

KANDHI, VAMSIKRISHNA, Ph.D. Identification, Quantification and Investigation of Anti-inflammatory Effects of *Echinacea purpurea* Constituents. (2012)
Directed by Dr. Nadja B. Cech. 263 pp.

Echinacea is among the top selling botanical medicines in the United States. Clinical trials have yielded contradictory reports on the efficacy of *Echinacea* preparations for treatment of colds, influenza, and inflammation, perhaps due to inconsistency in quality control and lack of information as to which constituents are responsible for their activity. Our overall goal with this research was to develop and apply mass spectrometry techniques to better understand the relationship between chemical composition of *Echinacea* extracts and their biological activity. This objective was achieved through three separate aims. **(1)** To determine whether *in vitro* anti-inflammatory activity of *Echinacea purpurea* extracts could be correlated with the presence of the alkylamides or caffeic acid derivatives, which have previously been reported to be bioactive. The ability of these extracts to inhibit production of TNF-alpha and PGE₂ from influenza A-infected RAW 264.7 macrophage-like cells was assessed. Chemical analysis of the extracts revealed variations in levels of alkylamides, caftaric acid, and cichoric acid. The biological activity of these extracts, however, did not correlate with concentrations of any of these compounds. **(2)** To investigate the effects of *Echinacea purpurea* preparations and their constituents on protein expression by immune cells *in vitro*. Stable isotope labeling with amino acid in cell culture (SILAC), a quantitative proteomics approach, was employed to measure changes in protein expression by activated RAW 264.7 macrophage-

type cells exposed to an *Echinacea purpurea* extract and several of its constituents. The extract and several isolated alkylamides were observed to block expression of a number of proteins, some of which were directly or indirectly involved in inflammation. **(3)** To develop new analytical methods to analyze bacterial lipoproteins. Lipoproteins are commonly found in aqueous *Echinacea* extracts and have pronounced immunostimulatory activity *in vitro*. These compounds are large and polydisperse, making them very difficult to characterize analytically. A new liquid chromatography – mass spectrometry (LC-MS) analytical method was developed and employed to analyze lipoproteins from *E. coli* and from an endophyte isolated from *Echinacea purpurea* seeds.

IDENTIFICATION, QUANTIFICATION AND INVESTIGATION OF ANTI-
INFLAMMATORY EFFECTS OF *ECHINACEA PURPUREA*
CONSTITUENTS

by

Vamsikrishna Kandhi

A Dissertation Submitted to
the Faculty of The Graduate School at
The University of North Carolina at Greensboro
in Partial Fulfillment
of the Requirements for the Degree
Doctor of Philosophy

Greensboro
2012

Approved by

Committee Chair

To my Wife,
Thank you for your love, encouragement, and support.

APPROVAL PAGE

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ACKNOWLEDGEMENTS

I would like to express my deepest gratitude to Dr. Nadja B. Cech for her support through my work at UNCG. I learned valuable lessons from Dr. Cech and I will always be grateful for her guidance. I would also like to thank my other committee members Dr. Gregory M. Raner, Dr. Scott M. Laster Dr. Vincent C. Henrich and Dr. Norman H. L. Chiu for their valuable comments and assistance through my graduate work. I would also like to thank all the Professors who have helped me at UNCG.

Without my family and friends, I would not be where I am today. Thanks go to my parents, and my sister and my brother. They were there every step of the way supporting me and helping and for always being there for me.

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CHAPTER I

INTRODUCTION

1.1 Introduction to *Echinacea*

One of the most popular and top selling herbal medicines in the United States today are preparations from the plant genus *Echinacea*. *Echinacea* has been traditionally used by Native Americans to treat inflammation, colds, and headaches, and to heal wounds. The German commission E and the Canadian Natural Health Products Directorate recommended the use of *Echinacea* for common cold and cough (Blumenthal 1998). However, there are contradictory reports on the efficacy of *Echinacea* for the above stated pharmacological actions, with some studies showing positive results (Yale 2004, Merali 2003, Schulten 2001) and some showing no effect (Turner 2000, Turner 2005, Barrett 2010). One reason for these contradictory reports may be variations in the chemical composition of products tested. Proper quality control of *Echinacea* preparations should ensure consistency; however, there is currently a lack of information as to which constituents might be responsible for the effects of *Echinacea*, and the best techniques to optimize levels of these constituents in commercial *Echinacea* preparations. This lack of information is a problem because it prevents the development of *Echinacea* products with optimal

efficacy. The long-term goal of our research is to aid in the development of effective therapeutic preparations of *Echinacea*. The goals of this particular project are (1) To determine which constituents are responsible for the anti-inflammatory activity of *Echinacea purpurea* preparations and (2) to investigate the effects of *Echinacea purpurea* preparations and their constituents on protein expression by immune cells in vitro and (3) to develop new analytical methods to analyze immunostimulatory lipoproteins that are present in *Echinacea* extracts.

1.2 Review of Literature

Echinacea is a tropical perennial plant from the family Asteraceae that is commonly found in central and eastern North America. There are approximately nine species in the genus *Echinacea*. The three most commonly studied species of *Echinacea* are *Echinacea purpurea*, *Echinacea angustifolia* and *Echinacea pallida*. The major groups of compounds that have been reported as constituents of *Echinacea* are alkylamides, caffeic acid derivatives (cichoric acid, caftaric acid and echinacoside), polysaccharides, and glycoproteins (Figure 1). Ethanol extracts of *Echinacea* contain high levels of alkylamides and phenolic compounds, and aqueous extracts contain hydrophilic compounds such as polysaccharides and glycoproteins (Matthias 2005). Alkylamides are the major lipophilic constituents of *Echinacea* and vary in distribution among different *Echinacea* species (Perry 1997). The roots of *Echinacea* are the plant parts that

contain the highest levels of alkylamides (Wills 1999). *Echinacea* extracts can have opposite effects depending up type of extract used.

1.3 Activity of Constituents from *Echinacea In Vitro*

The alkylamides and/or caffeic acid derivatives present in ethanolic *Echinacea* extracts are reported to have anti-inflammatory activity (Zhai 2009 and 2007). Polysaccharides and/or lipopolysaccharides (LPS) and lipoproteins present in aqueous *Echinacea* extracts are often assumed to be responsible for their immunostimulatory activity of *Echinacea* (Vohra 2009). These compounds might come from the *Echinacea* plant itself, or from bacteria that could be introduced into the preparation as contamination or could live in the plant as endophytes (Pugh 2008, Tamta 2008). Alkylamides of *Echinacea* are reported to influence the expression of TNF- α gene via the CB2 cannabinoid receptor (Gertsh 2004). The alkylamide dodeca-2Z, 4E-diene-8, 10-diynoic acid isobutylamide of *Echinacea purpurea* is reported to have anti-inflammatory activity (Chen 2005). Alkylamides of *Echinacea purpurea* have also been shown to have *in vitro* inhibitory action on cyclooxygenase-1 and cyclooxygenase-2 enzymes, which are responsible for inflammation (Clifford 2002). Inhibition of interleukin-2 (IL-2) production from jurkat T cells by alkylamides of *Echinacea* has also been observed (Sasagawa 2006). Synthetically derived caffeic acid and its ester derivatives are shown to have *in vitro* and *in vivo* anti-inflammatory activity (Da 2004).

1.4 Activity of Crude *Echinacea* Extracts *In Vitro*

Ethanollic extract of *Echinacea* containing alkylamides inhibited the prostaglandin E2 (PGE₂) production from lipopolysaccharide-stimulated RAW 264.7 cells (Lalone 2007). Ethanollic extract of *Echinacea* inhibit the production of proinflammatory cytokines (e.g., (TNF- α) and stimulate the production of anti-inflammatory cytokines (Senchina 2006, Chicca 2009). Ethanollic extract of *Echinacea* inhibited rhinovirus induced secretion of proinflammatory cytokines (e.g., interleukin-6 and interleukin-8). Ethanollic extract of *Echinacea* inhibit the production of inflammatory mediators (e.g., TNF- α , NO) from RAW 264.7 cells infected with *Salmonella enterica* bacteria (Zhai 2007). All the data published on ethanollic extract demonstrate anti-inflammatory activity.

1.5 Activity of Crude *Echinacea* Extracts *In Vivo*

There have been several studies focused on complex *Echinacea* extracts, which have had conflicting results (Yale 2004). Hydroalcoholic extracts of *Echinacea purpurea* containing known concentrations of alkylamides, cichoric acid and polysaccharides stimulated the phagocytic activity in macrophages in a dose dependent manner *in vivo* in Sprague Dawley rats (Basu 2002). However, oral administration of alcoholic *Echinacea* extracts had no effect on development of inflammation in murine peritoneal exudates cells (PECs) *in vivo* (Zhai 2007). Alkylamides are the only constituents of *Echinacea* that have been shown to be absorbed orally (Matthias 2005, Woelkart 2005). Ethanol extracts of *Echinacea*

were not effective against the treatment or decreasing the symptoms of common cold caused due to rhinovirus (Turner 2000, Turner 2005, Barrett 2010). Ethanol extracts of *Echinacea* lessens symptoms of common cold (Yale 2004).

1.5.1 Structures of compounds present in *Echinacea*

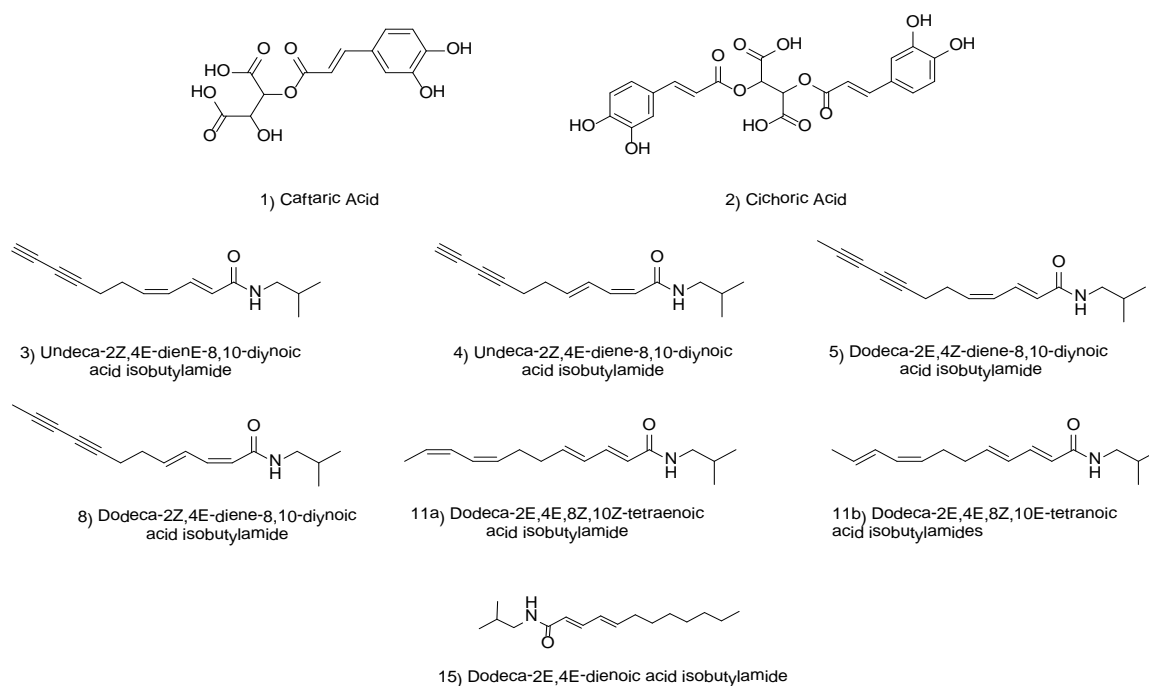


Figure 1. Structure of alkylamides (3-15), cichoric acid (2) and caftaric acid (1) commonly found in *Echinacea purpurea*

1.6 Mass Spectrometry

Mass spectrometry has become an essential tool for genomic and proteomics research. Since this dissertation is heavily focused on mass spectrometry, it is important to have some background information on mass spectrometry. The mass spectrometer measures the mass to charge (m/z) ratio

of ions. All mass spectrometers consists of three components: an ion source, which generates ions (ionization), a mass analyzer, which separates ions based on their m/z ratios and a detector, which measures the abundance of ions of a given m/z . Electrospray Ionization (ESI) and matrix assisted laser desorption/ionization (MALDI) are the most common ionization techniques used in proteomics. The most common mass analyzers used currently include ion-traps, quadrupoles, time of flight (TOF), and fourier transform mass analyzers (ion cyclotron resonance and orbitrap). Recently, hybrid instruments with different combinations of these mass analyzers have been developed. In this project, nano-electrospray ionization (Nano-ESI) coupled to a hybrid linear ion-trap-orbitrap mass spectrometer(LTQ-Orbitrap) as well as matrix assisted laser desorption/ionization (MALDI) –time of flight (ToF) mass spectrometer have been used.

1.6.1 Nano-Electrospray Ionization (Nano-ESI)

Electrospray ionization (ESI) is the most common soft ionization technique. The ESI technique was developed by John Fenn for analysis of macromolecules (Fenn 1989), and he was subsequently awarded the Nobel Prize in 2002. In this project, nano-ESI was used instead of conventional ESI. The only differences between these techniques are that nano-ESI operates at very low flow (100-500 nanoliters per min) and does not use inert gas to evaporate the solvent droplets.

In nano-ESI, mobile phase flows through a thin capillary tube at a nano liter per minute flow rate and several kV are applied between the metal contact to the capillary and the counter electrode. Hence, the liquid coming out of the capillary breaks into small droplets with charges accumulating at the surface of the droplets. Gas phase ions are formed from charged droplets, and two different mechanisms have been proposed for this: 1) Due to the large surface area, droplets evaporate, causing the charge density on their surfaces to increase. When the repulsive force of this charge overcomes surface tension, it results in columbic explosion and ions are released into the gas phase (Iribarne 1976). 2) The charged droplet evaporate, all the solvent escapes from droplet leaving behind charged gas phase ions (Dole 1968), which eventually enter the mass spectrometer.

1.6.2 Linear quadrupole ion trap coupled to orbitrap mass spectrometer (LTQ-Orbitrap)

The LTQ-Orbitrap is one of the most commonly used hybrid mass spectrometers in the proteomics field. It combines many of the advantages of linear quadrupole ion trap (LTQ) and orbitrap mass spectrometers. This hybrid instrument offers high sensitivity and fast scanning of the ion trap and the high resolution and outstanding mass accuracy of the orbitrap. The high resolution and high mass accuracy help in reducing the number of false positives and accomplishing true identification of the protein (Mann 2008).

The linear quadrupole ion trap can perform mass spectrometric analysis by itself or it can be connected to other mass analyzers as in hybrid mass spectrometer. In comparison to 3D ion traps, the LTQ has higher ion storage, higher ion trapping capacity, and increased scan rate. The LTQ used here contains two pairs of hyperbolic rods divided into 3 regions. The center region is larger than the other two. In the central region, a small slit is made at the Z axis on the rods, which allows ions to pass into the detector placed next to them. Ions are then trapped and ejected by a combination of direct current (dc), radio frequency (rf) and alternating current (ac). Three different DC voltages are applied to 3 different sections of rods to trap the ions in the axial direction. For radial trapping (X and Y direction), radio frequency of constant magnitude but opposite phase is applied to the two pairs of rods. For ion isolation, activation, and ejection of ions, alternating current is applied on X-electrode in two phases (Schwartz 2002).

The orbitrap is a new type of mass analyzer in the market, which was invented by Makarov (Makarov 2000). The orbitrap consists of a spindle shaped central electrode and barrel shaped outer electrode. In the orbitrap, electrostatic fields are used to trap ions, and the trapped ions orbit around the central electrode. The moving ions experience electrostatic attraction towards the central spindle electrode, which is balanced by the centrifugal force that allows ions to revolve around the central electrode in orbit. These ions oscillate while revolving

around the central electrode. The oscillations produce image current on the outer halves of the electrode. Fourier transform, a mathematical operation, is employed to convert image current in to frequencies, which in turn give information about mass to charge (m/z) ratios of ions (Scigelova 2006).

The peptide ions formed from the nanospray source enter the mass spectrometer through a heated metal capillary. These ions from the heated metal capillary then enter the LTQ ion trap mass spectrometer. The linear quadrupole ion trap (LTQ) is in the front end of hybrid mass spectrometer (LTQ-Orbitrap). It can perform MS and MS^n analysis with high sensitivity and excellent resolving power and mass accuracy. The LTQ isolates the peptides of interest, fragments them, and records the MS/MS spectra of the peptides. The number of ions transferred into the orbitrap mass spectrometer is determined with automatic gain control (AGC), which affects the resolution and sensitivity of the orbitrap. After exiting the LTQ, ions are transferred into a C-trap (rf only quadrupole), where they are packed into small packets prior to being injected in to orbitrap (Scigelova 2006).

1.7 Mass Spectrometry Based Proteomics

1.7.1 Proteomics

Proteomics is a science that focuses on the identification, characterization and quantification of all proteins in a cell. There are two fundamental approaches

to study proteomics by mass spectrometry, bottom-up, also known as shotgun proteomics and top-down. The top-down approach aims to determine the entire sequence of protein of interest. In top-down, intact protein molecular ions are introduced in to mass spectrometer and are subjected to fragmentation in the gas phase. One of the advantages of the top-down approach is that complete protein sequence coverage can be obtained. Also, it gives information about posttranslational modifications (PTMs) and eliminates time consuming protein digestion step. One of the limitation of top-down is that multiple charged proteins generates complex mass spectra, which limits analysis to simple mixture or single protein. It also requires high resolution mass spectrometers like FT-ICR and orbitrap and large proteins over 50 kDa are hard to fragment. Furthermore, online coupling of top-down techniques with a separation technique is difficult, and bioinformatics for the top-down technique is not very well developed. The bottom-up or shotgun proteomics approach aims to determine a protein of interest by a few amino acid sequences. In shotgun proteomics, first the protein or mixture of proteins is enzymatically cleaved into peptides, and then peptide molecular ions are introduced into the mass spectrometer. Some of the advantages of the bottom-up approach are that online coupling of with liquid chromatography is possible, and methods for separation of peptides are very well developed. Also, bioinformatics software for bottom-up proteomics is well developed and available commercially. Some of the limitations of bottom-up proteomics include that obtaining complete protein sequence is difficult and

information about posttranslational modifications (PTMs) is lost. For reasons mentioned above, shotgun proteomics is effective especially in the field expression proteomics. All of the research in this project employs shotgun proteomics.

1.7.2 Shotgun proteomics

In shotgun proteomics, the identification of proteins in sample mixtures is accomplished using liquid chromatography and mass spectrometry systems. The complexity of protein samples is high if they come from biological origin; hence analysis of these complex samples requires sophisticated analytical instruments (Washburn 2001). LC-MS/MS is a technique of choice for shotgun proteomics studies because of its high throughput and sensitivity. With this technique, enzymatic digestion of a complex protein sample into peptides is performed, and the peptides are separated by liquid chromatography. These separated peptides are then analyzed with the mass spectrometer. The resulting mass spectrometric data is used to identify the proteins with the help of a database search (Zhang 2010). Shotgun proteomics can be done by using liquid chromatography and electrospray ionization (ESI) MS/MS mass spectrometry or liquid chromatography and matrix assisted laser desorption/ ionization (MALDI) MS/MS mass spectrometry. In short, these two techniques are called LC/ESI/MS/MS and LC/MALDI/MS/MS. These two techniques have their own advantages and disadvantages. The advantage of the electrospray method in shotgun proteomics

is that it can easily be coupled to LC, whereas with MALDI-TOF, there is change of state of sample from liquid to solid. One advantage with MALDI-TOF is that it enables higher throughput because the chromatographic separation step is eliminated (Verberkmoes 2005). There are some differences in selectivity with the two different ionization techniques. ESI is good for ionization of aliphatic and hydroxyl amino acids, whereas MALDI favors basic and aromatic amino acids (Stapels 2004). For this reason, MALDI and ESI are complementary, and a combination of LC-ESI-MS/MS and LC-MALDI-MS/MS techniques results in a better sequence coverage than would be achieved with either technique alone.

1.8 Quantitative Proteomics

Quantitative proteomics by mass spectrometry involves at least one additional separation step prior to analysis by the mass spectrometer. Typically, this consists of C18 reverse phase separation by liquid chromatography and/or gel electrophoresis. Quantitation by mass spectrometry can be either absolute or relative, and the methods by which both can be accomplished are discussed below.

1.8.1 Absolute quantitation

To quantify the test sample, a known amount of synthetic peptide is used as an internal standard. This technique is known as absolute quantitation of protein (AQUA) (Gygi 2003). A major advantage of this technique is that true

protein concentrations can be determined which enables comparisons between different proteins in the same sample. The major disadvantage is that unknown samples cannot be quantified because of lack of standards.

1.8.2 Relative quantitation

Most commonly, only relative quantitation is accomplished in proteomics. Comparing expression levels of the same protein in different samples under different conditions, e.g., treated verses untreated samples, normal verses disease conditions, is called relative quantitation. There are two major approaches to relative quantification. The first employs labeling, and the second is label free. Labeling can involve either metabolic labeling or chemical labeling.

1.8.2.1 Chemical labeling

For chemical labeling, stable isotopes are incorporated into the proteins or peptides by a chemical reaction. Isotope containing reagents react with N or C terminal residues or reactive amino acids of proteins or peptides (Bentscheff 2007). The advantage with chemical labeling is this technique can be applied to any kind of samples, including tissue, blood, bio-fluids etc. The disadvantages include that it is expensive and that inconsistency in sampling can occur because of incomplete labeling.

Isotope coded affinity tag (ICAT) is one of the first commercialized chemical labeling techniques that was applied for quantifying differentially expressed proteins (Gygi 1999). The ICAT reagent consists of three units: 1) an affinity tag (biotin), which helps in isolating ICAT labeled peptides by avidin affinity chromatography, 2) a linkage group, which may contain either light or heavy isotopes, and 3) a thiol specific reactive group that interacts with only cysteines. In a typical experiment, test and control samples are mixed with either light or heavy ICAT reagent. Then, both samples are mixed together and digested, and cysteine containing peptides are collected by affinity chromatography and analyzed by LC-MS. The resulting MS data is then subjected to search for isotopes differing by eight mass units (Heavy ICAT tag is chemically modified with 8 stable isotopes of either carbon (^{13}C) or hydrogen (^2H)). Quantification is done by comparing intensities of these two isotopes. An advantage of the ICAT technique is that it increases the abundance of cysteine containing amino acids in the sample, which in turn decreases the complexity of sample. This is also a disadvantage because only cysteine containing peptides are quantified. Another disadvantage of ICAT is that it cannot be used to compare more than two samples.

The isobaric tag for relative and absolute quantitation (iTRAQ) technique is another labeling technique employed for quantitative proteomics. This technique was developed by Pappin in 2004. This technique can be used for

relative and absolute quantitation of 4 experimental conditions in one analysis. The iTRAQ reagent consists of a reporter group (m/z 114-117), a balance group (28-31Da) and a reactive group. All iTRAQ reagents have the same mass (145Da), but they differ in composition of balance group and reporter group. With the iTRAQ technique, the protein from control and test samples is digested. Peptides are reacted with suitable iTRAQ reagents and the samples are combined and subjected to LC-MS/MS analysis. Quantitation is performed in the MS/MS mode by comparing the intensities of fragments from reporter groups (Ross 2004). Advantages of iTRAQ over ICAT is that reagents used are isobars, so the same peptides from each sample show up as one peak in MS spectrum, this reduces complexity in MS spectrum and increases signal intensity especially of non-abundant proteins and more proteome coverage. It also increases the sensitivity of quantification, since quantification is done at MS/MS level where chemical noise is minimum. A disadvantage of iTRAQ is the need for a high resolution mass spectrometer.

Oxygen isotope (^{18}O) labeling is another technique for quantitative proteomics developed by Mirgorodskaya. With this technique, peptides are incubated with trypsin in ^{18}O water. ^{18}O atoms from water are enzymatically transferred to the C-termini of the peptides. Relative quantitation can then be accomplished by comparing intensities of light ^{16}O with heavy ^{18}O ions in the mass spectrum (Mirgorodskaya 2000). Advantages of this technique are that it

is simple, inexpensive, and any protein sample can be labeled. A major disadvantage is that it is prone to sample handling errors, and is, therefore, not very reproducible.

1.8.2.2 Metabolic labeling

With metabolic labeling, stable isotopes are incorporated in the proteins during cell growth. The major advantage of metabolic labeling is that all proteins can be labeled. Examples of metabolic labeling are stable isotope labeling with amino acids in cell culture (SILAC) (Ong 2002) and incorporation of ^{15}N (Wu 2004). SILAC is the most routinely used metabolic labeling technique for quantification of proteins. This SILAC technique was developed by Dr. Mann's group (Ong 2002). The advantages of SILAC over other labeling techniques include: 1) all proteins can be labeled, 2) complete labeling can be achieved, 3) more peptide coverage can be accomplished than is possible with labeling techniques, 4) SILAC is suitable for comparing more than two samples, 5) several labeled peptides identifying the same protein improves statistics and confidence in protein quantitation, 6) minimized handling and instrumental errors, 7) the mass differences of peptides are known in advance. Due to all these advantages, we chose to use the SILAC technique for our study. However, there also some disadvantages of SILAC as well. These include 1) the technique is generally only be applied to cultured cells (*in vivo* SILAC experiments are possible but very expensive and laborious), 2) the incorporation of amino acids in

cell culture is a time consuming process, 3) some type of cells cannot incorporate certain amino acids. With SILAC, cells are grown in either media containing natural amino acids (light media) or stable isotopically labeled non-radioactive form of amino acids (heavy media). Protein extracted from these cells is labeled as either light or heavy protein. The most commonly used isotopes in SILAC are carbon-13 (^{13}C) and nitrogen-15 (^{15}N). Any of the 20 essential amino acids can be used for labeling, but the most common amino acids are lysine and arginine. These amino acids make a good choice because the protease most often employed for digestion (trypsin) cleaves at the C-terminus of these amino acids.

For SILAC, cells are grown in light and heavy media for 5 to 6 generations for complete incorporation of labeled amino acids. Typically, control cells are grown in heavy media and experimental or test cells are grown in light media. After the experiment, the cells are lysed and the protein is extracted, quantified using the bicinchoninic acid assay (BCA) (Smith 1985), and combined at a 1:1 ratio (heavy: light). These mixed lysates undergo fractionation either by SDS-PAGE or chromatography or both, followed by digestion. Digested proteins are then subjected to mass spectrometric analysis. Quantification is accomplished by comparing the mass spectrometric signal intensities for heavy peptides ending with either lysine or arginine with those of light peptides.

1.8.3. Label free quantitation

Label free approaches include spectral counting and chromatographic peak intensity measurement. Advantages with label free methods are that they are simple, inexpensive, and not limited by number of samples and the kind of sample. Disadvantages with label free methods are that it is difficult to measure minor differences between samples and this technique needs many LC-MS replicates per sample.

For spectral counting, quantification is done by counting the number of MS/MS spectra of peptides identifying the protein (Liu 2004). A disadvantage of this approach is that it requires high resolution mass spectrometers. Accurate mass measurement of peptide molecular ions increases confidence of identification of MS/MS spectra especially for quantifying low abundant proteins. For chromatographic peak intensity measurement, quantification is done by measuring the chromatographic peak areas of peptides identifying a particular protein (Chelius 2002). A disadvantage of this approach is that it needs highly reproducible LC-MS chromatograms, which in turn need robust liquid chromatography systems. With good instrumentation and software, label free methods are definitely an alternative for labeling strategies.

1.9 Protein Identification and Database Searching

The important step in mass spectrometry based proteomics is protein identification from raw mass spectra. This is usually done by searching mass spectrometric data in database search engines like SEQUEST (Thermo Scientific) and MASCOT (Matrix Science). During the database search, the experimental mass spectra are compared with theoretical mass spectra present in the database. The theoretical mass spectra are generated by *in silico* digestion of proteins sequences, which vary depending on the enzyme of interest. For each peptide, experimental m/z values of the precursor ion and fragments ions are compared with theoretical values to make a correct identification of the protein. Based on the similarity between experimental and theoretical fragmentation spectra, this software assigns a score to each individual peptide. This score indicates correctness of the match. The Mascot score is calculated by a formula called $-10 \cdot \log(P)$, where P is the absolute probability that the resulting match can be a random event (Weatherly 2005). There is always a chance of incorrect identification of peptides that are called false positives. To control false positives, the strategy called target-decoy search is used. The mass spectral data is searched against both forward the sequences and reverse sequences present in the database. The identified peptides are then processed by a false discovery rate (FDR) filter, which estimates the extent of false positives in the search.

1.10 Chromatography Used in Shotgun Proteomics

The major liquid chromatography system used in shotgun proteomics is nano-liquid chromatography (nano-LC), which employs columns with an internal diameter ranging between 10-100 μm . Nano-liquid chromatography was used in this project for separation of peptide mixtures. The later technique offers higher efficiency, sensitivity, resolution and selectivity in comparison to conventional liquid chromatography. Thus, nano-liquid chromatography requires smaller sample sizes (in proteomics studies sample size is always limited), generates less solvent waste, and is highly compatible with modern mass spectrometers because of their low flow rates. Another major advantage is that almost all of the sample from column enters the mass spectrometer, which improves sensitivity as compared to conventional liquid chromatography approaches (Hernandez-Borges 2007).

CHAPTER II

IDENTIFY AND QUANTIFY CONSTITUENTS RESPONSIBLE FOR THE ANTI-INFLAMMATORY ACTIVITY OF *ECHINACEA PURPUREA* CONSTITUENTS

2.1 ABSTRACT

Rationale: The goals of this study were to identify and quantify constituents present in the *Echinacea purpurea* extracts, to test these extracts for in vitro anti-inflammatory activity, and to determine if the *in vitro* anti-inflammatory activity of these extracts correlated with presence of the alkylamides and/or caffeic acid derivatives.

Methods: Seventeen dormant *Echinacea purpurea* samples were collected from different locations of North Carolina. The roots were dried, powdered, and extracted with 75% ethanol. The extracts were then precipitated with 95% ethanol (1:1) to remove immunostimulatory compounds. Liquid chromatography - mass spectrometry (LC-MS) was used to identify the extract components based on retention time, fragmentation pattern, and mass to charge ratio (m/z), and quantification was accomplished based on peak area. The compounds were eluted from a reversed phase C18 column using an acetonitrile and water

gradient. Electrospray ionization (ESI) on an ion trap mass spectrometer was used to acquire the data in positive ion mode and negative ion mode. Immunomodulatory activity of the extracts was evaluated based on their ability to alter the production of PGE₂ and TNF- α from RAW 264.7 macrophage type cells infected with influenza A Strain PR/8/34 virus. The Pearson test was conducted to correlate anti-inflammatory activity extract with concentrations of alkylamides and caffeic acid derivatives.

Results: Alkylamides and caffeic acid derivatives, purported bioactive constituents of *Echinacea purpurea*, were successfully identified in all the extracts using the LC-MS technique in the positive ion and negative ion modes, respectively. The major alkylamide 11a/b (dodeca-2E, 4E, 8Z, 10E/Z-tetraenoic acid isobutylamide), cafteric acid and cichoric acid were quantified in all of the extracts. A range of anti-inflammatory activity was displayed by the seventeen different extracts, with extract seven being the most active one. The correlation between anti-inflammatory activity (ability to suppress production of TNF- α) and the presence of alkylamides was only very weak, and there was no correlation with this activity and the concentration of caffeic acid derivatives.

Conclusion: *Echinacea purpurea* extracts have anti-inflammatory activity *in vitro*. Further bioactivity-directed fractionation studies are needed to identify

constituents other than alkylamides and caffeic acid derivatives that may be responsible for the anti-inflammatory activity of *Echinacea purpurea*, or to eliminate extract components that mask the anti-inflammatory activity of the alkylamides and/or caffeic acid derivatives.

2.2 Introduction

Clinical trials conducted on *Echinacea* for anti-inflammatory activity resulted in contradictory reports, with some studies showing positive effect (Yale 2004, Merali 2003, Schulten 2001) and some showing no effect (Turner 2000, Turner 2005). One of the reasons for this is due to lack of information as to which constituents might be responsible for the anti-inflammatory effects of *Echinacea*. This lack of information is a problem because it prevents the development of *Echinacea* products with optimal efficacy. The goal of this project is to determine which constituents are responsible for the anti-inflammatory activity of *Echinacea purpurea* preparations. In this study, we sought to quantify the levels of alkylamides and caffeic acid derivatives in different extracts of *Echinacea purpurea* collected from seventeen different cultivation sites across North Carolina. Our goal was to determine if the levels of these compounds could be correlated with anti-inflammatory activity of extracts.

2.3 Experimental

2.3.1 Preparation of extracts

Dormant *Echinacea purpurea* roots were collected from seventeen different cultivation sites across North Carolina and voucher specimens were retained and submitted to the North Carolina Herbarium (CB# 3280, Coker Hall, University of North Carolina, Chapel Hill, NC 27599-3280) (Cech 2010). The roots were thoroughly washed, air dried at 38°C, and powdered. The powdered roots were subjected to maceration with 75% ethanol for one week at a 1:5 plant material to solvent ratio (w/v). After maceration, a hydraulic press was used to press the extracts and the extract was filtered through a 0.2- μ M membrane sterile filter under vacuum in a laminar flow hood and stored in sterile bottle at 2-8°C. The extracts were screened for endotoxin (lipopolysaccharide) using the limulus amoebocyte lysate (LAL) assay. The LAL test results showed that the extracts were endotoxin free with an acceptable sensitivity of 0.25 EU/mL. Ethanol precipitation was performed to remove ethanol insoluble compounds and create an alkylamide-enriched extracts. The ethanol precipitation was done by adding ethanol (95%) to the existing extracts at a ratio of 1 mL extract: 1 mL ethanol (95%). The resulting ethanol concentration of the extract was 85%. The ethanol precipitated extract was centrifuged to remove precipitate and the remaining supernatant was stored and labeled as “precipitated extract.” Alkylamide 11a/b (dodeca-2E, 4E, 8Z, 10E/Z-tetraenoic acid isobutylamide)

(Chapter 1, Figure 1) was obtained from Gaia herbs (Brevard, NC, USA) and caferic acid and cichoric acid (Chapter 1, Figure 1) were purchased from Chromadex (Santa Ana, CA, USA).

2.3.2 LC-MS method

Reversed phase liquid chromatography coupled with electrospray ionization mass spectrometry (ESI-MS) was employed for the analysis of the precipitated extracts of *Echinacea purpurea*. An HP1100 Liquid Chromatography system (Agilent, Palo Alto, CA, USA) equipped with a C18 column (50mm x 2.1 mm, 110 Å pore size, 3µm particle size, Grace, Deerfield, IL, USA) and a precolumn filter (0.5 µm) (MacMod analytical, Chadds Ford, PA, USA) was used. A gradient elution was performed at a flow rate of 0.2 mL/min with water and acetonitrile as mobile phase solvent system. Solvent A consists of nanopure water (1% acetic acid) and solvent B consists of acetonitrile (Pharmaco-AAPER, Shelbyville, KY, USA). Alkylamides and caffeic acid derivatives were analyzed separately in two different runs. For alkylamides, the solvent composition was as follows: t= 0-4 min, a constant composition of A-B (90:10,v/v); for t = 4-15 min, a linear gradient from A-B (90:10,v/v) to A-B (60:40, v/v): for 15-30 min, a linear gradient from A-B (60:40,v/v) to A-B (40:60,v/v); for t=30-35 min, a constant composition of A-B (90:10,v/v). For caffeic acid derivatives, the solvent composition was: t = 0-39 min, a linear gradient from A-B (90:10, v/v) to A-B (50-

50, v/v); for t = 39-43 min, a constant composition of A-B (90:10, v/v). An ion trap mass spectrometer (LCQ Advantage, Thermo Fisher, San Jose, CA, USA) with electrospray ionization (ESI) source at the front end was used for the analysis. The mass spectrometric analysis was performed over a scan range of 50-2000, with capillary, spray, and tube lens offset voltages being 3V, 4.5KV, and -60V, respectively. Analysis of alkylamides was performed in the positive ion mode while analysis of caffeic acid derivatives was performed in the negative ion mode.

2.3.3 Anti-inflammatory activity

The ability of the extracts to influence production of PGE₂ and TNF- α was evaluated with cultured RAW 264.7 cells as described in paper by Cech. et. al (Cech 2010). The cells were cultured in Dulbecco's Modified Eagle's Medium (DMEM) with 4mM L-glutamine, 1.5 g/L sodium bicarbonate, and 4.5 g/L glucose, with 10% fetal calf serum (FCS). The supernatants from cell cultures were collected from 24 well cell culture plates seeded with 1.5×10^5 cells per well in 1 mL culture media. Cells were treated with influenza A Strain PR/8/34 virus 30 minutes prior to addition of extracts. The extracts were added directly into the cell media (6.7 μ L of non-precipitated extracts or 5.8 μ L of precipitated extracts) of 1 mL well volume. The final ethanol percentage was 0.5% in precipitated and non-precipitated extracts, which was far below toxic level. After the treatment, supernatants were collected and stored at -80°C after centrifugation at 8,000 rpm

for 2 min. Later these supernatants were tested for anti-inflammatory activity by ELISA.

2.4 Results and Discussion

The seventeen dormant root samples of *E. purpurea* were obtained from seventeen different regions of North Carolina. Ethanol extracts of these samples were screened for induction of TNF- α production from non-infected RAW 264.7 cells (Figure 2A) and cells that had been exposed to virus (Figure 2B). In non-infected cells, most of the *E. purpurea* extracts had no effect, while some extracts did increase TNF- α production from RAW 264.7 cells. TNF- α production from RAW 264.7 cells treated with influenza A strain was suppressed by *E. purpurea* extracts, but the degree of suppression varied with different extracts (Figure 2B). The extracts that showed stimulatory action in non-exposed cells had the same effect in virus-exposed cells.

The same extracts listed in Table 1 were precipitated with ethanol to remove lipoproteins and lipopolysaccharides. These compounds might be present in *Echinacea* and may be responsible for production of inflammatory cytokines in macrophage cells (Pugh 2008). The precipitated extracts were then screened for the same activities in virus exposed and non-exposed cells. Results show that ethanol precipitation removed the most of the TNF- α stimulatory

activity of the extracts (Figure 2C and D). Extract number 7 showed strong inhibitory action against TNF- α production (Figure 2D). All these extracts were also screened for their effect on PGE₂ production by RAW 264.7 cells (Figure 3). In non-exposed cells, the only extract that stimulated PGE₂ production was extract number 12 (Figure 3A), whereas in virus exposed cells, many of these extracts increased the production of PGE₂ (Figure 3B). After ethanol precipitation, several extracts suppressed PGE₂ production in treated cells, with extract 7 showing the most pronounced suppressive effect against PGE₂ production (Figure 3D).

