine + [^{35}S]cysteine at 25°C . Following incubation, the medium was removed and the discs resuspended in 100 μL of lysis buffer.

2.3 Two-dimensional gel electrophoresis

Analytical 2-DE was performed as described by O'Farrell [9, 10] with some modifications [11]. Briefly, the first dimension for resolving acidic proteins (IEF) was performed on 230×2.3 mm 4% w/v polyacrylamide gels containing 2% carrier ampholytes (1.6% pH 5–7; 0.4%, pH 3.5–10) at 1200 V for 20 h. Basic proteins (NEPHGE) were resolved on 150×2.3 mm 4% w/v polyacrylamide gels containing 2% carrier ampholytes (1% pH 7–9; 1% pH 8–9.5) at 400 V for 4.5 h. The second dimension employed a 15% polyacrylamide gel (24×24 cm) run overnight at 18°C . The gels were processed for fluorography [12], dried, and exposed at -70°C for varying periods (4, 24, 96 and 240 h). Approximately 10^6 TCA-precipitable cpm [^{35}S]methionine + [^{35}S]cysteine were routinely applied to each gel. For preparative gels we used proteins prepared from 2 mL of Schneider cultures. The cell suspension was centrifuged and the cells were sonicated, treated with DNase and RNase [13], and passed several times through a narrow gauge needle. The sample was then lyophilized and resuspended in 2 mL of lysis buffer. Gels were stained with Coomassie Brilliant Blue and silver nitrate.

2.4 Computer analysis of 2-D patterns

The fluorograms were digitized at 176×176 μm resolution with a GS-800 calibrated densitometer Bio-Rad, and the resulting 2-D images merged and analyzed with PDQUEST™ software (V. 5.1; Bio-Rad).

2.5 In-gel digestion

Coomassie- or silver-stained protein spots were excised and digested with trypsin (Promega, Madison, WI, CA, USA). After washing three times for 40 min with 100 μL 50 mM ammonium bicarbonate and 50% methanol, the gel pieces were dried and swollen in digestion buffer (20 mM ammonium bicarbonate and 40 ng/ μL trypsin), and incubated at 37°C for 16 h. Peptides were extracted twice by 20 min incubation in 35 μL of 50% ACN in 0.1% TFA. The resulting peptide extracts were pooled, concentrated in a vacuum centrifuge and stored at -20°C .

2.6 Mass spectrometry analysis

Dried samples were dissolved in 10 μL of 30% ACN and 0.1% TFA. Equal volumes (0.5 μL) of peptide and matrix solution were mixed and crystallized on the sample plate.

The matrix solution consisted of 3 mg CHCA dissolved in 1 mL of a solution containing 50% ACN and 0.1% TFA. Peptides were analyzed with the Applied Biosystems 4700 proteomics analyzer (Applied Biosystems, Framingham, MA, USA) with TOF/TOF ion optics. MS spectra were obtained in reflectron mode using an acceleration voltage of 1 kV. Desorption and ionization was performed with an Nd:YAG laser operating at 355 nm, and the final mass spectrum was produced by averaging 3600 laser shots. The products of trypsin autodigestion were used for internal calibration. All MS/MS sequencing analyses were performed using the same equipment.

2.7 Protein identification using the *Drosophila* database

The first step in protein identification consisted of mass fingerprinting. The monoisotopic peptide mass fingerprinting data obtained from MALDI-TOF were then used to search for candidates in the Swiss-Prot/TrEMBL nonredundant protein database (<http://us.expasy.org/tools/peptident.html>).

3 Results

3.1 General pattern of protein synthesis in *Drosophila* wing imaginal discs

Figure 1A shows a wing imaginal disc of a wild-type third instar larvae of *D. melanogaster* (strain Vallecas) after dissection. Extensive studies of transplantation of imaginal disc fragments have shown that much of the patterning information needed to make the adult appendages has been elaborated in the disc by the end of the third larval instar; given regions of the disc reproducibly develop into particular parts of the adult appendage [14]. These studies have given rise to fate maps in which the spatial pattern of the adult appendages can be projected back onto the disc. Figure 1B and 1C are fate maps of the wing imaginal disc, and Fig. 1D representative fluorograms (after 96 h of exposure) of 2-D gel of acidic and basic polypeptides from wing imaginal discs of mature larvae. For quantification, four different exposures of the gels were merged and analyzed by computer with the PDQUEST™ system, and each polypeptide was assigned a number in the database. In this way we compiled a database of 1492 [³⁵S]methionine + [³⁵S]cysteine labeled polypeptides (1226 acidic, IEF and 266 basic, NEPHGE). This constitutes our reference wing imaginal disc database.

3.2 The protein pattern of Schneider cells

Cultures of Schneider cells were labeled with [³⁵S]methionine + [³⁵S]cysteine for 2 h as described in Section 2.1. Polypeptides were separated on 2-D gels and analyzed with the

PDQUEST™ software. A total of 824 polypeptides (608 acidic (IEF) and 216 basic (NEPHGE)) were identified, numbered and quantified as described in Section 3.1 for wing imaginal discs. We compared the Schneider 2-D pattern with our wing imaginal discs database and also ran samples containing a mixture of wing imaginal discs and Schneider cells. From these comparisons we concluded that the two systems have 634 polypeptides in common (461 IEF and 173 NEPHGE), and 190 polypeptides (147 IEF and 43 NEPHGE) were detected only in the Schneider cells. Although it is beyond the scope of this study to give a detailed comparative analysis of the two systems, it should be emphasized that there were appreciable differences in the levels of some of the shared polypeptides. Three hundred and sixty-three polypeptides (269 IEF and 94 NEPHGE) were expressed at similar levels in the two systems, whereas 197 polypeptides (152 IEF and 45 NEPHGE) were more highly expressed (at least two-fold) in the Schneider cells, and 74 polypeptides (40 IEF and 34 NEPHGE) in the discs. The shared polypeptides were of most interest to us, and Fig. 2 reproduces a small region of the IEF gels of wing imaginal discs (Fig. 2A) and Schneider cells (Fig. 2B) in which it is possible to see some of the shared polypeptides.

3.3 Isolation of proteins for MALDI-TOF

We took advantage of the shared proteins to isolate sufficient amounts of some of them to perform MALDI-TOF analysis of their tryptic peptides. After calibration with Coomassie blue stained 2-D gels, we ran preparative gels with precise amounts of polypeptides from the Schneider cells together with small amounts of [³⁵S]-labeled polypeptides from wing imaginal discs. The gels were stained with Coomassie or silver nitrate, dried and exposed to X-ray film. The autoradiograms displayed only spots derived from the wing imaginal discs, but large amounts of comigrating unlabeled proteins derived from the cell line. We then ran new preparative 2-D gels and after staining picked some of these spots and subjected them to in-gel digestion with trypsin followed by MALDI-TOF analysis. We were able to identify 100 spots from the preparative gels (81 acidic and 19 basic) in the database. In all the cases analyzed we could confirm the information obtained from the peptide mass fingerprinting by MS/MS using MALDI-TOF/TOF. A total of 417 MS/MS spectra were analyzed. All the wing imaginal discs proteins identified in this study are listed in Tables 1 and 2 ordered by SSP number. Molecular weight, pI, names, identified sequence tags, abundance relative and Flybase accession numbers are also included. Figure 3A shows, as an example, the MALDI-TOF spectrum of the tryptic digest of acidic polypeptide SSP 3303 identified as enolase (EC 4.2.1.11) and Fig. 3B reproduces a detail of the fragmentation spectrum of peak 1764.91 corresponding to polypeptide AAVPSGASTGV-HEALELR.

Figure 1. (A) Wing imaginal disc of late third instar larvae of *Drosophila melanogaster*. Schematic diagrams of an imaginal wing disc from late third instar larvae (B) and of the heminotum and wing that will give rise to metamorphosis (C). The fates of different regions of the disc are indicated by similar colouring of the corresponding adult structures. Noncoloured regions, such as the presumptive ventral wing surface, thoracic pleura and postnotum, correspond to structures not represented in (C), or regions of uncertain fate. Large circles in (C) represent notum macrochaete and the largest sensilla campaniformia in the wing. Small circles denote notum microchaetae and other sensory organs. (D) 2-DE maps (IEF, and NEPHGE) of total [^{35} S]methionine + [^{35} S]cysteine-labeled polypeptides from wing imaginal discs of late third instar larvae. Cells were pulse labeled for 1 h with [^{35} S]methionine + [^{35} S]cysteine (1 mCi/mL) and processed as described in Section 2.1. A total of 10^6 TCA-precipitable cpm were applied *per* gel and 1492 polypeptides were separated and quantified. The pH ranges were 9.0 (left) to 7.5 (right) in the basic gels and 7.0 (left) to 4.4 (right) in the acidic gels.

4 Discussion

This study is part of a major effort in our laboratory to monitor developmental changes in *Drosophila* polypeptides involved in cell proliferation and differentiation. We have shown previously that the quantitative 2-D wing imaginal disc database can be used to detect differences in the protein

patterns associated with specific mutations and stages of development. The limiting factor in such studies is identification of the polypeptides of interest, which is almost impossible using only wing imaginal discs as material. We considered this problem ten years ago but the circumstances then were unfavorable as the *Drosophila* genome had not yet been sequenced and classic Edman degradation was the only

Figure 2. Two-dimensional gel of acidic (IEF) [^{35}S]methionine + [^{35}S]cysteine-labelled polypeptides from wing imaginal disc (A) and Schneider cells (B). Only a small region of the gel is shown. The pH ranges from 5.6 (left) to 4.6 (right). Arrows indicate some of the polypeptides common to the two samples.

available approach for identifying polypeptides [15]. Peptide mass fingerprinting by MALDI-TOF MS is an excellent technique for identifying proteins in 2-D gels, especially in the case of well-defined genomes such as that of *Drosophila*.

In the present work we have used the Schneider cell line as our source for purifying some wing disc proteins, taking advantage of the possibility of obtaining large numbers of cultured cells. This cell line is stable and has no tendency to differentiate morphologically during serial passage. It may express a set of differentiated functions characteristic of a cell type normally found during some stage of *Drosophila* development beyond that of the original cell line, or its gene expression pattern may have no counterpart in normal development. Regardless of its present state, the cell line was found to share more than 600 polypeptides with the wing imaginal disc. The present experimental approach has enabled us to identify 100 spots by PMF, and to identify them from their MS/MS spectra. We determined a total of 417 internal sequences. Tables 1 and 2 list the polypeptides identified in the database and include the corresponding accession numbers in the *Drosophila* genome database (<http://flybase.bio.indiana.edu>), which is possibly the most complete currently available database of a eukaryotic organism, in which one can find extensive genetic and molecular information about each polypeptide.

The 100 identified polypeptides represent 6.7% of the 1492 polypeptides recorded in the database. As the database is quantitative, the 81 polypeptides identified in the acidic gels (IEF) constitute 16.9% of the 'counts' of the database. Tubulin alpha chain (SSP 7507) is the major polypeptide with 4401 cpm while CG 1354 (SSP 1414) is the rarest, with 82 cpm. In the basic gels (NEPHGE), the 19 polypeptides identified constitute 13.7% of the counts loaded on the gel with cyclophilin (SSP 1004) the major one with 7310 cpm and Tudor (SSP 5201) the most minor, with 471 cpm. Tables 1 and 2 also include the abundances of all the identified polypeptides relative to the sum of the radioactivity in all the spots of the gel. We loaded 10^6 cpm on the IEF gels and recovered 644 000 cpm in the total of 1226 acidic spots detected, while on NEPHGE gels we recovered 242 000 cpm in the 266 spots detected. Taken together these data indicate that we detected in our database practically 90% of the radioactivity applied to the gels.