To correlate the levels of constituents present in the *Echinacea* extracts with their anti-inflammatory activity, a quantitative analysis was performed on alkylamides 11a/b, caftaric acid and cichoric acid (Table 1). A Pearson test was conducted to evaluate the correlation between levels of *Echinacea* constituents (alkylamides 11 a/b, caftaric acid and cichoric acid) and concentrations of PGE₂ and TNF- α in the cell media.

The Pearson test results shows that there is weak correlation or no correlation between alkylamide 11a/b concentration in precipitated extracts and levels of TNF- α (R = -0.608, p=0.03) and PGE₂ (R = -0.496, p = 0.04, Pearson) expressed in the cell media. Similar results were observed with caftaric acid and

cichoric acid. No correlation ($p < 0.05$) was observed between levels of PGE₂ and TNF- α and in precipitated extracts concentrations of caftaric acid and cichoric acid (caftaric acid and TNF- α , $R = -0.173$, $p = 0.6$; caftaric acid and PGE₂, $R = -0.225$, $p = 0.4$, for cichoric acid and TNF- α , $R = -0.133$, $p = 0.7$; cichoric acid and PGE₂, $R = -0.025$, $p = 0.9$). The Pearson test was also performed on other alkylamides (3, 4, 5, 8 and 15 chapter 1, Figure 1) present in the extracts other than alkylamides 11 a/b. For the other alkylamides, the correlation was performed based on HPLC peak area (Figure 4) of alkylamides (rather than concentration, since no standards were available) and levels of PGE₂ or TNF- α expressed in the cell media (data not shown) (Cech 2010). There was no correlation ($p < 0.5$) between these parameters.

2.5 Conclusion

The results obtained from the experiments performed in this study were enough to demonstrate that some (but not all) *Echinacea purpurea* extracts have anti-inflammatory activity. However, these experiments do not provide conclusive evidence of which constituents of the *Echinacea purpurea* extracts are responsible for this activity, or to the precise mode of action of these constituents. Further bioactivity directed fractionation studies are needed to identify other constituents other than alkylamides and caffeic acid derivatives responsible for the anti-inflammatory activity of *Echinacea purpurea*, or find ways

to eliminate the components in the extracts that mask the anti-inflammatory activity of the extract.

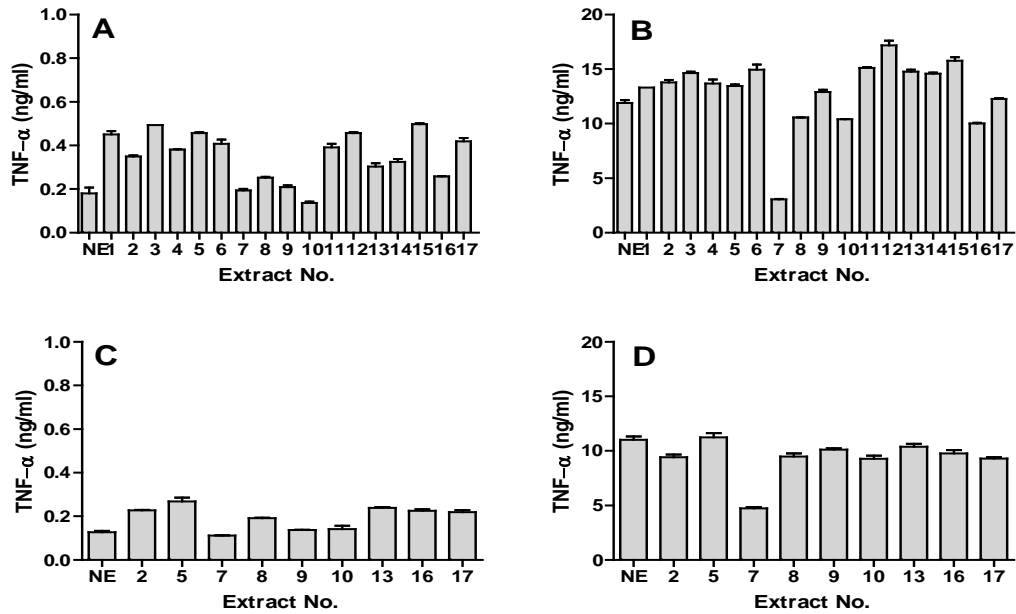


Figure 2. TNF- α Production from RAW 264.7 macrophages upon treatment with crude extracts of *Echinacea purpurea*. *E. purpurea* extracts were added to 1 mL culture of cells by itself (A and C) or cells exposed to influenza strain A/PR8/34 (B and D) (moi=5). After 24 hours, supernatants were collected. Cells were infected 30 min before the addition of *E. purpurea* extracts (panel B and D). Results in panel B and D were obtained after addition of 6.7 μ l of 75% ethanol extracts to treated cells, whereas in panels C and D, 5.8 μ l of 85% precipitated ethanol extracts were used. The concentrations of dodecatetraenoic acid isobutylamide (11a/b) ranged from 5-22 μ M (Table 1). For control samples, equal amount of ethanol was added instead of extracts. The results shown here are means \pm SEM of two ELISA experiments done independently. Data for this figure were collected in Scott Laster's laboratory at NC State University by D. Eads using extracts prepared and characterized by V. Kandhi. These results were published in *International Immunopharmacology* (Cech, 2010).

Table 1. Assay concentrations of alkylamides and caffeic acid derivatives achieved after treatment with different plant samples (note, samples are diluted 172 times upon addition to the sample wells).

Sample #	Concentration Alkylamide 11a/b		Concentration Caftaric acid		Concentration Cichoric Acid	
	μM	$\mu\text{g/mL}$	μM	$\mu\text{g/mL}$	μM	$\mu\text{g/mL}$
01	22.0	5.4	2.9	0.16	2.9	0.24
02	11.0	2.7	4.1	0.22	4.6	0.38
03	16.8	4.2	2.9	0.16	3.5	0.28
04	16.2	4.0	3.5	0.19	3.5	0.28
05	13.3	3.3	3.5	0.19	1.7	0.14
06	9.3	2.3	7.5	0.41	12.2	1.00
07	22.0	5.4	3.5	0.19	2.9	0.24
08	11.6	2.9	5.2	0.28	4.1	0.33
09	10.4	2.6	2.9	0.16	2.9	0.24
10	9.3	2.3	4.1	0.22	2.3	0.19
11	5.2	1.3	2.9	0.16	2.3	0.19
12	4.6	1.1	2.3	0.12	2.3	0.19
13	14.5	3.6	2.9	0.16	2.9	0.24
14	11.0	2.7	4.6	0.25	7.0	0.57
15	20.3	5.0	3.5	0.19	7.0	0.57
16	10.4	2.6	7.5	0.41	8.7	0.71
17	17.4	4.3	3.5	0.19	7.0	0.57

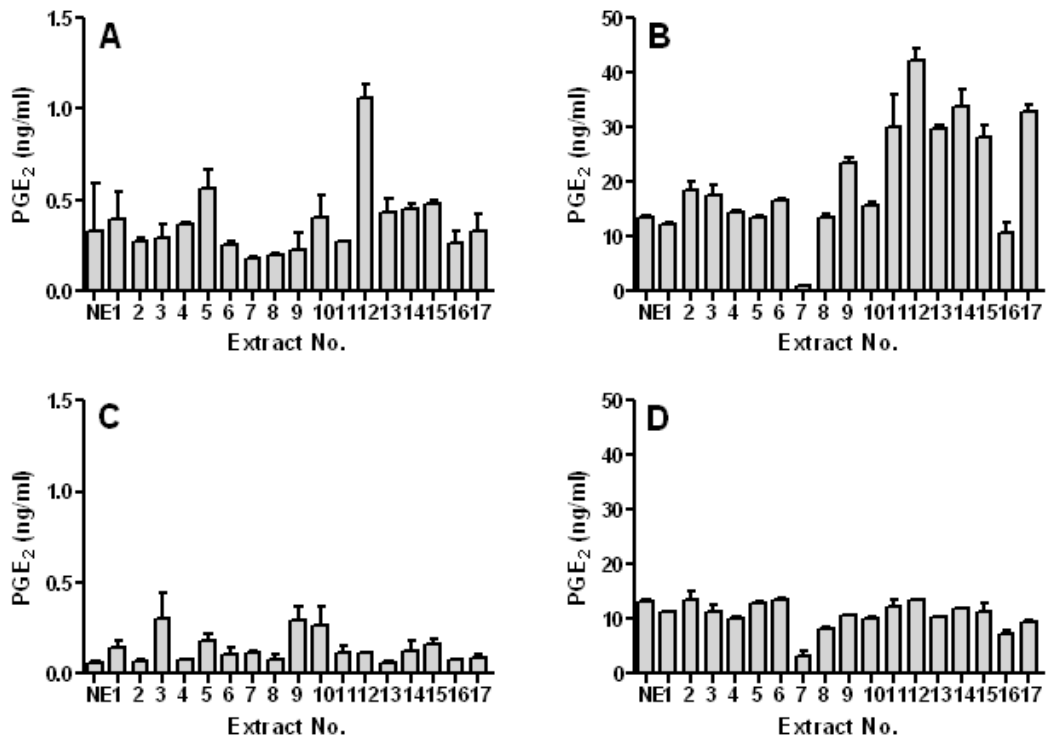


Figure 3. PGE₂ Production from RAW 264.7 cells upon treatment with crude extracts of *Echinacea purpurea*. All the conditions were identical to were shown in Figure 2, except that ELISA was conducted for PGE₂ instead of TNF- α . As with the data shown in Figure 2, except that ELISA was conducted for PGE₂ instead of TNF- α . As with the data shown in Figure 2, these results were obtained by D. Eads using extracts prepared by V. Kandhi.

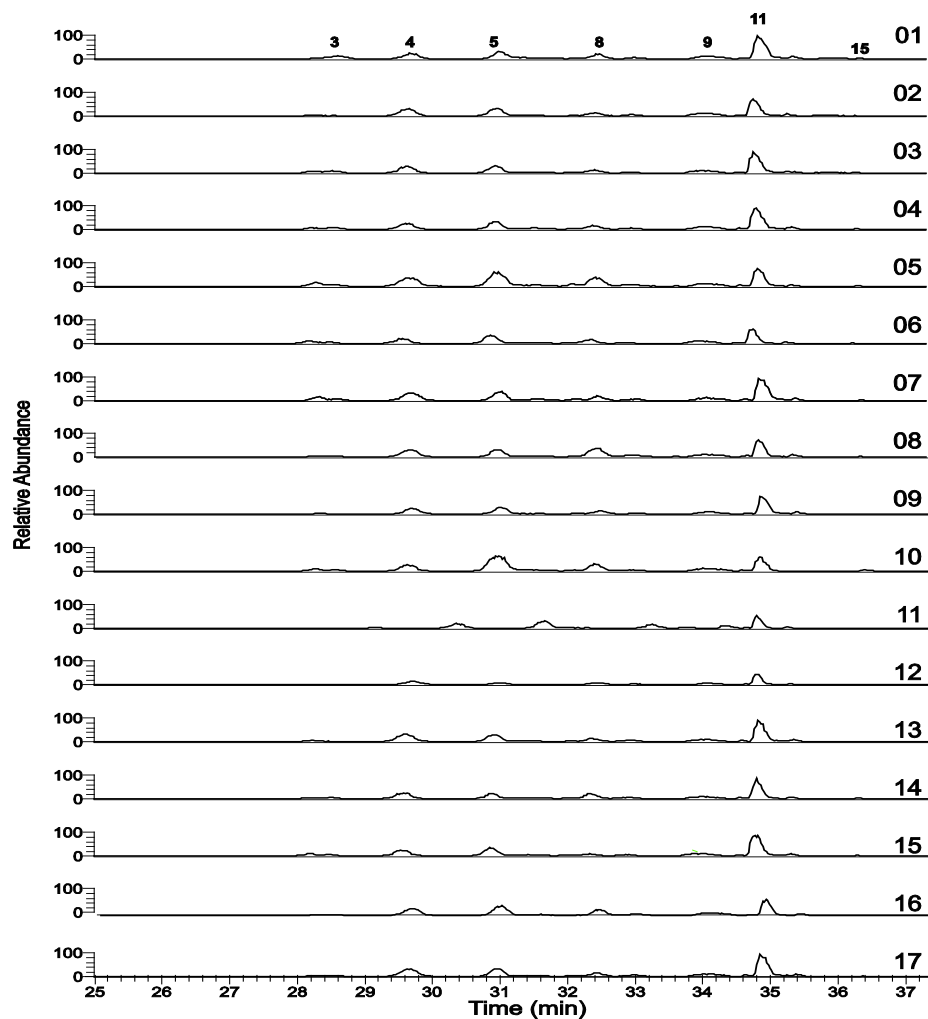


Figure 4. LC-ESI-MS base peak chromatograms comparing alkylamide profiles in different root extracts of *Echinacea*. LC-MS analysis was performed in positive ion mode. All the extracts have the similar alkylamide profile; extract two which is inactive has the same same alkylamide profile as the extract seven, which is the most active one.

CHAPTER III

**QUANTITATIVE PROTEOMICS USING SILAC TO INVESTIGATE THE
IMMUNOMODULATORY EFFECTS OF *ECHINACEA PURPUREA***

3.1 Abstract

Rationale: *Echinacea purpurea* and its constituents are known to have anti-inflammatory properties. *Echinacea purpurea* is one of the most popular herbal medicines in the United States. However, lack of knowledge regarding *Echinacea's* mechanism of action confounds the development of clinical trials to evaluate its efficacy. In this present study, we used proteomics to evaluate the effect on *Echinacea* extracts on Lipopolysaccharide (LPS) induced inflammatory conditions in Raw 264.7 macrophages in vitro.

Methods: Quantitative proteomics was employed to gain mechanistic insight into the *in vitro* immunomodulatory effects of *Echinacea*. Stable isotope labeling with amino acid in cell culture (SILAC) was employed to identify and quantify proteins in RAW 264.7 macrophage-type cells exposed to *Echinacea purpurea* extracts and lipopolysaccharide (LPS). Samples were analyzed by nanoLC (Eksigent)-MS/MS (LTQ-Orbitrap XL, Thermo Scientific).measurements using the orbitrap

mass spectrometer resulted in the identification and quantification of a number of proteins. Some of the proteins identified were involved directly or indirectly in immunomodulation. Three experiments (biological replicates) were performed. A total of 1013 proteins were identified in experiment 1, out of which 10 proteins were upregulated with LPS (Log_2 ratio >1), 834 proteins were identified in experiment 2, out of which 36 proteins were upregulated with LPS (Log_2 ratio >1), and 978 proteins were identified in experiment 3, out of which 8 proteins were upregulated with LPS (Log_2 ratio >1). LPS stimulation led to increased expression of a number of proteins involved in inflammation (prostaglandin synthase, immune-responsive gene 1, MARKS-related protein, Nuclear factor NF-kappa-B p100 subunit protein, and H-2 class I histocompatibility antigen. *Echinacea* extracts stimulation led to increased expression of coronin 1C protein (Log_2 ratio >1). Expression of several of the LPS-induced proteins was regulated by the *Echinacea* extract. The *Echinacea* extract completely blocked LPS-induced production of prostaglandin G/H synthase 2, partially blocked MARCKS-related protein, nuclear factor NF-kappa-B p100 subunit protein, and H-2 class I histocompatibility antigen, and caused differential regulation of immune-responsive gene 1 (this last protein was upregulated in experiment 2 and downregulated in experiment 1). Of these observations, the influence on prostaglandin G/H synthase 2 is particularly relevant given that this protein generates prostaglandin E from prostaglandin H₂, and is a target of anti-

inflammatory drugs such as aspirin. Furthermore; MARCKS related protein expression has been shown to be upregulated in macrophage cells upon LPS stimulation. These results suggest MARCKS related protein plays an important role in functioning of stimulated macrophages. Thus, the influence of *Echinacea* on these proteins is consistent with an anti-inflammatory mode of action. Both alkylamides, alkylamide 11 a/b (dodeca-2E, 4E, 8Z, 10E/Z-tetraenoic acid isobutylamide) and alkylamide 15 (dodeca-2E, 4E-dienoic acid isobutylamide) at a concentration of 54µg/ml also suppressed the inflammatory proteins listed above. The degree of suppression on these LPS induced proteins was greater for alkylamide 15 as compared to alkylamide 11a/b. This last finding was consistent with our earlier experiments conducted using ELISA techniques to monitor the effects of alkylamides on secretion of cytokines and chemokines by macrophage-type cells *in vitro*.

Conclusions: *Echinacea purpurea* and its alkylamide constituents have anti-inflammatory activity *in vitro* against LPS-induced inflammation in Raw 264.7 cells. They appear to exert their anti-inflammatory action on several different pathways. For example suppression of PGE₂ protein by extracts indicates that the arachidonic acid pathway is targeted, and upregulation of coronin 1C protein by extracts indicates influences on phagocytic and bactericidal pathways. Finally, influence of the *Echinacea* on the antigen presentation pathway is

indicated by suppression of H-2 class I histocompatibility antigen. Altogether, this research study increased our understanding of mechanism of action of *Echinacea purpurea*.

3.2 Introduction

In this study, a proteomic approach was used to better understand how *Echinacea* extract and its constituents act on immune cells. In recent years, mass spectrometry has become a powerful tool in proteomics, especially in functional proteomics, to study the concentration changes in normal and diseased states and also to understand the particular proteins and pathways involved in diseased states. This also helps to understand the signaling between the proteins and mechanism of action of drugs. Recent developments in the quantitative proteomics field have made it easier to monitor concentration changes in complex protein samples.

In these experiments, a particular type of quantitative proteomics, stable isotope labeling with amino acids in cell culture (SILAC) (Ong 2002), was employed to study changes in protein secretion by RAW 264.7 macrophage-type cells under various treatment conditions. The cells were treated with bacterial lipopolysaccharide (LPS) to mimic an inflammatory condition, and also with ethanolic *Echinacea* extracts and isolated alkylamides (major components of

ethanolic extracts of *Echinacea*). The objective of these studies was to gain insight into mechanism by which *Echinacea* extracts and isolated alkyalmides from *Echinacea* interact with immune cells *in vitro*. Towards this objective, our goals were to measure the influences *Echinacea* and components thereof on protein expression by activated RAW 264.7 macrophage cells.

RAW 264.7 macrophage cells are very well studied to understand how the immune system responds to inflammatory conditions (Fujiwara 2005). Macrophages are an important component of the immune system, and the first line of defense against infection. Macrophages are involved in phagocytosis, antigen presentation, and immunomodulation. Macrophages are important in initiating, maintaining and resolving inflammation. In these experiments, the macrophages were treated with LPS (lipopolysaccharide) to mimic an infection. Lipopolysaccharide (LPS) or endotoxin is a very important structural component present in the outer membrane of Gram-negative bacteria. Among the different pathogen-associated molecular patterns (PAMPs) of bacteria, LPS is the one that has been studied the most. LPS is known to activate the TLR4 (Toll Like Receptors 4) receptor, and this activation leads to release of pro-inflammatory cytokines (TNF- α , IFN- γ , IL-1) from macrophages. Imbalance in LPS regulation can lead to acute or chronic inflammation (Fujiwara 2005).

The general structure of gram negative lipopolysaccharide consists of a lipid A moiety, an O-polysaccharide moiety, and the core polysaccharide. The lipid A part of LPS is highly hydrophobic, and is bound to core polysaccharide by a covalent bond. Lipid A consist of β -D-GlcN-(1-6)- α -D-GlcN disaccharide with two phosphoryl groups. Four acyl chains are attached to this structure either by ester or amide linkage. The endotoxicity of LPS is due to the lipid A moiety. The endotoxicity of LPS depends on a number of factors including number, length of acyl chain and the phosphorylation state of the disaccharide backbone. The O-polysaccharide portion of LPS (also called O-chain or O-antigen) is composed of repeating sugar units, primarily hexoses. These repeating units differ by type of sugar, sequence, substitution and chemical linkage in different strains. Host antibody responses target the O-polysaccharide part of LPS. This core polysaccharide portion of LPS can be divided into an outer and an inner core. The inner core is present adjacent to lipid A and is characterized by the presence of highly conserved, unusual sugars, 3-deoxy-Dmanno-octulosonic acid (Kdo) and L-glycero-D-manno heptose. The outer core is composed of mainly hexoses and hexamines (Erridge 2002).

3.3 Materials and Methods

RAW 264.7 cells were purchased from American Type Culture Collection (ATCC). SILAC Dulbecco's Modified Eagle's Medium (DMEM) media without

lysine and arginine, L-Lysine-2HCl, L-Arginine-HCl, $^{13}\text{C}_6$ L- Arginine-HCl, and $^{13}\text{C}_6$, $^{15}\text{N}_2$ L-Lysine-2HCl were purchased from Thermo Scientific. Dialyzed fetal bovine serum was purchased from GIBCO (Invitrogen, CA). Lipopolysaccharide (LPS) from *Salmonella minnesota* R595 was purchased from List Biological Laboratories (Cambell, CA). Trypsin, (TPCK treated, from bovine pancreas, sigma –T1426) and formic acid were purchased from Sigma-Aldrich. Optima LC-MS-grade acetonitrile and water was purchased from Fisher Scientific. Alkylamide standards, alkylamide 11a/b (dodeca-2E, 4E, 8Z, 10E/Z-tetraenoic acid isobutylamide) and alkylamide15 (dodeca-2E, 4E-dienoic acid isobutylamide) were purchased from Gaia Herbs (Brevard, NC)

3.3.1 Cell culture media

RAW 264.7 cells were cultured in SILAC-DMEM media with 10% dialysed Fetal Bovine Serum (FBS). The incubator conditions are maintained at 5% CO_2 and 37°C . Light SILAC DMEM media contains L-Lysine-2HCl 0.798mM and L-Arginine-HCl 0.397mM. Heavy SILAC DMEM contains $^{13}\text{C}_6$ L- Arginine-HCl (0.397mM), and $^{13}\text{C}_6$, $^{15}\text{N}_2$ L-Lysine-2HCl (0.798mM).

3.3.2 Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC)

RAW 264.7 cells were cultured in either light SILAC DMEM media containing L-Lysine-2HCl, L-Arginine-HCl or heavy SILAC DMEM media

containing $^{13}\text{C}_6$ L- Arginine-HCl, $^{13}\text{C}_6$, $^{15}\text{N}_2$ L-Lysine-2HCl. Cells were allowed to grow for six doublings for complete incorporation of isotopes (Ong 2002). Three independent SILAC experiments were performed to study effects of *Echinacea* extracts and its constituents (alkylamides) on LPS stimulated RAW 264.7 macrophage cells, which serve as biological replicates. In all experiments, heavy cells (grown in heavy media) were treated with 0.5% ethanol which is the vehicle control. Light cells (grown in light media) were treated with *Echinacea* extracts, its constituents (alkylamides) and LPS by itself and in combinations of them. In experiment 1, light cell were treated with $1\mu\text{g}/\text{mL}$ lipopolysaccharide (LPS), $5.8\mu\text{L}/\text{mL}$ *Echinacea* extract, and $1\mu\text{g}/\text{mL}$ LPS+ $5.8\mu\text{L}/\text{mL}$ *Echinacea* extract. One of the questions to be resolved is what effect LPS and extract have on RAW 264.7 cells. Another question that has to be resolved is, will the extract oppose LPS induced protein. In experiment 2, all the conditions are same as in experiment 1, except for an additional treatment, which include isolated constituent of *Echinacea*, a major alkylamide, alkylamide 11a/b, at a concentration of $5.4\mu\text{g}/\text{mL}$. One of the questions that have to be resolved in this experiment is to see if these results are reproducible. Also, what effect alkylamide 11 a/b (dodeca-2E, 4E, 8Z, 10E/Z-tetraenoic acid isobutylamide) have on LPS induced proteins. In experiment 3, all the conditions are same as in experiment 2, except for an additional treatment, which include isolated constituent of *Echinacea* alkylamide, alkylamide 15 (dodeca-2E, 4E-dienoic acid

isobutylamide) along with alkylamide 11 a/b at a concentration of 54 $\mu\text{g}/\text{mL}$. Treatment was continued for a period of 16 hr. Then, cells were harvested and lysed with RIPA (Thermo Scientific) cell lysis buffer (50mM Tris-HCL (pH 8.0), 150mM NaCl, and 0.1% SDS, CA-630 (NP-40), and 0.5% sodium deoxycholate) under cold conditions 4°C. The whole lysate mixture was centrifuged at 3500 rpm and the top layer containing proteins was collected quantified using the BCA assay (Bio-rad) (Section 2.2.4). The protein extracted from light and heavy cells are mixed in equal proportions and analyzed by LC-MS technique. The intensity of the light and heavy peptide is used to estimate relative protein concentrations in two types of cell states. Intensity of light peptide precursor ion is divided by heavy peptide precursor ions, the ratios are then Log_2 transformed. The Log_2 ratio of value 1 indicates a two-fold increase in light peptide precursor ion intensity when compared to heavy peptide precursor ions (reference precursor ion).

3.3.3 Extraction of protein

RAW 264.7 macrophage cells were scraped from the T-25 flask and 7 mL of medium containing cells are removed and centrifuged at 3500 rpm. The pellet was washed with 0.01M phosphate buffer saline (PBS). The pellet was then resuspended in PBS and centrifuged at 3500 rpm. Lysis buffer (RIPA Buffer1 X, 25mM Tris.Hcl, pH 7.6, 150mM Nacl, 1% SDS) was used to lyse the cells and

extract protein. The pellet with lysis buffer was subjected to alternative vortexing for 30 seconds and incubating on ice for 1 min, and this process was repeated for a total of 30 min. The whole lysate mixture was centrifuged at 3500 rpm and the top layer containing proteins was collected and bottom layer (cell wall debris) was discarded. The top layer containing protein was quantified using the BCA assay, as described in the next section.

3.3.4 Quantitation by Bicinchonic Acid Assay (BCA)

The bicinchonic acid assay is a spectrophotometric assay for colorimetric detection and quantitation of total protein in a sample. This assay is based on reduction of cupric ion Cu^{+2} to cuprous ion Cu^{+1} by the protein present in the sample in an alkaline medium. Two molecules of BCA then bind with one Cu^{+1} to give a purple colored complex that shows strong absorbance at 562nm. Some of the advantages of BCA assay are that it is simple, sensitive, and resistant to detergents and measures a wide range of protein concentration.

Table 2. Concentration of protein in samples.

Sample	Concentration in mg/ml
LPS	6.9
LPS+ <i>Echinacea</i> extract 7	7.5
<i>Echinacea</i> extract 7	8.6

Table 3. Concentration of protein in samples.

Sample	Concentration in mg/ml
LPS	2.2
LPS+ <i>Echinacea</i> extract 7	1.9
<i>Echinacea</i> extract 7	2.6
LPS+ alkylamide 11 a/b	1.9

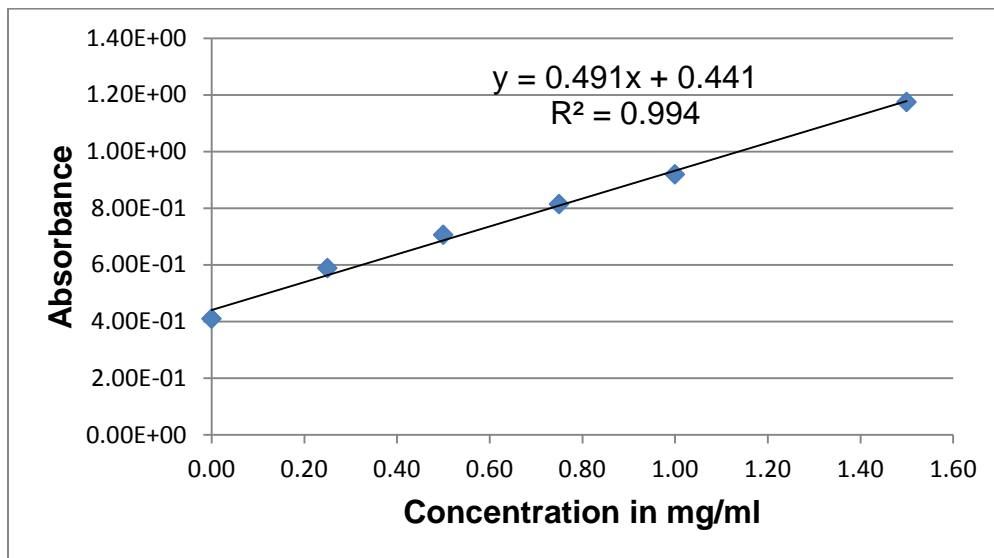
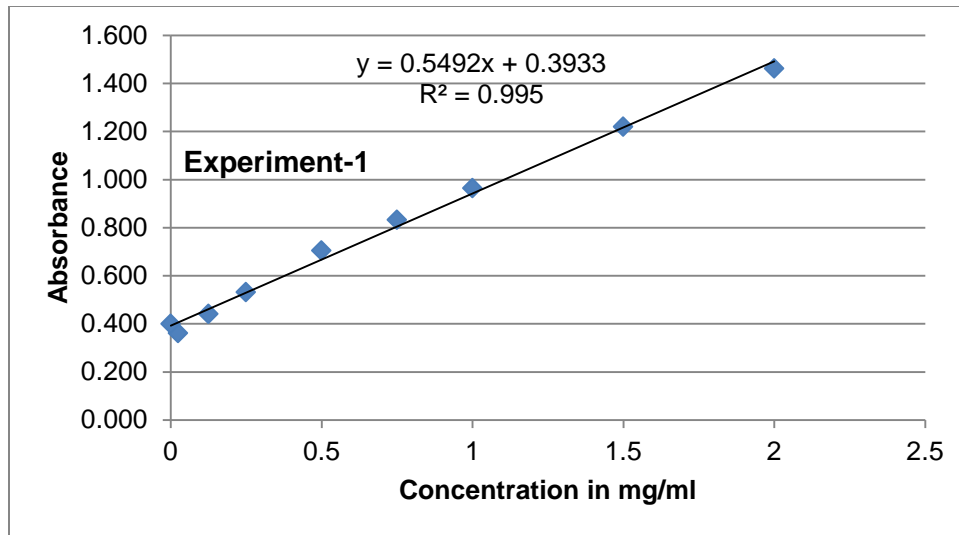


Figure 5. Calibration curves of BSA using BCA assay. Concentration is plotted on X-axis and absorbance at 562 is plotted on Y-axis. The tables on the side show concentration of protein in respective samples as determined with the calibration curves.

3.3.5 Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis (SDS-PAGE) and coomassie G-250 staining

Equal quantities of SILAC heavy (25 µg) and SILAC light (25 µg) protein were combined and mixed with laemmli buffer contain β mercaptoethanol (BIO RAD, Hercules, CA, USA), and boiled at 95⁰C for 5 mins. Samples were then cooled on ice for 5 minutes and separated by gradient SDS-PAGE (criterion™ precast gels, 10-20% Tris-HCL, 1.0mm 12+2 well comb (BIO-RAD) at a constant applied voltage of 200V. The gel was rinsed with nanopure water for 5 min, and then immersed in Coomassie G-250 Stain (Bio-Safe™ Coomassie G-259 stain, BIO RAD) and gently shaken in gel rocker (VWR rocker) at ten tilts per min for 45 mins. The gel was then rinsed with nanopure water, immersed in nanopure water, and left to de-stain for overnight. After this time, the gel was rinsed one more time with nanopure water in preparation for cutting.

3.3.6 In-gel digestion

Each gel lane was cut into 12 gel pieces and treated with a 1:1 ratio of 100mM ammonium bicarbonate and acetonitrile mixture (total volume 150 µL) for 30 minutes. These gel pieces were then treated with 10mM Dithiothreitol (DTT) (Sigma, 646563) (150 µL) for 30 minutes at 56°C and with 55mM iodoacetamide (IAM) (Sigma-A3221) for 20 minutes in the dark. Each of the above steps was followed by dehydration with acetonitrile (200 µL). The gel pieces were incubated

with 5 µg/mL trypsin (trypsin from bovine pancreas-Sigma T1426) (150 µL) overnight at 37°C. Digestion was quenched using 150 µL of water: acetonitrile: formic acid (33:66:2) at 37°C for 30 minutes. Then the supernatant is transferred to a new eppendorf tube. The gel pieces were then subjected to dehydration with acetonitrile followed by hydration with 100mM ammonium bicarbonate and acetonitrile mixture at a ratio of 2:1 for 15 minutes followed by dehydration with acetonitrile. All the supernatants from hydration and dehydration steps were transferred to new eppendorf tube. The supernatants were dried down and reconstituted in 100mM ammonium bicarbonate.

3.3.7 Nano-LC-NSI-MS/MS analysis

All LC-MS/MS experiments were conducted using an Eksigent NanoLC Ultra 2D (Eksigent, Dublin, USA) system coupled online to a LTQ-orbitrap mass spectrometer (LTQ XLThermo Fisher Scientific). The peptide mixtures were separated using a C18 reverse phase nano-LC column (Integra fit C18 75µm ID X 10cm long, new objective) at a flow rate of 300nL/min. The mass spectrometric analysis was performed in both the MS mode and the MS/MS mode using data dependent scanning. Full scan MS analyses were performed using the orbitrap mass analyzer at mass range of 400-1600. For MS/MS, the eight most intense ions from the previous full scan were subjected to collisionally induced dissociation (CID) in the linear ion trap. Peptides were first injected on trap

column (Integra fit sample trap column, new objective) where concentration and desalting occurs at a 2 μ l/min flow rate with 2% solvent B. The peptides were eluted from nano-LC column at a flow rate of 300nL/min. A linear gradient of 2-40% solvent B over a period of 90 minutes, 40-95% B from 90-94 minutes, 95% B from 94 to 104 minutes, 95 to 5% B from 104-108 minutes, and 5% B from 108 to 120 minutes were employed. Here solvent A is 2% acetonitrile in water with 0.1% formic acid and solvent B is 2% water in acetonitrile with 0.1% formic acid.

3.3.8 Lock mass internal calibration

The LTQ Orbitrap instrument has a unique option called internal calibration by lock mass, which helps to achieve less than 1 ppm mass accuracy throughout the run time. This option uses ions generated from ambient air by the electrospray process. These ions are called lock mass ions. We have used protonated polydimethylcyclsiloxane ($\text{Si}(\text{CH}_3)_2\text{O}$) with mass m/z 445.1200 in the MS mode as our lock mass ion. The lock mass ions are isolated by the linear quadrupole ion trap, stored in the C-trap where they are mixed with rest of the analyte ions, and transferred in to orbitrap. The calibration is adjusted based on the frequencies of lock mass to achieve internal calibration and improved mass accuracy for the peptide ions (Olsen 2005).

3.3.9 Data analysis

Protein identification was accomplished using Mascot Daemon software version 2.3.2 (Matrix Science) Mascot Distiller version 2.4.2.0 (64 bit) was used to generate a peak list from Thermo Excalibur LC-MS Files (which have the .RAW extension). The peak list generated was used to search against a mouse (*Mus musculus*) protein database (concatenated forward and reverse data base) using Mascot software. Concatenated forward and reverse database is a database which has both forward or normal sequence and reverse sequence compared to the forward sequence. Reverse database should not have any peptide match and doing this eliminates false positives and increase confidence in the identification of proteins. The search was performed using a precursor ion mass tolerance of ± 5 ppm and fragment ion mass tolerance of ± 0.6 Da. Carbamidomethylation of cysteine was used as fixed modification. Methionine oxidation, deamidation of glutamine and asparagine were used as variable modifications. Quantitation of SILAC data was accomplished using ProteoIQ software version 1.2 (Bioinquire) with 1% false discovery rate (FDR). Log_2 ratios are calculated based on intensities of light and heavy protein. These ratios are used to indicate changes in protein expression. Intensity of light peptide precursor ion is divided by heavy peptide precursor ions the ratios are then Log_2 transformed. The Log_2 ratio of value 1 indicates two-fold increase in light peptide precursor ion intensity when compared to heavy peptide precursor ions

(reference precursor ion). The \log_2 ratio of -10 indicates that the protein was present in control sample but not detected in light sample. (It was down regulated so much in the treated cells that we were not able to detect it with the mass spectrometer.) Ingenuity Pathway Analysis (IPA) (Ingenuity Systems Inc.) commercial software was employed to analyze and understand proteomics data. IPA was used to determine the functions and significant pathways associated with the proteins.

3.3.10 Preparation of *Echinacea* extracts

Dormant roots of *Echinacea purpurea* were harvested from 17 different cultivation sites in North Carolina, between the months of February and May 2008. The age of the plants varied from 2-10 years at the time of harvest and voucher specimens were retained and submitted to the North Carolina Herbarium (CB# 3280, Coker Hall, University of North Carolina, Chapel Hill, NC 27599-3280). The voucher number for extract 7 is NCU585851. The roots were thoroughly washed, air dried at 38°C and powdered. The powdered roots were subjected to maceration with 75% ethanol for one week at a 1:5 plant material to solvent ratio (w/v). After maceration, a hydraulic press was used to press the extract. The resulting extract was then filter-sterilized through a 0.2- μ M membrane sterile filter under vacuum in a laminar flow hood and stored in sterile bottle at 2-8°C. The extract was screened for endotoxin (lipopolysaccharide)

using the limulus amoebocyte lysate (LAL) assay. The LAL test results showed that the extract was endotoxin free (tolerance of 0.25 EU/mL). Ethanol precipitation was performed to remove ethanol insoluble compounds and create an alkylamide-enriched extract. The ethanol precipitation was done by adding ethanol (95%) to the existing extracts at a ratio of 1 mL extract: 1 mL ethanol (95%). The resulting ethanol concentration of extract was 85%. The resulting extract after ethanol precipitation was centrifuged to remove precipitate and the remaining supernatant was stored and labeled as “precipitated extract.” Precipitated extract were used for all the studies conducted in this project.