The genes encoded the detected polypeptides mapped over the four *Drosophila* chromosomes in proportion consistent with the chromosome size: 47 polypeptides on chromosome 2, 37 on chromosome 3, 15 on the X chromosome and only one on chromosome 4. All cellular organelles were represented in the subcellular location of the identified polypeptides. Our data thus validate the methods of sample preparation and extraction used. Mitochondria are the organelles most highly represented with 11 polypeptides identified.

In most cases analyzed the experimental pI and M_r values were in good agreement with the theoretical values for the proteins identified. Only four spots showed significant discrepancies in their isoelectric points. Thus the acidic proteins SSP 0024 and SSP 0410 whose theoretical pI values are 8.69 and 8.22 respectively, appeared at the basic end of the IEF gels, with experimental pI values near 7.0. Similarly the basic polypeptides SSP 5201 and SSP 7502 with theoretical pI values of 6.44 and 6.10 respectively, appeared at the acidic end of the basic gels, with experimental pI values of 7.5. We detected no protein fragments; in each case the identified spots corresponded to a full-length polypeptide. In certain cases the same protein was found in several spots. Such multiple spots could stem from highly similar isoforms, or post-translational modifications. Three instances where two spots contained the same polypeptide were detected in the acidic gels: polypeptides SSP 5406 and SSP 6401 were identified as CG 8983 (Erp60), and polypeptides SSP 8204 and SSP 8209 as annexin IX. Finally, polypeptides SSP 9102 and SSP 9106 were identified as 14-3-3 & Epsilon. The proteins identified in this study cover a wide spectrum of biological functions. For example, 15 are involved in biosynthetic pathways (two in amino acid, three in nucleic acid, seven in carbohydrate and three in lipid metabolism), and 14 are enzymes involved in aspects of energy generation (10 glycolysis, one pentose phosphate, and three tricarboxylic pathway). We also identified five proteins involved in protein synthesis, and six in signal transduction. For example, SSP 3105 IEF was identified as CG1803, a polypeptide homo-

Figure 3. (A) MALDI-TOF MS spectra of the tryptic digest of acidic polypeptide SSP 3303. The labeled peaks represent 8 of the 17 peptides matched to *D. melanogaster*. The peptides analyzed by MALDI-TOF/TOF MS are also indicated with its sequences underlined. (B) A small detail of the MS/MS spectrum of the 1764.91 Da peptide that was matched to the sequence AAVPSGASTGVHEALELR.

logue of regucalcin that is involved in calcium-mediated signaling and in anterior/posterior axis specification in *Drosophila*. In addition we identified five cytoskeletal proteins, six in the proteasome and four in the chaperonin T-complex.

5 Concluding remarks

The major benefit of this study is to increase the number of identified proteins in the database so that those proteins that change when the database is used for comparative purposes

in developmental or morphogenetic studies can be identified. For example some time ago we used the wing database to evaluate changes in the pattern of protein synthesis in the wing imaginal discs of *Drosophila* mutants with abnormal wing disc development [8]. At that time it was impossible to identify any of the polypeptides of interest; these could only be identified by their coordinates. Now we are able to say that one of those spots, SSP 7108 IEF, has been identified as ubiquitin C-terminal hydrolase (Uch-L3). That protein appears to be phosphorylated in the tumor suppressor mutants analyzed. It is in this kind of application that the database promises to be most useful.

Using preparative comigration gels of *Drosophila* wing imaginal discs and Schneider cell proteins, we believe that it should be possible to identify at least 300 proteins on 10–12 preparative gels. This effort is underway, together with characterization of the nuclear and mitochondrial subproteomes. The availability of sequence information for such a large proportion of the proteins observed in 2-D gels should enhance the usefulness of the 2-D gel database, and will be helpful in subsequent studies of *Drosophila* development and morphogenesis.

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7 Addendum

Table 1. Identification by MALDI-TOF and MALDI-TOF/TOF MS of acidic polypeptides (IEF) recorded in the *Drosophila* wing imaginal disc database

SSP no.	kDa/pI	N /% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
0024	22.1/8.69	9/46.9	1332.72 1358.67 2004.08	ELALKPQGEGYK DTNGSQFFITTK DVVIANSGLTPVSEAFSVAK	CG 2852	0.43	0034753
0025	17.1/7.83	5/33.3	1390.74 1469.71	TFIMVKPDGVQR NIIHGSDAVESA EK	ABNORMAL WING DISCS awd	0.39	0000150
0026	24.7/7.66	7/35.6	1214.61 1294.62 1784.92 2066.12	NLQYYDISAK FNVWDTAGQEK SNYNFEKPFLWLAR YVATLGVEVHPLIFHTNR	CG 1404 PROTEIN (RAN 10 A)	0.31	0020255
0103	27.1/7.55	9/36.5	1156.60 1160.59 1189.54 1425.77	HITIFSPEGR LYQVEYAFK TDPAGYFSGFK NIVPETVTHLFR	PROTEASOME & ALPHA 6 SUBUNIT	0.21	0026781
0206	35.6/7.14	13/37.7	1329.54 1485.64 1670.87	DEDTNYGYPOK DEDTNYGYPOKR TVEELRPEVVSPTSK	RECEPTOR OF ACTIVATED PROTEIN KINASE C1 (RAC K1)	0.02	0020618