3.4 Experimental Design

Figure 6 shows the overall quantitative proteomics approach for stable isotope labeling with amino acids in cell culture (SILAC). RAW 264.7 macrophage like cells were cultured in either light SILAC DMEM media containing L-Lysine-2HCl and L-Arginine-HCl or heavy SILAC DMEM media containing $^{13}\text{C}_6$ L- Arginine-HCl and $^{13}\text{C}_6$, $^{15}\text{N}_2$ L-Lysine-2HCl. Cells were allowed to grow for six doublings for complete incorporation of isotopes. The cells grown in heavy SILAC DMEM media were treated with 0.5% ethanol (vehicle control) and cells grown in SILAC light DMEM media were stimulated with 1) $1\mu\text{g/ml}$ of lipopolysaccharide (LPS), 2) *Echinacea* extract 7, which is the most active extract in our earlier experiment (Cech 2010). Out of seventeen extracts

tested, extract 7 showed the most anti-inflammatory activity. Extract 7 suppressed the production of Prostaglandin E₂ (PGE₂) and tumor necrosis factor alpha (TNF- α) (Cech 2010) when compared to other extracts. 3) LPS+ *Echinacea* extract 7, 4) alkylamide-11a/b, 5) alkylamide-11a/b + LPS, for time the period of 16 hours. Then, cells were harvested and lysed with lysis buffer. The whole lysate mixture was centrifuged and the top layer containing proteins was collected and quantified using BCA assay (Figure 5) (Thermo Scientific). Equal quantities of treated and untreated protein are combined and separated by a gradient SDS-PAGE (Figure 7). Coomassie stain was used to visualize the protein bands in SDS-PAGE. Each gel lane was cut into 12 gel pieces and in-gel digestion was performed and peptides were separated by nano-liquid chromatography and mass spectrometric analysis was performed using LTQ-orbitrap mass spectrometer.

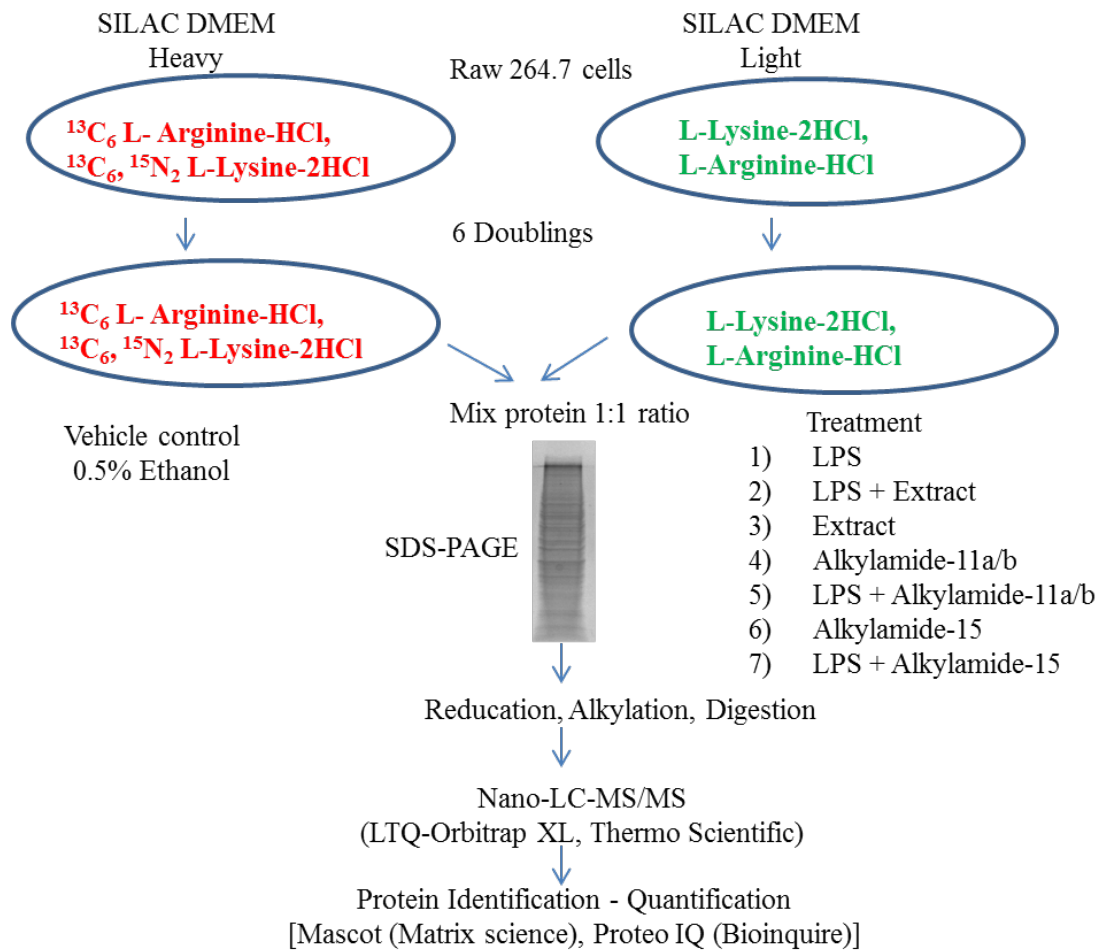


Figure 6. Schematic representation of SILAC approach combined to mass spectrometric analysis for the relative quantitation of protein extracted from RAW 264.7 cells.

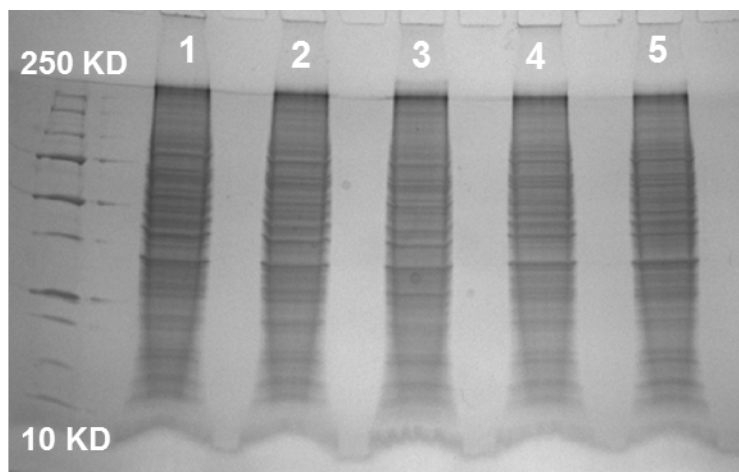


Figure 7. SILAC samples separated by SDS-PAGE. Each lane shows separation of protein extracted from RAW 264.7 cells by 10-20% gradient SDS-PAGE. The gel was stained by Coomassie Brilliant Blue stain to visualize the gel lane. The left most lane show molecular mass marker ranging for 10-250 kDa. Gel lanes contain the following combinations of heavy and light in 1:1 ratio. Lane 1 contains heavy protein (vehicle control, RAW 264.7 cells treated with 0.5% ethanol) and light protein (Raw 264.7 cells treated with LPS). Lane 2 contains heavy protein (vehicle control, RAW 264.7 cells treated with 0.5% ethanol) and light protein (RAW 264.7 cells treated with *Echinacea* extract 7). Lane 3 contains heavy protein (vehicle control RAW 264.7 cells treated with 0.5% ethanol) and light protein (cells treated with LPS + *Echinacea* extract 7). Lane 4 contains heavy protein (vehicle control RAW 264.7 cells treated with 0.5% ethanol) and light protein (RAW 264.7 cells treated with alkyalmide 11 a/b). Lane 5 contains heavy protein (vehicle control RAW 264.7 cells treated with 0.5% ethanol) and light protein (RAW 264.7 cells treated with alkyalmide 11 a/b + LPS).

3.5 Results and Discussion

The LC-MS chromatogram in Figure 8 shows separation of peptides obtained from in-gel digestion of protein extracted from RAW 264.7 cells. The various peaks in LC-MS chromatograms represent peptides of different masses.

These peptides elute from nano-LC columns at different times based on their affinities towards the C18 stationary phase in the column. The peptides are then identified by mass spectra (MS) generated by the mass spectrometer (Figure 9). These peptides are fragmented in mass spectrometer and mass spectra of the fragments (MS/MS) are recorded, which gives the structural information of the peptides (Figure 10). Both MS and MS/MS data were searched against mouse Swiss-Prot data base using MASCOT search engine to get the protein identification. All the proteins identified were quantified by ProteoIQ software.

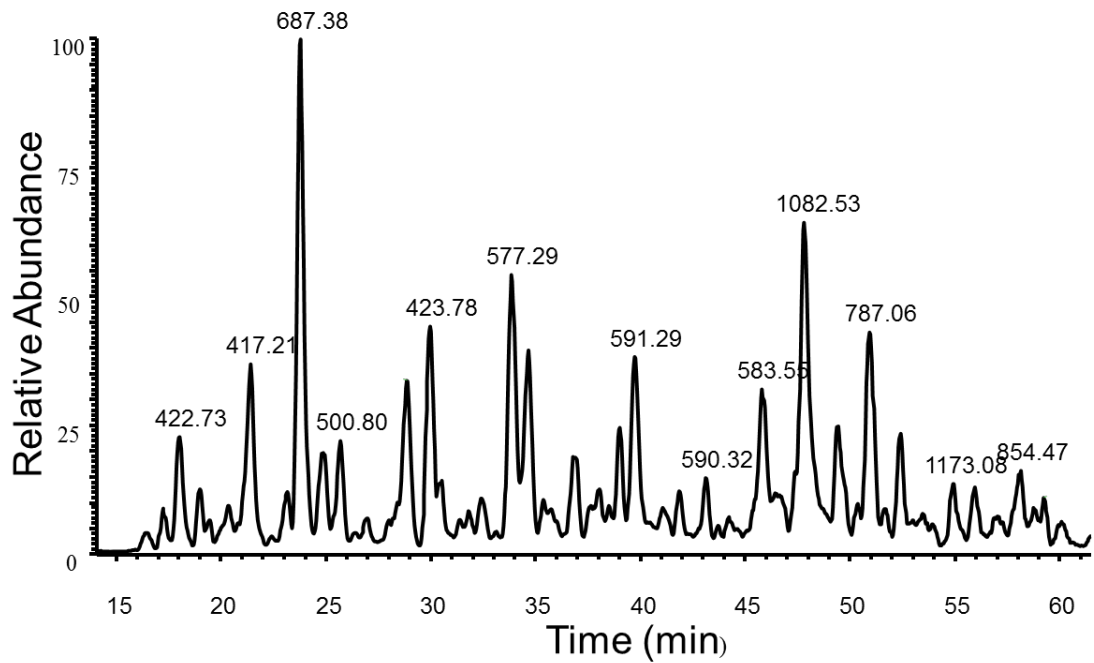


Figure 8. Nano-LC-MS base peak chromatogram that plots the signal for the most intense ion at any given time versus time. This figure shows the nano-LC elution profile of a digested complex protein sample from RAW 264.7 macrophage-type cells. Each peak corresponds to the elution of one or several peptides. The mass spectrum of peak eluted at 38.8 min is shown in Figure 7.

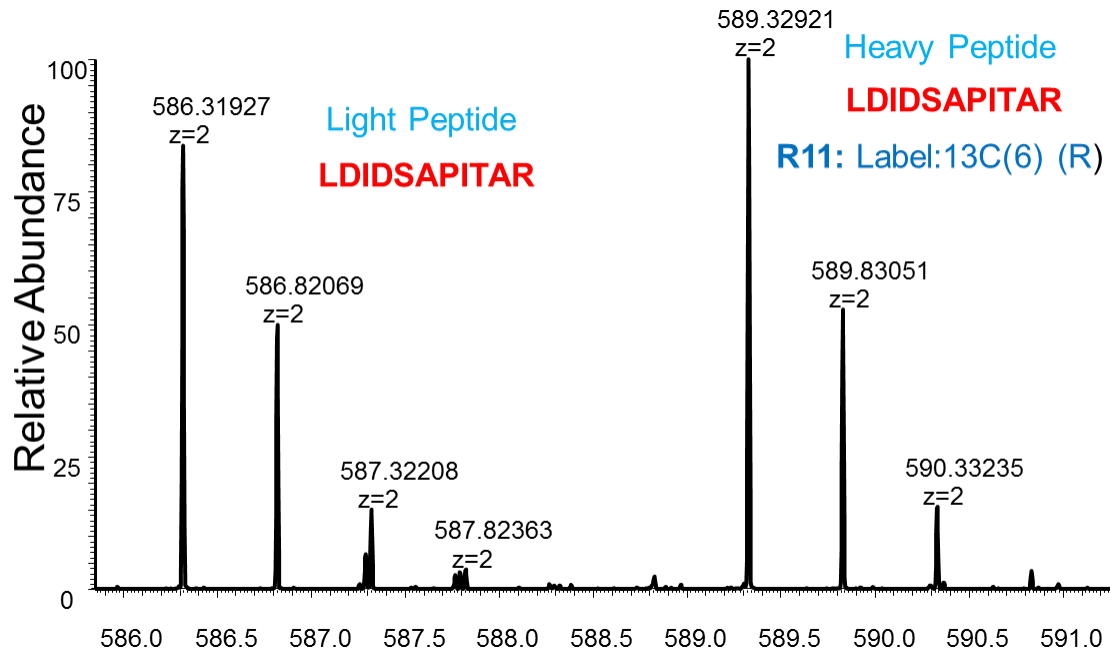


Figure 9. Mass spectrum of SILAC pair of peptides LDIDSAPITAR eluted at 38.8 minutes. The light peptide and heavy peptides have the same amino acid sequence but the light peptide has $^{12}\text{C}_6$ -arginine whereas the heavy peptide has $^{13}\text{C}_6$ -arginine, which introduces 6 Da mass differences. Due to doubly charged peptides, we see a 3 Da mass difference in this figure. Relative quantitation is performed by comparison of mass spectra ion intensity ratios of light and heavy peptide isotope pairs.

3.5.1 Identification of proteins by proteomics

Three independent SILAC experiments were performed using separate batches of cells, and repeating the entire process from protein extraction, analysis with LC-MS, and protein database searching for identification. Experiment 1 led to identification of 1014 proteins, experiment 2 led to identification of 834 proteins and experiment 3 led to identification of 978 proteins.

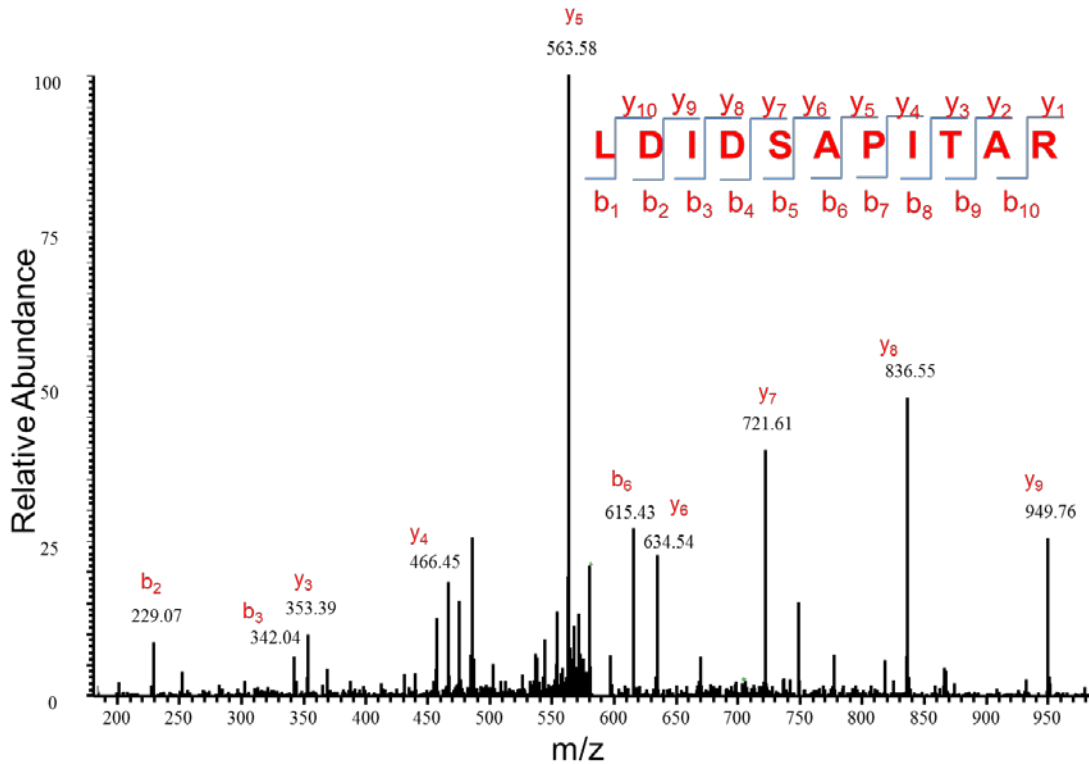


Figure 10. MS/MS spectrum of heavy peptide LDIDSAPITAR of m/z 589.32921 (molecular mass of 1178.6). Peptide backbone cleavage by collisionally induced dissociation (CID) gives rise to peptide internal fragments. The most common fragment ions are b ions and y ions. If the charge is retained on N-terminus, ions are called b ions (immonium ions), and if charge is retained on C-terminus ions, they are called y ions (amino-acylium ions).

Overall, across all different treatment conditions for both experiment one and experiment two, 671 proteins were observed consistently. This demonstrates that there is reproducibility in the SILAC technique. Some of these proteins include proteins related to growth and maintenance, such as cytoskeleton proteins like macrophage capping proteins, actin related proteins,

and gelsolin. In addition, oxidative stress related proteins were also detected, including superoxide dismutase and peroxiredoxin. Finally, and most important to this study, a number of proteins involved in the inflammatory response were identified, including prostaglandin G/H synthase 2 and NF- κ B protein. Cytokines are produced in the cells at a concentration of low ng/mL to pg/mL concentrations (Angel 2012). These concentration levels are below the lower limit of quantification using one dimensional LC-MS/MS analysis, which is the reason why they could not be detected in our experiments.

3.5.2 Effect of lipopolysaccharide on RAW 264.7 cells

The SILAC experiment was repeated three time (Tables 4 and 5 page 69, 74) using the same procedure and protocol starting from cell culture, gel electrophoresis and LC-MS/MS analysis to address the reproducibility of the SILAC technique and protein expression. These separate experiments were conducted several months apart using separate batches of cells. The data were processed so that only proteins that were consistently upregulated or downregulated upon treatment with LPS in experiments were included in Tables 4 and 5, respectively. Stimulation of RAW 264.7 cells with LPS led to the upregulation of 115 proteins with $\text{Log}_2 > 0$ (Table 4, Page No 66) and down regulation of 281 proteins $\text{Log}_2 < 0$ (Table 5, Page No 71) in comparison to RAW 264.7 cells treated with 0.5% ethanol (vehicle control, untreated). Positive values

in the tables indicate that protein was expressed more (upregulated) in treated than in untreated. To obtain the numerical values in the tables, the intensities of the mass spectral signals for the light peptide precursor ions are divided by the intensities of the heavy peptide precursor ions and the ratios are then Log_2 transformed. The Log_2 ratio of value 1 indicates a two-fold increase in light peptide precursor ion intensity when compared to heavy peptide precursor ions (reference precursor ion).

Some of the proteins that were upregulated in response to treatment with LPS, such as integrin $\alpha 3$, heat shock protein, immune-responsive gene 1 protein, and nucleophosmin, were consistent with literature reports of proteins upregulated with LPS treatment (Dhungana 2009, Zhang 2006). More importantly, since LPS mimics an infection, it was expected that some of the proteins observed to be upregulated would be those known to be involved in the inflammatory response. Consistent with this prediction, we observed upregulation of prostaglandin G/H synthase 2, which mediates formation of prostaglandins from arachidonic acid (Eschwege 2004). The prostaglandins are potent mediators of inflammation (Banion 1999). In addition, we observed upregulation of nuclear factor NF-kappa-B p100 subunit protein, a subunit of transcription factor NF- κ B. NF- κ B, when activated, stimulates synthesis of many proinflammatory cytokines and chemokines (Lappas 2002). LPS stimulation of

immune cells led to upregulation of nuclear factor NF-kappa-B p100 subunit protein expression (De 1998), and upregulation of H-2 class I histocompatibility antigen, the function of which is to present antigens to other immune cells (Behl 2012). Finally, we observed an increase in the level of myristoylated alanine-rich C-kinase substrate (MARCKS) related protein in response to treatment with LPS. MARCKS related protein plays an important role in functioning of stimulated macrophages (Chun 2009).

There were 281 proteins which appeared to be expressed less in cells stimulated with LPS in comparison to untreated (vehicle control) (Table 5, Page No 74). These proteins show negative values in Table 5 (Log_2 of a number less than one becomes negative). Many of these proteins display Log_2 values of -10 in either or both experiments 1 and 2. A value of -10 indicates that the protein was detected in the control cells (heavy labeled) but not the treated (light) cells. It is possible that this could occur because the protein was so down-regulated in the treated cells that it could no longer be detected. This could be a biologically relevant and interesting conclusion. However, it is also possible that instrumental/methodological shortcomings (i.e. dynamic range limitations) are responsible for the failure to detect some proteins in the treated samples. If the treatment causes some proteins (i.e. prostaglandin G/H synthase 2) to be highly upregulated, this may swamp out the signal in the mass spectrometer, making it

difficult to detect other low-abundance proteins in the treated cells than the untreated cells. For this reason, we have not tried to draw conclusions from the data showing which proteins which were down regulated, and have focused rather on comparisons of upregulated proteins in treated and untreated cells.

3.5.3 Effects of *Echinacea* extract 7 on RAW 264.7 cells

Stimulation of RAW 264.7 cells with *Echinacea purpurea* (treated) led to the upregulation of 100 proteins (Table 8, page 103) and down regulation of 300 proteins (Table 9, page 107) consistently in both experiments 1 and 2 in comparison to RAW 264.7 cells treated with 0.5% ethanol (untreated). When the data from both experiment 1 and 2 are combined, the only protein which was upregulated consistently with Log_2 (ratio >1) is Coronin-1C. Coronin-1 is an actin binding protein associated with phagocytosis (Yan 2007), a process by which immune cells remove pathogens. *Echinacea* extracts enhances bacterial phagocytosis (Zhai 2007).

3.5.4 Effects of *Echinacea* extract 7 on LPS induced proteins in RAW 264.7 cells

Table 19 (page 195) shows comparison of level of protein expression in LPS stimulated RAW 264.7 cells by itself and in presence of *Echinacea purpurea* extract 7. *Echinacea* extract 7 showed suppressive effects on the several LPS

induced proteins in both experiments 1 and 2. Our focus was on the proteins which were upregulated more than two-fold upon LPS stimulation and involved in inflammation.

The effect of *Echinacea* extract 7 on LPS induced proteins was compared in each experiment separately. In both the experiments, the \log_2 values were different, but the trend was the same in most of the proteins. The different value in different experiments could be due to biological factors (different batches of cells may behave differently, even when the growth conditions are theoretically the same) or differences in instrumental response. With regards to differences in instrument response, the use of the heavy labeled protein as an internal control within each lane of the gel corrects for such variations *within that lane of the gel*. However, in this section, we wished to compare the levels of protein expressed by LPS treated and *Echinacea* treated cells, which were in different lanes of the gel (each with its own internal, heavy labeled control). There are some limitations to such comparisons, given that each excised gel piece is analyzed separately, and instrument response may vary somewhat from run to run. Further follow up experiments using other bioanalytical techniques such as Western blotting or ELISA could be useful to validate the results observed in these experiments. In addition, it could be useful to perform a future SILAC experiment where the control (heavy) cells are treated with both LPS and vehicle, while the light

(treated) cells are exposed to LPS and *Echinacea*. This would allow the influence of *Echinacea* on LPS stimulated cells to be evaluated in a single gel lane, although the information about the influence of LPS on untreated cells would be lost. Ultimately, despite the aforementioned caveats, the results shown here were replicated by several independent experiments, and provide useful insights into pathways that may be altered in response to treatment with the *Echinacea* extract.

Out of 115 proteins induced by LPS in both experiment 1 and 2, 90% of proteins appeared to be suppressed by *Echinacea* extract 7. The most obvious and important of these effects was that the *Echinacea* extract completely blocked (Log₂ value -10) prostaglandin G/H synthase 2 production. As mentioned in the previous section, prostaglandin G/H synthase 2 production was strongly induced by LPS, but the prostaglandin G/H synthase 2 enzyme was not detected in cells exposed to both LPS and *Echinacea* extract (Table 19). These results are significant because prostaglandin G/H synthase 2 is part of the arachidonic acid pathway, which produces prostaglandins that cause inflammation. prostaglandin G/H synthase 2 converts prostaglandin H₂ (PGH₂) to prostaglandin E₂ (PGE₂) (Eschwege 2004). *Echinacea* extract inhibited secretion of PGE₂ from RAW 264.7 cells macrophage cells stimulated with influenza A virus (Cech 2010). The reason we found out in this experiment is that *Echinacea* extracts inhibit

secretion of PGE₂ from RAW 264.7 cells macrophage cells stimulated with influenza A virus by inhibiting prostaglandin G/H synthase 2 enzyme. Several non-steroidal anti-inflammatory agents (NSAIDs) inhibit prostaglandin production by inhibiting prostaglandin G/H synthase 2.

The *Echinacea* extract appeared to partially block production of myristoylated alanine-rich C-kinase substrate (MARCKS) related protein and Nuclear factor NF-kappa-B p100 subunit protein. Here by partially blocked we mean that the Log₂ value of the protein in presence of LPS and *Echinacea* extract was less than the Log₂ value of the protein in the presence of LPS alone. These results are significant given that MARCKS related protein expression level has been shown to be upregulated in RAW 264.7 cells upon LPS stimulation (Chun 2009). Furthermore, nuclear factor NF-kappa-B p100 subunit protein is a subunit of transcription factor NF-κB. The NF-κB transcription factor is active in conditions like inflammation, and is responsible for transcription of proinflammatory cytokines and chemokines (Lappas 2002).

The influence of *Echinacea* on immune-responsive gene 1 proteins was inconsistent (Log₂ value of protein in presence of LPS and *Echinacea* extract 7 was less than Log₂ value of protein in presence of LPS alone in experiment 2, but greater in experiment 1). The exact function of this protein is not known, but it was reported in the literature to be upregulated upon LPS stimulation in RAW

264.7 cells. Collectively, these observations are suggestive of anti-inflammatory action of *Echinacea*. Extract 7 appear to exert their anti-inflammatory action by targeting several different pathways. Effect on arachidonic acid pathway is indicated by suppression of PGE₂ protein by extract 7. Effect on phagocytic and bactericidal pathways is indicated by upregulation of coronin 1C protein by extract 7. Effect on antigen presentation pathway is indicated by suppression on H-2 class I histocompatibility antigen.

3.5.5 Effects of individual alkylamides on LPS-induced proteins in RAW

264.7 cells

Given that alkylamides have previously been reported as anti-inflammatory constituents of *Echinacea purpurea* (Cech 2010), it was of interest to compare the activities of individual alkylamides to that of the crude *E. purpurea* extract. We included a separate treatment with the most abundant alkylamide produced by *Echinacea* (alkylamide 11 a/b) (dodeca-2E, 4E, 8Z, 10E/Z-tetraenoic acid isobutylamide) (Chapter 1, Figure 1) in combination with LPS in the second experiment. At the concentration evaluated (5.4 µg/ml), the alkylamide did not shown any suppressive effect on LPS induced proteins in comparison to extract 7 (Table 24, Page No 202). Thus, we performed an additional SILAC experiment (again using a separate batch of cells, and repeating the entire procedure) to evaluate the activity of alkylamides at higher

concentrations (54 μ g/mL). In this repeat experiment, we included both alkylamide 11a/b and alkylamide 15 (dodeca-2E, 4E-dienoic acid isobutylamide) (Chapter 1, Figure 1). This second alkylamide was selected because it showed the most potent anti-inflammatory effects of among four alkylamides tested in our previous studies (Cech 2010). At this higher concentration, both alkylamides 11 a/b and alkylamide 15 suppressed approximately 50 proteins of the 55 LPS induced proteins ($\text{Log}_2 > 2$) (Table 24). Proteins suppressed by the high alkylamide concentration included prostaglandin G/H synthase 2, MARCKS related protein, Nuclear factor NF-kappa-B p100 subunit protein, immune suppressive gene 1, and H-2 class I histocompatibility antigen. As mentioned previously, all of these proteins are involved in inflammation. The alkylamides at 54 μ g/ml were more effective than the extract; although this may have been a concentration effect (extract was tested at 5.8 μ l/ml total alkylamide content, while pure alkylamides were tested at 54 μ g/ml.) Interestingly, the extent of suppression on LPS induced proteins was greater for alkylamide 15 in comparison to alkylamide 11 a/b. These findings are consistent with our previous experiments (Cech 2010), in which alkylamide 15 was more potent than alkylamide 11a/b at suppressing PGE₂ and TNF – alpha production by macrophage type cells stimulated with influenza virus.

3.6 Conclusion

Three independent SILAC experiments were successfully performed to study the protein expression in RAW 264.7 cells. The proteome was successfully labeled using SILAC, which allowed us to identify and quantify number of proteins produced by the cells. High resolution and accurate mass measurements were acquired using an orbitrap mass spectrometer, which increased the confidence in identification. Mass accuracy of < 5 ppm throughout the run was maintained with the help of lock mass calibration. The Nano-LC-ESI-MS technique provided the efficiency, sensitivity, and resolution needed for the analysis.

LPS stimulation of RAW 264.7 cells led to upregulation of number of proteins involved in inflammation. Of these, proteins including prostaglandin G/H synthase 2, MARCKS related protein, and Nuclear factor NF-kappa-B p100 subunit protein and immune responsive gene 1 were suppressed in the presence of *Echinacea* extract 7. Both alkylamides 11 a/b and alkylamid 15 at individual concentrations of 54µg/ml were able to suppress LPS induced proteins. When compared to alkylamide 11 a/b, the extent of suppression was greater for alkylamide 15. All these above stated data suggest anti-inflammatory action of *Echinacea*. *Echinacea* and its constituents appear to exert their anti-inflammatory action by suppression of several different pathways, including the arachidonic

acid pathway and bactericidal and phagocytic pathways. Altogether, this research increases our understanding of mechanism of action of *Echinacea purpurea*, and provides a starting point for future focused experiments exploring the influence of *Echinacea* and its constituents on particular pathways related to inflammation.

3.7 Tables of Protein Expression Data

Table 4. List of proteins consistently upregulated in experiments 1 and 2.

Sequence Id	Sequence Name	Experiment2	Experiment 1
		lps log2 Ratio	lps log2 Ratio
sp O08807 PRDX4_MOUSE	Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	1.43	0.1
sp O08810 U5S1_MOUSE	116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1	0.32	0.38
sp O70456 1433S_MOUSE	14-3-3 protein sigma OS=Mus musculus GN=Sfn PE=1 SV=2	0.03	0.48
sp P03995 GFAP_MOUSE	Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4	1.44	0.25
sp P05555 ITAM_MOUSE	Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=2	0.98	0.74
sp P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	0.38	0.05
sp P09041 PGK2_MOUSE	Phosphoglycerate kinase 2 OS=Mus musculus GN=Pgk2 PE=1 SV=4	0.05	0.46
sp P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2	0.55	0.81
sp P09411 PGK1_MOUSE	Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4	0.18	0.41
sp P0C0S6 H2AZ_MOUSE	Histone H2A.Z OS=Mus musculus GN=H2afz PE=1 SV=2	1.14	0.17
sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=1 SV=1	0.55	0.54
sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	0.55	0.54
sp P10107 ANXA1_MOUSE	Annexin A1 OS=Mus musculus	0.15	0.26

	GN=Anxa1 PE=1 SV=2		
sp P10852 4F2_MOUSE	4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	0.74	0.74
sp P11835 ITB2_MOUSE	Integrin beta-2 OS=Mus musculus GN=Itgb2 PE=1 SV=2	0.39	0.49
sp P13020 GELS_MOUSE	Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	0.03	0.41
sp P14733 LMNB1_MOUSE	Lamin-B1 OS=Mus musculus GN=Lmb1 PE=1 SV=3	0.3	0.27
sp P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	0.39	0.58
sp P17156 HSP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2	0.44	0.56
sp P17751 TPIS_MOUSE	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	0.07	0.47
sp P17809 GTR1_MOUSE	Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=4	1.43	0.91
sp P17879 HS71B_MOUSE	Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3	0.18	0.59
sp P18760 COF1_MOUSE	Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3	0.02	0.16
sp P20029 GRP78_MOUSE	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	0.51	0.68
sp P21107 TPM3_MOUSE	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2	0.35	0.35
sp P22752 H2A1_MOUSE	Histone H2A type 1 OS=Mus musculus GN=Hist1h2ab PE=1 SV=3	0.97	0.09
sp P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	1.35	0.46
sp P26040 EZRI_MOUSE	Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	0.56	0.52
sp P26041 MOES_MOUSE	Moesin OS=Mus musculus GN=Msn PE=1 SV=3	0.71	0.58
sp P26043 RADI_MOUSE	Radixin OS=Mus musculus GN=Rdx PE=1 SV=3	0.39	0.56
sp P26443 DHE3_MOUSE	Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	0.01	0.27
sp P27661 H2AX_MOUSE	Histone H2A.x OS=Mus musculus GN=H2afx PE=1 SV=2	1.14	0.17
sp P28656 NP1L1_MOUSE	Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap111 PE=1 SV=2	0.02	0.49
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcks1 PE=1 SV=2	4.15	1.63
sp P29341 PABP1_MOUSE	Polyadenylate-binding protein 1	0.43	0.31

	OS=Mus musculus GN=Pabpc1 PE=1 SV=2		
sp P29351 PTN6_MOUSE	Tyrosine-protein phosphatase non-receptor type 6 OS=Mus musculus GN=Ptpn6 PE=1 SV=2	0.26	0.16
sp P35278 RAB5C_MOUSE	Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	0.44	0.16
sp P35700 PRDX1_MOUSE	Peroxioredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	1.52	0.11
sp P37040 NCPR_MOUSE	NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	0.9	4.01
sp P38647 GRP75_MOUSE	Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	0.11	0.23
sp P40124 CAP1_MOUSE	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	0.8	0.51
sp P45591 COF2_MOUSE	Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1	1.44	0.19
sp P46638 RB11B_MOUSE	Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3	0.18	0.2
sp P47915 RL29_MOUSE	60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2	0.24	0.45
sp P47955 RLA1_MOUSE	60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1	0.53	0.67
sp P48036 ANXA5_MOUSE	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	0.05	0.76
sp P54987 IRG1_MOUSE	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	3.58	3.1
sp P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	0.09	0.25
sp P58252 EF2_MOUSE	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	0.3	0.42
sp P58771 TPM1_MOUSE	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	0.36	0.37
sp P58774 TPM2_MOUSE	Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1	0.33	0.37
sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	1.36	0.42
sp P61027 RAB10_MOUSE	Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	0.09	0.23
sp P61089 UBE2N_MOUSE	Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1	0.04	0.03
sp P61957 SUMO2_MOUSE	Small ubiquitin-related modifier 2 OS=Mus musculus GN=Sumo2 PE=2 SV=1	3.1	0.17
sp P61982 1433G_MOUSE	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	0.19	0.37

sp P62492 RB11A_MOUSE	Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a PE=1 SV=3	0.18	0.2
sp P62737 ACTA_MOUSE	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	1.35	0.41
sp P62821 RAB1A_MOUSE	Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3	0.84	0.35
sp P62835 RAP1A_MOUSE	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=2 SV=1	1.47	0.38
sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=Rps27a PE=1 SV=2	0.55	0.45
sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Uba52 PE=1 SV=2	0.55	0.54
sp P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	0.45	0.55
sp P63101 1433Z_MOUSE	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	0.53	0.4
sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	1.36	0.42
sp P63268 ACTH_MOUSE	Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1	1.35	0.41
sp P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	1.35	0.41
sp P68134 ACTS_MOUSE	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	1.35	0.41
sp P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1	0.04	0.33
sp P97429 ANXA4_MOUSE	Annexin A4 OS=Mus musculus GN=Anxa4 PE=2 SV=4	0.58	1.15
sp P99029 PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2	2.23	1.13
sp Q00612 G6PD1_MOUSE	Glucose-6-phosphate 1- dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3	0.12	0.28
sp Q01853 TERA_MOUSE	Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4	0.04	0.32
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	4.89	3.6
sp Q3THS6 METHK2_MOUSE	S-adenosylmethionine synthase isoform type-2 OS=Mus musculus GN=Mat2a PE=2 SV=2	0.56	0.06
sp Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus musculus GN=H2afv PE=1 SV=3	1.14	0.17
sp Q61233 PLSL_MOUSE	Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4	0.3	0.41

sp Q61696 HS71A_MOUSE	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	0.18	0.59
sp Q61937 NPM_MOUSE	Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	0.3	0.31
sp Q62433 NDRG1_MOUSE	Protein NDRG1 OS=Mus musculus GN=Ndr1 PE=1 SV=1	2.05	0.82
sp Q64522 H2A2B_MOUSE	Histone H2A type 2-B OS=Mus musculus GN=Hist2h2ab PE=1 SV=3	1.14	0.17
sp Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac PE=1 SV=3	0.97	0.09
sp Q64727 VINC_MOUSE	Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	0.52	0.28
sp Q69Z7 MYOF_MOUSE	Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	0.96	1.27
sp Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus musculus GN=Hist2h2aa1 PE=1 SV=3	0.97	0.09
sp Q6IRU2 TPM4_MOUSE	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=3	0.32	0.76
sp Q71LX4 TLN2_MOUSE	Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	1.07	0.37
sp Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	0.26	0.36
sp Q80X90 FLNB_MOUSE	Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3	1.04	0.02
sp Q8BFU2 H2A3_MOUSE	Histone H2A type 3 OS=Mus musculus GN=Hist3h2a PE=1 SV=3	0.97	0.09
sp Q8BFZ3 ACTBL_MOUSE	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=1 SV=1	1.54	0.64
sp Q8BGQ7 SYAC_MOUSE	Alanyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1	0.18	0.23
sp Q8BTM8 FLNA_MOUSE	Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5	1.08	0.12
sp Q8CGP5 H2A1F_MOUSE	Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	0.97	0.09
sp Q8CGP6 H2A1H_MOUSE	Histone H2A type 1-H OS=Mus musculus GN=Hist1h2ah PE=1 SV=3	0.97	0.09
sp Q8CGP7 H2A1K_MOUSE	Histone H2A type 1-K OS=Mus musculus GN=Hist1h2ak PE=1 SV=3	0.97	0.09
sp Q8R1M2 H2AJ_MOUSE	Histone H2A.J OS=Mus musculus GN=H2afj PE=2 SV=1	0.97	0.09
sp Q8VDJ3 VIGLN_MOUSE	Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	0.15	0.38
sp Q91V41 RAB14_MOUSE	Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3	1.21	0.05
sp Q91XV3 BASP1_MOUSE	Brain acid soluble protein 1 OS=Mus musculus GN=Basp1 PE=1 SV=3	1.16	1.53
sp Q99J16 RAP1B_MOUSE	Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=2 SV=2	1.47	0.38
sp Q99PL5 RRBP1_MOUSE	Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=2 SV=2	0.29	0.37

sp Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	0.77	0.7
sp Q9CQS8 SC61B_MOUSE	Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3	3	1.02
sp Q9CQV8 1433B_MOUSE	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	0.02	0.31
sp Q9CXW3 CYBP_MOUSE	Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	0.07	0.27
sp Q9D1A2 CNDP2_MOUSE	Cytosolic non-specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1	1.28	0.78
sp Q9ER72 SYCC_MOUSE	Cysteinyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2	0.64	0.51
sp Q9ES52 SHIP1_MOUSE	Phosphatidylinositol-3,4,5- trisphosphate 5-phosphatase 1 OS=Mus musculus GN=Inpp5d PE=1 SV=2	0.74	0.1
sp Q9JMH6 TRXR1_MOUSE	Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txnrd1 PE=1 SV=3	1.75	0.71
sp Q9R1P4 PSA1_MOUSE	Proteasome subunit alpha type-1 OS=Mus musculus GN=Psma1 PE=1 SV=1	0.11	0.38
sp Q9WTK5 NFKB2_MOUSE E	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	2.49	1.04
sp Q9WVK4 EHD1_MOUSE	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	2.09	0.61
sp Q9Z172 SUMO3_MOUSE	Small ubiquitin-related modifier 3 OS=Mus musculus GN=Sumo3 PE=2 SV=1	3.1	0.17
sp Q9Z1Q5 CLIC1_MOUSE	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	0.24	0.3

Table 5. List of LPS suppressed proteins consistently in experiment 2 and 1.

Sequence Id	Sequence Name	LPS Ratio Expt-2	LPS Ratio Expt- 1
sp O55131 SEPT7_MOUSE	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	-10	-10
sp O70152 DPM1_MOUSE	Dolichol-phosphate mannosyltransferase OS=Mus musculus GN=Dpm1 PE=2 SV=1	-10	-10
sp O88844 IDHC_MOUSE	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=Idh1 PE=1 SV=2	-10	-0.89

sp P01895 HA1Y_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus GN=H2-D1 PE=2 SV=1	-10	-10
sp P01896 HA1Z_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus PE=1 SV=1	-10	-10
sp P01942 HBA_MOUSE	Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2	-10	-10
sp P03930 ATP8_MOUSE	ATP synthase protein 8 OS=Mus musculus GN=Mtstp8 PE=1 SV=1	-10	-10
sp P08752 GNAI2_MOUSE	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5	-10	-0.6
sp P24369 PIIB_MOUSE	Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=2 SV=2	-10	-10
sp P26516 PSD7_MOUSE	26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	-10	-10
sp P28738 KIF5C_MOUSE	Kinesin heavy chain isoform 5C OS=Mus musculus GN=Kif5c PE=1 SV=3	-10	-0.1
sp P29758 OAT_MOUSE	Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1	-10	-0.05
sp P33175 KIF5A_MOUSE	Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3	-10	-0.1
sp P49717 MCM4_MOUSE	DNA replication licensing factor MCM4 OS=Mus musculus GN=Mcm4 PE=2 SV=1	-10	-10
sp P50396 GDIA_MOUSE	Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3	-10	-0.24
sp P50516 VATA_MOUSE	V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2	-10	-10
sp P53986 MOT1_MOUSE	Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	-10	-10
sp P54071 IDHP_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	-10	-0.61
sp P54775 PRS6B_MOUSE	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2	-10	-0.35
sp P56135 ATPK_MOUSE	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=1 SV=3	-10	-10
sp P57722 PCBP3_MOUSE	Poly(rC)-binding protein 3 OS=Mus musculus GN=Pcbp3 PE=2 SV=3	-10	-0.37
sp P60867 RS20_MOUSE	40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	-10	-0.34
sp P61161 ARP2_MOUSE	Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	-10	-0.15
sp P62082 RS7_MOUSE	40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	-10	-0.39
sp P62717 RL18A_MOUSE	60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	-10	-0.77
sp P62806 H4_MOUSE	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	-10	-0.06
sp P62830 RL23_MOUSE	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	-10	-0.52
sp P62855 RS26_MOUSE	40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=2 SV=3	-10	-0.35
sp P67984 RL22_MOUSE	60S ribosomal protein L22 OS=Mus musculus	-10	-0.42

	GN=Rpl22 PE=2 SV=2		
sp P68040 GBLP_MOUSE	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3	-10	-0.63
sp P68433 H31_MOUSE	Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	-10	-1.03
sp P84084 ARF5_MOUSE	ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=2 SV=2	-10	-10
sp P84228 H32_MOUSE	Histone H3.2 OS=Mus musculus GN=Hist1h3b PE=1 SV=2	-10	-1.03
sp P84244 H33_MOUSE	Histone H3.3 OS=Mus musculus GN=H3f3a PE=1 SV=2	-10	-1.03
sp P86048 RL10L_MOUSE	60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=1	-10	-0.59
sp P97310 MCM2_MOUSE	DNA replication licensing factor MCM2 OS=Mus musculus GN=Mcm2 PE=1 SV=3	-10	-3.13
sp Q04646 ATNG_MOUSE	Sodium/potassium-transporting ATPase subunit gamma OS=Mus musculus GN=Fxyd2 PE=2 SV=2	-10	-0.13
sp Q09014 NCF1_MOUSE	Neutrophil cytosol factor 1 OS=Mus musculus GN=Ncf1 PE=1 SV=3	-10	-0.75
sp Q3U9G9 LBR_MOUSE	Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	-10	-1.07
sp Q501J6 DDX17_MOUSE	Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	-10	-0.22
sp Q5SUR0 PUR4_MOUSE	Phosphoribosylformylglycinamide synthase OS=Mus musculus GN=Pfas PE=2 SV=1	-10	-0.63
sp Q5SW19 K0664_MOUSE	Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 PE=2 SV=2	-10	-0.29
sp Q5XJY5 COPD_MOUSE	Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=2 SV=2	-10	-10
sp Q60875 ARHG2_MOUSE	Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 PE=1 SV=4	-10	-0.79
sp Q60931 VDAC3_MOUSE	Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	-10	-0.44
sp Q60932 VDAC1_MOUSE	Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	-10	-0.05
sp Q61390 TCPW_MOUSE	T-complex protein 1 subunit zeta-2 OS=Mus musculus GN=Cct6b PE=2 SV=4	-10	-0.43
sp Q61820 RANT_MOUSE	GTP-binding nuclear protein Ran, testis-specific isoform OS=Mus musculus GN=Rasl2-9 PE=2 SV=1	-10	-0.47
sp Q61990 PCBP2_MOUSE	Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	-10	-0.58
sp Q62351 TFR1_MOUSE	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	-10	-10
sp Q62425 NDUA4_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Mus musculus GN=Ndufa4 PE=1 SV=2	-10	-10
sp Q641P0 ARP3B_MOUSE	Actin-related protein 3B OS=Mus musculus GN=Actr3b PE=2 SV=1	-10	-0.58
sp Q64518 AT2A3_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium	-10	-0.28

	ATPase 3 OS=Mus musculus GN=Atp2a3 PE=2 SV=3		
sp Q64521 GPDM_MOUSE	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus GN=Gpd2 PE=1 SV=2	-10	-10
sp Q64674 SPEE_MOUSE	Spermidine synthase OS=Mus musculus GN=Srm PE=2 SV=1	-10	-0.06
sp Q6P1B1 XPP1_MOUSE	Xaa-Pro aminopeptidase 1 OS=Mus musculus GN=Xpnpep1 PE=2 SV=1	-10	-10
sp Q6ZWU9 RS27_MOUSE	40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3	-10	-1.03
sp Q6ZWV3 RL10_MOUSE	60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3	-10	-0.59
sp Q6ZWY3 RS27L_MOUSE	40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=2 SV=3	-10	-1.28
sp Q7M6Y3 PICA_MOUSE	Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus GN=Picalm PE=1 SV=1	-10	-10
sp Q7TQI3 OTUB1_MOUSE	Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2	-10	-10
sp Q8BG32 PSD11_MOUSE	26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psm11 PE=1 SV=3	-10	-0.03
sp Q8BH04 PCKGM_MOUSE	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=2 SV=1	-10	-10
sp Q8BMJ2 SYLC_MOUSE	Leucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Lars PE=2 SV=2	-10	-0.59
sp Q8BP47 SYNC_MOUSE	Asparaginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Nars PE=1 SV=2	-10	-0.24
sp Q8BU30 SYIC_MOUSE	Isoleucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=lars PE=2 SV=2	-10	-0.81
sp Q8BWW3 ERF1_MOUSE	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Elf1 PE=1 SV=4	-10	-0.03
sp Q8QZY1 EIF3L_MOUSE	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Elf3l PE=1 SV=1	-10	-0.07
sp Q8R0W0 EPIPL_MOUSE	Epiplakin OS=Mus musculus GN=Eppk1 PE=1 SV=2	-10	-0.6
sp Q8R429 AT2A1_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1	-10	-0.28
sp Q8VDP4 K1967_MOUSE	Protein KIAA1967 homolog OS=Mus musculus PE=1 SV=2	-10	-0.22
sp Q8VIJ6 SFPQ_MOUSE	Splicing factor, proline- and glutamine-rich OS=Mus musculus GN=Sfpq PE=1 SV=1	-10	-0.51
sp Q91VR2 ATPG_MOUSE	ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	-10	-10
sp Q921F2 TADBP_MOUSE	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	-10	-10
sp Q99JY0 ECHB_MOUSE	Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	-10	-0.62
sp Q99JY9 ARP3_MOUSE	Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3	-10	-0.58
sp Q99LC5 ETFA_MOUSE	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1	-10	-0.54

	SV=2		
sp Q99LX0 PARK7_MOUSE	Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	-10	-10
sp Q99MR6 SRRT_MOUSE	Serrate RNA effector molecule homolog OS=Mus musculus GN=Srrt PE=1 SV=1	-10	-0.04
sp Q9BDB7 IF44L_MOUSE	Interferon-induced protein 44-like OS=Mus musculus GN=IFI44L PE=2 SV=2	-10	-0.78
sp Q9CPU0 LGUL_MOUSE	Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=3	-10	-10
sp Q9CQ65 MTAP_MOUSE	S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=2 SV=1	-10	-10
sp Q9CQI6 COTL1_MOUSE	Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3	-10	-0.3
sp Q9CR16 PPID_MOUSE	Peptidyl-prolyl cis-trans isomerase D OS=Mus musculus GN=Ppid PE=1 SV=3	-10	-10
sp Q9CR62 M2OM_MOUSE	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus GN=Slc25a11 PE=1 SV=3	-10	-10
sp Q9CXT8 MPPB_MOUSE	Mitochondrial-processing peptidase subunit beta OS=Mus musculus GN=Pmpcb PE=2 SV=1	-10	-0.23
sp Q9CY57 FOP_MOUSE	Friend of PRMT1 protein OS=Mus musculus GN=Fop PE=1 SV=2	-10	-10
sp Q9CY64 BIEA_MOUSE	Biliverdin reductase A OS=Mus musculus GN=Blvra PE=2 SV=1	-10	-0.79
sp Q9D0I9 SYRC_MOUSE	Arginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Rars PE=2 SV=2	-10	-1.37
sp Q9D1G1 RAB1B_MOUSE	Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	-10	-0.18
sp Q9DAS9 GBG12_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Mus musculus GN=Gng12 PE=1 SV=3	-10	-0.01
sp Q9DCC4 P5CR3_MOUSE	Pyrroline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycl1 PE=2 SV=2	-10	-10
sp Q9DCC8 TOM20_MOUSE	Mitochondrial import receptor subunit TOM20 homolog OS=Mus musculus GN=Tom20 PE=1 SV=1	-10	-10
sp Q9DCL9 PUR6_MOUSE	Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4	-10	-0.62
sp Q9DCX2 ATP5H_MOUSE	ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	-10	-10
sp Q9EQP2 EHD4_MOUSE	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	-10	-0.14
sp Q9JJI8 RL38_MOUSE	60S ribosomal protein L38 OS=Mus musculus GN=Rpl38 PE=2 SV=3	-10	-10
sp Q9JLJ5 ELOV1_MOUSE	Elongation of very long chain fatty acids protein 1 OS=Mus musculus GN=Elolv1 PE=2 SV=1	-10	-0.57
sp Q9JMA1 UBP14_MOUSE	Ubiquitin carboxyl-terminal hydrolase 14 OS=Mus musculus GN=Usp14 PE=1 SV=3	-10	-0.13
sp Q9QXK3 COPG2_MOUSE	Coatamer subunit gamma-2 OS=Mus musculus GN=Copg2 PE=2 SV=1	-10	-10
sp Q9QYJ0 DNJA2_MOUSE	DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1	-10	-10
sp Q9QZE5 COPG_MOUSE	Coatamer subunit gamma OS=Mus musculus GN=Copg PE=2 SV=1	-10	-0.86

sp Q9WUM4 COR1C_MOUSE	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	-10	-10
sp Q9Z2I8 SUCB2_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Suclg2 PE=2 SV=3	-10	-10
sp A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn PE=1 SV=1	-7.6	-10
sp P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus GN=Lyz2 PE=1 SV=2	-3.06	-0.41
sp P17897 LYZ1_MOUSE	Lysozyme C-1 OS=Mus musculus GN=Lyz1 PE=1 SV=1	-3.06	-0.33
sp P25206 MCM3_MOUSE	DNA replication licensing factor MCM3 OS=Mus musculus GN=Mcm3 PE=1 SV=2	-1.7	-1.12
sp P43276 H15_MOUSE	Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	-1.64	-0.3
sp Q91ZX7 LRP1_MOUSE	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	-1.55	-0.9
sp P97311 MCM6_MOUSE	DNA replication licensing factor MCM6 OS=Mus musculus GN=Mcm6 PE=1 SV=1	-1.51	-10
sp Q91VD9 NDUS1_MOUSE	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2	-1.23	-10
sp P49718 MCM5_MOUSE	DNA replication licensing factor MCM5 OS=Mus musculus GN=Mcm5 PE=2 SV=1	-1.22	-1.3
sp Q922D8 C1TC_MOUSE	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4	-1.21	-1.81
sp P57759 ERP29_MOUSE	Endoplasmic reticulum resident protein 29 OS=Mus musculus GN=Erp29 PE=1 SV=2	-1.2	-0.03
sp P30681 HMGB2_MOUSE	High mobility group protein B2 OS=Mus musculus GN=Hmgb2 PE=1 SV=3	-1.16	-0.12
sp Q9QZD8 DIC_MOUSE	Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=2 SV=2	-1.16	-1.01
sp P43275 H11_MOUSE	Histone H1.1 OS=Mus musculus GN=Hist1h1a PE=2 SV=2	-1.1	-0.3
sp Q9Z1W8 AT12A_MOUSE	Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=3	-1.1	-1.11
sp Q9WV27 AT1A4_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Mus musculus GN=Atp1a4 PE=1 SV=3	-1.08	-0.98
sp O54879 HMGB3_MOUSE	High mobility group protein B3 OS=Mus musculus GN=Hmgb3 PE=2 SV=3	-1.07	-10
sp Q8BHN3 GANAB_MOUSE	Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1	-1.07	-0.08
sp Q9D3B1 HACD2_MOUSE	3-hydroxyacyl-CoA dehydratase 2 OS=Mus musculus GN=Ptplb PE=2 SV=1	-1.06	-0.75
sp P10404 ENV1_MOUSE	MLV-related proviral Env polyprotein OS=Mus musculus PE=2 SV=3	-1.03	-0.47
sp Q9D8E6 RL4_MOUSE	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	-1.03	-0.64
sp P00405 COX2_MOUSE	Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1	-1.01	-0.4
sp Q8VDN2 AT1A1_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	-1.01	-0.57

sp P17918 PCNA_MOUSE	Proliferating cell nuclear antigen OS=Mus musculus GN=Pcna PE=1 SV=2	-1	-0.34
sp P50247 SAHH_MOUSE	Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	-1	-0.44
sp Q6GQT9 NOMO1_MOUSE	Nodal modulator 1 OS=Mus musculus GN=Nomo1 PE=1 SV=1	-0.99	-0.35
sp Q9DB20 ATPO_MOUSE	ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	-0.99	-0.12
sp P11370 ENV2_MOUSE	Retrovirus-related Env polyprotein from Fv-4 locus OS=Mus musculus GN=Fv4 PE=1 SV=2	-0.98	-0.47
sp Q9DB77 QCR2_MOUSE	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcr2 PE=1 SV=1	-0.98	-0.65
sp Q6PIC6 AT1A3_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Mus musculus GN=Atp1a3 PE=1 SV=1	-0.97	-0.86
sp Q9CZ13 QCR1_MOUSE	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcr1 PE=1 SV=2	-0.96	-0.35
sp Q64436 ATP4A_MOUSE	Potassium-transporting ATPase alpha chain 1 OS=Mus musculus GN=Atp4a PE=1 SV=3	-0.95	-1.17
sp P07091 S10A4_MOUSE	Protein S100-A4 OS=Mus musculus GN=S100a4 PE=1 SV=1	-0.92	-0.22
sp P15864 H12_MOUSE	Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	-0.92	-0.17
sp P43277 H13_MOUSE	Histone H1.3 OS=Mus musculus GN=Hist1h1d PE=1 SV=2	-0.92	-0.15
sp Q6PIE5 AT1A2_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Mus musculus GN=Atp1a2 PE=1 SV=1	-0.91	-0.76
sp Q07133 H1T_MOUSE	Histone H1t OS=Mus musculus GN=Hist1h1t PE=2 SV=4	-0.84	-0.07
sp Q9DCT2 NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=2	-0.84	-0.86
sp Q6ZQ38 CAND1_MOUSE	Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	-0.79	-0.65
sp P43274 H14_MOUSE	Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2	-0.78	-0.19
sp Q9D0K2 SCOT1_MOUSE	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial OS=Mus musculus GN=Oxct1 PE=1 SV=1	-0.78	-0.11
sp Q9DBG6 RPN2_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	-0.76	-0.26
sp P62827 RAN_MOUSE	GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3	-0.74	-0.49
sp O35129 PHB2_MOUSE	Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	-0.7	-0.75
sp P67778 PHB_MOUSE	Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	-0.68	-0.58
sp Q9CQA3 DHSB_MOUSE	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=Sdhb PE=1 SV=1	-0.68	-0.48
sp P51410 RL9_MOUSE	60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=2 SV=2	-0.64	-0.57

sp Q6ZWN5 RS9_MOUSE	40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	-0.61	-0.65
sp Q9CQQ7 AT5F1_MOUSE	ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	-0.61	-0.55
sp Q68FL6 SYMC_MOUSE	Methionyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Mars PE=2 SV=1	-0.6	-10
sp Q8VEM8 MPCP_MOUSE	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	-0.6	-0.39
sp P18572 BASI_MOUSE	Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	-0.57	-10
sp Q9CR57 RL14_MOUSE	60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=2 SV=3	-0.57	-0.56
sp Q9CW03 SMC3_MOUSE	Structural maintenance of chromosomes protein 3 OS=Mus musculus GN=Smc3 PE=1 SV=2	-0.57	-0.74
sp Q5SWU9 ACACA_MOUSE	Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	-0.56	-1.03
sp P19096 FAS_MOUSE	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	-0.55	-0.76
sp P51881 ADT2_MOUSE	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	-0.55	-0.72
sp Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=4	-0.55	-0.96
sp P48962 ADT1_MOUSE	ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	-0.54	-0.71
sp Q8VDW0 DX39A_MOUSE	ATP-dependent RNA helicase DDX39A OS=Mus musculus GN=Ddx39a PE=2 SV=1	-0.54	-0.34
sp P97807 FUMH_MOUSE	Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3	-0.53	-10
sp Q61598 GDIB_MOUSE	Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	-0.51	-0.18
sp Q921H8 THIKA_MOUSE	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=2 SV=1	-0.51	-0.59
sp Q9Z1N5 DX39B_MOUSE	Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1	-0.51	-0.35
sp Q9Z1Q9 SYVC_MOUSE	Valyl-tRNA synthetase OS=Mus musculus GN=Vars PE=2 SV=1	-0.51	-0.23
sp Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	-0.5	-0.73
sp Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	-0.5	-10
sp Q8K2B3 DHSA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	-0.5	-0.48
sp Q9CQ60 PGL_MOUSE	6-phosphogluconolactonase OS=Mus musculus GN=Pgls PE=2 SV=1	-0.5	-0.35
sp Q9D1R9 RL34_MOUSE	60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=3 SV=2	-0.5	-0.59
sp P62264 RS14_MOUSE	40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	-0.49	-0.46
sp Q8K1B8 URP2_MOUSE	Fermitin family homolog 3 OS=Mus musculus GN=Fermt3 PE=1 SV=1	-0.49	-0.67
sp P80317 TCPZ_MOUSE	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	-0.48	-0.43
sp Q9D0E1 HNRPM_MOUSE	Heterogeneous nuclear ribonucleoprotein M	-0.48	-0.3

	OS=Mus musculus GN=Hnrrnpm PE=1 SV=3		
sp P60335 PCBP1_MOUSE	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	-0.46	-0.3
sp Q9WUA2 SYFB_MOUSE	Phenylalanyl-tRNA synthetase beta chain OS=Mus musculus GN=Farsb PE=2 SV=2	-0.46	-0.78
sp Q61033 LAP2A_MOUSE	Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmpo PE=1 SV=4	-0.45	-10
sp Q6PDI5 ECM29_MOUSE	Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=3	-0.45	-0.41
sp P62281 RS11_MOUSE	40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3	-0.43	-0.81
sp P54116 STOM_MOUSE	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	-0.42	-0.03
sp P56480 ATPB_MOUSE	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	-0.42	-0.65
sp Q920E5 FPPS_MOUSE	Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps PE=2 SV=1	-0.42	-0.84
sp P62245 RS15A_MOUSE	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=2 SV=2	-0.41	-10
sp Q60930 VDAC2_MOUSE	Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2	-0.41	-0.45
sp Q8VCT3 AMPB_MOUSE	Aminopeptidase B OS=Mus musculus GN=Rnpep PE=2 SV=2	-0.41	-10
sp P27659 RL3_MOUSE	60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=3	-0.4	-1.15
sp P61255 RL26_MOUSE	60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=2 SV=1	-0.4	-0.45
sp Q3V132 ADT4_MOUSE	ADP/ATP translocase 4 OS=Mus musculus GN=Slc25a31 PE=2 SV=1	-0.4	-0.65
sp Q922F4 TBB6_MOUSE	Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	-0.4	-0.76
sp Q9D0B0 SRSF9_MOUSE	Serine/arginine-rich splicing factor 9 OS=Mus musculus GN=Srsf9 PE=1 SV=1	-0.38	-0.11
sp Q8C0C7 SYFA_MOUSE	Phenylalanyl-tRNA synthetase alpha chain OS=Mus musculus GN=Farsa PE=2 SV=1	-0.37	-10
sp P62702 RS4X_MOUSE	40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	-0.36	-0.54
sp Q9DCH4 EIF3F_MOUSE	Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Eif3f PE=1 SV=2	-0.36	-0.15
sp P47962 RL5_MOUSE	60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	-0.35	-0.2
sp P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	-0.35	-0.72
sp P21550 ENOB_MOUSE	Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	-0.34	-0.1
sp P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	-0.34	-0.22
sp Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	-0.34	-0.17
sp Q9ERD7 TBB3_MOUSE	Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	-0.34	-0.6

sp Q9D6R2 IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	-0.33	-0.34
sp Q1HFZ0 NSUN2_MOUSE	tRNA (cytosine(34)-C(5))-methyltransferase OS=Mus musculus GN=Nsun2 PE=1 SV=2	-0.32	-0.58
sp O09167 RL21_MOUSE	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	-0.31	-0.65
sp P61358 RL27_MOUSE	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=2 SV=2	-0.31	-0.07
sp P80313 TCPH_MOUSE	T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	-0.31	-0.23
sp Q7TMM9 TBB2A_MOUSE	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	-0.31	-0.69
sp Q8BFR5 EFTU_MOUSE	Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	-0.31	-0.54
sp Q8CGK3 LONM_MOUSE	Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE=1 SV=2	-0.31	-0.21
sp Q9CWF2 TBB2B_MOUSE	Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1	-0.31	-0.69
sp P41105 RL28_MOUSE	60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	-0.3	-0.58
sp P84104 SRSF3_MOUSE	Serine/arginine-rich splicing factor 3 OS=Mus musculus GN=Srsf3 PE=1 SV=1	-0.3	-0.2
sp Q99K10 ACON_MOUSE	Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	-0.3	-0.37
sp Q9DBT5 AMPD2_MOUSE	AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1	-0.3	-0.08
sp Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	-0.3	-10
sp P14115 RL27A_MOUSE	60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=5	-0.29	-0.53
sp P14148 RL7_MOUSE	60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	-0.29	-0.6
sp P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	-0.29	-0.05
sp P19253 RL13A_MOUSE	60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	-0.29	-0.47
sp P47963 RL13_MOUSE	60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	-0.29	-0.53
sp Q61753 SERA_MOUSE	D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	-0.29	-0.63
sp Q6PB66 LPPRC_MOUSE	Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	-0.29	-0.25
sp Q64514 TPP2_MOUSE	Tripeptidyl-peptidase 2 OS=Mus musculus GN=Tpp2 PE=2 SV=3	-0.28	-0.25
sp P62754 RS6_MOUSE	40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	-0.27	-0.66
sp P62918 RL8_MOUSE	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	-0.27	-0.42
sp Q9CXW4 RL11_MOUSE	60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4	-0.26	-0.49
sp Q61029 LAP2B_MOUSE	Lamina-associated polypeptide 2, isoforms	-0.24	-10

	beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4		
sp P12970 RL7A_MOUSE	60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	-0.23	-0.75
sp P62242 RS8_MOUSE	40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	-0.23	-0.65
sp P63323 RS12_MOUSE	40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2	-0.23	-0.03
sp Q9CU62 SMC1A_MOUSE	Structural maintenance of chromosomes protein 1A OS=Mus musculus GN=Smc1a PE=1 SV=4	-0.23	-0.41
sp Q9Z110 P5CS_MOUSE	Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=Aldh18a1 PE=2 SV=2	-0.23	-10
sp P05213 TBA1B_MOUSE	Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2	-0.21	-0.71
sp P17183 ENOG_MOUSE	Gamma-enolase OS=Mus musculus GN=Eno2 PE=1 SV=2	-0.21	-0.08
sp P23116 EIF3A_MOUSE	Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=Eif3a PE=1 SV=5	-0.21	-0.27
sp P68369 TBA1A_MOUSE	Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	-0.21	-0.7
sp P68372 TBB2C_MOUSE	Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	-0.21	-0.72
sp P68373 TBA1C_MOUSE	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1	-0.21	-0.69
sp Q9CZM2 RL15_MOUSE	60S ribosomal protein L15 OS=Mus musculus GN=Rpl15 PE=2 SV=4	-0.2	-0.63
sp P53657 KPYR_MOUSE	Pyruvate kinase isozymes R/L OS=Mus musculus GN=Pklr PE=2 SV=1	-0.19	-0.01
sp Q9CQR2 RS21_MOUSE	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=2 SV=1	-0.19	-0.04
sp P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	-0.17	-0.19
sp P62301 RS13_MOUSE	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	-0.17	-0.01
sp Q62167 DDX3X_MOUSE	ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3	-0.17	-0.34
sp Q8BL97 SRSF7_MOUSE	Serine/arginine-rich splicing factor 7 OS=Mus musculus GN=Srsf7 PE=1 SV=1	-0.16	-0.78
sp Q9CRB9 CHCH3_MOUSE	Coiled-coil-helix-coiled-coil-helix domain- containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1 SV=1	-0.16	-0.05
sp O35737 HNRH1_MOUSE	Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnp1 PE=1 SV=3	-0.15	-10
sp P25444 RS2_MOUSE	40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	-0.15	-0.44
sp P70333 HNRH2_MOUSE	Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrnp2 PE=1 SV=1	-0.15	-10
sp P97351 RS3A_MOUSE	40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	-0.15	-0.25
sp Q9Z2X1 HNRPF_MOUSE	Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnrnpf PE=1 SV=3	-0.15	-10
sp O08788 DCTN1_MOUSE	Dynactin subunit 1 OS=Mus musculus GN=Dctn1 PE=1 SV=3	-0.14	-10

sp P05214 TBA3_MOUSE	Tubulin alpha-3 chain OS=Mus musculus GN=Tuba3a PE=1 SV=1	-0.13	-0.69
sp P35980 RL18_MOUSE	60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=3	-0.13	-0.52
sp P52480 KPYM_MOUSE	Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	-0.13	-0.15
sp P62631 EF1A2_MOUSE	Elongation factor 1-alpha 2 OS=Mus musculus GN=Eef1a2 PE=1 SV=1	-0.13	-0.18
sp P80318 TCPG_MOUSE	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	-0.13	-0.28
sp Q68FD5 CLH_MOUSE	Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	-0.13	-0.5
sp Q9CPR4 RL17_MOUSE	60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=2 SV=3	-0.13	-0.85
sp P11983 TCPA_MOUSE	T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3	-0.12	-0.5
sp Q9QXX4 CMC2_MOUSE	Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1	-0.11	-10
sp O70133 DHX9_MOUSE	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	-0.1	-0.64
sp P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	-0.1	-0.22
sp Q8VEK3 HNRPU_MOUSE	Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrpu PE=1 SV=1	-0.1	-0.34
sp Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2	-0.09	-0.65
sp P14131 RS16_MOUSE	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV=4	-0.08	-0.46
sp O08756 HCD2_MOUSE	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17b10 PE=1 SV=4	-0.07	-0.61
sp Q9EPU0 RENT1_MOUSE	Regulator of nonsense transcripts 1 OS=Mus musculus GN=Upf1 PE=1 SV=2	-0.07	-0.39
sp P60764 RAC3_MOUSE	Ras-related C3 botulinum toxin substrate 3 OS=Mus musculus GN=Rac3 PE=1 SV=1	-0.06	-0.21
sp P63001 RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	-0.06	-0.21
sp P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	-0.05	-0.28
sp Q61879 MYH10_MOUSE	Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	-0.05	-0.66
sp Q99NB9 SF3B1_MOUSE	Splicing factor 3B subunit 1 OS=Mus musculus GN=Sf3b1 PE=1 SV=1	-0.05	-0.27
sp Q05144 RAC2_MOUSE	Ras-related C3 botulinum toxin substrate 2 OS=Mus musculus GN=Rac2 PE=2 SV=1	-0.04	-0.46
sp Q7TPV4 MBB1A_MOUSE	Myb-binding protein 1A OS=Mus musculus GN=Mybbp1a PE=1 SV=2	-0.04	-0.17
sp P16381 DDX3L_MOUSE	Putative ATP-dependent RNA helicase PI10 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	-0.03	-0.34
sp P62267 RS23_MOUSE	40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3	-0.03	-0.59
sp Q6URW6 MYH14_MOUSE	Myosin-14 OS=Mus musculus GN=Myh14 PE=1 SV=1	-0.02	-0.72

sp Q8VDD5 MYH9_MOUSE	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-0.01	-0.67
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Table 6. List of *Echinacea* extract 7 and LPS induced proteins consistently.

Sequence Id	Sequence Name	LPS+ <i>Echinacea</i> extract 7 Ratio- Expt- 2	LPS+ <i>Echinacea</i> extract 7 Ratio- Expt-1
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcksl1 PE=1 SV=2	3.42	0.93
sp P99029 PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2	2.52	0.38
sp P35700 PRDX1_MOUSE	Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	2.5	0.78
sp P05555 ITAM_MOUSE	Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=2	1.65	0.13
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	1.41	0.71
sp P03995 GFAP_MOUSE	Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4	1.26	0.48
sp P17809 GTR1_MOUSE	Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=4	1.03	0.86
sp P10852 4F2_MOUSE	4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	1	0.34
sp Q69ZN7 MYOF_MOUSE	Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	0.93	1.47
sp Q9D1A2 CNDP2_MOUSE	Cytosolic non-specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1	0.82	0.24
sp Q80X90 FLNB_MOUSE	Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3	0.8	0.06
sp Q9CY57 FOP_MOUSE	Friend of PRMT1 protein OS=Mus musculus GN=Fop PE=1 SV=2	0.74	0.14
sp P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	0.67	0.06
sp P20029 GRP78_MOUSE	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	0.61	0.35
sp P26041 MOES_MOUSE	Moesin OS=Mus musculus GN=Msn PE=1 SV=3	0.49	0.12
sp Q00612 G6PD1_MOUSE	Glucose-6-phosphate 1-dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3	0.49	0.32
sp P26040 EZRI_MOUSE	Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	0.48	0.12
sp P26043 RADI_MOUSE	Radixin OS=Mus musculus GN=Rdx	0.48	0.01

	PE=1 SV=3		
sp P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2	0.46	0.26
sp P62835 RAP1A_MOUSE	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=2 SV=1	0.46	0.03
sp Q99J16 RAP1B_MOUSE	Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=2 SV=2	0.46	0.03
sp P17156 HSP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2	0.42	0.1
sp P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	0.38	0.08
sp Q71LX4 TLN2_MOUSE	Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	0.29	0.15
sp P07901 HS90A_MOUSE	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	0.25	0.38
sp Q60692 PSB6_MOUSE	Proteasome subunit beta type-6 OS=Mus musculus GN=Psm6 PE=1 SV=3	0.24	0.18
sp Q9ER72 SYCC_MOUSE	CysteinyI-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2	0.24	0.33
sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=1 SV=1	0.19	0.29
sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	0.19	0.29
sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=Rps27a PE=1 SV=2	0.19	0.25
sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Uba52 PE=1 SV=2	0.19	0.29
sp P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	0.15	0.18
sp P48036 ANXA5_MOUSE	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	0.13	0.23
sp P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	0.12	0.13
sp P58252 EF2_MOUSE	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	0.12	0.02
sp Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	0.12	0.25
sp P62821 RAB1A_MOUSE	Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3	0.1	0.19
sp P61982 1433G_MOUSE	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	0.07	0.06
sp Q3THS6 METHK2_MOUSE	S-adenosylmethionine synthase isoform type-2 OS=Mus musculus GN=Mat2a PE=2 SV=2	0.07	0.08
sp P0C0S6 H2AZ_MOUSE	Histone H2A.Z OS=Mus musculus GN=H2afz PE=1 SV=2	0.04	0.03
sp P27661 H2AX_MOUSE	Histone H2A.x OS=Mus musculus GN=H2afx PE=1 SV=2	0.04	0.03

sp Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus musculus GN=H2afv PE=1 SV=3	0.04	0.03
sp Q64522 H2A2B_MOUSE	Histone H2A type 2-B OS=Mus musculus GN=Hist2h2ab PE=1 SV=3	0.04	0.03

Table 7. List of *Echinacea* extract 7 and LPS suppressed proteins consistently in experiment 2 and 1.