6 References

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Table 1. Continued

SSP no.	kDa/pI	N [% ^{a)}]	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
0410	54.5/8.22	18/32.9	1026.59	AVDSLVPGR	BELLWETHER (blw) ATP SYNTHASE ALPHA CHAIN	0.16	0011211
			1438.84	GIRPAINVGLSVSR			
			1472.79	GKHALIYDDLK			
			1553.72	EAYPGDVFYLHSR			
			1610.86	TGAIVDVPVGDELLGR			
1309	35.5/6.60	7/28.9	1205.60	VIGSGTNLDSSR	ECDYSONE-INDUCIBLE GENE L3 Imp L3	0.03	0001258
			1250.65	QVVD SAYEVIK			
			1526.83	QILTPTEVEQLQK			
			1750.83	NPQITASTDFAASANSR			
1414	44.9/6.26	9/26.2	1216.64	DLEIISEELR	CG 1354	0.01	0030151
			1560.75	NYTVEDGDIIFK			
			1701.78	FEDWNAHDIEALNK			
			1813.90	GLQLEYFFTAGPDEVK			
			2010.94	AFEDPDVTHVEGEVDPVR			
1503	63.0/6.33	22/44	1081.61	HLYVPTVPR	CG 8036	0.21	0037607
			1464.72	KIDSDLEGHPTPR			
			1594.80	TVAFVSTFATFFTR			
			1646.84	SGPPSVLIDMFGISAR			
2002	17.1/6.73	8/59.5	973.55	YVIFYIR	TWINSTAR (tsr)	0.40	0011726
			1145.57	QIDVETVADR			
			1353.65	YIQATDLSEASR			
			1612.74	NAEYDQFLEDIQK			
2111	23.8/6.75	7/22.5	945.46	APADPEAFKK	GLUTATHIONE S TRANSFERASE D1 GstD1	0.01	0001149
			1062.61	AIQVYLVEK			
			1850.04	LLNLQAGEHLKPEFLK			
2115	20.2/6.10	9/41.6	793.42	IQNYQK	ATP SYNTHASE, SUBUNIT d	0.06	0016120
			1248.55	EQLEAEAQGH			
			1372.77	LVPVAGLVDSFQK			
			1545.79	IAQSSINWSALAER			
2318	35.9/6.21	13/41.5	1108.59	REDLFITSK	CG 6048	0.02	0036182
2508	56.4/6.07	9/27.9	1157.59	SDKGGNPDLVR	CG 17259	0.27	0031497
			1390.68	GSEKAEVGVDEK			
			1513.77	VEQFVLTSPHDNK			
			1732.92	YLIATSEQPIAAYHR			
2512	55.6/6.24	12/27.6	1141.56	AFEAYNEGLK	HSP 70/HSP 90 Organizing Protein Homolog	0.39	0024352
			1179.56	FQEALEDAEK			
			1360.74	YDPTNAILLOGR			
			1568.80	AEEEEKEQGNLFFK			
			1774.91	ALELDPNNAEAIEGYR			
2701	94.3/6.18	18/21	760.38	FYAFGR	ELONGATION FACTOR 2b (EF-2b)	0.41	0000559
			999.56	GGGQIIPTR			
			1092.56	VNFTVDEIR			
			1340.69	DLVFITHPDQR			
2710	105.7/6.05	29/33.2	1011.53	AVIHGDPFR	CG 14476	0.25	0027588
			1092.60	LEALVGSTFR			
			1112.49	DNNYFFHR			
			1439.68	DLIHYGNWEHR			
3103	24.7/5.96	8/39.1	1139.61	IAVHQPEFAK	PEROXIREDOXIN 2540 Prx2540-2	0.65	0033518
			1140.63	ALFIISPDHK			
			1341.71	VVATPANWTPGTK			
			1520.75	LGQTVPNFEADTTK			

Table 1. Continued

SSP no.	kDa/pI	N /% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
3105	33.6/6.02	16/50.2	1175.53	YIGDEFEFR	CG 1803 REGUCALCIN HOMOLOGUE	0.08	0030362
			1295.61	FDQPAPAGTTYK			
			1470.79	VVIVNWDGVSPSAK			
			1556.71	FYYIDTTDYEK			
			1692.73	SYDYDFETGVASNP			
3205	31.0/6.10	9/43	1325.60	HSYDTTYPVSR	PROTEASOME 35 kDa SUBUNIT Pros 35	0.09	0003151
			1353.69	DPEVLVATEQRP			
			1664.86	RPYGVGLLVAGYDER			
			2049.87	NDDDDDRPSPPEEPAAGPR			
3303	46.5/6.10	17/52.7	1100.48	DGQYDLDFK	ENOLASE (Eno)	0.12	0000579
			1238.67	LANLYKEFIK			
			1764.91	AAVPSGASTGVHEALELR			
			1860.96	GNPTVEVDLTTELGLFR			
			2252.13	SGETEDSFIGDLVVGLSTGQIK			
3403	59.3/5.97	13/33.8	1477.76	VVDAEWQILYNK	CG 8351	0.37	0037632
			1521.81	QVKPFVEEGVHPR			
			1565.79	LPIGDVATQYFADR			
			1807.91	VTGGSLEESQLVSGVAFK			
3405	53.2/5.93	11/29	1752.94	GLVDDLNLNPNAGVTQK	THIOREDOXIN REDUCTASE-1 Trxr-1	0.11	0020653
			2063.08	VEYINGLGSFVDSHTLLAK			
			2443.17	YPDIPGAVEYGITSDDLFSLDR			
			2585.36	SGLTINTLINTVGIHPTTAEFTR			
4001	26.6/6.0	11/51	1279.65	IQYGGSVTAANAK	TRIOSE PHOSPHATE ISOMERASE (Tpi)	0.08	0003738
			1363.70	AIFGESDALIAEK			
			1567.77	DIGADWWILGHSEK			
			1683.83	TATPDQAQEVHAFK			
4108	26.0/5.92	11/49.6	1231.64	NVLPAAEVQYK	VACUOLAR H⁺ ATPase 26 kDa E SUBUNIT	0.06	0015324
			1311.62	NQSEYETVLTK			
			1523.85	LDLISQQLVPEIR			
			1597.77	VREDHVSSVLDDAR			
			1660.83	AQINQNVLFIDEK			
4111	25.1/5.88	7/27.4	1170.61	GEHLTPFLK	CG 16936	0.07	0027590
			1265.66	LHLDSGHLFAR			
			2124.01	LAELPYYQEVNGDGADLK			
			2280.12	RLAELPYYQEVNGDGADLK			
4201	35.7/5.77	9/26.2	930.48	HAIDVGYR	CG 10638	0.09	0036290
			1120.63	REDIFLVTK			
			1177.61	YVDDNTLLPK			
			1521.77	SIGVSNFNSEQLAR			
			1884.89	HIDTAYFYQNEAEVKG			
4207	36.8/5.66	12/32	1343.67	HIDTAPVYGNEK	CG 2767 (LD 24679 p)	0.09	0037537
			1566.82	SENITVTAYSPLGSK			
			1927.11	VPPVSNRPHEVEPTIKK			
			2116.17	IRPANNOIEHHVYLQQR			
4301	48.9/5.93	19/48	1034.56	RVEEFNLK	ISOCITRATE DEHYDROGENASE ldh	0.05	0001248
			1466.88	LVTGWQKPIVIGR			
			1523.68	EYEAAGIWEYHR			
			1693.85	ETSTNPIASIFAWTR			
			1718.82	DYQETFEFINTLAK			
			2599.36	SQILPFLDIELHTYDLGIENR			