Sequence Id	Sequence Name	LPS+ <i>Echinacea</i> extract 7 Ratio- Expt2	LPS+ <i>Echinacea</i> extract 7 Ratio- Expt1
sp O08528 HXK2_MOUSE	Hexokinase-2 OS=Mus musculus GN=Hk2 PE=1 SV=1	-10	-0.26
sp O08547 SC22B_MOUSE	Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3	-10	-0.15
sp O08756 HCD2_MOUSE	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17b10 PE=1 SV=4	-10	-0.48
sp O08788 DCTN1_MOUSE	Dynactin subunit 1 OS=Mus musculus GN=Dctn1 PE=1 SV=3	-10	-0.7
sp O09167 RL21_MOUSE	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	-10	-0.46
sp O54734 OST48_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddost PE=1 SV=2	-10	-10
sp O54879 HMGB3_MOUSE	High mobility group protein B3 OS=Mus musculus GN=Hmgb3 PE=2 SV=3	-10	-10
sp O55131 SEPT7_MOUSE	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	-10	-10
sp O55143 AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	-10	-0.23
sp O70152 DPM1_MOUSE	Dolichol-phosphate mannosyltransferase OS=Mus musculus GN=Dpm1 PE=2 SV=1	-10	-10
sp O70456 1433S_MOUSE	14-3-3 protein sigma OS=Mus musculus GN=Sfn PE=1 SV=2	-10	-0.02
sp O88531 PPT1_MOUSE	Palmitoyl-protein thioesterase 1 OS=Mus musculus GN=Ppt1 PE=2 SV=2	-10	-10
sp O88844 IDHC_MOUSE	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=ldh1 PE=1 SV=2	-10	-1.01
sp P00342 LDHC_MOUSE	L-lactate dehydrogenase C chain OS=Mus musculus GN=Ldhc PE=1 SV=2	-10	-0.05
sp P00375 DYR_MOUSE	Dihydrofolate reductase OS=Mus musculus GN=Dhfr PE=1 SV=3	-10	-0.11
sp P01895 HA1Y_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus GN=H2-D1 PE=2 SV=1	-10	-0.14
sp P01896 HA1Z_MOUSE	H-2 class I histocompatibility antigen, alpha	-10	-0.14

	chain (Fragment) OS=Mus musculus PE=1 SV=1		
sp P01942 HBA_MOUSE	Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2	-10	-10
sp P05063 ALDOC_MOUSE	Fructose-bisphosphate aldolase C OS=Mus musculus GN=Aldoc PE=1 SV=4	-10	-0.4
sp P07724 ALBU_MOUSE	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	-10	-10
sp P08228 SODC_MOUSE	Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=2	-10	-10
sp P08553 NFM_MOUSE	Neurofilament medium polypeptide OS=Mus musculus GN=Nefm PE=1 SV=4	-10	-10
sp P08752 GNAI2_MOUSE	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5	-10	-0.78
sp P10404 ENV1_MOUSE	MLV-related proviral Env polyprotein OS=Mus musculus PE=2 SV=3	-10	-0.54
sp P11370 ENV2_MOUSE	Retrovirus-related Env polyprotein from Fv-4 locus OS=Mus musculus GN=Fv4 PE=1 SV=2	-10	-0.65
sp P11983 TCPA_MOUSE	T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3	-10	-0.51
sp P12265 BGLR_MOUSE	Beta-glucuronidase OS=Mus musculus GN=Gusb PE=2 SV=1	-10	-0.37
sp P12787 COX5A_MOUSE	Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2	-10	-0.05
sp P16125 LDHB_MOUSE	L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2	-10	-0.21
sp P19246 NFB_MOUSE	Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE=1 SV=3	-10	-10
sp P20108 PRDX3_MOUSE	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Mus musculus GN=Prdx3 PE=1 SV=1	-10	-0.04
sp P21619 LMNB2_MOUSE	Lamin-B2 OS=Mus musculus GN=Lmnb2 PE=1 SV=2	-10	-0.2
sp P23492 PNPH_MOUSE	Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2	-10	-10
sp P24369 PPIB_MOUSE	Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=2 SV=2	-10	-0.01
sp P24547 IMDH2_MOUSE	Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh2 PE=1 SV=2	-10	-0.15
sp P25206 MCM3_MOUSE	DNA replication licensing factor MCM3 OS=Mus musculus GN=Mcm3 PE=1 SV=2	-10	-0.99
sp P26516 PSD7_MOUSE	26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	-10	-0.43
sp P26638 SYSC_MOUSE	Seryl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Sars PE=2 SV=3	-10	-0.3
sp P27659 RL3_MOUSE	60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=3	-10	-0.47
sp P28738 KIF5C_MOUSE	Kinesin heavy chain isoform 5C OS=Mus musculus GN=Kif5c PE=1 SV=3	-10	-0.09

sp P29387 GBB4_MOUSE	Guanine nucleotide-binding protein subunit beta-4 OS=Mus musculus GN=Gnb4 PE=2 SV=4	-10	-10
sp P29758 OAT_MOUSE	Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1	-10	-0.15
sp P32067 LA_MOUSE	Lupus La protein homolog OS=Mus musculus GN=Ssb PE=2 SV=1	-10	-0.26
sp P33175 KIF5A_MOUSE	Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3	-10	-0.09
sp P34022 RANG_MOUSE	Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	-10	-0.28
sp P37040 NCPR_MOUSE	NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	-10	-2.98
sp P42208 SEPT2_MOUSE	Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2	-10	-0.2
sp P42225 STAT1_MOUSE	Signal transducer and activator of transcription 1 OS=Mus musculus GN=Stat1 PE=1 SV=1	-10	-10
sp P43276 H15_MOUSE	Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	-10	-0.62
sp P46638 RB11B_MOUSE	Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3	-10	-0.59
sp P46660 AINX_MOUSE	Alpha-internexin OS=Mus musculus GN=Ina PE=1 SV=2	-10	-10
sp P47753 CAZA1_MOUSE	F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=Capza1 PE=1 SV=4	-10	-0.25
sp P47754 CAZA2_MOUSE	F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=Capza2 PE=1 SV=3	-10	-0.25
sp P47955 RLA1_MOUSE	60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1	-10	-0.04
sp P47962 RL5_MOUSE	60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	-10	-0.39
sp P49312 ROA1_MOUSE	Heterogeneous nuclear ribonucleoprotein A1 OS=Mus musculus GN=Hnrnpa1 PE=1 SV=2	-10	-10
sp P49717 MCM4_MOUSE	DNA replication licensing factor MCM4 OS=Mus musculus GN=Mcm4 PE=2 SV=1	-10	-1.4
sp P49718 MCM5_MOUSE	DNA replication licensing factor MCM5 OS=Mus musculus GN=Mcm5 PE=2 SV=1	-10	-0.97
sp P50247 SAHH_MOUSE	Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	-10	-0.49
sp P50396 GDIA_MOUSE	Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3	-10	-0.31
sp P50516 VATA_MOUSE	V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2	-10	-0.18
sp P53026 RL10A_MOUSE	60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	-10	-0.1
sp P53986 MOT1_MOUSE	Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	-10	-0.7
sp P54071 IDHP_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	-10	-0.68
sp P54775 PRS6B_MOUSE	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2	-10	-0.19

sp P56135 ATPK_MOUSE	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=1 SV=3	-10	-0.3
sp P57722 PCBP3_MOUSE	Poly(rC)-binding protein 3 OS=Mus musculus GN=Pcbp3 PE=2 SV=3	-10	-0.38
sp P57759 ERP29_MOUSE	Endoplasmic reticulum resident protein 29 OS=Mus musculus GN=Erp29 PE=1 SV=2	-10	-0.19
sp P60335 PCBP1_MOUSE	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	-10	-0.35
sp P60867 RS20_MOUSE	40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	-10	-0.36
sp P61161 ARP2_MOUSE	Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	-10	-0.44
sp P61358 RL27_MOUSE	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=2 SV=2	-10	-0.04
sp P61979 HNRPK_MOUSE	Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrpk PE=1 SV=1	-10	-0.21
sp P62082 RS7_MOUSE	40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	-10	-0.41
sp P62192 PRS4_MOUSE	26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	-10	-0.17
sp P62245 RS15A_MOUSE	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=2 SV=2	-10	-3.33
sp P62274 RS29_MOUSE	40S ribosomal protein S29 OS=Mus musculus GN=Rps29 PE=2 SV=2	-10	-0.14
sp P62301 RS13_MOUSE	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	-10	-0.14
sp P62315 SMD1_MOUSE	Small nuclear ribonucleoprotein Sm D1 OS=Mus musculus GN=Snrpd1 PE=2 SV=1	-10	-0.27
sp P62320 SMD3_MOUSE	Small nuclear ribonucleoprotein Sm D3 OS=Mus musculus GN=Snrpd3 PE=1 SV=1	-10	-0.05
sp P62492 RB11A_MOUSE	Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a PE=1 SV=3	-10	-0.59
sp P62806 H4_MOUSE	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	-10	-0.28
sp P62827 RAN_MOUSE	GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3	-10	-0.47
sp P62830 RL23_MOUSE	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	-10	-0.45
sp P62855 RS26_MOUSE	40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=2 SV=3	-10	-0.44
sp P63242 IF5A1_MOUSE	Eukaryotic translation initiation factor 5A-1 OS=Mus musculus GN=Eif5a PE=1 SV=2	-10	-0.1
sp P63276 RS17_MOUSE	40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	-10	-0.34
sp P67984 RL22_MOUSE	60S ribosomal protein L22 OS=Mus musculus GN=Rpl22 PE=2 SV=2	-10	-0.42
sp P68040 GBLP_MOUSE	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3	-10	-0.58
sp P68433 H31_MOUSE	Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	-10	-0.94
sp P80317 TCPZ_MOUSE	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	-10	-0.39

sp P84084 ARF5_MOUSE	ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=2 SV=2	-10	-10
sp P84228 H32_MOUSE	Histone H3.2 OS=Mus musculus GN=Hist1h3b PE=1 SV=2	-10	-0.94
sp P84244 H33_MOUSE	Histone H3.3 OS=Mus musculus GN=H3f3a PE=1 SV=2	-10	-0.94
sp P86048 RL10L_MOUSE	60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=1	-10	-0.53
sp P97310 MCM2_MOUSE	DNA replication licensing factor MCM2 OS=Mus musculus GN=Mcm2 PE=1 SV=3	-10	-1.14
sp P97311 MCM6_MOUSE	DNA replication licensing factor MCM6 OS=Mus musculus GN=Mcm6 PE=1 SV=1	-10	-0.85
sp Q04447 KCRB_MOUSE	Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1	-10	-0.26
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	-10	-10
sp Q06185 ATP5I_MOUSE	ATP synthase subunit e, mitochondrial OS=Mus musculus GN=Atp5i PE=1 SV=2	-10	-0.19
sp Q1HFZ0 NSUN2_MOUSE	tRNA (cytosine(34)-C(5))-methyltransferase OS=Mus musculus GN=Nsun2 PE=1 SV=2	-10	-0.45
sp Q3U9G9 LBR_MOUSE	Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	-10	-0.57
sp Q3UM45 PP1R7_MOUSE	Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2	-10	-0.21
sp Q501J6 DDX17_MOUSE	Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	-10	-0.33
sp Q5SWU9 ACACA_MOUSE	Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	-10	-1.5
sp Q5XJY5 COPD_MOUSE	Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=2 SV=2	-10	-10
sp Q60668 HNRPD_MOUSE	Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=Hnrnpd PE=1 SV=2	-10	-0.37
sp Q60864 STIP1_MOUSE	Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1	-10	-0.21
sp Q60931 VDAC3_MOUSE	Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	-10	-10
sp Q60932 VDAC1_MOUSE	Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	-10	-0.2
sp Q61011 GBB3_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Mus musculus GN=Gnb3 PE=1 SV=2	-10	-10
sp Q61029 LAP2B_MOUSE	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4	-10	-10
sp Q61033 LAP2A_MOUSE	Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmpo PE=1 SV=4	-10	-10
sp Q61335 BAP31_MOUSE	B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=3	-10	-10
sp Q61390 TCPW_MOUSE	T-complex protein 1 subunit zeta-2 OS=Mus musculus GN=Cct6b PE=2 SV=4	-10	-0.42

sp Q61598 GDIB_MOUSE	Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	-10	-0.37
sp Q61768 KINH_MOUSE	Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=3	-10	-0.2
sp Q61820 RANT_MOUSE	GTP-binding nuclear protein Ran, testis-specific isoform OS=Mus musculus GN=Rasl2-9 PE=2 SV=1	-10	-0.52
sp Q61990 PCBP2_MOUSE	Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	-10	-0.51
sp Q62351 TFR1_MOUSE	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	-10	-0.1
sp Q62425 NDUA4_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Mus musculus GN=Ndufa4 PE=1 SV=2	-10	-0.74
sp Q62446 FKBP3_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Mus musculus GN=Fkbp3 PE=1 SV=2	-10	-10
sp Q641P0 ARP3B_MOUSE	Actin-related protein 3B OS=Mus musculus GN=Actr3b PE=2 SV=1	-10	-0.26
sp Q64514 TPP2_MOUSE	Tripeptidyl-peptidase 2 OS=Mus musculus GN=Tpp2 PE=2 SV=3	-10	-0.31
sp Q64516 GLPK_MOUSE	Glycerol kinase OS=Mus musculus GN=Gk PE=2 SV=2	-10	-10
sp Q64518 AT2A3_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Mus musculus GN=Atp2a3 PE=2 SV=3	-10	-0.29
sp Q64674 SPEE_MOUSE	Spermidine synthase OS=Mus musculus GN=Srm PE=2 SV=1	-10	-10
sp Q68FD5 CLH_MOUSE	Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	-10	-0.43
sp Q68FL6 SYMC_MOUSE	Methionyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Mars PE=2 SV=1	-10	-0.39
sp Q6PDI5 ECM29_MOUSE	Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=3	-10	-0.65
sp Q6ZWU9 RS27_MOUSE	40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3	-10	-1.3
sp Q6ZWV3 RL10_MOUSE	60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3	-10	-0.53
sp Q6ZX6 IF2A_MOUSE	Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3	-10	-0.02
sp Q6ZWY3 RS27L_MOUSE	40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=2 SV=3	-10	-1.29
sp Q7M6Y3 PICA_MOUSE	Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus GN=Picalm PE=1 SV=1	-10	-0.95
sp Q7TMK9 HNRPQ_MOUSE	Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncrip PE=1 SV=2	-10	-0.18
sp Q7TQI3 OTUB1_MOUSE	Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2	-10	-0.53
sp Q8BFR5 EFTU_MOUSE	Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	-10	-0.44
sp Q8BG32 PSD11_MOUSE	26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psm11	-10	-10

	PE=1 SV=3		
sp Q8BGY2 IF5A2_MOUSE	Eukaryotic translation initiation factor 5A-2 OS=Mus musculus GN=Eif5a2 PE=2 SV=3	-10	-0.1
sp Q8BH04 PCKGM_MOUSE	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=2 SV=1	-10	-0.35
sp Q8BKC5 IPO5_MOUSE	Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	-10	-0.22
sp Q8BMK4 CKAP4_MOUSE	Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=2 SV=2	-10	-10
sp Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	-10	-0.75
sp Q8BP47 SYNC_MOUSE	Asparaginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Nars PE=1 SV=2	-10	-0.19
sp Q8BWY3 ERF1_MOUSE	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Etf1 PE=1 SV=4	-10	-0.29
sp Q8C0C7 SYFA_MOUSE	Phenylalanyl-tRNA synthetase alpha chain OS=Mus musculus GN=Farsa PE=2 SV=1	-10	-10
sp Q8C166 CPNE1_MOUSE	Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1	-10	-10
sp Q8CGK3 LONM_MOUSE	Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE=1 SV=2	-10	-0.3
sp Q8C143 MYL6B_MOUSE	Myosin light chain 6B OS=Mus musculus GN=Myl6b PE=2 SV=1	-10	-0.14
sp Q8JZQ9 EIF3B_MOUSE	Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1	-10	-0.35
sp Q8K2Q2 GSTO2_MOUSE	Glutathione S-transferase omega-2 OS=Mus musculus GN=Gsto2 PE=2 SV=1	-10	-10
sp Q8K4Z3 AIBP_MOUSE	Apolipoprotein A-I-binding protein OS=Mus musculus GN=Apoa1bp PE=1 SV=1	-10	-10
sp Q8QZY1 EIF3L_MOUSE	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1	-10	-0.19
sp Q8R0W0 EPIPL_MOUSE	Epiplakin OS=Mus musculus GN=Eppk1 PE=1 SV=2	-10	-0.36
sp Q8R1F1 NIBL1_MOUSE	Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=1 SV=2	-10	-10
sp Q8R429 AT2A1_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1	-10	-0.09
sp Q8VCT3 AMPB_MOUSE	Aminopeptidase B OS=Mus musculus GN=Rnpep PE=2 SV=2	-10	-0.18
sp Q8VDJ3 VIGLN_MOUSE	Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	-10	-0.19
sp Q8VDP4 K1967_MOUSE	Protein KIAA1967 homolog OS=Mus musculus PE=1 SV=2	-10	-0.46
sp Q8VHX6 FLNC_MOUSE	Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	-10	-0.04
sp Q8VIJ6 SFPQ_MOUSE	Splicing factor, proline- and glutamine-rich OS=Mus musculus GN=Sfpq PE=1 SV=1	-10	-0.53

sp Q91V92 ACLY_MOUSE	ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	-10	-1.06
sp Q91VI7 RINI_MOUSE	Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1	-10	-0.17
sp Q91VR2 ATPG_MOUSE	ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	-10	-10
sp Q91ZX7 LRP1_MOUSE	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	-10	-0.54
sp Q920E5 FPPS_MOUSE	Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps PE=2 SV=1	-10	-0.49
sp Q921M7 FA49B_MOUSE	Protein FAM49B OS=Mus musculus GN=Fam49b PE=2 SV=1	-10	-10
sp Q99020 ROAA_MOUSE	Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculus GN=Hnrnpab PE=1 SV=1	-10	-0.09
sp Q99JY0 ECHB_MOUSE	Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	-10	-10
sp Q99KC8 VMA5A_MOUSE	von Willebrand factor A domain-containing protein 5A OS=Mus musculus GN=Vwa5a PE=1 SV=2	-10	-0.67
sp Q99LC5 ETFA_MOUSE	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2	-10	-0.36
sp Q99LP6 GRPE1_MOUSE	GrpE protein homolog 1, mitochondrial OS=Mus musculus GN=Grpel1 PE=1 SV=1	-10	-10
sp Q99LX0 PARK7_MOUSE	Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	-10	-0.67
sp Q99MN1 SYK_MOUSE	Lysyl-tRNA synthetase OS=Mus musculus GN=Kars PE=1 SV=1	-10	-0.08
sp Q99MR6 SRRT_MOUSE	Serrate RNA effector molecule homolog OS=Mus musculus GN=Srrt PE=1 SV=1	-10	-10
sp Q99NB9 SF3B1_MOUSE	Splicing factor 3B subunit 1 OS=Mus musculus GN=Sf3b1 PE=1 SV=1	-10	-0.29
sp Q99PL5 RRBP1_MOUSE	Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=2 SV=2	-10	-0.16
sp Q9BDB7 IF44L_MOUSE	Interferon-induced protein 44-like OS=Mus musculus GN=IF44L PE=2 SV=2	-10	-10
sp Q9CPU0 LGUL_MOUSE	Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=3	-10	-10
sp Q9CQ60 6PGL_MOUSE	6-phosphogluconolactonase OS=Mus musculus GN=Pgls PE=2 SV=1	-10	-0.52
sp Q9CQ65 MTAP_MOUSE	S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=2 SV=1	-10	-10
sp Q9CQI6 COTL1_MOUSE	Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3	-10	-0.54
sp Q9CQR2 RS21_MOUSE	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=2 SV=1	-10	-0.22
sp Q9CR62 M2OM_MOUSE	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus GN=Slc25a11 PE=1 SV=3	-10	-10
sp Q9CRB9 CHCH3_MOUSE	Coiled-coil-helix-coiled-coil-helix domain- containing protein 3, mitochondrial OS=Mus	-10	-10

	musculus GN=Chchd3 PE=1 SV=1		
sp Q9CW03 SMC3_MOUSE	Structural maintenance of chromosomes protein 3 OS=Mus musculus GN=Smc3 PE=1 SV=2	-10	-0.55
sp Q9CXW3 CYBP_MOUSE	Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	-10	-10
sp Q9CY64 BIEA_MOUSE	Biliverdin reductase A OS=Mus musculus GN=Blvra PE=2 SV=1	-10	-10
sp Q9CZY3 UB2V1_MOUSE	Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=1 SV=1	-10	-10
sp Q9D0B0 SRSF9_MOUSE	Serine/arginine-rich splicing factor 9 OS=Mus musculus GN=Srsf9 PE=1 SV=1	-10	-10
sp Q9D0I9 SYRC_MOUSE	Arginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Rars PE=2 SV=2	-10	-0.3
sp Q9D1G1 RAB1B_MOUSE	Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	-10	-0.69
sp Q9D2M8 UB2V2_MOUSE	Ubiquitin-conjugating enzyme E2 variant 2 OS=Mus musculus GN=Ube2v2 PE=2 SV=4	-10	-10
sp Q9D3D9 ATPD_MOUSE	ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5d PE=1 SV=1	-10	-0.27
sp Q9D4D4 TKTL2_MOUSE	Transketolase-like protein 2 OS=Mus musculus GN=Tktl2 PE=2 SV=1	-10	-10
sp Q9DBG6 RPN2_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	-10	-0.32
sp Q9DCC8 TOM20_MOUSE	Mitochondrial import receptor subunit TOM20 homolog OS=Mus musculus GN=Tom20 PE=1 SV=1	-10	-10
sp Q9DCH4 EIF3F_MOUSE	Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Eif3f PE=1 SV=2	-10	-10
sp Q9DCL9 PUR6_MOUSE	Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4	-10	-0.57
sp Q9EPU0 RENT1_MOUSE	Regulator of nonsense transcripts 1 OS=Mus musculus GN=Upf1 PE=1 SV=2	-10	-0.39
sp Q9EQP2 EHD4_MOUSE	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	-10	-0.5
sp Q9ES52 SHIP1_MOUSE	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1 OS=Mus musculus GN=Inpp5d PE=1 SV=2	-10	-0.31
sp Q9JHU9 INO1_MOUSE	Inositol-3-phosphate synthase 1 OS=Mus musculus GN=Isyna1 PE=2 SV=1	-10	-0.03
sp Q9JII6 AK1A1_MOUSE	Alcohol dehydrogenase [NADP+] OS=Mus musculus GN=Akr1a1 PE=1 SV=3	-10	-0.06
sp Q9JJ28 FLII_MOUSE	Protein flightless-1 homolog OS=Mus musculus GN=Flil PE=1 SV=1	-10	-0.38
sp Q9JJI8 RL38_MOUSE	60S ribosomal protein L38 OS=Mus musculus GN=Rpl38 PE=2 SV=3	-10	-0.45
sp Q9JKF1 IQGA1_MOUSE	Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=1	-10	-0.16
sp Q9JM76 ARPC3_MOUSE	Actin-related protein 2/3 complex subunit 3 OS=Mus musculus GN=Arpc3 PE=1 SV=3	-10	-0.27
sp Q9JMA1 UBP14_MOUSE	Ubiquitin carboxyl-terminal hydrolase 14	-10	-0.42

	OS=Mus musculus GN=Usp14 PE=1 SV=3		
sp Q9QXK3 COPG2_MOUSE	Coatomer subunit gamma-2 OS=Mus musculus GN=Copg2 PE=2 SV=1	-10	-10
sp Q9QXX4 CMC2_MOUSE	Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1	-10	-0.46
sp Q9QYJ0 DNJA2_MOUSE	DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1	-10	-0.33
sp Q9QZD8 DIC_MOUSE	Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=2 SV=2	-10	-10
sp Q9QZE5 COPG_MOUSE	Coatomer subunit gamma OS=Mus musculus GN=Copg PE=2 SV=1	-10	-0.24
sp Q9R1P0 PSA4_MOUSE	Proteasome subunit alpha type-4 OS=Mus musculus GN=Psm4 PE=1 SV=1	-10	-0.06
sp Q9R1Q7 PLP2_MOUSE	Proteolipid protein 2 OS=Mus musculus GN=Plp2 PE=2 SV=1	-10	-0.15
sp Q9WTI7 MYO1C_MOUSE	Myosin-1c OS=Mus musculus GN=Myo1c PE=1 SV=2	-10	-0.85
sp Q9WUM4 COR1C_MOUSE	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	-10	-0.9
sp Q9WV32 ARC1B_MOUSE	Actin-related protein 2/3 complex subunit 1B OS=Mus musculus GN=Arpc1b PE=1 SV=4	-10	-0.27
sp Q9Z110 P5CS_MOUSE	Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=Aldh18a1 PE=2 SV=2	-10	-0.68
sp Q9Z2I8 SUCB2_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Suc1g2 PE=2 SV=3	-10	-10
sp Q9Z2U1 PSA5_MOUSE	Proteasome subunit alpha type-5 OS=Mus musculus GN=Psm5 PE=1 SV=1	-10	-0.02
sp Q9Z2X1 HNRPF_MOUSE	Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnrnpf PE=1 SV=3	-10	-0.47
sp Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	-2.74	-1.33
sp P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus GN=Lyz2 PE=1 SV=2	-1.96	-0.24
sp P17897 LYZ1_MOUSE	Lysozyme C-1 OS=Mus musculus GN=Lyz1 PE=1 SV=1	-1.96	-0.29
sp P11438 LAMP1_MOUSE	Lysosome-associated membrane glycoprotein 1 OS=Mus musculus GN=Lamp1 PE=1 SV=2	-1.91	-0.29
sp Q35737 HNRH1_MOUSE	Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnp1 PE=1 SV=3	-1.76	-0.63
sp P70333 HNRH2_MOUSE	Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrnp2 PE=1 SV=1	-1.76	-0.7
sp Q6ZQ38 CAND1_MOUSE	Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	-1.61	-0.54
sp P45376 ALDR_MOUSE	Aldose reductase OS=Mus musculus GN=Akr1b1 PE=1 SV=3	-1.48	-0.18
sp Q8VC28 AK1CD_MOUSE	Aldo-keto reductase family 1 member C13	-1.43	-1.13

	OS=Mus musculus GN=Akr1c13 PE=1 SV=2		
sp Q9DB77 QCR2_MOUSE	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	-1.39	-0.59
sp P63158 HMGB1_MOUSE	High mobility group protein B1 OS=Mus musculus GN=Hmgb1 PE=1 SV=2	-1.35	-0.3
sp Q9D0K2 SCOT1_MOUSE	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial OS=Mus musculus GN=Oxct1 PE=1 SV=1	-1.33	-0.22
sp P17918 PCNA_MOUSE	Proliferating cell nuclear antigen OS=Mus musculus GN=Pcna PE=1 SV=2	-1.32	-0.4
sp Q9D3B1 HACD2_MOUSE	3-hydroxyacyl-CoA dehydratase 2 OS=Mus musculus GN=Ptplb PE=2 SV=1	-1.31	-1.39
sp Q8BMF3 MAON_MOUSE	NADP-dependent malic enzyme, mitochondrial OS=Mus musculus GN=Me3 PE=1 SV=2	-1.26	-0.28
sp Q921H8 THIKA_MOUSE	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=2 SV=1	-1.26	-0.47
sp Q9CWWY9 RIP_MOUSE	RPA-interacting protein OS=Mus musculus GN=Rpain PE=2 SV=1	-1.26	-0.37
sp P48722 HS74L_MOUSE	Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2	-1.22	-0.11
sp Q9DCT2 NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=2	-1.17	-1.06
sp Q8BK67 RCC2_MOUSE	Protein RCC2 OS=Mus musculus GN=Rcc2 PE=2 SV=1	-1.15	-0.4
sp Q9WV27 AT1A4_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Mus musculus GN=Atp1a4 PE=1 SV=3	-1.15	-0.56
sp Q9Z1W8 AT12A_MOUSE	Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=3	-1.15	-0.58
sp P30681 HMGB2_MOUSE	High mobility group protein B2 OS=Mus musculus GN=Hmgb2 PE=1 SV=3	-1.13	-0.54
sp P06801 MAOX_MOUSE	NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=2	-1.11	-0.31
sp P07091 S10A4_MOUSE	Protein S100-A4 OS=Mus musculus GN=S100a4 PE=1 SV=1	-1.09	-0.47
sp Q9EQU5 SET_MOUSE	Protein SET OS=Mus musculus GN=Set PE=1 SV=1	-1.09	-0.18
sp Q64436 ATP4A_MOUSE	Potassium-transporting ATPase alpha chain 1 OS=Mus musculus GN=Atp4a PE=1 SV=3	-1.08	-0.59
sp Q99K51 PLST_MOUSE	Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	-1.06	-0.01
sp Q9D0E1 HNRPM_MOUSE	Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrnrm PE=1 SV=3	-1.02	-0.41
sp Q8VDN2 AT1A1_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	-0.99	-0.53
sp Q91VD9 NDUS1_MOUSE	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2	-0.99	-10

sp P23116 EIF3A_MOUSE	Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=Eif3a PE=1 SV=5	-0.98	-0.39
sp Q62095 DDX3Y_MOUSE	ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2	-0.97	-0.44
sp Q8R1B4 EIF3C_MOUSE	Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1	-0.94	-0.27
sp P14152 MDHC_MOUSE	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	-0.93	-0.32
sp Q9DCX2 ATP5H_MOUSE	ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	-0.93	-0.56
sp P63038 CH60_MOUSE	60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	-0.92	-0.06
sp Q5SUR0 PUR4_MOUSE	Phosphoribosylformylglycinamide synthase OS=Mus musculus GN=Pfas PE=2 SV=1	-0.92	-0.54
sp O35381 AN32A_MOUSE	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Mus musculus GN=Anp32a PE=1 SV=1	-0.9	-0.31
sp Q64G17 AN32C_MOUSE	Putative acidic leucine-rich nuclear phosphoprotein 32 family member C OS=Mus musculus GN=Anp32c PE=5 SV=3	-0.9	-0.29
sp Q922D8 C1TC_MOUSE	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4	-0.9	-0.69
sp Q9EST5 AN32B_MOUSE	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Mus musculus GN=Anp32b PE=1 SV=1	-0.9	-0.31
sp Q6PIC6 AT1A3_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Mus musculus GN=Atp1a3 PE=1 SV=1	-0.89	-0.6
sp Q6PIE5 AT1A2_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Mus musculus GN=Atp1a2 PE=1 SV=1	-0.89	-0.57
sp Q9CWJ9 PUR9_MOUSE	Bifunctional purine biosynthesis protein PURH OS=Mus musculus GN=Atic PE=1 SV=2	-0.88	-0.09
sp Q9D8E6 RL4_MOUSE	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	-0.86	-0.54
sp Q9DCC4 P5CR3_MOUSE	Pyrroline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycrl PE=2 SV=2	-0.84	-0.47
sp P09055 ITB1_MOUSE	Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	-0.82	-0.11
sp P97807 FUMH_MOUSE	Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3	-0.81	-10
sp Q921F2 TADBP_MOUSE	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	-0.8	-0.63
sp Q8VEK3 HNRPU_MOUSE	Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1	-0.79	-0.45
sp Q9CPQ1 COX6C_MOUSE	Cytochrome c oxidase subunit 6C OS=Mus musculus GN=Cox6c PE=1 SV=3	-0.79	-0.12
sp P43275 H11_MOUSE	Histone H1.1 OS=Mus musculus GN=Hist1h1a PE=2 SV=2	-0.76	-0.73
sp P19096 FAS_MOUSE	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	-0.75	-0.77

sp O70133 DHX9_MOUSE	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	-0.74	-0.83
sp P14131 RS16_MOUSE	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV=4	-0.74	-0.45
sp P16381 DDX3L_MOUSE	Putative ATP-dependent RNA helicase P110 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	-0.73	-0.44
sp P70296 PEBP1_MOUSE	Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3	-0.73	-0.24
sp Q62167 DDX3X_MOUSE	ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3	-0.73	-0.35
sp Q9Z1Q9 SYVC_MOUSE	Valyl-tRNA synthetase OS=Mus musculus GN=Vars PE=2 SV=1	-0.73	-0.42
sp P67778 PHB_MOUSE	Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	-0.72	-0.52
sp P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	-0.71	-0.71
sp O35326 SRSF5_MOUSE	Serine/arginine-rich splicing factor 5 OS=Mus musculus GN=Srsf5 PE=1 SV=1	-0.7	-0.15
sp O88569 ROA2_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	-0.7	-0.07
sp P17742 PPIA_MOUSE	Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2	-0.7	-0.23
sp Q8VE97 SRSF4_MOUSE	Serine/arginine-rich splicing factor 4 OS=Mus musculus GN=Srsf4 PE=2 SV=1	-0.7	-0.15
sp Q61937 NPM_MOUSE	Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	-0.68	-0.02
sp Q8VDW0 DX39A_MOUSE	ATP-dependent RNA helicase DDX39A OS=Mus musculus GN=Ddx39a PE=2 SV=1	-0.68	-0.44
sp Q8VEM8 MPCP_MOUSE	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	-0.68	-0.43
sp Q9Z1N5 DX39B_MOUSE	Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1	-0.68	-0.36
sp P70349 HINT1_MOUSE	Histidine triad nucleotide-binding protein 1 OS=Mus musculus GN=Hint1 PE=1 SV=3	-0.67	-0.22
sp Q99K10 ACON_MOUSE	Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	-0.67	-0.37
sp Q6GQT9 NOMO1_MOUSE	Nodal modulator 1 OS=Mus musculus GN=Nomo1 PE=1 SV=1	-0.66	-0.27
sp P05214 TBA3_MOUSE	Tubulin alpha-3 chain OS=Mus musculus GN=Tuba3a PE=1 SV=1	-0.65	-0.74
sp P54116 STOM_MOUSE	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	-0.65	-0.34
sp P56480 ATPB_MOUSE	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	-0.65	-0.69
sp Q7TMM9 TBB2A_MOUSE	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	-0.65	-0.69
sp Q91YQ5 RPN1_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=2 SV=1	-0.65	-0.03
sp Q9CWF2 TBB2B_MOUSE	Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1	-0.65	-0.69

sp Q9ERD7 TBB3_MOUSE	Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	-0.65	-0.65
sp Q9CZX8 RS19_MOUSE	40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=3	-0.64	-0.05
sp P61082 UBC12_MOUSE	NEDD8-conjugating enzyme Ubc12 OS=Mus musculus GN=Ube2m PE=2 SV=1	-0.63	-0.17
sp Q9CXT8 MPPB_MOUSE	Mitochondrial-processing peptidase subunit beta OS=Mus musculus GN=Pmpcb PE=2 SV=1	-0.63	-0.38
sp Q9CZ13 QCR1_MOUSE	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2	-0.63	-0.52
sp Q9D6F9 TBB4_MOUSE	Tubulin beta-4 chain OS=Mus musculus GN=Tubb4 PE=1 SV=3	-0.63	-0.67
sp P40142 TKT_MOUSE	Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1	-0.62	-0.19
sp P68372 TBB2C_MOUSE	Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	-0.62	-0.69
sp P00920 CAH2_MOUSE	Carbonic anhydrase 2 OS=Mus musculus GN=Ca2 PE=1 SV=4	-0.6	-0.35
sp Q07133 H1T_MOUSE	Histone H1t OS=Mus musculus GN=Hist1h1t PE=2 SV=4	-0.6	-0.9
sp Q9CU62 SMC1A_MOUSE	Structural maintenance of chromosomes protein 1A OS=Mus musculus GN=Smc1a PE=1 SV=4	-0.6	-0.64
sp P62281 RS11_MOUSE	40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3	-0.59	-0.65
sp P80314 TCPB_MOUSE	T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	-0.59	-0.15
sp Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	-0.59	-0.91
sp Q8BU30 SYIC_MOUSE	Isoleucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=lars PE=2 SV=2	-0.59	-0.49
sp P05213 TBA1B_MOUSE	Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2	-0.58	-0.8
sp P68369 TBA1A_MOUSE	Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	-0.58	-0.8
sp P68373 TBA1C_MOUSE	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1	-0.58	-0.79
sp P43274 H14_MOUSE	Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2	-0.57	-0.82
sp P80315 TCPD_MOUSE	T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	-0.57	-0.3
sp Q60597 ODO1_MOUSE	2-oxoglutarate dehydrogenase, mitochondrial OS=Mus musculus GN=Ogdh PE=1 SV=3	-0.57	-0.18
sp Q8BHN3 GANAB_MOUSE	Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1	-0.57	-0.25
sp P09405 NUCL_MOUSE	Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2	-0.56	-0.12
sp Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=4	-0.56	-0.66
sp Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	-0.56	-0.16

sp O09131 GSTO1_MOUSE	Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto1 PE=2 SV=2	-0.55	-0.45
sp P10107 ANXA1_MOUSE	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	-0.54	-0.09
sp P48962 ADT1_MOUSE	ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	-0.54	-0.74
sp P70168 IMB1_MOUSE	Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2	-0.53	-0.17
sp Q9WTM5 RUVB2_MOUSE	RuvB-like 2 OS=Mus musculus GN=Ruvbl2 PE=2 SV=3	-0.52	-1.01
sp P14206 RSSA_MOUSE	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	-0.5	-0.17
sp P68368 TBA4A_MOUSE	Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1	-0.5	-0.7
sp P84104 SRSF3_MOUSE	Serine/arginine-rich splicing factor 3 OS=Mus musculus GN=Srsf3 PE=1 SV=1	-0.5	-0.86
sp Q61656 DDX5_MOUSE	Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=Ddx5 PE=1 SV=2	-0.5	-0.41
sp P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	-0.49	-0.26
sp P62242 RS8_MOUSE	40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	-0.49	-0.53
sp Q61753 SERA_MOUSE	D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	-0.49	-0.45
sp P15864 H12_MOUSE	Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	-0.48	-0.77
sp P43277 H13_MOUSE	Histone H1.3 OS=Mus musculus GN=Hist1h1d PE=1 SV=2	-0.48	-0.77
sp Q9CQA3 DHBS_MOUSE	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=Sdhb PE=1 SV=1	-0.48	-0.9
sp P42932 TCPQ_MOUSE	T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3	-0.46	-0.18
sp P51881 ADT2_MOUSE	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	-0.46	-0.71
sp P21550 ENOB_MOUSE	Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	-0.45	-0.13
sp P50580 PA2G4_MOUSE	Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3	-0.45	-0.08
sp Q9CPR4 RL17_MOUSE	60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=2 SV=3	-0.45	-0.45
sp A2AQ07 TBB1_MOUSE	Tubulin beta-1 chain OS=Mus musculus GN=Tubb1 PE=1 SV=1	-0.44	-0.73
sp P10639 THIO_MOUSE	Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3	-0.44	-0.01
sp Q09014 NCF1_MOUSE	Neutrophil cytosol factor 1 OS=Mus musculus GN=Ncf1 PE=1 SV=3	-0.44	-0.39
sp Q60875 ARHG2_MOUSE	Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 PE=1 SV=4	-0.44	-0.33
sp Q922F4 TBB6_MOUSE	Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	-0.44	-0.69
sp Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy chain 1	-0.44	-0.66