Table 1. Continued

SSP no.	kDa/pI	N /% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
4306	48.5/5.75	16/37	1205.70	YQIHIPLPPK	Rpt1	0.15	0028687
			1536.84	QILQNEQPLOVAR			
			1761.88	TMLELINQLDGFDP			
			1869.92	ESDTGLAPPALWDLAADK			
4401	59.3/5.97	12/24.4	1365.61	GGAEQFLEETER	CG 8351	0.06	0037632
			1521.80	QVKPFVEEGVHPR			
			1565.79	LPIGDVATQYFADR			
			1807.94	VTGGSLEESQLVSGVAFK			
4404	47.3/5.82	9/24.5	1021.62	HIILLAEGR	ADENOSYLHOMO-CYSTEINASE Ahcy13	0.01	0014455
			1216.63	VADISLAEWGR			
			1495.79	ILDEEVASLHLEK			
			2165.06	QATYLGVSQTGPFKPDHYR			
4702	107.7/5.77	23/26.5	1017.50	LKATIDNDK	ALANYL-tRNA SYNTHASE	0.21	0027094
			1422.67	SVFDEVYPDPVR			
			1640.78	FENQFVNEITSGQK			
			1672.84	TITIALADGGTPDNTGR			
			2060.99	TNFYAESGGQIYDQGALVK			
5211	30.6/5.61	13/34.2	1134.55	RGHGAIFYNGR	CG 9391	0.01	0037063
			1184.67	VLTQFNPLPR			
			1438.66	FIGEESSGAEGVK			
			1696.95	RVLAAATPELAQEISK			
			1743.96	VTELGLVYNPILEQR			
5305	40.2/5.46	9/27	2050.02	FVAEGEPHIDGEPGLIVR	CG 4164	0.18	0031256
5406	55.2/5.62	17/38.1	1114.57	YSVSGYPTLK	Erp60	0.55	0033663
			1248.61	NFDDLVINNGK			
			1375.67	FGHSSEKEVLDK			
			1407.60	QDEVSQDYNGPR			
			1532.70	FEGSSESDLSTFVK			
			1582.68	DTTLFGYFSDSDSK			
5408	58.0/5.60	16/36.4	1090.58	EAIAIEAFAR	CG 7033	0.32	0030086
			1316.63	GATQQLDEADR			
			1840.90	QLIYNYPEQLFADAR			
5410	46.7/5.48	17/42.5	764.43	FLDTLR	CaBP1	0.17	0025678
			1168.49	ASDAQEYDGGGR			
			1279.61	TASDIVSWASDK			
			1411.75	KPAIVSVDPWDGK			
			1879.91	VGSVNADADSTLSGQFGVR			
5501	76.2/5.62	12/22	1309.67	LLEQPDVQPDR	CYTOCHROME P450 REDUCTASE (Cpr)	0.28	0015623
			1598.88	TALTHYLEITAIPR			
			1650.86	LHSIQNQRPPFDAK			
			1820.98	LHPTDVHVTAVLVEYK			
6001	21.7/5.52	6/33	920.50	GLFIIDDK	THIOREDOXIN PEROXIDASE (Jafrac1)	0.16	0040309
			1211.67	QITVNDLPGGR			
			1212.64	LVQAFQYTDK			
			1610.76	DYGVLDDEETGIPFR			
6103	30.3/5.55	11/44.6	1349.68	SFGEAGDGLVELR	LETHAL (2) 37 Cc	0.08	0002031
			1452.86	ILYRPIPDQLPK			
			1485.73	IYTILGQDYDER			
			1617.87	AVVAQFDAGELITQR			
			1800.00	LASIISAEGDAEAAGLLAK			