	OS=Mus musculus GN=Dync1h1 PE=1 SV=2		
sp P62717 RL18A_MOUSE	60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	-0.43	-0.59
sp Q6PB66 LPPRC_MOUSE	Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrprrc PE=1 SV=2	-0.43	-0.48
sp P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	-0.42	-1.02
sp P47757 CAPZB_MOUSE	F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb PE=1 SV=3	-0.42	-10
sp P62918 RL8_MOUSE	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	-0.42	-0.47
sp P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	-0.41	-0.32
sp P47915 RL29_MOUSE	60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2	-0.41	-0.06
sp P62259 1433E_MOUSE	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	-0.41	-0.04
sp P62702 RS4X_MOUSE	40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	-0.41	-0.56
sp O70250 PGAM2_MOUSE	Phosphoglycerate mutase 2 OS=Mus musculus GN=Pgam2 PE=1 SV=3	-0.39	-0.1
sp P62900 RL31_MOUSE	60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=2 SV=1	-0.39	-0.46
sp Q6ZWN5 RS9_MOUSE	40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	-0.39	-0.53
sp Q9CR57 RL14_MOUSE	60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=2 SV=3	-0.39	-0.39
sp P25444 RS2_MOUSE	40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	-0.38	-0.44
sp Q9DB20 ATPO_MOUSE	ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	-0.38	-0.46
sp P17183 ENOG_MOUSE	Gamma-enolase OS=Mus musculus GN=Eno2 PE=1 SV=2	-0.37	-0.18
sp Q6PDM2 SRSF1_MOUSE	Serine/arginine-rich splicing factor 1 OS=Mus musculus GN=Srsf1 PE=1 SV=3	-0.37	-10
sp P14069 S10A6_MOUSE	Protein S100-A6 OS=Mus musculus GN=S100a6 PE=1 SV=3	-0.35	-0.07
sp P57776 EF1D_MOUSE	Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3	-0.35	-0.14
sp P12970 RL7A_MOUSE	60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	-0.34	-0.54
sp P47963 RL13_MOUSE	60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	-0.34	-0.45
sp Q8BP67 RL24_MOUSE	60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=2 SV=2	-0.34	-0.65
sp Q9DBT5 AMPD2_MOUSE	AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1	-0.34	-0.37
sp P80316 TCPE_MOUSE	T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	-0.33	-0.35
sp Q9CQQ7 AT5F1_MOUSE	ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	-0.33	-0.76

sp P19253 RL13A_MOUSE	60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	-0.32	-0.51
sp Q3V132 ADT4_MOUSE	ADP/ATP translocase 4 OS=Mus musculus GN=Slc25a31 PE=2 SV=1	-0.32	-0.63
sp Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	-0.32	-10
sp P63323 RS12_MOUSE	40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2	-0.31	-0.24
sp Q9CXW4 RL11_MOUSE	60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4	-0.3	-0.51
sp P80313 TCPH_MOUSE	T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	-0.29	-0.4
sp Q9D1R9 RL34_MOUSE	60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=3 SV=2	-0.29	-0.43
sp Q7TPV4 MBB1A_MOUSE	Myb-binding protein 1A OS=Mus musculus GN=Mybbp1a PE=1 SV=2	-0.28	-0.27
sp P60122 RUVB1_MOUSE	RuvB-like 1 OS=Mus musculus GN=Ruvbl1 PE=1 SV=1	-0.27	-0.27
sp P61089 UBE2N_MOUSE	Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1	-0.27	-0.15
sp P62849 RS24_MOUSE	40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1	-0.27	-1.18
sp Q8K2B3 DHSA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	-0.27	-0.63
sp P99027 RLA2_MOUSE	60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3	-0.26	-0.14
sp Q64433 CH10_MOUSE	10 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspe1 PE=1 SV=2	-0.26	-0.09
sp Q91VC3 IF4A3_MOUSE	Eukaryotic initiation factor 4A-III OS=Mus musculus GN=Eif4a3 PE=2 SV=3	-0.26	-0.35
sp Q9CZM2 RL15_MOUSE	60S ribosomal protein L15 OS=Mus musculus GN=Rpl15 PE=2 SV=4	-0.26	-0.46
sp P35979 RL12_MOUSE	60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	-0.25	-0.06
sp P62751 RL23A_MOUSE	60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=1 SV=1	-0.25	-0.23
sp Q64524 H2B2E_MOUSE	Histone H2B type 2-E OS=Mus musculus GN=Hist2h2be PE=1 SV=3	-0.25	-10
sp Q8CGP0 H2B3B_MOUSE	Histone H2B type 3-B OS=Mus musculus GN=Hist3h2bb PE=1 SV=3	-0.25	-10
sp Q9D2U9 H2B3A_MOUSE	Histone H2B type 3-A OS=Mus musculus GN=Hist3h2ba PE=1 SV=3	-0.25	-10
sp Q9D6R2 IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	-0.25	-0.54
sp Q9R0Q7 TEBP_MOUSE	Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1	-0.25	-0.01
sp Q9DAS9 GBG12_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Mus musculus GN=Gng12 PE=1 SV=3	-0.23	-1.52
sp P26443 DHE3_MOUSE	Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	-0.22	-0.47

sp P10853 H2B1F_MOUSE	Histone H2B type 1-F/J/L OS=Mus musculus GN=Hist1h2bf PE=1 SV=2	-0.21	-0.53
sp P10854 H2B1M_MOUSE	Histone H2B type 1-M OS=Mus musculus GN=Hist1h2bm PE=1 SV=2	-0.21	-0.53
sp P70696 H2B1A_MOUSE	Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba PE=2 SV=3	-0.21	-10
sp Q64475 H2B1B_MOUSE	Histone H2B type 1-B OS=Mus musculus GN=Hist1h2bb PE=1 SV=3	-0.21	-0.53
sp Q64478 H2B1H_MOUSE	Histone H2B type 1-H OS=Mus musculus GN=Hist1h2bh PE=1 SV=3	-0.21	-0.53
sp Q64525 H2B2B_MOUSE	Histone H2B type 2-B OS=Mus musculus GN=Hist2h2bb PE=1 SV=3	-0.21	-0.53
sp Q6ZWY9 H2B1C_MOUSE	Histone H2B type 1-C/E/G OS=Mus musculus GN=Hist1h2bc PE=1 SV=3	-0.21	-0.53
sp Q8CGP1 H2B1K_MOUSE	Histone H2B type 1-K OS=Mus musculus GN=Hist1h2bk PE=1 SV=3	-0.21	-0.53
sp Q8CGP2 H2B1P_MOUSE	Histone H2B type 1-P OS=Mus musculus GN=Hist1h2bp PE=1 SV=3	-0.21	-0.53
sp Q9D8N0 EF1G_MOUSE	Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3	-0.21	-0.03
sp P10630 IF4A2_MOUSE	Eukaryotic initiation factor 4A-II OS=Mus musculus GN=Eif4a2 PE=2 SV=2	-0.2	-0.28
sp P53657 KPYR_MOUSE	Pyruvate kinase isozymes R/L OS=Mus musculus GN=Pklr PE=2 SV=1	-0.2	-0.27
sp P60843 IF4A1_MOUSE	Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=2 SV=1	-0.2	-0.3
sp P80318 TCPG_MOUSE	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	-0.2	-0.31
sp P84099 RL19_MOUSE	60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	-0.2	-0.27
sp P48678 LMNA_MOUSE	Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	-0.19	-0.16
sp P62858 RS28_MOUSE	40S ribosomal protein S28 OS=Mus musculus GN=Rps28 PE=2 SV=1	-0.18	-0.09
sp P35980 RL18_MOUSE	60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=3	-0.17	-0.45
sp P70372 ELAV1_MOUSE	ELAV-like protein 1 OS=Mus musculus GN=Elavl1 PE=1 SV=2	-0.17	-0.39
sp P52480 KPYM_MOUSE	Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	-0.16	-0.32
sp P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	-0.15	-0.24
sp P14148 RL7_MOUSE	60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	-0.15	-0.53
sp P62267 RS23_MOUSE	40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3	-0.15	-0.42
sp P17710 HXK1_MOUSE	Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3	-0.14	-0.45
sp Q9D1Q4 DPM3_MOUSE	Dolichol-phosphate mannosyltransferase subunit 3 OS=Mus musculus GN=Dpm3 PE=2 SV=1	-0.14	-0.98
sp Q9ERK4 XPO2_MOUSE	Exportin-2 OS=Mus musculus GN=Cse1l PE=2 SV=1	-0.14	-0.24

sp Q9R1P4 PSA1_MOUSE	Proteasome subunit alpha type-1 OS=Mus musculus GN=Psm1 PE=1 SV=1	-0.14	-0.04
sp O08749 DLDH_MOUSE	Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Did PE=1 SV=2	-0.13	-0.12
sp P41105 RL28_MOUSE	60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	-0.13	-0.58
sp P62264 RS14_MOUSE	40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	-0.13	-0.31
sp P62754 RS6_MOUSE	40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	-0.12	-0.61
sp Q61233 PLSL_MOUSE	Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4	-0.12	-0.08
sp P14733 LMNB1_MOUSE	Lamin-B1 OS=Mus musculus GN=Lmnb1 PE=1 SV=3	-0.11	-0.48
sp P17751 TPIS_MOUSE	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	-0.11	-0.01
sp Q14C59 TM11B_MOUSE	Transmembrane protease serine 11B OS=Mus musculus GN=Tmprss11b PE=2 SV=2	-0.1	-0.22
sp Q61699 HS105_MOUSE	Heat shock protein 105 kDa OS=Mus musculus GN=Hsp1 PE=1 SV=2	-0.1	-0.12
sp P18760 COF1_MOUSE	Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3	-0.09	-0.2
sp P60764 RAC3_MOUSE	Ras-related C3 botulinum toxin substrate 3 OS=Mus musculus GN=Rac3 PE=1 SV=1	-0.09	-0.34
sp P63001 RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	-0.09	-0.34
sp P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1	-0.09	-0.05
sp P68510 1433F_MOUSE	14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	-0.09	-0.1
sp P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	-0.07	-0.32
sp O89053 COR1A_MOUSE	Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5	-0.05	-0.75
sp Q8VDD5 MYH9_MOUSE	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-0.05	-0.55
sp Q921M3 SF3B3_MOUSE	Splicing factor 3B subunit 3 OS=Mus musculus GN=Sf3b3 PE=2 SV=1	-0.04	-0.17
sp P14115 RL27A_MOUSE	60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=5	-0.02	-0.49
sp P22752 H2A1_MOUSE	Histone H2A type 1 OS=Mus musculus GN=Hist1h2ab PE=1 SV=3	-0.01	-0.15
sp Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac PE=1 SV=3	-0.01	-0.15
sp Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus musculus GN=Hist2h2aa1 PE=1 SV=3	-0.01	-0.15
sp Q8BFU2 H2A3_MOUSE	Histone H2A type 3 OS=Mus musculus GN=Hist3h2a PE=1 SV=3	-0.01	-0.15
sp Q8CGP5 H2A1F_MOUSE	Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	-0.01	-0.15
sp Q8CGP6 H2A1H_MOUSE	Histone H2A type 1-H OS=Mus musculus	-0.01	-0.15

	GN=Hist1h2ah PE=1 SV=3		
sp Q8CGP7 H2A1K_MOUSE	Histone H2A type 1-K OS=Mus musculus GN=Hist1h2ak PE=1 SV=3	-0.01	-0.15
sp Q8R1M2 H2AJ_MOUSE	Histone H2A.J OS=Mus musculus GN=H2afj PE=2 SV=1	-0.01	-0.15

Table 8. List of *Echinacea* extract 7 induced proteins consistently in experiment 2 and 1.

Sequence Id	Sequence Name	<i>Echinacea</i> extract 7 Ratio EXPT-1	<i>Echinacea</i> extract 7 Ratio EXPT-2
sp Q9WUM4 COR1C_MOUSE	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	2.13	1.65
sp P62852 RS25_MOUSE	40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=2 SV=1	0.87	0.04
sp P13020 GELS_MOUSE	Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	0.56	0.58
sp Q9JMH6 TRXR1_MOUSE	Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txnrd1 PE=1 SV=3	0.55	1.17
sp P25444 RS2_MOUSE	40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	0.48	0.03
sp Q6P1B1 XPP1_MOUSE	Xaa-Pro aminopeptidase 1 OS=Mus musculus GN=Xpnpep1 PE=2 SV=1	0.44	0.57
sp P97324 G6PD2_MOUSE	Glucose-6-phosphate 1-dehydrogenase 2 OS=Mus musculus GN=G6pd2 PE=2 SV=3	0.39	0.58
sp Q93092 TALDO_MOUSE	Transaldolase OS=Mus musculus GN=Taldo1 PE=1 SV=2	0.38	0.37
sp Q9DBJ1 PGAM1_MOUSE	Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3	0.38	0.5
sp Q00612 G6PD1_MOUSE	Glucose-6-phosphate 1-dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3	0.36	0.53
sp P24452 CAPG_MOUSE	Macrophage-capping protein OS=Mus musculus GN=Capg PE=1 SV=2	0.35	0.05
sp Q9CR16 PPID_MOUSE	Peptidyl-prolyl cis-trans isomerase D OS=Mus musculus GN=Ppid PE=1 SV=3	0.35	0.03
sp P16125 LDHB_MOUSE	L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2	0.34	2.94
sp Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	0.34	0.42
sp O70250 PGAM2_MOUSE	Phosphoglycerate mutase 2 OS=Mus musculus GN=Pgam2 PE=1 SV=3	0.33	0.33
sp P48036 ANXA5_MOUSE	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	0.31	0.03
sp P06745 G6PI_MOUSE	Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=1 SV=4	0.3	0.51

sp P17751 TPIS_MOUSE	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	0.3	0.23
sp P18572 BASI_MOUSE	Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	0.3	0.01
sp P05201 AATC_MOUSE	Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Got1 PE=1 SV=3	0.29	0.12
sp O08709 PRDX6_MOUSE	Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3	0.28	0.78
sp P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2	0.28	0.06
sp Q60864 STIP1_MOUSE	Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1	0.27	0.23
sp P00342 LDHC_MOUSE	L-lactate dehydrogenase C chain OS=Mus musculus GN=Ldhc PE=1 SV=2	0.26	2.94
sp P09041 PGK2_MOUSE	Phosphoglycerate kinase 2 OS=Mus musculus GN=Pgk2 PE=1 SV=4	0.26	1.7
sp P16110 LEG3_MOUSE	Galectin-3 OS=Mus musculus GN=Lgals3 PE=1 SV=3	0.26	0.4
sp P35700 PRDX1_MOUSE	Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	0.26	1.32
sp P60122 RUVB1_MOUSE	RuvB-like 1 OS=Mus musculus GN=Ruvbl1 PE=1 SV=1	0.26	0.1
sp Q9JII6 AK1A1_MOUSE	Alcohol dehydrogenase [NADP+] OS=Mus musculus GN=Akr1a1 PE=1 SV=3	0.26	0.35
sp P60766 CDC42_MOUSE	Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2	0.25	0.54
sp P17879 HS71B_MOUSE	Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3	0.24	0.52
sp P57776 EF1D_MOUSE	Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3	0.24	0.11
sp P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	0.24	0.42
sp Q61696 HS71A_MOUSE	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	0.24	0.52
sp P14152 MDHC_MOUSE	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	0.23	0.12
sp Q9R1P0 PSA4_MOUSE	Proteasome subunit alpha type-4 OS=Mus musculus GN=Psm4 PE=1 SV=1	0.23	0.37
sp P35278 RAB5C_MOUSE	Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	0.22	0.23
sp P37040 NCPR_MOUSE	NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	0.22	0.18
sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=1 SV=1	0.21	0.05
sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	0.21	0.05
sp P21550 ENOB_MOUSE	Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	0.21	1.23
sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=Rps27a PE=1 SV=2	0.21	0.05
sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40	0.21	0.05

	OS=Mus musculus GN=Uba52 PE=1 SV=2		
sp P70296 PEBP1_MOUSE	Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3	0.21	0.01
sp P17183 ENOG_MOUSE	Gamma-enolase OS=Mus musculus GN=Eno2 PE=1 SV=2	0.2	0.42
sp P26883 FKB1A_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=2 SV=2	0.2	0.19
sp P09411 PGK1_MOUSE	Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4	0.19	0.56
sp P50580 PA2G4_MOUSE	Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3	0.19	0.18
sp P40124 CAP1_MOUSE	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	0.17	0.53
sp P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	0.16	0.02
sp Q7TMK9 HNRPQ_MOUSE	Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncrip PE=1 SV=2	0.16	0.16
sp Q9DCD0 6PGD_MOUSE	6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=2 SV=3	0.16	0.37
sp P06801 MAOX_MOUSE	NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=2	0.15	0.04
sp P07901 HS90A_MOUSE	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	0.15	0.27
sp P15532 NDKA_MOUSE	Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 PE=1 SV=1	0.15	0.02
sp Q61937 NPM_MOUSE	Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	0.15	0.15
sp Q9ER72 SYCC_MOUSE	Cysteinyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2	0.15	0.32
sp P03995 GFAP_MOUSE	Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4	0.14	1.8
sp Q01768 NDKB_MOUSE	Nucleoside diphosphate kinase B OS=Mus musculus GN=Nme2 PE=1 SV=1	0.13	0.02
sp Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	0.13	0.28
sp P63325 RS10_MOUSE	40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1	0.12	0.49
sp Q922Q8 LRC59_MOUSE	Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=2 SV=1	0.12	0.26
sp Q9R1P4 PSA1_MOUSE	Proteasome subunit alpha type-1 OS=Mus musculus GN=Pma1 PE=1 SV=1	0.12	0.5
sp P40142 TKT_MOUSE	Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1	0.11	0.32
sp Q9EQU5 SET_MOUSE	Protein SET OS=Mus musculus GN=Set PE=1 SV=1	0.11	0.3
sp P05064 ALDOA_MOUSE	Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	0.1	0.47

sp P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	0.1	0.24
sp Q9JHU9 INO1_MOUSE	Inositol-3-phosphate synthase 1 OS=Mus musculus GN=Isyna1 PE=2 SV=1	0.1	0.19
sp P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	0.09	0.73
sp P50396 GDIA_MOUSE	Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3	0.09	0.76
sp P53657 KPYR_MOUSE	Pyruvate kinase isozymes R/L OS=Mus musculus GN=Pklr PE=2 SV=1	0.09	0.12
sp P62962 PROF1_MOUSE	Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	0.09	0.36
sp P35979 RL12_MOUSE	60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	0.08	0.32
sp P62270 RS18_MOUSE	40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=2 SV=3	0.08	0.11
sp P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1	0.08	0.24
sp Q78PY7 SND1_MOUSE	Staphylococcal nuclease domain- containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1	0.08	0.25
sp Q8QZY1 EIF3L_MOUSE	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1	0.08	0.16
sp Q9CWH6 PSA7L_MOUSE	Proteasome subunit alpha type-7-like OS=Mus musculus GN=Pasma8 PE=2 SV=1	0.08	0.24
sp Q9Z2U0 PSA7_MOUSE	Proteasome subunit alpha type-7 OS=Mus musculus GN=Pasma7 PE=1 SV=1	0.08	0.24
sp P62259 1433E_MOUSE	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	0.07	0.22
sp P52480 KPYM_MOUSE	Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	0.05	0.43
sp P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	0.04	0.46
sp P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	0.04	0.56
sp P17156 HSP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2	0.04	0.43
sp P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	0.04	0.74
sp P58771 TPM1_MOUSE	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	0.04	0.42
sp P58774 TPM2_MOUSE	Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1	0.04	0.42
sp P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	0.04	0.4
sp Q8BGQ7 SYAC_MOUSE	Alanyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1	0.04	0.46
sp Q9CQV8 1433B_MOUSE	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	0.04	0.18

sp P58252 EF2_MOUSE	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	0.03	0.38
sp P62274 RS29_MOUSE	40S ribosomal protein S29 OS=Mus musculus GN=Rps29 PE=2 SV=2	0.03	0.37
sp P63001 RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	0.03	0.14
sp Q61598 GDIB_MOUSE	Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	0.03	0.25
sp O08810 U5S1_MOUSE	116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1	0.02	0.37
sp P63101 1433Z_MOUSE	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	0.02	0.13
sp P68510 1433F_MOUSE	14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	0.02	0.13
sp Q501J6 DDX17_MOUSE	Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	0.02	0.1
sp Q6ZWX6 IF2A_MOUSE	Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3	0.02	0.14
sp P26041 MOES_MOUSE	Moesin OS=Mus musculus GN=Msn PE=1 SV=3	0.01	0.49

Table 9. List of *Echinacea* extract 7 Suppressed proteins consistently in experiment 2 and 1.

Sequence Id	Sequence Name	<i>Echinacea</i> extract 7 Ratio-Expt-2	<i>Echinacea</i> extract 7 Ratio-Expt-1
sp O08528 HXK2_MOUSE	Hexokinase-2 OS=Mus musculus GN=Hk2 PE=1 SV=1	-10	-0.07
sp O08547 SC22B_MOUSE	Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3	-10	-10
sp O08756 HCD2_MOUSE	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17b10 PE=1 SV=4	-10	-0.09
sp O08788 DCTN1_MOUSE	Dynactin subunit 1 OS=Mus musculus GN=Dctn1 PE=1 SV=3	-10	-0.57
sp O09167 RL21_MOUSE	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	-10	-0.14
sp O54879 HMGB3_MOUSE	High mobility group protein B3 OS=Mus musculus GN=Hmgb3 PE=2 SV=3	-10	-10
sp O55143 AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	-10	-0.25
sp O70133 DHX9_MOUSE	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	-10	-0.65
sp O70152 DPM1_MOUSE	Dolichol-phosphate mannosyltransferase OS=Mus musculus GN=Dpm1 PE=2 SV=1	-10	-0.14

sp O88531 PPT1_MOUSE	Palmitoyl-protein thioesterase 1 OS=Mus musculus GN=Ppt1 PE=2 SV=2	-10	-0.47
sp P00405 COX2_MOUSE	Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1	-10	-0.17
sp P01895 HA1Y_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus GN=H2-D1 PE=2 SV=1	-10	-0.11
sp P01896 HA1Z_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus PE=1 SV=1	-10	-0.11
sp P01900 HA12_MOUSE	H-2 class I histocompatibility antigen, D-D alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=1	-10	-0.11
sp P01942 HBA_MOUSE	Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2	-10	-10
sp P03930 ATP8_MOUSE	ATP synthase protein 8 OS=Mus musculus GN=Mtatp8 PE=1 SV=1	-10	-0.56
sp P05555 ITAM_MOUSE	Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=2	-10	-0.17
sp P06800 PTPRC_MOUSE	Receptor-type tyrosine-protein phosphatase C OS=Mus musculus GN=Ptprc PE=1 SV=3	-10	-0.23
sp P07724 ALBU_MOUSE	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	-10	-10
sp P08553 NFM_MOUSE	Neurofilament medium polypeptide OS=Mus musculus GN=Nefm PE=1 SV=4	-10	-10
sp P10404 ENV1_MOUSE	MLV-related proviral Env polyprotein OS=Mus musculus PE=2 SV=3	-10	-0.05
sp P11370 ENV2_MOUSE	Retrovirus-related Env polyprotein from Fv-4 locus OS=Mus musculus GN=Fv4 PE=1 SV=2	-10	-0.01
sp P15331 PERI_MOUSE	Peripherin OS=Mus musculus GN=Prph PE=1 SV=2	-10	-10
sp P19246 NFH_MOUSE	Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE=1 SV=3	-10	-10
sp P23492 PNPH_MOUSE	Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2	-10	-10
sp P26516 PSD7_MOUSE	26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	-10	-0.04
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcks1 PE=1 SV=2	-10	-10
sp P29387 GBB4_MOUSE	Guanine nucleotide-binding protein subunit beta-4 OS=Mus musculus GN=Gnb4 PE=2 SV=4	-10	-10
sp P30416 FKBP4_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus GN=Fkbp4 PE=1 SV=5	-10	-0.03
sp P31001 DESM_MOUSE	Desmin OS=Mus musculus GN=Des PE=1 SV=3	-10	-10
sp P42225 STAT1_MOUSE	Signal transducer and activator of transcription 1 OS=Mus musculus GN=Stat1 PE=1 SV=1	-10	-10
sp P46638 RB11B_MOUSE	Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3	-10	-0.55

sp P46660 AINX_MOUSE	Alpha-internexin OS=Mus musculus GN=Ina PE=1 SV=2	-10	-10
sp P47754 CAZA2_MOUSE	F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=Capza2 PE=1 SV=3	-10	-0.03
sp P51410 RL9_MOUSE	60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=2 SV=2	-10	-0.49
sp P53986 MOT1_MOUSE	Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	-10	-0.33
sp P54987 IRG1_MOUSE	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	-10	-10
sp P61358 RL27_MOUSE	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=2 SV=2	-10	-0.15
sp P62301 RS13_MOUSE	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	-10	-0.1
sp P62492 RB11A_MOUSE	Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a PE=1 SV=3	-10	-0.55
sp P62830 RL23_MOUSE	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	-10	-0.31
sp P62849 RS24_MOUSE	40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1	-10	-0.38
sp P62880 GBB2_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Mus musculus GN=Gnb2 PE=1 SV=3	-10	-0.01
sp P62900 RL31_MOUSE	60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=2 SV=1	-10	-0.25
sp P68040 GBLP_MOUSE	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3	-10	-0.28
sp P86048 RL10L_MOUSE	60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=1	-10	-0.27
sp P97310 MCM2_MOUSE	DNA replication licensing factor MCM2 OS=Mus musculus GN=Mcm2 PE=1 SV=3	-10	-0.58
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	-10	-10
sp Q3THS6 METK2_MOUSE	S-adenosylmethionine synthase isoform type-2 OS=Mus musculus GN=Mat2a PE=2 SV=2	-10	-0.22
sp Q3U9G9 LBR_MOUSE	Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	-10	-0.41
sp Q3UM45 PP1R7_MOUSE	Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2	-10	-0.1
sp Q3V3R1 C1TM_MOUSE	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Mus musculus GN=Mthfd1l PE=1 SV=2	-10	-0.13
sp Q5SW19 K0664_MOUSE	Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 PE=2 SV=2	-10	-0.01
sp Q5SWU9 ACACA_MOUSE	Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	-10	-0.59
sp Q60668 HNRPD_MOUSE	Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=Hnrpd PE=1 SV=2	-10	-0.08
sp Q60875 ARHG2_MOUSE	Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 PE=1 SV=4	-10	-0.24

sp Q60931 VDAC3_MOUSE	Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	-10	-0.11
sp Q60932 VDAC1_MOUSE	Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	-10	-0.13
sp Q61011 GBB3_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Mus musculus GN=Gnb3 PE=1 SV=2	-10	-10
sp Q61029 LAP2B_MOUSE	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4	-10	-0.02
sp Q61335 BAP31_MOUSE	B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=3	-10	-0.02
sp Q61820 RANT_MOUSE	GTP-binding nuclear protein Ran, testis-specific isoform OS=Mus musculus GN=Rasl2-9 PE=2 SV=1	-10	-0.12
sp Q62351 TFR1_MOUSE	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	-10	-0.2
sp Q62433 NDRG1_MOUSE	Protein NDRG1 OS=Mus musculus GN=Ndr1 PE=1 SV=1	-10	-10
sp Q64436 ATP4A_MOUSE	Potassium-transporting ATPase alpha chain 1 OS=Mus musculus GN=Atp4a PE=1 SV=3	-10	-0.19
sp Q64514 TPP2_MOUSE	Tripeptidyl-peptidase 2 OS=Mus musculus GN=Tpp2 PE=2 SV=3	-10	-0.64
sp Q64516 GLPK_MOUSE	Glycerol kinase OS=Mus musculus GN=Gk PE=2 SV=2	-10	-10
sp Q64518 AT2A3_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Mus musculus GN=Atp2a3 PE=2 SV=3	-10	-0.25
sp Q64674 SPEE_MOUSE	Spermidine synthase OS=Mus musculus GN=Srm PE=2 SV=1	-10	-0.02
sp Q68FL6 SYMC_MOUSE	Methionyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Mars PE=2 SV=1	-10	-0.1
sp Q69ZN7 MYOF_MOUSE	Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	-10	-10
sp Q6PDI5 ECM29_MOUSE	Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=3	-10	-0.09
sp Q6ZQ38 CAND1_MOUSE	Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	-10	-0.26
sp Q6ZWU9 RS27_MOUSE	40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3	-10	-0.8
sp Q6ZWW3 RL10_MOUSE	60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3	-10	-0.27
sp Q6ZWY3 RS27L_MOUSE	40S ribosomal protein S27-like OS=Mus musculus GN=Rps271 PE=2 SV=3	-10	-0.89
sp Q76MZ3 2AAA_MOUSE	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3	-10	-0.01
sp Q7M6Y3 PICA_MOUSE	Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus	-10	-10

	GN=Picalm PE=1 SV=1		
sp Q7TQI3 OTUB1_MOUSE	Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2	-10	-0.24
sp Q8BG32 PSD11_MOUSE	26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psm11 PE=1 SV=3	-10	-10
sp Q8BH04 PCKGM_MOUSE	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=2 SV=1	-10	-10
sp Q8BKC5 IPO5_MOUSE	Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	-10	-0.07
sp Q8BMJ2 SYLC_MOUSE	Leucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Lars PE=2 SV=2	-10	-0.27
sp Q8BMK4 CKAP4_MOUSE	Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=2 SV=2	-10	-10
sp Q8BP47 SYNC_MOUSE	Asparaginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Nars PE=1 SV=2	-10	-0.22
sp Q8BWY3 ERF1_MOUSE	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Elf1 PE=1 SV=4	-10	-0.01
sp Q8K2Q2 GSTO2_MOUSE	Glutathione S-transferase omega-2 OS=Mus musculus GN=Gsto2 PE=2 SV=1	-10	-10
sp Q8K4Z3 AIBP_MOUSE	Apolipoprotein A-I-binding protein OS=Mus musculus GN=Apoa1bp PE=1 SV=1	-10	-0.19
sp Q8R0W0 EPIPL_MOUSE	Epiplakin OS=Mus musculus GN=Eppk1 PE=1 SV=2	-10	-0.13
sp Q8R429 AT2A1_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1	-10	-0.35
sp Q8VCT3 AMPB_MOUSE	Aminopeptidase B OS=Mus musculus GN=Rnpep PE=2 SV=2	-10	-0.42
sp Q8VDJ3 VIGLN_MOUSE	Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	-10	-0.05
sp Q8VDP4 K1967_MOUSE	Protein KIAA1967 homolog OS=Mus musculus PE=1 SV=2	-10	-0.05
sp Q91V92 ACLY_MOUSE	ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	-10	-0.37
sp Q91VR2 ATPG_MOUSE	ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	-10	-0.73
sp Q921E2 RAB31_MOUSE	Ras-related protein Rab-31 OS=Mus musculus GN=Rab31 PE=1 SV=1	-10	-0.06
sp Q921F2 TADBP_MOUSE	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	-10	-10
sp Q921M7 FA49B_MOUSE	Protein FAM49B OS=Mus musculus GN=Fam49b PE=2 SV=1	-10	-0.3
sp Q99JY0 ECHB_MOUSE	Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	-10	-10
sp Q99KC8 VMA5A_MOUSE	von Willebrand factor A domain-containing protein 5A OS=Mus musculus GN=Vwa5a PE=1 SV=2	-10	-0.18
sp Q99LC5 ETFA_MOUSE	Electron transfer flavoprotein subunit alpha,	-10	-0.29

	mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2		
sp Q99LX0 PARK7_MOUSE	Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	-10	-0.08
sp Q9CQ65 MTAP_MOUSE	S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=2 SV=1	-10	-10
sp Q9CQI6 COTL1_MOUSE	Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3	-10	-0.22
sp Q9CQR2 RS21_MOUSE	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=2 SV=1	-10	-0.07
sp Q9CR62 M2OM_MOUSE	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus GN=Slc25a11 PE=1 SV=3	-10	-0.44
sp Q9CRB9 CHCH3_MOUSE	Coiled-coil-helix-coiled-coil-helix domain- containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1 SV=1	-10	-0.34
sp Q9CW03 SMC3_MOUSE	Structural maintenance of chromosomes protein 3 OS=Mus musculus GN=Smc3 PE=1 SV=2	-10	-0.62
sp Q9CWY9 RIP_MOUSE	RPA-interacting protein OS=Mus musculus GN=Rpain PE=2 SV=1	-10	-10
sp Q9CXT8 MPPB_MOUSE	Mitochondrial-processing peptidase subunit beta OS=Mus musculus GN=Pmpcb PE=2 SV=1	-10	-0.3
sp Q9CXW3 CYBP_MOUSE	Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	-10	-0.02
sp Q9CY64 BIEA_MOUSE	Biliverdin reductase A OS=Mus musculus GN=Blvra PE=2 SV=1	-10	-10
sp Q9CZY3 UB2V1_MOUSE	Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=1 SV=1	-10	-0.06
sp Q9D0E1 HNRPM_MOUSE	Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrpm PE=1 SV=3	-10	-0.07
sp Q9D1R9 RL34_MOUSE	60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=3 SV=2	-10	-0.23
sp Q9D2M8 UB2V2_MOUSE	Ubiquitin-conjugating enzyme E2 variant 2 OS=Mus musculus GN=Ube2v2 PE=2 SV=4	-10	-0.06
sp Q9D3D9 ATPD_MOUSE	ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5d PE=1 SV=1	-10	-0.12
sp Q9DBG6 RPN2_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	-10	-0.2
sp Q9DCC8 TOM20_MOUSE	Mitochondrial import receptor subunit TOM20 homolog OS=Mus musculus GN=Tom20 PE=1 SV=1	-10	-10
sp Q9DCH4 EIF3F_MOUSE	Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Eif3f PE=1 SV=2	-10	-0.29
sp Q9EPU0 RENT1_MOUSE	Regulator of nonsense transcripts 1 OS=Mus musculus GN=Upf1 PE=1 SV=2	-10	-0.11
sp Q9EQP2 EHD4_MOUSE	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	-10	-0.74
sp Q9ES52 SHIP1_MOUSE	Phosphatidylinositol-3,4,5-trisphosphate 5- phosphatase 1 OS=Mus musculus	-10	-0.26

	GN=Inpp5d PE=1 SV=2		
sp Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2	-10	-0.3
sp Q9JIK5 DDX21_MOUSE	Nucleolar RNA helicase 2 OS=Mus musculus GN=Ddx21 PE=1 SV=3	-10	-0.29
sp Q9JJ28 FLII_MOUSE	Protein flightless-1 homolog OS=Mus musculus GN=Flil PE=1 SV=1	-10	-0.14
sp Q9JM76 ARPC3_MOUSE	Actin-related protein 2/3 complex subunit 3 OS=Mus musculus GN=Arpc3 PE=1 SV=3	-10	-0.03
sp Q9JMA1 UBP14_MOUSE	Ubiquitin carboxyl-terminal hydrolase 14 OS=Mus musculus GN=Usp14 PE=1 SV=3	-10	-0.06
sp Q9QXX4 CMC2_MOUSE	Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1	-10	-0.21
sp Q9QYJ0 DNJA2_MOUSE	DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1	-10	-10
sp Q9QZD8 DIC_MOUSE	Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=2 SV=2	-10	-0.09
sp Q9R1Q7 PLP2_MOUSE	Proteolipid protein 2 OS=Mus musculus GN=Plp2 PE=2 SV=1	-10	-0.09
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	-10	-10
sp Q9VVK4 EHD1_MOUSE	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	-10	-10
sp Q9Z110 P5CS_MOUSE	Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=Aldh18a1 PE=2 SV=2	-10	-0.47
sp Q9Z1Q5 CLIC1_MOUSE	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	-10	-0.05
sp Q9Z2I8 SUCB2_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Suc1g2 PE=2 SV=3	-10	-10
sp A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn PE=1 SV=1	-9.52	-10
sp Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	-3.35	-1.24
sp P25206 MCM3_MOUSE	DNA replication licensing factor MCM3 OS=Mus musculus GN=Mcm3 PE=1 SV=2	-3.06	-0.41
sp Q8CGK3 LONM_MOUSE	Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE=1 SV=2	-2.3	-0.12
sp P80317 TCPZ_MOUSE	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	-2.04	-0.18
sp P63038 CH60_MOUSE	60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	-2	-0.12
sp Q8VCH0 THIKB_MOUSE	3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1	-1.96	-0.06
sp Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	-1.91	-0.21
sp Q91VD9 NDUS1_MOUSE	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2	-1.79	-0.05

sp Q9WV27 AT1A4_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Mus musculus GN=Atp1a4 PE=1 SV=3	-1.74	-0.21
sp Q9DB77 QCR2_MOUSE	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	-1.66	-0.35
sp Q9D0K2 SCOT1_MOUSE	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial OS=Mus musculus GN=Oxct1 PE=1 SV=1	-1.59	-0.18
sp Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	-1.55	-0.28
sp Q9CZ13 QCR1_MOUSE	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2	-1.48	-0.3
sp Q6PIE5 AT1A2_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Mus musculus GN=Atp1a2 PE=1 SV=1	-1.44	-0.19
sp Q8VDN2 AT1A1_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	-1.34	-0.2
sp Q9DCX2 ATP5H_MOUSE	ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	-1.32	-0.34
sp P62806 H4_MOUSE	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	-1.3	-0.08
sp P54071 IDHP_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	-1.27	-0.23
sp P56480 ATPB_MOUSE	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	-1.26	-0.34
sp Q922D8 C1TC_MOUSE	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4	-1.2	-0.93
sp P68433 H31_MOUSE	Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	-1.17	-10
sp P84228 H32_MOUSE	Histone H3.2 OS=Mus musculus GN=Hist1h3b PE=1 SV=2	-1.17	-10
sp P84244 H33_MOUSE	Histone H3.3 OS=Mus musculus GN=H3f3a PE=1 SV=2	-1.17	-10
sp Q99MN1 SYK_MOUSE	Lysyl-tRNA synthetase OS=Mus musculus GN=Kars PE=1 SV=1	-1.17	-10
sp Q9JKR6 HYOU1_MOUSE	Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1	-1.17	-0.18
sp Q6PIC6 AT1A3_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Mus musculus GN=Atp1a3 PE=1 SV=1	-1.16	-0.22
sp P67778 PHB_MOUSE	Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	-1.15	-0.36
sp Q9D3B1 HACD2_MOUSE	3-hydroxyacyl-CoA dehydratase 2 OS=Mus musculus GN=Ptplb PE=2 SV=1	-1.14	-10
sp Q8CGP0 H2B3B_MOUSE	Histone H2B type 3-B OS=Mus musculus GN=Hist3h2bb PE=1 SV=3	-1.13	-0.35
sp Q9D2U9 H2B3A_MOUSE	Histone H2B type 3-A OS=Mus musculus GN=Hist3h2ba PE=1 SV=3	-1.13	-0.35
sp P97807 FUMH_MOUSE	Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3	-1.12	-10

sp Q9Z1W8 AT12A_MOUSE	Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=3	-1.12	-0.21
sp Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	-1.09	-0.39
sp P10853 H2B1F_MOUSE	Histone H2B type 1-F/J/L OS=Mus musculus GN=Hist1h2bf PE=1 SV=2	-1.08	-0.37
sp P10854 H2B1M_MOUSE	Histone H2B type 1-M OS=Mus musculus GN=Hist1h2bm PE=1 SV=2	-1.08	-0.37
sp P70696 H2B1A_MOUSE	Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba PE=2 SV=3	-1.08	-0.29
sp Q64475 H2B1B_MOUSE	Histone H2B type 1-B OS=Mus musculus GN=Hist1h2bb PE=1 SV=3	-1.08	-0.37
sp Q64478 H2B1H_MOUSE	Histone H2B type 1-H OS=Mus musculus GN=Hist1h2bh PE=1 SV=3	-1.08	-0.37
sp Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac PE=1 SV=3	-1.08	-0.17
sp Q64525 H2B2B_MOUSE	Histone H2B type 2-B OS=Mus musculus GN=Hist2h2bb PE=1 SV=3	-1.08	-0.37
sp Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus musculus GN=Hist2h2aa1 PE=1 SV=3	-1.08	-0.17
sp Q6ZWY9 H2B1C_MOUSE	Histone H2B type 1-C/E/G OS=Mus musculus GN=Hist1h2bc PE=1 SV=3	-1.08	-0.37
sp Q8CGP2 H2B1P_MOUSE	Histone H2B type 1-P OS=Mus musculus GN=Hist1h2bp PE=1 SV=3	-1.08	-0.37
sp O08749 DLDH_MOUSE	Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2	-1.07	-0.25
sp P22752 H2A1_MOUSE	Histone H2A type 1 OS=Mus musculus GN=Hist1h2ab PE=1 SV=3	-1.06	-0.17
sp Q8BFU2 H2A3_MOUSE	Histone H2A type 3 OS=Mus musculus GN=Hist3h2a PE=1 SV=3	-1.06	-0.17
sp Q8CGP5 H2A1F_MOUSE	Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	-1.06	-0.17
sp Q8CGP6 H2A1H_MOUSE	Histone H2A type 1-H OS=Mus musculus GN=Hist1h2ah PE=1 SV=3	-1.06	-0.17
sp Q8CGP7 H2A1K_MOUSE	Histone H2A type 1-K OS=Mus musculus GN=Hist1h2ak PE=1 SV=3	-1.06	-0.17
sp Q8R1M2 H2AJ_MOUSE	Histone H2A.J OS=Mus musculus GN=H2afj PE=2 SV=1	-1.06	-0.17
sp Q9DBT5 AMPD2_MOUSE	AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1	-1.06	-0.03
sp P20491 FCERG_MOUSE	High affinity immunoglobulin epsilon receptor subunit gamma OS=Mus musculus GN=Fcer1g PE=1 SV=1	-1.05	-0.08
sp Q9DCT2 NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=2	-1.03	-0.08
sp Q64524 H2B2E_MOUSE	Histone H2B type 2-E OS=Mus musculus GN=Hist2h2be PE=1 SV=3	-1.01	-0.35
sp P50518 VATE1_MOUSE	V-type proton ATPase subunit E 1 OS=Mus musculus GN=Atp6v1e1 PE=1 SV=2	-1	-0.27
sp Q8CGP1 H2B1K_MOUSE	Histone H2B type 1-K OS=Mus musculus GN=Hist1h2bk PE=1 SV=3	-1	-0.37

sp Q64522 H2A2B_MOUSE	Histone H2A type 2-B OS=Mus musculus GN=Hist2h2ab PE=1 SV=3	-0.95	-0.15
sp P27661 H2AX_MOUSE	Histone H2A.x OS=Mus musculus GN=H2afx PE=1 SV=2	-0.91	-0.15
sp Q9D1G1 RAB1B_MOUSE	Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	-0.9	-0.04
sp Q64433 CH10_MOUSE	10 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspe1 PE=1 SV=2	-0.87	-0.09
sp Q8BFR5 EFTU_MOUSE	Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	-0.86	-0.28
sp P0C0S6 H2AZ_MOUSE	Histone H2A.Z OS=Mus musculus GN=H2afz PE=1 SV=2	-0.82	-0.15
sp Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus musculus GN=H2afv PE=1 SV=3	-0.82	-0.15
sp P54116 STOM_MOUSE	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	-0.81	-0.42
sp Q3TW96 UAP1L_MOUSE	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Mus musculus GN=Uap1l1 PE=2 SV=1	-0.79	-10
sp Q6PB66 LPPRC_MOUSE	Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	-0.75	-0.29
sp P12787 COX5A_MOUSE	Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2	-0.74	-0.04
sp Q9ERK4 XPO2_MOUSE	Exportin-2 OS=Mus musculus GN=Cse1l PE=2 SV=1	-0.73	-0.23
sp Q8VEM8 MPCP_MOUSE	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	-0.72	-0.34
sp Q91ZX7 LRP1_MOUSE	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	-0.72	-0.11
sp Q99KI0 ACON_MOUSE	Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	-0.72	-0.2
sp Q07133 H1T_MOUSE	Histone H1t OS=Mus musculus GN=Hist1h1t PE=2 SV=4	-0.69	-0.72
sp Q35129 PHB2_MOUSE	Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	-0.68	-0.32
sp Q5SUR0 PUR4_MOUSE	Phosphoribosylformylglycinamide synthase OS=Mus musculus GN=Pfas PE=2 SV=1	-0.68	-0.21
sp P80315 TCPD_MOUSE	T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	-0.67	-0.03
sp Q06185 ATP5I_MOUSE	ATP synthase subunit e, mitochondrial OS=Mus musculus GN=Atp5i PE=1 SV=2	-0.67	-0.07
sp P43276 H15_MOUSE	Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	-0.66	-0.46
sp P43274 H14_MOUSE	Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2	-0.64	-0.67
sp Q9Z2X1 HNRPF_MOUSE	Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnmpf PE=1 SV=3	-0.64	-0.4

sp P15864 H12_MOUSE	Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	-0.63	-0.57
sp P63276 RS17_MOUSE	40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	-0.63	-0.19
sp P43277 H13_MOUSE	Histone H1.3 OS=Mus musculus GN=Hist1h1d PE=1 SV=2	-0.62	-0.57
sp P48962 ADT1_MOUSE	ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	-0.61	-0.42
sp Q9CQQ7 AT5F1_MOUSE	ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	-0.61	-0.41
sp P56135 ATPK_MOUSE	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=1 SV=3	-0.6	-0.12
sp Q921H8 THIKA_MOUSE	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=2 SV=1	-0.6	-0.1
sp Q99LP6 GRPE1_MOUSE	GrpE protein homolog 1, mitochondrial OS=Mus musculus GN=Grpel1 PE=1 SV=1	-0.6	-10
sp Q61753 SERA_MOUSE	D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	-0.59	-0.23
sp P08113 ENPL_MOUSE	Endoplasmic reticulum protein OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	-0.58	-0.07
sp Q8K2B3 DHSA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	-0.58	-0.09
sp Q9CQA3 DHSB_MOUSE	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=Sdhb PE=1 SV=1	-0.58	-0.36
sp Q62095 DDX3Y_MOUSE	ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2	-0.56	-0.14
sp Q9DB20 ATPO_MOUSE	ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	-0.56	-0.25
sp P43275 H11_MOUSE	Histone H1.1 OS=Mus musculus GN=Hist1h1a PE=2 SV=2	-0.55	-0.84
sp Q99K51 PLST_MOUSE	Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	-0.54	-0.1
sp Q99NB9 SF3B1_MOUSE	Splicing factor 3B subunit 1 OS=Mus musculus GN=Sf3b1 PE=1 SV=1	-0.54	-0.2
sp P51881 ADT2_MOUSE	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	-0.53	-0.41
sp Q9D6R2 IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	-0.52	-0.18
sp P17710 HXK1_MOUSE	Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3	-0.51	-0.32
sp P16381 DDX3L_MOUSE	Putative ATP-dependent RNA helicase PI10 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	-0.5	-0.34
sp P42208 SEPT2_MOUSE	Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2	-0.5	-0.16
sp Q62167 DDX3X_MOUSE	ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3	-0.5	-0.31
sp Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=4	-0.49	-0.3
sp Q8VC28 AK1CD_MOUSE	Aldo-keto reductase family 1 member C13 OS=Mus musculus GN=Akr1c13 PE=1	-0.49	-1.3