Table 1. Continued

SSP no.	kDa/pI	N /% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
6104	29.6/5.49	8/29	908.53	FINFVLR	CG 10688	0.13	0036300
			1332.75	YLSELDVPIKR			
			1712.73	TEPGGNDYEIYSDPR			
			1736.81	SVVTPEFEFFYSR			
6203	44.0/5.46	9/28	1238.63	GENIVLAYCEK	CG 8309	0.07	0033902
			1332.67	TGGAPQWEQLR			
			1360.72	LFNNLDTASPLR			
			1537.74	LPAYVQFYEDHR			
6205	32.6/5.43	11/49	1205.59	NSPSYSLYFK	NUCLEOSOME REMODELING FACTOR – 38 kDa (NURF – 38)	0.11	0016687
			1320.70	TIYNMVEVPR			
			1544.78	NADFANTIIAETHK			
			1575.77	GDNDPIDVIEIGYR			
			1847.90	IPDGKPENQFAFNGDAK			
6207	41.7/5.40	12/32	1125.58	AAFAPHPTTGR	CG 5854	0.16	0039130
			1203.62	DFGYVLQHPK			
			1216.70	LPVVGIGDKR			
			1607.82	ELANIDDLSTVVR			
			1875.98	NLATYLLDNELAQEIR			
6301	49.9/5.51	16/39.3	1017.50	YGLEPPGER	GDP DISSOCIATION INHIBITOR (Gdi)	0.25	0004868
			1314.69	NFLIYVQDFR			
			1590.80	NTQDFTGHALALFR			
			1648.78	DDEYLNPAVNTIR			
			1898.93	NFLIYVQDFREDDPK			
			2060.00	YYGGESASITPLEELFQR			
6302	48.6/5.43	11/27.8	1103.65	ILVATNLFGR	HELICASE AT 25E	0.41	0014189
			1243.74	DFLKPEILR			
			1310.64	GTYSIHSSGFR			
			1663.93	LTLHGLQQHYVNLK			
6303	45.8/5.43	14/43.7	1114.69	VLITDDLAR	EUKARYOTIC INITIATION FACTOR 4A (eIF-4A)	0.11	0001942
			1324.68	GFKDQIQDVFK			
			1387.72	GRDVIAQAQSGTGK			
			1491.74	GVAINFITDDRR			
			1813.91	GIYGYGFEKPSAIQQR			
6304	51.8/5.67	14/34	1134.62	IPLHELEQR	CG 3731	0.20	0038271
			1290.72	RIPLHELEQR			
			1467.70	ADLTDYIQTHYK			
			2150.03	VASEDSGASTATVGLWIDAGSR			
			2460.19	SQTDLELEVENLGAHLNAYTSR			
6401	55.2/5.62	14/33.8	1582.69	DTTLFGYFSDSDSK	CG 8983 (Erp60)	0.04	0033663
			1675.78	MDATANDVPPEFNVR			
			2174.08	YALKDEFSVENLQDFVEK			
6413	41.5/5.30	9/23	976.45	AGFAGDDAPR	ACTIN 5C	0.29	0000042
			1132.53	GYSFTTTAER			
			1515.75	IWHHTFYNELR			
			1790.90	SYELPDGOVITIGNER			
			1954.09	VAPEEHPVLLTEAPLNPK			
6502	68.4/5.32	14/31.2	1567.77	LDEILEFANSNFR	CG 10602	0.19	0032721
			1723.87	RLDEILEFANSNFR			
			1968.92	DFQSALYDYFIDTDKK			
			2000.01	YLEDLFGGPTVFEPFLR			
			2496.24	IDYETSSASGLQWLNPTQTLGK			

Table 1. Continued

SSP no.	kDa/pI	N [% ^a]	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
6615	71.1/5.36	17/35	1487.69	TTPSYVAFTDTER	HEAT SHOCK PROTEIN 70-4	0.02	0001219
			1691.71	STAGDTHLGGEDFDNR			
			2774.32	QTQTFTTYSNQPGLVLIQVYEGER			
6709	88.5/5.31	19/28.4	1243.65	TADSPVQISAVR	HSC 70 CB PROTEIN (LD 32979 P) Hsc 70Cb	0.17	0026418
			1495.73	SGGIETLANDYSLR			
			1537.90	ALLDAAQIAGLNVLRL			
			1640.74	SDYEQGPAAFDLKL			
			1860.94	NDPHVQHELTSLPAR			
			2588.33	LIEQVFNKPASTTLNQDEAVSR			
7006	17.5/4.98	6/40.9	1226.64	VPEGELGEQLR	EUKARYOTIC TRANSLATION INITIATION FACTOR 5A (eIF 5A)	0.41	0034967
			1359.70	VHVMGIDIFSNNK			
			1711.88	EDLKVPEGELGEQLR			
			2682.32	EDLQLIAISDDSFLLMTESGDLR			
7102	27.6/5.46	11/57.3	1201.65	QQFEQAIPLK	PROTEASOME SUBUNIT ALPHA TYPE 3.7	0.15	0023175
			1566.78	TDELVESAGEIYYK			
			1707.92	VTGGLHLINPSELTEK			
			2074.06	NIGMAVAGLVADGNFVADIAR			
7105	23.2/5.28	7/36.1	825.47	VFHIGPR	PROTEASOME SUBUNIT BETA TYPE 3	0.30	0026380
			1455.74	FGIQAQTISTDFK			
			1748.93	FGPYFIEPVVAGLDPK			
			1777.98	MFLGLTGLQTDILTVR			
7108	37.6/5.12	18/60	1186.60	TYIEYEIQK	UCH-L3	0.14	0011327
			1450.81	VVLDRENIFFAK			
			1540.89	NLEPIHGLIFLFK			
			1825.98	SEQNWIDVVRPIEK			
			1968.92	KDDDVYHFVGYMPIGGR			
7207	36.1/5.17	8/34	1244.55	SYASGGEDGFVR	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 2 (eIF-3 BETA) (Trip1)	0.10	0015834
			1600.77	FFHLIYEEEFAR			
			1693.84	GHFGPINSLAFHPDGK			
			1705.82	DQKPNVWYSLNGER			
			1824.80	TSNFSFSGNQAAAYSTDK			
7304	47.8/5.20	18/46	1124.66	VDILDALLR	RPT5 Tat-binding protein-1	0.22	0028684
			1466.73	KIEFPHNNEAR			
			1662.89	GAYFLPVIGLVDAEK			
			1868.92	DSYLILETLPAEYDAR			
			2096.06	TMLELLNQLDGFSSSTADIK			
7402	54.5/5.25	16/43	1341.61	NFISQGNENR	VACUOLAR ATP SYNTHASE SUBUNIT B (Vha 55)	0.31	0005671
			1520.79	AVVQVFEGTSGIDAK			
			1582.89	QIYPPVNVLPSSLR			
			1896.88	GFPGYMYTDLATIER			
7404	59.4/5.19	20/37.5	1013.52	LFDLYQSK	CG 8258	0.25	0033342
			1135.60	FANALEVFPK			
			1257.59	FVEGDVTYAEK			
			1263.69	KFANALEVFPK			
			1496.73	LGITTAEISDGYEK			
			1655.76	QYGQEDFLNDLVSK			
7412	46.6/5.16	14/36	1237.63	VVDLTEDTFAK	CG1837	0.02	0030329
			1584.82	ELSAPAEADLGEVKR			
7507	49.8/5.00	11/30.4	1071.60	EIVDLVDR	TUBULIN ALPHA CHAIN	0.68	0003884
			1410.77	QLFHPEQLITGK			
			1718.88	NLDIERPTYTNLNR			
			1785.00	IHFPLVITYAPVISAELK			