	SV=2		
sp P10107 ANXA1_MOUSE	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	-0.48	-0.03
sp P80316 TCPE_MOUSE	T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	-0.47	-0.02
sp Q9DAS9 GBG12_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Mus musculus GN=Gng12 PE=1 SV=3	-0.47	-0.35
sp P30681 HMGB2_MOUSE	High mobility group protein B2 OS=Mus musculus GN=Hmgb2 PE=1 SV=3	-0.46	-0.07
sp P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	-0.46	-0.13
sp P38647 GRP75_MOUSE	Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	-0.45	-0.07
sp P60335 PCBP1_MOUSE	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	-0.45	-0.02
sp P97351 RS3A_MOUSE	40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	-0.45	-0.24
sp Q62425 NDUA4_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Mus musculus GN=Ndufa4 PE=1 SV=2	-0.45	-0.36
sp P54775 PRS6B_MOUSE	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2	-0.43	-0.29
sp P26443 DHE3_MOUSE	Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	-0.41	-10
sp Q3V132 ADT4_MOUSE	ADP/ATP translocase 4 OS=Mus musculus GN=Slc25a31 PE=2 SV=1	-0.38	-0.38
sp Q8JZQ9 EIF3B_MOUSE	Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1	-0.36	-0.06
sp Q9D8E6 RL4_MOUSE	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	-0.36	-0.3
sp O54734 OST48_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddost PE=1 SV=2	-0.35	-0.13
sp P62245 RS15A_MOUSE	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=2 SV=2	-0.35	-1.68
sp O35326 SRSF5_MOUSE	Serine/arginine-rich splicing factor 5 OS=Mus musculus GN=Srsf5 PE=1 SV=1	-0.34	-0.12
sp Q8VE97 SRSF4_MOUSE	Serine/arginine-rich splicing factor 4 OS=Mus musculus GN=Srsf4 PE=2 SV=1	-0.34	-0.12
sp P34022 RANG_MOUSE	Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	-0.33	-0.08
sp Q8C0C7 SYFA_MOUSE	Phenylalanyl-tRNA synthetase alpha chain OS=Mus musculus GN=Farsa PE=2 SV=1	-0.33	-0.19
sp P84104 SRSF3_MOUSE	Serine/arginine-rich splicing factor 3 OS=Mus musculus GN=Srsf3 PE=1 SV=1	-0.31	-0.55
sp P29341 PABP1_MOUSE	Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=2	-0.3	-0.1
sp P97311 MCM6_MOUSE	DNA replication licensing factor MCM6 OS=Mus musculus GN=Mcm6 PE=1 SV=1	-0.29	-10
sp Q9DCC4 P5CR3_MOUSE	Pyrraline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycr1 PE=2 SV=2	-0.29	-0.05

sp O35737 HNRH1_MOUSE	Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3	-0.28	-0.4
sp P70333 HNRH2_MOUSE	Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrnph2 PE=1 SV=1	-0.28	-10
sp Q04447 KCRB_MOUSE	Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1	-0.27	-10
sp Q8VEK3 HNRPU_MOUSE	Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1	-0.26	-0.27
sp Q9ERD7 TBB3_MOUSE	Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	-0.25	-0.24
sp P14206 RSSA_MOUSE	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	-0.23	-0.15
sp P68372 TBB2C_MOUSE	Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	-0.23	-0.23
sp Q9CZU6 CISY_MOUSE	Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	-0.21	-0.97
sp Q9D1Q4 DPM3_MOUSE	Dolichol-phosphate mannosyltransferase subunit 3 OS=Mus musculus GN=Dpm3 PE=2 SV=1	-0.21	-0.32
sp P11983 TCPA_MOUSE	T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3	-0.2	-0.2
sp P80318 TCPG_MOUSE	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	-0.19	-0.15
sp Q922F4 TBB6_MOUSE	Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	-0.19	-0.24
sp P62082 RS7_MOUSE	40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	-0.17	-0.22
sp P70168 IMB1_MOUSE	Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2	-0.17	-0.01
sp Q7TMM9 TBB2A_MOUSE	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	-0.17	-0.23
sp Q9CWF2 TBB2B_MOUSE	Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1	-0.17	-0.23
sp Q9WUU7 CATZ_MOUSE	Cathepsin Z OS=Mus musculus GN=Ctsz PE=2 SV=1	-0.17	-0.08
sp P14131 RS16_MOUSE	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV=4	-0.16	-0.19
sp O88569 ROA2_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	-0.15	-0.11
sp P08752 GNAI2_MOUSE	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5	-0.14	-0.07
sp P53026 RL10A_MOUSE	60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	-0.14	-0.08
sp P62918 RL8_MOUSE	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	-0.14	-0.25
sp P27659 RL3_MOUSE	60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=3	-0.12	-0.05
sp P31254 UBA1Y_MOUSE	Ubiquitin-like modifier-activating enzyme 1 Y OS=Mus musculus GN=Ube1ay PE=2 SV=2	-0.1	-0.16

sp P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	-0.09	-0.28
sp Q9D6F9 TBB4_MOUSE	Tubulin beta-4 chain OS=Mus musculus GN=Tubb4 PE=1 SV=3	-0.09	-0.21
sp Q8C166 CPNE1_MOUSE	Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1	-0.05	-10
sp P50247 SAHH_MOUSE	Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	-0.04	-0.09
sp Q8VDM4 PSMD2_MOUSE	26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psm2 PE=1 SV=1	-0.04	-0.28
sp P08003 PDIA4_MOUSE	Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=3	-0.03	-10
sp P70372 ELAV1_MOUSE	ELAV-like protein 1 OS=Mus musculus GN=Elav1 PE=1 SV=2	-0.03	-0.5
sp Q14C59 TM11B_MOUSE	Transmembrane protease serine 11B OS=Mus musculus GN=Tmprss11b PE=2 SV=2	-0.03	-10
sp Q80UM7 MOGS_MOUSE	Mannosyl-oligosaccharide glucosidase OS=Mus musculus GN=Mogs PE=2 SV=1	-0.02	-0.37
sp P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	-0.01	-0.09

Table 10. List of alkylamide- 11 a/b induced proteins in experiment 2.

Sequence Id	Sequence Name	alkylamide- 11 a/b Expt- 2
sp A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn PE=1 SV=1	5.96
sp Q9BDB7 IF44L_MOUSE	Interferon-induced protein 44-like OS=Mus musculus GN=IFI44L PE=2 SV=2	3.77
sp P61957 SUMO2_MOUSE	Small ubiquitin-related modifier 2 OS=Mus musculus GN=Sumo2 PE=2 SV=1	2.54
sp Q9Z172 SUMO3_MOUSE	Small ubiquitin-related modifier 3 OS=Mus musculus GN=Sumo3 PE=2 SV=1	2.54
sp P19246 NFH_MOUSE	Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE=1 SV=3	2.18
sp P03995 GFAP_MOUSE	Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4	1.98
sp P08551 NFL_MOUSE	Neurofilament light polypeptide OS=Mus musculus GN=Nefl PE=1 SV=5	1.98
sp P45591 COF2_MOUSE	Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1	1.98
sp Q6ZWX6 IF2A_MOUSE	Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3	1.89
sp P29387 GGB4_MOUSE	Guanine nucleotide-binding protein subunit beta-4 OS=Mus musculus GN=Gnb4 PE=2 SV=4	1.61
sp Q61011 GGB3_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Mus musculus GN=Gnb3 PE=1 SV=2	1.61
sp P42225 STAT1_MOUSE	Signal transducer and activator of transcription 1 OS=Mus musculus GN=Stat1 PE=1 SV=1	1.06

sp P63276 RS17_MOUSE	40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	0.92
sp Q61093 CY24B_MOUSE	Cytochrome b-245 heavy chain OS=Mus musculus GN=Cybb PE=2 SV=1	0.8
sp Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2	0.78
sp P62874 GGB1_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Mus musculus GN=Gnb1 PE=1 SV=3	0.62
sp P62880 GGB2_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Mus musculus GN=Gnb2 PE=1 SV=3	0.62
sp Q9WVK4 EHD1_MOUSE	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	0.62
sp P13020 GELS_MOUSE	Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	0.54
sp Q91XV3 BASP1_MOUSE	Brain acid soluble protein 1 OS=Mus musculus GN=Basp1 PE=1 SV=3	0.44
sp P20152 VIME_MOUSE	Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	0.43
sp Q6IRU2 TPM4_MOUSE	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=3	0.37
sp Q9D6R2 IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=ldh3a PE=1 SV=1	0.37
sp P97429 ANXA4_MOUSE	Annexin A4 OS=Mus musculus GN=Anxa4 PE=2 SV=4	0.36
sp Q3THS6 METK2_MOUSE	S-adenosylmethionine synthase isoform type-2 OS=Mus musculus GN=Mat2a PE=2 SV=2	0.35
sp Q8K4Z3 AIBP_MOUSE	Apolipoprotein A-I-binding protein OS=Mus musculus GN=Apoa1bp PE=1 SV=1	0.34
sp P34884 MIF_MOUSE	Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2	0.33
sp Q71LX4 TLN2_MOUSE	Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	0.33
sp O88531 PPT1_MOUSE	Palmitoyl-protein thioesterase 1 OS=Mus musculus GN=Ppt1 PE=2 SV=2	0.31
sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	0.29
sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	0.29
sp Q8BFZ3 ACTBL_MOUSE	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=1 SV=1	0.28
sp Q1HFZ0 NSUN2_MOUSE	tRNA (cytosine(34)-C(5))-methyltransferase OS=Mus musculus GN=Nsun2 PE=1 SV=2	0.27
sp P47915 RL29_MOUSE	60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2	0.25
sp P62737 ACTA_MOUSE	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	0.25
sp P63268 ACTH_MOUSE	Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1	0.25
sp P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	0.25
sp P68134 ACTS_MOUSE	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	0.25
sp Q6P1B1 XPP1_MOUSE	Xaa-Pro aminopeptidase 1 OS=Mus musculus GN=Xpnpep1 PE=2 SV=1	0.24
sp Q8BH59 CMC1_MOUSE	Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus musculus GN=Slc25a12 PE=1 SV=1	0.22

sp Q8BTM8 FLNA_MOUSE	Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5	0.22
sp P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	0.21
sp Q9CQ60 6PGL_MOUSE	6-phosphogluconolactonase OS=Mus musculus GN=Pgls PE=2 SV=1	0.2
sp Q9D1G1 RAB1B_MOUSE	Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	0.19
sp P63325 RS10_MOUSE	40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1	0.18
sp Q61768 KINH_MOUSE	Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=3	0.18
sp O08709 PRDX6_MOUSE	Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3	0.16
sp O88844 IDHC_MOUSE	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=ldh1 PE=1 SV=2	0.16
sp Q8R1F1 NIBL1_MOUSE	Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=1 SV=2	0.16
sp Q99KC8 VMA5A_MOUSE	von Willebrand factor A domain-containing protein 5A OS=Mus musculus GN=Vwa5a PE=1 SV=2	0.16
sp Q9EPU0 RENT1_MOUSE	Regulator of nonsense transcripts 1 OS=Mus musculus GN=Upf1 PE=1 SV=2	0.16
sp P35278 RAB5C_MOUSE	Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	0.15
sp Q61233 PLSL_MOUSE	Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4	0.15
sp P62267 RS23_MOUSE	40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3	0.14
sp Q99K51 PLST_MOUSE	Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	0.14
sp Q99NB9 SF3B1_MOUSE	Splicing factor 3B subunit 1 OS=Mus musculus GN=Sf3b1 PE=1 SV=1	0.14
sp P26516 PSD7_MOUSE	26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	0.12
sp P62137 PP1A_MOUSE	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE=1 SV=1	0.11
sp O08756 HCD2_MOUSE	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17b10 PE=1 SV=4	0.1
sp P29351 PTN6_MOUSE	Tyrosine-protein phosphatase non-receptor type 6 OS=Mus musculus GN=Ptpn6 PE=1 SV=2	0.1
sp Q7M6Y3 PICA_MOUSE	Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus GN=Picalm PE=1 SV=1	0.1
sp Q8K1B8 URP2_MOUSE	Fermitin family homolog 3 OS=Mus musculus GN=Fermt3 PE=1 SV=1	0.1
sp P40124 CAP1_MOUSE	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	0.08
sp Q80X90 FLNB_MOUSE	Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3	0.08
sp O89053 COR1A_MOUSE	Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5	0.07
sp Q8BL97 SRSF7_MOUSE	Serine/arginine-rich splicing factor 7 OS=Mus musculus GN=Srsf7 PE=1 SV=1	0.06
sp Q9D6F9 TBB4_MOUSE	Tubulin beta-4 chain OS=Mus musculus GN=Tubb4 PE=1 SV=3	0.06
sp O08810 U5S1_MOUSE	116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1	0.05

sp Q921M7 FA49B_MOUSE	Protein FAM49B OS=Mus musculus GN=Fam49b PE=2 SV=1	0.05
sp Q9ERD7 TBB3_MOUSE	Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	0.05
sp Q9QXS1 PLEC_MOUSE	Plectin OS=Mus musculus GN=Plec PE=1 SV=2	0.05
sp Q9Z1Q5 CLIC1_MOUSE	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	0.05
sp P54775 PRS6B_MOUSE	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2	0.04
sp P62264 RS14_MOUSE	40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	0.04
sp P99029 PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2	0.04
sp Q922F4 TBB6_MOUSE	Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	0.04
sp Q99JY9 ARP3_MOUSE	Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3	0.04
sp P28656 NP1L1_MOUSE	Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap111 PE=1 SV=2	0.03
sp Q7TMM9 TBB2A_MOUSE	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	0.03
sp Q9CWF2 TBB2B_MOUSE	Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1	0.03
sp P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	0.02
sp Q9JHU9 INO1_MOUSE	Inositol-3-phosphate synthase 1 OS=Mus musculus GN=Isyna1 PE=2 SV=1	0.02
sp P26040 EZRI_MOUSE	Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	0.01
sp P26043 RADI_MOUSE	Radixin OS=Mus musculus GN=Rdx PE=1 SV=3	0.01

Table 11. List of alkylamide-11a/b suppressed proteins in experiment 2.

Sequence Id	Sequence Name	alkylamide-11a/b Ratio Expt-2
sp P01942 HBA_MOUSE	Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2	-10
sp P03930 ATP8_MOUSE	ATP synthase protein 8 OS=Mus musculus GN=Mtatp8 PE=1 SV=1	-10
sp P05555 ITAM_MOUSE	Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=2	-10
sp P07724 ALBU_MOUSE	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	-10
sp P10639 THIO_MOUSE	Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3	-10
sp P10853 H2B1F_MOUSE	Histone H2B type 1-F/J/L OS=Mus musculus GN=Hist1h2bf PE=1 SV=2	-10
sp P10854 H2B1M_MOUSE	Histone H2B type 1-M OS=Mus musculus GN=Hist1h2bm PE=1 SV=2	-10
sp P11438 LAMP1_MOUSE	Lysosome-associated membrane glycoprotein 1	-10

	OS=Mus musculus GN=Lamp1 PE=1 SV=2	
sp P12787 COX5A_MOUSE	Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2	-10
sp P14069 S10A6_MOUSE	Protein S100-A6 OS=Mus musculus GN=S100a6 PE=1 SV=3	-10
sp P15331 PERI_MOUSE	Peripherin OS=Mus musculus GN=Prph PE=1 SV=2	-10
sp P15379 CD44_MOUSE	CD44 antigen OS=Mus musculus GN=Cd44 PE=1 SV=3	-10
sp P19783 COX41_MOUSE	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Mus musculus GN=Cox4i1 PE=1 SV=2	-10
sp P20491 FCERG_MOUSE	High affinity immunoglobulin epsilon receptor subunit gamma OS=Mus musculus GN=Fcer1g PE=1 SV=1	-10
sp P24547 IMDH2_MOUSE	Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh2 PE=1 SV=2	-10
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcks1 PE=1 SV=2	-10
sp P28738 KIF5C_MOUSE	Kinesin heavy chain isoform 5C OS=Mus musculus GN=Kif5c PE=1 SV=3	-10
sp P33175 KIF5A_MOUSE	Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3	-10
sp P42208 SEPT2_MOUSE	Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2	-10
sp P43276 H15_MOUSE	Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	-10
sp P47753 CAZA1_MOUSE	F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=Capza1 PE=1 SV=4	-10
sp P47754 CAZA2_MOUSE	F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=Capza2 PE=1 SV=3	-10
sp P47955 RLA1_MOUSE	60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1	-10
sp P49717 MCM4_MOUSE	DNA replication licensing factor MCM4 OS=Mus musculus GN=Mcm4 PE=2 SV=1	-10
sp P53986 MOT1_MOUSE	Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	-10
sp P54987 IRG1_MOUSE	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	-10
sp P56135 ATPK_MOUSE	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=1 SV=3	-10
sp P57716 NICA_MOUSE	Nicastrin OS=Mus musculus GN=Ncstn PE=1 SV=3	-10
sp P61358 RL27_MOUSE	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=2 SV=2	-10
sp P62274 RS29_MOUSE	40S ribosomal protein S29 OS=Mus musculus GN=Rps29 PE=2 SV=2	-10
sp P62320 SMD3_MOUSE	Small nuclear ribonucleoprotein Sm D3 OS=Mus musculus GN=Snrpd3 PE=1 SV=1	-10
sp P62806 H4_MOUSE	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	-10
sp P62821 RAB1A_MOUSE	Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3	-10
sp P62858 RS28_MOUSE	40S ribosomal protein S28 OS=Mus musculus GN=Rps28 PE=2 SV=1	-10

sp P67984 RL22_MOUSE	60S ribosomal protein L22 OS=Mus musculus GN=Rpl22 PE=2 SV=2	-10
sp P70696 H2B1A_MOUSE	Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba PE=2 SV=3	-10
sp P99027 RLA2_MOUSE	60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3	-10
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	-10
sp Q501J6 DDX17_MOUSE	Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	-10
sp Q61033 LAP2A_MOUSE	Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmpo PE=1 SV=4	-10
sp Q61543 GSLG1_MOUSE	Golgi apparatus protein 1 OS=Mus musculus GN=Glg1 PE=1 SV=1	-10
sp Q62425 NDUA4_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Mus musculus GN=Ndufa4 PE=1 SV=2	-10
sp Q62433 NDRG1_MOUSE	Protein NDRG1 OS=Mus musculus GN=Ndrp1 PE=1 SV=1	-10
sp Q64475 H2B1B_MOUSE	Histone H2B type 1-B OS=Mus musculus GN=Hist1h2bb PE=1 SV=3	-10
sp Q64478 H2B1H_MOUSE	Histone H2B type 1-H OS=Mus musculus GN=Hist1h2bh PE=1 SV=3	-10
sp Q64516 GLPK_MOUSE	Glycerol kinase OS=Mus musculus GN=Gk PE=2 SV=2	-10
sp Q64524 H2B2E_MOUSE	Histone H2B type 2-E OS=Mus musculus GN=Hist2h2be PE=1 SV=3	-10
sp Q64525 H2B2B_MOUSE	Histone H2B type 2-B OS=Mus musculus GN=Hist2h2bb PE=1 SV=3	-10
sp Q64727 VINC_MOUSE	Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	-10
sp Q69Z97 MYOF_MOUSE	Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	-10
sp Q6PDI5 ECM29_MOUSE	Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=3	-10
sp Q6ZUW9 RS27_MOUSE	40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3	-10
sp Q6ZWY3 RS27L_MOUSE	40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=2 SV=3	-10
sp Q6ZWY9 H2B1C_MOUSE	Histone H2B type 1-C/E/G OS=Mus musculus GN=Hist1h2bc PE=1 SV=3	-10
sp Q8BH04 PCKGM_MOUSE	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=2 SV=1	-10
sp Q8BMK4 CKAP4_MOUSE	Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=2 SV=2	-10
sp Q8BP47 SYNC_MOUSE	Asparaginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Nars PE=1 SV=2	-10
sp Q8BU30 SYIC_MOUSE	Isoleucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=lars PE=2 SV=2	-10
sp Q8CGP0 H2B3B_MOUSE	Histone H2B type 3-B OS=Mus musculus GN=Hist3h2bb PE=1 SV=3	-10
sp Q8CGP1 H2B1K_MOUSE	Histone H2B type 1-K OS=Mus musculus GN=Hist1h2bk PE=1 SV=3	-10

sp Q8CGP2 H2B1P_MOUSE	Histone H2B type 1-P OS=Mus musculus GN=Hist1h2bp PE=1 SV=3	-10
sp Q8QZY1 EIF3L_MOUSE	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=EIF3L PE=1 SV=1	-10
sp Q8R0W0 EPIPL_MOUSE	Epiplakin OS=Mus musculus GN=Eppk1 PE=1 SV=2	-10
sp Q8VCT3 AMPB_MOUSE	Aminopeptidase B OS=Mus musculus GN=Rnpep PE=2 SV=2	-10
sp Q8VDJ3 VIGLN_MOUSE	Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	-10
sp Q8VHX6 FLNC_MOUSE	Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	-10
sp Q91VC9 GHITM_MOUSE	Growth hormone-inducible transmembrane protein OS=Mus musculus GN=Ghitm PE=2 SV=1	-10
sp Q99JB2 STML2_MOUSE	Stomatin-like protein 2 OS=Mus musculus GN=Stoml2 PE=1 SV=1	-10
sp Q99LP6 GRPE1_MOUSE	GrpE protein homolog 1, mitochondrial OS=Mus musculus GN=Grpel1 PE=1 SV=1	-10
sp Q99MN1 SYK_MOUSE	Lysyl-tRNA synthetase OS=Mus musculus GN=Kars PE=1 SV=1	-10
sp Q9CQS8 SC61B_MOUSE	Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3	-10
sp Q9CY57 FOP_MOUSE	Friend of PRMT1 protein OS=Mus musculus GN=Fop PE=1 SV=2	-10
sp Q9CZY3 UB2V1_MOUSE	Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=1 SV=1	-10
sp Q9D0I9 SYRC_MOUSE	Arginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Rars PE=2 SV=2	-10
sp Q9D2M8 UB2V2_MOUSE	Ubiquitin-conjugating enzyme E2 variant 2 OS=Mus musculus GN=Ube2v2 PE=2 SV=4	-10
sp Q9D2U9 H2B3A_MOUSE	Histone H2B type 3-A OS=Mus musculus GN=Hist3h2ba PE=1 SV=3	-10
sp Q9D4D4 TKTL2_MOUSE	Transketolase-like protein 2 OS=Mus musculus GN=Tktl2 PE=2 SV=1	-10
sp Q9DAS9 GBG12_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Mus musculus GN=Gng12 PE=1 SV=3	-10
sp Q9DBG6 RPN2_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	-10
sp Q9DCC8 TOM20_MOUSE	Mitochondrial import receptor subunit TOM20 homolog OS=Mus musculus GN=Tom20 PE=1 SV=1	-10
sp Q9EQP2 EHD4_MOUSE	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	-10
sp Q9JII6 AK1A1_MOUSE	Alcohol dehydrogenase [NADP+] OS=Mus musculus GN=Akr1a1 PE=1 SV=3	-10
sp Q9JIK5 DDX21_MOUSE	Nucleolar RNA helicase 2 OS=Mus musculus GN=Ddx21 PE=1 SV=3	-10
sp Q9JJ28 FLII_MOUSE	Protein flightless-1 homolog OS=Mus musculus GN=Flil PE=1 SV=1	-10
sp Q9JJI8 RL38_MOUSE	60S ribosomal protein L38 OS=Mus musculus GN=Rpl38 PE=2 SV=3	-10
sp Q9JLJ5 ELOV1_MOUSE	Elongation of very long chain fatty acids protein 1 OS=Mus musculus GN=Elol1 PE=2 SV=1	-10

sp Q9JMH6 TRXR1_MOUSE	Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txnrd1 PE=1 SV=3	-10
sp Q9QXK3 COPG2_MOUSE	Coatomer subunit gamma-2 OS=Mus musculus GN=Copg2 PE=2 SV=1	-10
sp Q9QXX4 CMC2_MOUSE	Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1	-10
sp Q9QXZ0 MACF1_MOUSE	Microtubule-actin cross-linking factor 1 OS=Mus musculus GN=Macf1 PE=1 SV=2	-10
sp Q9QZD8 DIC_MOUSE	Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=2 SV=2	-10
sp Q9QZE5 COPG_MOUSE	Coatomer subunit gamma OS=Mus musculus GN=Copg PE=2 SV=1	-10
sp Q9R1Q7 PLP2_MOUSE	Proteolipid protein 2 OS=Mus musculus GN=Plp2 PE=2 SV=1	-10
sp Q9WTI7 MYO1C_MOUSE	Myosin-Ic OS=Mus musculus GN=Myo1c PE=1 SV=2	-10
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	-10
sp Q9WUA2 SYFB_MOUSE	Phenylalanyl-tRNA synthetase beta chain OS=Mus musculus GN=Farsb PE=2 SV=2	-10
sp Q9WUA3 K6PP_MOUSE	6-phosphofructokinase type C OS=Mus musculus GN=Pfkp PE=1 SV=1	-10
sp Q9Z0X1 AIFM1_MOUSE	Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifm1 PE=1 SV=1	-10
sp Q9Z110 P5CS_MOUSE	Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus GN=Aldh18a1 PE=2 SV=2	-10
sp Q62446 FKBP3_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Mus musculus GN=Fkbp3 PE=1 SV=2	-2.52
sp Q14C59 TM11B_MOUSE	Transmembrane protease serine 11B OS=Mus musculus GN=Tmprss11b PE=2 SV=2	-1.93
sp Q9CQI6 COTL1_MOUSE	Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3	-1.88
sp Q9D3B1 HACD2_MOUSE	3-hydroxyacyl-CoA dehydratase 2 OS=Mus musculus GN=Ptp1b PE=2 SV=1	-1.76
sp Q9D1M7 FKBP11_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP11 OS=Mus musculus GN=Fkbp11 PE=2 SV=1	-1.65
sp Q8VEM8 MPCP_MOUSE	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	-1.6
sp O70133 DHX9_MOUSE	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	-1.54
sp Q6GQT9 NOMO1_MOUSE	Nodal modulator 1 OS=Mus musculus GN=Nomo1 PE=1 SV=1	-1.41
sp O70152 DPM1_MOUSE	Dolichol-phosphate mannosyltransferase OS=Mus musculus GN=Dpm1 PE=2 SV=1	-1.27
sp Q62351 TFR1_MOUSE	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	-1.26
sp Q9D0K2 SCOT1_MOUSE	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial OS=Mus musculus GN=Oxct1 PE=1 SV=1	-1.26
sp O08795 GLU2B_MOUSE	Glucosidase 2 subunit beta OS=Mus musculus GN=Prkcsh PE=1 SV=1	-1.18
sp P24369 PPIB_MOUSE	Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=2 SV=2	-1.17
sp P10605 CATB_MOUSE	Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	-1.16

sp Q9ERK4 XPO2_MOUSE	Exportin-2 OS=Mus musculus GN=Cse1l PE=2 SV=1	-1.09
sp Q64433 CH10_MOUSE	10 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspe1 PE=1 SV=2	-1.06
sp Q9Z2l8 SUCB2_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Suclg2 PE=2 SV=3	-1.04
sp P08003 PDIA4_MOUSE	Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=3	-1.02
sp P10852 4F2_MOUSE	4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	-1
sp Q8BFR5 EFTU_MOUSE	Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	-0.99
sp Q8BHN3 GANAB_MOUSE	Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1	-0.99
sp Q9WV27 AT1A4_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Mus musculus GN=Atp1a4 PE=1 SV=3	-0.99
sp Q9Z1W8 AT12A_MOUSE	Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=3	-0.99
sp Q9CZ13 QCR1_MOUSE	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2	-0.98
sp Q8C166 CPNE1_MOUSE	Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1	-0.97
sp O08807 PRDX4_MOUSE	Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	-0.95
sp P22752 H2A1_MOUSE	Histone H2A type 1 OS=Mus musculus GN=Hist1h2ab PE=1 SV=3	-0.95
sp Q64436 ATP4A_MOUSE	Potassium-transporting ATPase alpha chain 1 OS=Mus musculus GN=Atp4a PE=1 SV=3	-0.95
sp Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac PE=1 SV=3	-0.95
sp Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus musculus GN=Hist2h2aa1 PE=1 SV=3	-0.95
sp Q8BFU2 H2A3_MOUSE	Histone H2A type 3 OS=Mus musculus GN=Hist3h2a PE=1 SV=3	-0.95
sp Q8CGP5 H2A1F_MOUSE	Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	-0.95
sp Q8CGP6 H2A1H_MOUSE	Histone H2A type 1-H OS=Mus musculus GN=Hist1h2ah PE=1 SV=3	-0.95
sp Q8CGP7 H2A1K_MOUSE	Histone H2A type 1-K OS=Mus musculus GN=Hist1h2ak PE=1 SV=3	-0.95
sp Q8R1M2 H2AJ_MOUSE	Histone H2A.J OS=Mus musculus GN=H2afj PE=2 SV=1	-0.95
sp Q8VDN2 AT1A1_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	-0.95
sp Q9DB77 QCR2_MOUSE	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	-0.94
sp O35129 PHB2_MOUSE	Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	-0.93
sp Q9DB20 ATPO_MOUSE	ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	-0.93
sp Q9DCX2 ATP5H_MOUSE	ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	-0.93
sp P67778 PHB_MOUSE	Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	-0.92

sp P14211 CALR_MOUSE	Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	-0.91
sp P45377 ALD2_MOUSE	Aldose reductase-related protein 2 OS=Mus musculus GN=Akr1b8 PE=1 SV=2	-0.91
sp P54116 STOM_MOUSE	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	-0.91
sp Q6PIC6 AT1A3_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Mus musculus GN=Atp1a3 PE=1 SV=1	-0.91
sp Q8JZQ9 EIF3B_MOUSE	Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1	-0.91
sp Q06185 ATP5I_MOUSE	ATP synthase subunit e, mitochondrial OS=Mus musculus GN=Atp5i PE=1 SV=2	-0.9
sp Q6PIE5 AT1A2_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Mus musculus GN=Atp1a2 PE=1 SV=1	-0.9
sp Q8VC28 AK1CD_MOUSE	Aldo-keto reductase family 1 member C13 OS=Mus musculus GN=Akr1c13 PE=1 SV=2	-0.9
sp P12265 BGLR_MOUSE	Beta-glucuronidase OS=Mus musculus GN=Gusb PE=2 SV=1	-0.88
sp P17809 GTR1_MOUSE	Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=4	-0.88
sp P05202 AATM_MOUSE	Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1	-0.87
sp P27773 PDIA3_MOUSE	Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2	-0.87
sp Q9CQ7 AT5F1_MOUSE	ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	-0.86
sp O54734 OST48_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddost PE=1 SV=2	-0.85
sp P0C0S6 H2AZ_MOUSE	Histone H2A.Z OS=Mus musculus GN=H2afz PE=1 SV=2	-0.84
sp P27661 H2AX_MOUSE	Histone H2A.x OS=Mus musculus GN=H2afx PE=1 SV=2	-0.84
sp Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus musculus GN=H2afv PE=1 SV=3	-0.84
sp Q60692 PSB6_MOUSE	Proteasome subunit beta type-6 OS=Mus musculus GN=Psm6 PE=1 SV=3	-0.84
sp Q64521 GPDM_MOUSE	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus GN=Gpd2 PE=1 SV=2	-0.84
sp Q64522 H2A2B_MOUSE	Histone H2A type 2-B OS=Mus musculus GN=Hist2h2ab PE=1 SV=3	-0.84
sp P21300 ALD1_MOUSE	Aldose reductase-related protein 1 OS=Mus musculus GN=Akr1b7 PE=2 SV=4	-0.83
sp P35564 CALX_MOUSE	Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	-0.83
sp Q9DCT2 NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=2	-0.83
sp Q9CPQ1 COX6C_MOUSE	Cytochrome c oxidase subunit 6C OS=Mus musculus GN=Cox6c PE=1 SV=3	-0.82
sp P18572 BASI_MOUSE	Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	-0.81
sp P63038 CH60_MOUSE	60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	-0.81
sp Q91VR2 ATPG_MOUSE	ATP synthase subunit gamma, mitochondrial OS=Mus	-0.8

	musculus GN=Atp5c1 PE=1 SV=1	
sp Q9CXT8 MPPB_MOUSE	Mitochondrial-processing peptidase subunit beta OS=Mus musculus GN=Pmpcb PE=2 SV=1	-0.79
sp P08113 ENPL_MOUSE	Endoplasmic reticulum chaperone protein OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	-0.78
sp P48962 ADT1_MOUSE	ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	-0.78
sp P51881 ADT2_MOUSE	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	-0.78
sp Q61335 BAP31_MOUSE	B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=3	-0.78
sp P45376 ALDR_MOUSE	Aldose reductase OS=Mus musculus GN=Akr1b1 PE=1 SV=3	-0.77
sp P56480 ATPB_MOUSE	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	-0.77
sp Q64518 AT2A3_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Mus musculus GN=Atp2a3 PE=2 SV=3	-0.77
sp Q8R429 AT2A1_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1	-0.77
sp Q91VD9 NDUS1_MOUSE	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2	-0.77
sp P08249 MDHM_MOUSE	Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3	-0.76
sp Q922R8 PDIA6_MOUSE	Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3	-0.76
sp P08228 SODC_MOUSE	Superoxide dismutase [Cu-Zn] OS=Mus musculus GN=Sod1 PE=1 SV=2	-0.75
sp Q60597 ODO1_MOUSE	2-oxoglutarate dehydrogenase, mitochondrial OS=Mus musculus GN=Ogdh PE=1 SV=3	-0.75
sp Q01768 NDKB_MOUSE	Nucleoside diphosphate kinase B OS=Mus musculus GN=Nme2 PE=1 SV=1	-0.74
sp P68433 H31_MOUSE	Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	-0.73
sp P84228 H32_MOUSE	Histone H3.2 OS=Mus musculus GN=Hist1h3b PE=1 SV=2	-0.73
sp P84244 H33_MOUSE	Histone H3.3 OS=Mus musculus GN=H3f3a PE=1 SV=2	-0.73
sp P00405 COX2_MOUSE	Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1	-0.72
sp P63242 IF5A1_MOUSE	Eukaryotic translation initiation factor 5A-1 OS=Mus musculus GN=Eif5a PE=1 SV=2	-0.72
sp Q64514 TPP2_MOUSE	Tripeptidyl-peptidase 2 OS=Mus musculus GN=Tpp2 PE=2 SV=3	-0.72
sp Q8BGY2 IF5A2_MOUSE	Eukaryotic translation initiation factor 5A-2 OS=Mus musculus GN=Eif5a2 PE=2 SV=3	-0.72
sp Q9CXW3 CYBP_MOUSE	Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	-0.72
sp O54879 HMGB3_MOUSE	High mobility group protein B3 OS=Mus musculus GN=Hmgb3 PE=2 SV=3	-0.71
sp Q9CR62 M2OM_MOUSE	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus GN=Slc25a11 PE=1 SV=3	-0.71
sp Q60931 VDAC3_MOUSE	Voltage-dependent anion-selective channel protein 3	-0.7