Table 1. Continued

SSP no.	kDa/pI	N /% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
			1824.99	VGINYQPPTVVPGGDLAK			
			1993.89	TVGGGDDSFNTFFSETGAGK			
7603	68.2/5.19	24/46.9	1403.72	VASWEFNPLNVK	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A ISOFORM 2 (Vha 68-2)	0.18	0020367
7702	88.8/5.24	23 / 39.3	1256.64	EIDIGIPDATGR	TER 94	0.32	0024923
			1542.83	LDQLIYIPLPDDK	TRANSITIONAL ENDOPLASMIC		
			1823.91	ELQELVQYPVEHPDK	RETICULUM ATPase		
8106	28.2/4.90	11/41	1165.58	YLAEVATGDAR	14-3-3 & ZETA	0.44	0004907
			1549.74	SVTETGVELSNEER			
			2157.99	QAFDDIAELDTLNEDSYK			
8112	15.1/4.97	4/36	773.39	FFFGGAK	CYTOCHROME b5	0.03	0033189
			1031.54	IGELVESER			
			1776.73	DATENFEDVGHSNDAR			
			1952.87	SEPTWSTEQQTEESSVK			
8204	35.9/4.99	13/34	929.44	IDYFSEER	ANNEXIN IX	0.25	0000083
			1418.68	TIAQFYEQSFGK			
			1911.93	QIFLEYENLSGNDIEK			
8209	35.9/4.99	11/29.9	929.43	IDYFSEER	ANNEXIN IX	0.04	0000083
			1418.69	TIAQFYEQSFGK			
			1911.93	QIFLEYENLSGNDIEK			
8404	54.1/4.93	16/37	1367.74	IINVIGEPIDER	ATP SYNTHASE BETA CHAIN	0.30	0010217
			1406.68	AHGGYSVFAGVGER			
			1439.78	VALTGLTVAEYFR			
			1677.92	LVLEVAQHLGENTVR			
8504	50.1/4.76	15/47.2	1053.60	YLTVAAIER	TUBULIN BETA-1 CHAIN at 56D	0.26	0003887
			1130.58	FPGQLNADLR			
			1620.81	LHFFMPGFAPLTSR			
			1958.97	GHYTEGAELVDSVLDVVR			
8709	90.2/4.93	25/36.5	1141.56	FTFQTEVNR	GLYCOPROTEIN 93	0.25	0039562
			1284.67	YSQFINFPIR			
			1434.71	QEHIIYYIAGANR			
			1580.70	EEAQDFLEEDTVR			
			2236.07	DSSEPLTQTHFIAEGEVTFK			
9002	19.6/4.66	7/52	1048.53	SPDQVDIFK	CG 4800 : TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)	0.29	0037874
			1412.72	LVDDVIYEVYVK			
			1595.81	EINGDSVPVLMFFK			
9102	29.7/4.68	11/44	1189.66	DSTLIMQLLR	14-3-3 & EPSILON (SUPPRESSOR OF Ras 3-9)	0.42	0020238
			1229.57	YLAEFATGSDR			
			2087.96	AAFDDAIAELDTLSEESYK			
			2331.19	LGLALNFSVFYIEILNSPDR			
9106	29.1/4.74	10/30	1229.57	YLAEFATGSDR	14-3-3 & EPSILON	0.41	0020238
			1357.66	YLAEFATGSDRK			
9114	23.9/4.74	11/49.1	1434.67	NGFISHDEFSGPK	Fkbp 13	0.02	0010470
			1648.87	DQPFTFQLGAGQVIK			
			2503.21	FDSSFDRDQPFTFQLGAGQVIK			
9115	24.1/4.40	10/50.2	1130.56	HIASFEEAER	ELONGATION FACTOR 1 & BETA	0.04	0028737
			1233.64	AFGDVTTPOGLK			
			2090.01	ELNAFLADNSYISGYTPSK			
			2101.01	IEEFEDFVQSVDAIAFNK			

Table 1. Continued

SSP no.	kDa/pI	N /% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
9401	53.8/4.70	24/54.4	1095.50	SGSPVEYSGGR	PROTEIN DISULFIDE ISOMERASE	0.30	0014002
			1105.61	SHLLFFVSR			
			1388.73	QLAPIYDQLAEK			
			1507.75	SVFEGELNEENLK			
			1519.79	VEEGVLVATVDNFK			
			1749.85	VDAIVEGELAEQYAVR			
9402	48.6/4.75	11/29.1	1153.65	RLHVWDLSK	CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT (Caf 1)	0.16	0015610
			1471.72	TPSSDVLVFDYTK			
			1654.68	SDNAAESFDDAVEER			
9505	44.9/4.38	11/35	974.45	EAQDEVQR	CALRETICULIN	0.45	0005585
			1787.87	FVLTPGTFYNDAAEDK			
			2021.05	SGTIFDNVLITDDVELAAK			

a) N = Number of matched peptides; % = Coverage of full length protein by tryptic peptides

Table 2. Identification by MALDI-TOF AND MALDI-TOF/TOF MS of basic polypeptides (NEPHGE) recorded in the *Drosophila* wing imaginal disc database

SSP no.	kDa/pI	N/% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
1004	17.9/8.43	9/44.8	1055.52	IESYGSQSGK	CYCLOPHILIN 1	3.02	0004432
			1183.59	KIESYGSQSGK			
			1800.86	SIYGNKFPDENFELK			
1102	26.9/9.12	9/38	1198.69	AAVVGMTLPIAR	3-HYDROXYACYL-CoA DEHYDROGENASE TYPE II (SCULLY)	0.46	0021765
			1358.72	NAVSLVTGGASGLGR			
			1385.74	QGASVILADLPSSK			
			1757.80	LSAGLMGANEPNQDGQR			
1201	35.3/8.56	10/35.5	1369.74	GAAQNIIPASTGAAK	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE II	1.78	0001092
			1495.85	VPTPNVSVVDLTVR			
			1546.82	GTVAEEGGFLVVNGQK			
			1763.80	LISWYDNEFGYSNR			
1202	31.5/8.88	7/27.8	1210.72	NVGIVTLNRPK	CG 18645	0.38	0033879
			1381.68	TFHATFSTADRK			
			1766.86	EAVNTAYETTLQGLK			
			1869.98	FGQPEIALGTIPGAGGTQR			
1302	48.1/8.69	11/24.8	1267.65	GLYSNPPVHGAR	CG 4233	0.09	0031380
			1276.58	DHSVYLTNDGR			
			1370.72	IAAEILNNEDLR			
			1487.74	DDNTQPFVLPSVR			
			1511.78	HNVTASISGTGALR			
1401	41.6/8.73	11/32.4	1085.55	TAFGTGGSLK	YIPPEE INTERACTING PROTEIN 2	0.14	0040064
			1302.71	ITGHLVHELQR			
			1373.72	GINQTQLQTTAAK			
			1450.74	ERVDEFSLLSQK			
			1860.98	LNVNGGAIALGHPLGASGR			

Table 2. Continued

SSP no.	kDa/pI	N/% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abundance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
1404	44.6/7.84	10/26	1155.55	TELHHFESR	CG 8507	0.11	0037756
			1183.62	HLHAEHALQK			
			1208.59	SFENDLNTLR			
			1312.65	EANDPHFQQVK			
			1640.82	LVSSGPHSQDFIEPK			
2102	22.1/8.69	11/52.7	1104.53	QIENSATDAR	CG 2852	1.55	0034753
			1169.58	FEDENFKLK			
			1358.66	DTNGSQFFITTK			
			2004.09	DVVIANSGLTPVSEAFSVAK			
2203	35.3/8.25	8/26	833.47	IGINGFGR	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	0.13	0001091
			1495.84	VPTPNVSVVDLTVR			
			1546.81	GTVAEAGGFLVVNGQK			
			1763.79	LISWYDNEFGYSNR			
2206	38.6/7.10	15/44	1230.62	VDITDREQVR	CG 12030	0.13	0035147
			1317.67	YFNPVGAHISGR			
			1534.71	FVYSSSATVYGEPK			
			1608.84	DYIHIVDLAEGHVK			
			2148.00	RPSLSVYGSDFPDHDGTGVR			
2401	51.5/8.89	12/27	945.51	SQVQQLSR	CG 3861 CITRATE SYNTHASE	0.15	0026708
			1093.67	ALGLPIERPCK			
			1439.77	SGQVVPGYGHAVLR			
			1542.77	HLPEDETFLQVSK			
			1688.86	ALVTETSVLDADEGIR			
2602	57.4/7.13	15/39	1014.52	EPGLGDWLK	PYRUVATE KINASE	0.73	0003178
			1526.82	LGYEHPVAIALDTK			
			1690.94	GVNLPGPVVDLPVASEK			
			1895.99	GAGTIDASHAAAIAVEAATK			
2801	85.3/8.49	26/35.3	1170.70	LNRPLTLSEK	ACONITASE	0.41	0010100
			1214.62	NGSWGVPDVAR			
			1457.81	IPFNVTGSEQIR			
			1625.75	WVAVGDENYGEGRSSR			
			1854.93	VLYSHLDDPANQDIVR			
3802	103.0/8.14	28/35.4	1128.63	VTGSPNLATLR	TUDOR – SN	0.08	0035121
			1205.68	VFFSSIRPPR			
			1365.69	TEAIVEFVASGSR			
			1425.81	QLVAEGLVLAERQ			
			1526.68	YGDITQDDAPEFR			
			2184.08	EGRPTAEQQTLIELEDQAR			
5201	30.5/6.44	12/44	1181.53	YQLDDDASVR	VOLTAGE-DEPENDENT ANION SELECTIVE CHANNEL (PORIN)	0.19	0004363
			1443.73	LTTNNFALGYTTK			
			1461.71	LSLEGNFAPQSGNK			
			1505.75	VNNASQVGLGYQQK			
			1950.87	TSSGIEFNTAGHSNQESGK			
5301	38.9/6.92	11/37	1502.71	LQDIGVENTEDNR	ALDOLASE	0.36	0000064
			1658.81	RLQDIGVENTEDNRR			
			1898.90	YVAGSAGAGSGSLFVANHAY			
			2128.10	IVPIVEPEVLPGDHDLDLR			
5501	43.9/7.01	12/30	1175.66	YTLAPVAAELK	PHOSPHOGLYCERATE KINASE	0.46	0003075
			1238.58	IGGSLFDEEGSK			

Table 2. Continued

SSP no.	kDa/pI	N/% ^{a)}	MS/MS		PROTEIN IDENTIFIED	Relative abun- dance	FLYBASE Accession No.
			MH ⁺	SEQUENCE TAG			
			1328.74	LSIENLDLAGKR			
			1634.78	LGDVYVNDAFGTAHR			
			1685.79	FYVEEEGKGLDASGGK			
7502	46.5/6.10	19/51.0	1100.49	DGQYDLDFK	ENOLASE	0.77	0000579
			1238.68	LANLYKEFIK			
			1471.67	DGQYDLDFKNEK			
			1764.92	AAVPSGASTGVHEALELR			
			2147.17	EILPVPAFNVINGGSHAGNK			
			2208.07	FGLDATAVGDEGGFAPNIQSNK			
8601	80.4/7.56	17/23.9	1192.59	NYLNADVEVR	CG 8256 I(2)K 05713	2.66	0022160
			1599.81	IHPEFPYIDAEIR			
			1668.80	TALVELDDFASGTSSR			
			1858.89	SFGDGDVSGEQLHEILR			

a) **N** = Number of matched peptides; % = Coverage of full length protein by tryptic peptides