	OS=Mus musculus GN=Vdac3 PE=1 SV=1	
sp Q99MR6 SRRT_MOUSE	Serrate RNA effector molecule homolog OS=Mus musculus GN=Srrt PE=1 SV=1	-0.7
sp P51150 RAB7A_MOUSE	Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2	-0.69
sp Q3V132 ADT4_MOUSE	ADP/ATP translocase 4 OS=Mus musculus GN=Slc25a31 PE=2 SV=1	-0.69
sp P62281 RS11_MOUSE	40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3	-0.68
sp Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	-0.68
sp Q80UM7 MOGS_MOUSE	Mannosyl-oligosaccharide glucosidase OS=Mus musculus GN=Mogs PE=2 SV=1	-0.67
sp Q91ZX7 LRP1_MOUSE	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	-0.67
sp Q9DCC4 P5CR3_MOUSE	Pyrroline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycr1 PE=2 SV=2	-0.67
sp P50518 VATE1_MOUSE	V-type proton ATPase subunit E 1 OS=Mus musculus GN=Atp6v1e1 PE=1 SV=2	-0.66
sp P97807 FUMH_MOUSE	Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3	-0.66
sp Q8K2B3 DHSA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	-0.66
sp Q99K85 SERC_MOUSE	Phosphoserine aminotransferase OS=Mus musculus GN=Psat1 PE=1 SV=1	-0.63
sp P20108 PRDX3_MOUSE	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Mus musculus GN=Prdx3 PE=1 SV=1	-0.62
sp P63323 RS12_MOUSE	40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2	-0.62
sp Q07133 H1T_MOUSE	Histone H1t OS=Mus musculus GN=Hist1h1t PE=2 SV=4	-0.62
sp Q922D8 C1TC_MOUSE	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4	-0.62
sp P57759 ERP29_MOUSE	Endoplasmic reticulum resident protein 29 OS=Mus musculus GN=Erp29 PE=1 SV=2	-0.61
sp Q3THE2 ML12B_MOUSE	Myosin regulatory light chain 12B OS=Mus musculus GN=My12b PE=1 SV=2	-0.61
sp Q8BWY3 ERF1_MOUSE	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Elf1 PE=1 SV=4	-0.61
sp Q91YQ5 RPN1_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=2 SV=1	-0.61
sp P30681 HMGB2_MOUSE	High mobility group protein B2 OS=Mus musculus GN=Hmgb2 PE=1 SV=3	-0.6
sp P61027 RAB10_MOUSE	Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	-0.6
sp Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	-0.6
sp Q9D1R9 RL34_MOUSE	60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=3 SV=2	-0.6
sp Q8BMF3 MAON_MOUSE	NADP-dependent malic enzyme, mitochondrial	-0.59

	OS=Mus musculus GN=Me3 PE=1 SV=2	
sp Q8CGK3 LONM_MOUSE	Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE=1 SV=2	-0.59
sp Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	-0.59
sp Q91V41 RAB14_MOUSE	Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3	-0.59
sp Q9CWY9 RIP_MOUSE	RPA-interacting protein OS=Mus musculus GN=Rpain PE=2 SV=1	-0.59
sp Q9CY64 BIEA_MOUSE	Biliverdin reductase A OS=Mus musculus GN=Blvra PE=2 SV=1	-0.59
sp Q8VIJ6 SFPQ_MOUSE	Splicing factor, proline- and glutamine-rich OS=Mus musculus GN=Sfpq PE=1 SV=1	-0.58
sp Q9CQR2 RS21_MOUSE	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=2 SV=1	-0.58
sp Q9D1Q4 DPM3_MOUSE	Dolichol-phosphate mannosyltransferase subunit 3 OS=Mus musculus GN=Dpm3 PE=2 SV=1	-0.57
sp Q60932 VDAC1_MOUSE	Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	-0.56
sp Q9DBT5 AMPD2_MOUSE	AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1	-0.56
sp P09055 ITB1_MOUSE	Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	-0.55
sp P15532 NDKA_MOUSE	Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 PE=1 SV=1	-0.55
sp P29758 OAT_MOUSE	Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1	-0.55
sp P62245 RS15A_MOUSE	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=2 SV=2	-0.55
sp P62900 RL31_MOUSE	60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=2 SV=1	-0.55
sp Q9CU62 SMC1A_MOUSE	Structural maintenance of chromosomes protein 1A OS=Mus musculus GN=Smc1a PE=1 SV=4	-0.55
sp P49312 ROA1_MOUSE	Heterogeneous nuclear ribonucleoprotein A1 OS=Mus musculus GN=Hnrnpa1 PE=1 SV=2	-0.54
sp Q8VEK3 HNRPU_MOUSE	Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrpu PE=1 SV=1	-0.53
sp P11983 TCPA_MOUSE	T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3	-0.52
sp Q8BGQ7 SYAC_MOUSE	Alanyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1	-0.52
sp Q9D3D9 ATPD_MOUSE	ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5d PE=1 SV=1	-0.52
sp P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	-0.51
sp Q04646 ATNG_MOUSE	Sodium/potassium-transporting ATPase subunit gamma OS=Mus musculus GN=Fxyd2 PE=2 SV=2	-0.51
sp Q3TW96 UAP1L_MOUSE	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Mus musculus GN=Uap111 PE=2 SV=1	-0.51
sp Q60930 VDAC2_MOUSE	Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2	-0.51
sp Q9CQN1 TRAP1_MOUSE	Heat shock protein 75 kDa, mitochondrial OS=Mus musculus GN=Trap1 PE=1 SV=1	-0.51

sp Q9CZU6 CISY_MOUSE	Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	-0.51
sp P07091 S10A4_MOUSE	Protein S100-A4 OS=Mus musculus GN=S100a4 PE=1 SV=1	-0.5
sp Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=4	-0.5
sp Q99JY0 ECHB_MOUSE	Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	-0.5
sp Q99PL5 RRBP1_MOUSE	Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=2 SV=2	-0.5
sp Q9CRB9 CHCH3_MOUSE	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1 SV=1	-0.5
sp Q9CW03 SMC3_MOUSE	Structural maintenance of chromosomes protein 3 OS=Mus musculus GN=Smc3 PE=1 SV=2	-0.5
sp O55143 AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	-0.48
sp P57776 EF1D_MOUSE	Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3	-0.48
sp Q8K2Q2 GSTO2_MOUSE	Glutathione S-transferase omega-2 OS=Mus musculus GN=Gsto2 PE=2 SV=1	-0.48
sp Q99LC5 ETFA_MOUSE	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2	-0.48
sp Q99LX0 PARK7_MOUSE	Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	-0.48
sp P38647 GRP75_MOUSE	Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	-0.47
sp P63158 HMGB1_MOUSE	High mobility group protein B1 OS=Mus musculus GN=Hmgb1 PE=1 SV=2	-0.47
sp P80316 TCPE_MOUSE	T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	-0.47
sp Q60605 MYL6_MOUSE	Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3	-0.47
sp Q8CI43 MYL6B_MOUSE	Myosin light chain 6B OS=Mus musculus GN=Myl6b PE=2 SV=1	-0.47
sp Q9JKR6 HYOU1_MOUSE	Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1	-0.47
sp P20029 GRP78_MOUSE	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	-0.46
sp P70296 PEBP1_MOUSE	Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3	-0.46
sp Q9CWJ9 PUR9_MOUSE	Bifunctional purine biosynthesis protein PURH OS=Mus musculus GN=Atic PE=1 SV=2	-0.46
sp O88569 ROA2_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	-0.45
sp Q5SUR0 PUR4_MOUSE	Phosphoribosylformylglycinamide synthase OS=Mus musculus GN=Pfas PE=2 SV=1	-0.45
sp Q9CQA3 DHSB_MOUSE	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=Sdhb PE=1 SV=1	-0.45
sp P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	-0.44

sp P17918 PCNA_MOUSE	Proliferating cell nuclear antigen OS=Mus musculus GN=Pcna PE=1 SV=2	-0.44
sp P21619 LMNB2_MOUSE	Lamin-B2 OS=Mus musculus GN=Lmnb2 PE=1 SV=2	-0.44
sp P27659 RL3_MOUSE	60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=3	-0.44
sp P48722 HS74L_MOUSE	Heat shock 70 kDa protein 4L OS=Mus musculus GN=Hspa4l PE=1 SV=2	-0.44
sp P62315 SMD1_MOUSE	Small nuclear ribonucleoprotein Sm D1 OS=Mus musculus GN=Snrpd1 PE=2 SV=1	-0.44
sp Q62465 VAT1_MOUSE	Synaptic vesicle membrane protein VAT-1 homolog OS=Mus musculus GN=Vat1 PE=1 SV=3	-0.44
sp Q64G17 AN32C_MOUSE	Putative acidic leucine-rich nuclear phosphoprotein 32 family member C OS=Mus musculus GN=Anp32c PE=5 SV=3	-0.44
sp O35381 AN32A_MOUSE	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Mus musculus GN=Anp32a PE=1 SV=1	-0.43
sp P17710 HXK1_MOUSE	Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3	-0.43
sp P62751 RL23A_MOUSE	60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=1 SV=1	-0.43
sp Q76MZ3 2AAA_MOUSE	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3	-0.43
sp Q99020 ROAA_MOUSE	Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculus GN=Hnrnpab PE=1 SV=1	-0.43
sp Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	-0.43
sp Q9ES52 SHIP1_MOUSE	Phosphatidylinositol-3,4,5-trisphosphate 5- phosphatase 1 OS=Mus musculus GN=Inpp5d PE=1 SV=2	-0.43
sp P09405 NUCL_MOUSE	Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2	-0.42
sp Q99KI0 ACON_MOUSE	Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	-0.42
sp Q9ER72 SYCC_MOUSE	Cysteinyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2	-0.42
sp Q9WTP6 KAD2_MOUSE	Adenylate kinase 2, mitochondrial OS=Mus musculus GN=Ak2 PE=1 SV=5	-0.42
sp O08547 SC22B_MOUSE	Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3	-0.41
sp P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus GN=Lyz2 PE=1 SV=2	-0.41
sp P17897 LYZ1_MOUSE	Lysozyme C-1 OS=Mus musculus GN=Lyz1 PE=1 SV=1	-0.41
sp P54071 IDHP_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	-0.41
sp Q3U9G9 LBR_MOUSE	Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	-0.41
sp Q61390 TCPW_MOUSE	T-complex protein 1 subunit zeta-2 OS=Mus musculus GN=Cct6b PE=2 SV=4	-0.41
sp Q61753 SERA_MOUSE	D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	-0.41

sp P50247 SAHH_MOUSE	Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	-0.4
sp P62301 RS13_MOUSE	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	-0.4
sp P62631 EF1A2_MOUSE	Elongation factor 1-alpha 2 OS=Mus musculus GN=Eef1a2 PE=1 SV=1	-0.4
sp Q61937 NPM_MOUSE	Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	-0.4
sp Q6ZWN5 RS9_MOUSE	40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	-0.4
sp Q91VW3 SH3L3_MOUSE	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Mus musculus GN=Sh3bgrl3 PE=1 SV=1	-0.4
sp P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2	-0.39
sp P17742 PPIA_MOUSE	Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2	-0.39
sp P25444 RS2_MOUSE	40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	-0.39
sp Q9CR57 RL14_MOUSE	60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=2 SV=3	-0.39
sp O55131 SEPT7_MOUSE	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	-0.38
sp O70435 PSA3_MOUSE	Proteasome subunit alpha type-3 OS=Mus musculus GN=Pma3 PE=1 SV=3	-0.38
sp P26443 DHE3_MOUSE	Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	-0.38
sp P26638 SYSC_MOUSE	Seryl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Sars PE=2 SV=3	-0.38
sp P61082 UBC12_MOUSE	NEDD8-conjugating enzyme Ubc12 OS=Mus musculus GN=Ube2m PE=2 SV=1	-0.38
sp P62827 RAN_MOUSE	GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3	-0.38
sp P86048 RL10L_MOUSE	60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=1	-0.38
sp Q6ZWV3 RL10_MOUSE	60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3	-0.38
sp Q8VDW0 DX39A_MOUSE	ATP-dependent RNA helicase DDX39A OS=Mus musculus GN=Ddx39a PE=2 SV=1	-0.38
sp Q9CZX8 RS19_MOUSE	40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=3	-0.38
sp Q9DCL9 PUR6_MOUSE	Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4	-0.38
sp P05201 AATC_MOUSE	Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Got1 PE=1 SV=3	-0.37
sp P26883 FKB1A_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=2 SV=2	-0.37
sp P49718 MCM5_MOUSE	DNA replication licensing factor MCM5 OS=Mus musculus GN=Mcm5 PE=2 SV=1	-0.37
sp P62918 RL8_MOUSE	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	-0.37
sp Q921H8 THIKA_MOUSE	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=2 SV=1	-0.37
sp Q6PDM2 SRSF1_MOUSE	Serine/arginine-rich splicing factor 1 OS=Mus musculus GN=Srsf1 PE=1 SV=3	-0.36

sp Q9EST5 AN32B_MOUSE	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Mus musculus GN=Anp32b PE=1 SV=1	-0.36
sp Q9R1P0 PSA4_MOUSE	Proteasome subunit alpha type-4 OS=Mus musculus GN=Psm4 PE=1 SV=1	-0.36
sp P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	-0.35
sp P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	-0.35
sp P43274 H14_MOUSE	Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2	-0.35
sp P62717 RL18A_MOUSE	60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	-0.35
sp Q7TQI3 OTUB1_MOUSE	Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2	-0.35
sp Q8VCH0 THIKB_MOUSE	3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1	-0.35
sp Q9QYJ0 DNJA2_MOUSE	DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1	-0.35
sp P47963 RL13_MOUSE	60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	-0.34
sp P48678 LMNA_MOUSE	Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	-0.34
sp P50516 VATA_MOUSE	V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2	-0.34
sp P51410 RL9_MOUSE	60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=2 SV=2	-0.34
sp Q61316 HSP74_MOUSE	Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1	-0.34
sp Q61599 GDIR2_MOUSE	Rho GDP-dissociation inhibitor 2 OS=Mus musculus GN=Arhgdib PE=1 SV=3	-0.34
sp Q6ZQ38 CAND1_MOUSE	Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	-0.34
sp Q7TPV4 MBB1A_MOUSE	Myb-binding protein 1A OS=Mus musculus GN=Mybbp1a PE=1 SV=2	-0.34
sp Q93092 TALDO_MOUSE	Transaldolase OS=Mus musculus GN=Taldo1 PE=1 SV=2	-0.34
sp Q9WTM5 RUVB2_MOUSE	RuvB-like 2 OS=Mus musculus GN=Ruvbl2 PE=2 SV=3	-0.34
sp Q9Z1N5 DX39B_MOUSE	Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1	-0.34
sp P62192 PRS4_MOUSE	26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	-0.33
sp P62702 RS4X_MOUSE	40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	-0.33
sp Q62095 DDX3Y_MOUSE	ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2	-0.33
sp Q8BP67 RL24_MOUSE	60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=2 SV=2	-0.33
sp Q9D8E6 RL4_MOUSE	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	-0.33
sp P19253 RL13A_MOUSE	60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	-0.32

sp P49722 PSA2_MOUSE	Proteasome subunit alpha type-2 OS=Mus musculus GN=Psm2 PE=1 SV=2	-0.32
sp P80317 TCPZ_MOUSE	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	-0.32
sp P84099 RL19_MOUSE	60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	-0.32
sp Q60668 HNRPD_MOUSE	Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=Hnrpd PE=1 SV=2	-0.32
sp Q68FL6 SYMC_MOUSE	Methionyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Mars PE=2 SV=1	-0.32
sp Q8BG32 PSD11_MOUSE	26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psm11 PE=1 SV=3	-0.32
sp Q91VI7 RINI_MOUSE	Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1	-0.32
sp O70251 EF1B_MOUSE	Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5	-0.31
sp P46638 RB11B_MOUSE	Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3	-0.31
sp P60122 RUVB1_MOUSE	RuvB-like 1 OS=Mus musculus GN=Ruvb1 PE=1 SV=1	-0.31
sp P62082 RS7_MOUSE	40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	-0.31
sp P62492 RB11A_MOUSE	Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a PE=1 SV=3	-0.31
sp P68040 GBLP_MOUSE	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3	-0.31
sp P97324 G6PD2_MOUSE	Glucose-6-phosphate 1-dehydrogenase 2 OS=Mus musculus GN=G6pd2 PE=2 SV=3	-0.31
sp Q07813 BAX_MOUSE	Apoptosis regulator BAX OS=Mus musculus GN=Bax PE=1 SV=1	-0.31
sp Q61598 GDIB_MOUSE	Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	-0.31
sp Q9CPR4 RL17_MOUSE	60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=2 SV=3	-0.31
sp P47911 RL6_MOUSE	60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3	-0.3
sp P62259 1433E_MOUSE	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	-0.3
sp Q68FD5 CLH_MOUSE	Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	-0.3
sp Q9CQV8 1433B_MOUSE	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	-0.3
sp Q9CXW4 RL11_MOUSE	60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4	-0.3
sp Q9D0E1 HNRPM_MOUSE	Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrpm PE=1 SV=3	-0.3
sp Q9DCN2 NB5R3_MOUSE	NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 PE=1 SV=3	-0.3
sp Q9JK81 MYG1_MOUSE	UPF0160 protein MYG1, mitochondrial OS=Mus musculus GN=Myg1 PE=2 SV=1	-0.3
sp Q9WV32 ARC1B_MOUSE	Actin-related protein 2/3 complex subunit 1B OS=Mus musculus GN=Arpc1b PE=1 SV=4	-0.3
sp Q9Z2U1 PSA5_MOUSE	Proteasome subunit alpha type-5 OS=Mus musculus	-0.3

	GN=Psm5 PE=1 SV=1	
sp O09167 RL21_MOUSE	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	-0.29
sp P10404 ENV1_MOUSE	MLV-related proviral Env polyprotein OS=Mus musculus PE=2 SV=3	-0.29
sp P11370 ENV2_MOUSE	Retrovirus-related Env polyprotein from Fv-4 locus OS=Mus musculus GN=Fv4 PE=1 SV=2	-0.29
sp P12970 RL7A_MOUSE	60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	-0.29
sp P14115 RL27A_MOUSE	60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=5	-0.29
sp P14148 RL7_MOUSE	60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	-0.29
sp P14152 MDHC_MOUSE	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	-0.29
sp P14733 LMNB1_MOUSE	Lamin-B1 OS=Mus musculus GN=Lmn1 PE=1 SV=3	-0.29
sp P53026 RL10A_MOUSE	60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	-0.29
sp P61979 HNRPK_MOUSE	Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrpk PE=1 SV=1	-0.29
sp Q6URW6 MYH14_MOUSE	Myosin-14 OS=Mus musculus GN=Myh14 PE=1 SV=1	-0.29
sp P00342 LDHC_MOUSE	L-lactate dehydrogenase C chain OS=Mus musculus GN=Ldhc PE=1 SV=2	-0.28
sp P31254 UBA1Y_MOUSE	Ubiquitin-like modifier-activating enzyme 1 Y OS=Mus musculus GN=Ube1ay PE=2 SV=2	-0.28
sp P41105 RL28_MOUSE	60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	-0.28
sp P62270 RS18_MOUSE	40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=2 SV=3	-0.28
sp Q01853 TERA_MOUSE	Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4	-0.28
sp Q02053 UBA1_MOUSE	Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus GN=Uba1 PE=1 SV=1	-0.28
sp Q9R0Q7 TEBP_MOUSE	Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1	-0.28
sp Q9Z1Q9 SYVC_MOUSE	Valyl-tRNA synthetase OS=Mus musculus GN=Vars PE=2 SV=1	-0.28
sp P07901 HS90A_MOUSE	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	-0.27
sp P32067 LA_MOUSE	Lupus La protein homolog OS=Mus musculus GN=Ssb PE=2 SV=1	-0.27
sp P70349 HINT1_MOUSE	Histidine triad nucleotide-binding protein 1 OS=Mus musculus GN=Hint1 PE=1 SV=3	-0.27
sp Q8BKC5 IPO5_MOUSE	Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	-0.27
sp Q9CR16 PPID_MOUSE	Peptidyl-prolyl cis-trans isomerase D OS=Mus musculus GN=Ppid PE=1 SV=3	-0.27
sp Q9QUM9 PSA6_MOUSE	Proteasome subunit alpha type-6 OS=Mus musculus GN=Psm6 PE=1 SV=1	-0.27
sp O09131 GSTO1_MOUSE	Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto1 PE=2 SV=2	-0.26
sp O70250 PGAM2_MOUSE	Phosphoglycerate mutase 2 OS=Mus musculus	-0.26

	GN=Pgam2 PE=1 SV=3	
sp P06801 MAOX_MOUSE	NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=2	-0.26
sp P08553 NFM_MOUSE	Neurofilament medium polypeptide OS=Mus musculus GN=Nefm PE=1 SV=4	-0.26
sp P11835 ITB2_MOUSE	Integrin beta-2 OS=Mus musculus GN=Itgb2 PE=1 SV=2	-0.26
sp P31001 DESM_MOUSE	Desmin OS=Mus musculus GN=Des PE=1 SV=3	-0.26
sp P46660 AINX_MOUSE	Alpha-internexin OS=Mus musculus GN=Ina PE=1 SV=2	-0.26
sp P47962 RL5_MOUSE	60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	-0.26
sp P70168 IMB1_MOUSE	Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2	-0.26
sp Q8BMJ2 SYLC_MOUSE	Leucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Lars PE=2 SV=2	-0.26
sp Q8VDD5 MYH9_MOUSE	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-0.26
sp Q922Q8 LRC59_MOUSE	Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=2 SV=1	-0.26
sp Q99L47 F10A1_MOUSE	Hsc70-interacting protein OS=Mus musculus GN=St13 PE=2 SV=1	-0.26
sp P35980 RL18_MOUSE	60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=3	-0.25
sp P42932 TCPQ_MOUSE	T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3	-0.25
sp Q61029 LAP2B_MOUSE	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4	-0.25
sp Q6ZQ06 QN1_MOUSE	Protein QN1 homolog OS=Mus musculus GN=Kiaa1009 PE=1 SV=2	-0.25
sp O08788 DCTN1_MOUSE	Dynactin subunit 1 OS=Mus musculus GN=Dctn1 PE=1 SV=3	-0.24
sp P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	-0.24
sp P16125 LDHB_MOUSE	L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2	-0.24
sp P50580 PA2G4_MOUSE	Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3	-0.24
sp P62242 RS8_MOUSE	40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	-0.24
sp P62852 RS25_MOUSE	40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=2 SV=1	-0.24
sp P97351 RS3A_MOUSE	40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	-0.24
sp Q5SWU9 ACACA_MOUSE	Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	-0.24
sp Q9EQU5 SET_MOUSE	Protein SET OS=Mus musculus GN=Set PE=1 SV=1	-0.24
sp P08752 GNAI2_MOUSE	Guanine nucleotide-binding protein G(i) subunit alpha- 2 OS=Mus musculus GN=Gnai2 PE=1 SV=5	-0.23
sp P48036 ANXA5_MOUSE	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	-0.23

sp P60764 RAC3_MOUSE	Ras-related C3 botulinum toxin substrate 3 OS=Mus musculus GN=Rac3 PE=1 SV=1	-0.23
sp P62754 RS6_MOUSE	40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	-0.23
sp P63001 RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	-0.23
sp P70372 ELAV1_MOUSE	ELAV-like protein 1 OS=Mus musculus GN=Elavl1 PE=1 SV=2	-0.23
sp P80315 TCPD_MOUSE	T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	-0.23
sp Q61879 MYH10_MOUSE	Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	-0.23
sp O70456 1433S_MOUSE	14-3-3 protein sigma OS=Mus musculus GN=Sfn PE=1 SV=2	-0.22
sp P00375 DYR_MOUSE	Dihydrofolate reductase OS=Mus musculus GN=Dhfr PE=1 SV=3	-0.22
sp P10630 IF4A2_MOUSE	Eukaryotic initiation factor 4A-II OS=Mus musculus GN=Eif4a2 PE=2 SV=2	-0.22
sp P16110 LEG3_MOUSE	Galectin-3 OS=Mus musculus GN=Lgals3 PE=1 SV=3	-0.22
sp P16381 DDX3L_MOUSE	Putative ATP-dependent RNA helicase PI10 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	-0.22
sp P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	-0.22
sp P37040 NCPR_MOUSE	NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	-0.22
sp P80314 TCPB_MOUSE	T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	-0.22
sp Q62167 DDX3X_MOUSE	ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3	-0.22
sp Q9CZM2 RL15_MOUSE	60S ribosomal protein L15 OS=Mus musculus GN=Rpl15 PE=2 SV=4	-0.22
sp P24452 CAPG_MOUSE	Macrophage-capping protein OS=Mus musculus GN=Capg PE=1 SV=2	-0.21
sp P60335 PCBP1_MOUSE	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	-0.21
sp P61089 UBE2N_MOUSE	Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1	-0.21
sp Q61990 PCBP2_MOUSE	Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	-0.21
sp Q9CQ65 MTAP_MOUSE	S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=2 SV=1	-0.21
sp P34022 RANG_MOUSE	Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	-0.2
sp Q00612 G6PD1_MOUSE	Glucose-6-phosphate 1-dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3	-0.2
sp Q9D8N0 EF1G_MOUSE	Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3	-0.2
sp P11499 HS90B_MOUSE	Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3	-0.19
sp P19096 FAS_MOUSE	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	-0.19
sp P60867 RS20_MOUSE	40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	-0.19

sp P63101 1433Z_MOUSE	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	-0.19
sp P80318 TCPG_MOUSE	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	-0.19
sp Q61699 HS105_MOUSE	Heat shock protein 105 kDa OS=Mus musculus GN=Hsph1 PE=1 SV=2	-0.19
sp Q8C0C7 SYFA_MOUSE	Phenylalanyl-tRNA synthetase alpha chain OS=Mus musculus GN=Farsa PE=2 SV=1	-0.19
sp Q9CPU0 LGUL_MOUSE	Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=3	-0.19
sp Q9Z2U0 PSA7_MOUSE	Proteasome subunit alpha type-7 OS=Mus musculus GN=Pspa7 PE=1 SV=1	-0.19
sp O08749 DLDH_MOUSE	Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2	-0.18
sp O35326 SRSF5_MOUSE	Serine/arginine-rich splicing factor 5 OS=Mus musculus GN=Srsf5 PE=1 SV=1	-0.18
sp P57722 PCBP3_MOUSE	Poly(rC)-binding protein 3 OS=Mus musculus GN=Pcbp3 PE=2 SV=3	-0.18
sp P70333 HNRH2_MOUSE	Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrph2 PE=1 SV=1	-0.18
sp Q8R1B4 EIF3C_MOUSE	Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1	-0.18
sp O08638 MYH11_MOUSE	Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	-0.17
sp P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	-0.17
sp Q3UM45 PP1R7_MOUSE	Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2	-0.17
sp Q61820 RANT_MOUSE	GTP-binding nuclear protein Ran, testis-specific isoform OS=Mus musculus GN=Rasl2-9 PE=2 SV=1	-0.17
sp Q7TMK9 HNRPQ_MOUSE	Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncrip PE=1 SV=2	-0.17
sp Q9DBJ1 PGAM1_MOUSE	Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3	-0.17
sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=1 SV=1	-0.16
sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	-0.16
sp P10107 ANXA1_MOUSE	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	-0.16
sp P15864 H12_MOUSE	Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	-0.16
sp P40142 TKT_MOUSE	Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1	-0.16
sp P43277 H13_MOUSE	Histone H1.3 OS=Mus musculus GN=Hist1h1d PE=1 SV=2	-0.16
sp P61255 RL26_MOUSE	60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=2 SV=1	-0.16
sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=Rps27a PE=1 SV=2	-0.16
sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Uba52 PE=1 SV=2	-0.16
sp P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus musculus GN=Ywhaq	-0.16

	PE=1 SV=1	
sp P68510 1433F_MOUSE	14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	-0.16
sp P84104 SRSF3_MOUSE	Serine/arginine-rich splicing factor 3 OS=Mus musculus GN=Srsf3 PE=1 SV=1	-0.16
sp P97461 RS5_MOUSE	40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=2 SV=3	-0.16
sp Q8VDM4 PSMD2_MOUSE	26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psm2 PE=1 SV=1	-0.16
sp Q91VC3 IF4A3_MOUSE	Eukaryotic initiation factor 4A-III OS=Mus musculus GN=Eif4a3 PE=2 SV=3	-0.16
sp P17183 ENOG_MOUSE	Gamma-enolase OS=Mus musculus GN=Eno2 PE=1 SV=2	-0.15
sp P17751 TPIS_MOUSE	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	-0.15
sp P17879 HS71B_MOUSE	Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3	-0.15
sp P23116 EIF3A_MOUSE	Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=Eif3a PE=1 SV=5	-0.15
sp P60843 IF4A1_MOUSE	Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=2 SV=1	-0.15
sp Q61696 HS71A_MOUSE	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	-0.15
sp Q64467 G3PT_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Mus musculus GN=Gapdhs PE=1 SV=1	-0.15
sp Q64674 SPEE_MOUSE	Spermidine synthase OS=Mus musculus GN=Srm PE=2 SV=1	-0.15
sp Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	-0.15
sp Q9D1A2 CNDP2_MOUSE	Cytosolic non-specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1	-0.15
sp Q9JKF1 IQGA1_MOUSE	Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=1	-0.15
sp P14131 RS16_MOUSE	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV=4	-0.14
sp P17156 HSP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2	-0.14
sp P30416 FKBP4_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus GN=Fkbp4 PE=1 SV=5	-0.14
sp P43275 H11_MOUSE	Histone H1.1 OS=Mus musculus GN=Hist1h1a PE=2 SV=2	-0.14
sp P80313 TCPH_MOUSE	T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	-0.14
sp Q5XJY5 COPD_MOUSE	Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=2 SV=2	-0.14
sp Q9DCD0 6PGD_MOUSE	6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=2 SV=3	-0.14
sp P01895 HA1Y_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus GN=H2-D1 PE=2 SV=1	-0.13
sp P01896 HA1Z_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus PE=1 SV=1	-0.13
sp P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus musculus	-0.13

	GN=Hspa1l PE=2 SV=4	
sp P18760 COF1_MOUSE	Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3	-0.13
sp P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	-0.13
sp P62830 RL23_MOUSE	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	-0.13
sp P62835 RAP1A_MOUSE	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=2 SV=1	-0.13
sp Q3U0V1 FUBP2_MOUSE	Far upstream element-binding protein 2 OS=Mus musculus GN=Khsrp PE=1 SV=2	-0.13
sp Q99Jl6 RAP1B_MOUSE	Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=2 SV=2	-0.13
sp Q9WUU7 CATZ_MOUSE	Cathepsin Z OS=Mus musculus GN=Ctsz PE=2 SV=1	-0.13
sp Q35737 HNRH1_MOUSE	Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrph1 PE=1 SV=3	-0.12
sp P14206 RSSA_MOUSE	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	-0.12
sp P35979 RL12_MOUSE	60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	-0.12
sp P62908 RS3_MOUSE	40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	-0.12
sp Q8VDP4 K1967_MOUSE	Protein KIAA1967 homolog OS=Mus musculus PE=1 SV=2	-0.12
sp Q920E5 FPPS_MOUSE	Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps PE=2 SV=1	-0.12
sp P05213 TBA1B_MOUSE	Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2	-0.11
sp P25206 MCM3_MOUSE	DNA replication licensing factor MCM3 OS=Mus musculus GN=Mcm3 PE=1 SV=2	-0.11
sp P35700 PRDX1_MOUSE	Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	-0.11
sp P52480 KPYM_MOUSE	Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	-0.11
sp Q8BK67 RCC2_MOUSE	Protein RCC2 OS=Mus musculus GN=Rcc2 PE=2 SV=1	-0.11
sp Q921F2 TADBP_MOUSE	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	-0.11
sp P01900 HA12_MOUSE	H-2 class I histocompatibility antigen, D-D alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=1	-0.1
sp P06800 PTPRC_MOUSE	Receptor-type tyrosine-protein phosphatase C OS=Mus musculus GN=Ptprc PE=1 SV=3	-0.1
sp P60766 CDC42_MOUSE	Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=2	-0.1
sp P62855 RS26_MOUSE	40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=2 SV=3	-0.1
sp P68369 TBA1A_MOUSE	Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	-0.1
sp Q05144 RAC2_MOUSE	Ras-related C3 botulinum toxin substrate 2 OS=Mus musculus GN=Rac2 PE=2 SV=1	-0.1
sp Q3V3R1 C1TM_MOUSE	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Mus musculus GN=Mthfd1l PE=1 SV=2	-0.1

sp Q91V92 ACLY_MOUSE	ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	-0.1
sp P21550 ENOB_MOUSE	Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	-0.09
sp P68373 TBA1C_MOUSE	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1	-0.09
sp P97310 MCM2_MOUSE	DNA replication licensing factor MCM2 OS=Mus musculus GN=Mcm2 PE=1 SV=3	-0.09
sp Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	-0.09
sp Q8VE97 SRSF4_MOUSE	Serine/arginine-rich splicing factor 4 OS=Mus musculus GN=Srsf4 PE=2 SV=1	-0.09
sp Q9CWH6 PSA7L_MOUSE	Proteasome subunit alpha type-7-like OS=Mus musculus GN=Psm8 PE=2 SV=1	-0.09
sp P05214 TBA3_MOUSE	Tubulin alpha-3 chain OS=Mus musculus GN=Tuba3a PE=1 SV=1	-0.08
sp P29341 PABP1_MOUSE	Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=2	-0.08
sp P50396 GDIA_MOUSE	Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3	-0.08
sp P97311 MCM6_MOUSE	DNA replication licensing factor MCM6 OS=Mus musculus GN=Mcm6 PE=1 SV=1	-0.08
sp Q04447 KCRB_MOUSE	Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1	-0.08
sp Q9R1P4 PSA1_MOUSE	Proteasome subunit alpha type-1 OS=Mus musculus GN=Psm1 PE=1 SV=1	-0.08
sp P00920 CAH2_MOUSE	Carbonic anhydrase 2 OS=Mus musculus GN=Ca2 PE=1 SV=4	-0.07
sp P58252 EF2_MOUSE	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	-0.07
sp P62849 RS24_MOUSE	40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1	-0.07
sp P68368 TBA4A_MOUSE	Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1	-0.07
sp Q78PY7 SND1_MOUSE	Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1	-0.07
sp O08528 HXK2_MOUSE	Hexokinase-2 OS=Mus musculus GN=Hk2 PE=1 SV=1	-0.06
sp P05064 ALDOA_MOUSE	Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	-0.06
sp P23492 PNPH_MOUSE	Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2	-0.06
sp P53657 KPYR_MOUSE	Pyruvate kinase isozymes R/L OS=Mus musculus GN=Pklr PE=2 SV=1	-0.06
sp P61982 1433G_MOUSE	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	-0.06
sp Q09014 NCF1_MOUSE	Neutrophil cytosol factor 1 OS=Mus musculus GN=Ncf1 PE=1 SV=3	-0.06
sp Q5SW19 K0664_MOUSE	Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 PE=2 SV=2	-0.06
sp Q60864 STIP1_MOUSE	Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1	-0.06
sp Q60875 ARHG2_MOUSE	Rho guanine nucleotide exchange factor 2 OS=Mus	-0.06

	musculus GN=Arhgef2 PE=1 SV=4	
sp Q9D0B0 SRSF9_MOUSE	Serine/arginine-rich splicing factor 9 OS=Mus musculus GN=Srsf9 PE=1 SV=1	-0.06
sp Q9DCH4 EIF3F_MOUSE	Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Elf3f PE=1 SV=2	-0.06
sp P05063 ALDOC_MOUSE	Fructose-bisphosphate aldolase C OS=Mus musculus GN=Aldoc PE=1 SV=4	-0.05
sp P09041 PGK2_MOUSE	Phosphoglycerate kinase 2 OS=Mus musculus GN=Pgk2 PE=1 SV=4	-0.05
sp P58771 TPM1_MOUSE	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	-0.05
sp P58774 TPM2_MOUSE	Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1	-0.05
sp Q61656 DDX5_MOUSE	Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=Ddx5 PE=1 SV=2	-0.05
sp Q9Z2X1 HNRPF_MOUSE	Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnrnpf PE=1 SV=3	-0.05
sp A2AQ07 TBB1_MOUSE	Tubulin beta-1 chain OS=Mus musculus GN=Tubb1 PE=1 SV=1	-0.04
sp P09411 PGK1_MOUSE	Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4	-0.04
sp P21107 TPM3_MOUSE	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2	-0.04
sp Q921E2 RAB31_MOUSE	Ras-related protein Rab-31 OS=Mus musculus GN=Rab31 PE=1 SV=1	-0.04
sp P61161 ARP2_MOUSE	Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	-0.03
sp Q6PB66 LPPRC_MOUSE	Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	-0.03
sp Q78ZA7 NP1L4_MOUSE	Nucleosome assembly protein 1-like 4 OS=Mus musculus GN=Nap1l4 PE=1 SV=1	-0.03
sp P26041 MOES_MOUSE	Moesin OS=Mus musculus GN=Msn PE=1 SV=3	-0.02
sp P47757 CAPZB_MOUSE	F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb PE=1 SV=3	-0.02
sp P62962 PROF1_MOUSE	Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	-0.01
sp P84084 ARF5_MOUSE	ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=2 SV=2	-0.01
sp Q641P0 ARP3B_MOUSE	Actin-related protein 3B OS=Mus musculus GN=Actr3b PE=2 SV=1	-0.01
sp Q9WUM4 COR1C_MOUSE	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	-0.01

Table 12. Effect of *Echinacea* extract 7 and alkylamide-11 a/b on LPS induced proteins.

Sequence Id	Sequence Name	LPS Ratio -2	LPS+ <i>Echinacea</i> extract 7 Ratio-2	alkylamid e-11 a/b +LPS Ratio-2	LPS Ratio -1	LPS+ <i>Echinacea</i> extract 7Ratio-1
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sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	4.89	-10	6.1	3.6	-10
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcks1 PE=1 SV=2	4.15	3.42	4.9	1.63	0.93
sp P54987 IRG1_MOUSE	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	3.58	-10	7.08	3.1	4.26
sp P61957 SUMO2_MOUSE	Small ubiquitin-related modifier 2 OS=Mus musculus GN=Sumo2 PE=2 SV=1	3.1	1.97	3.44	0.17	-0.12
sp Q9Z172 SUMO3_MOUSE	Small ubiquitin-related modifier 3 OS=Mus musculus GN=Sumo3 PE=2 SV=1	3.1	1.97	3.44	0.17	-0.12
sp Q9CQS8 SC61B_MOUSE	Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3	3	-10	-0.31	1.02	0.63
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	2.49	1.41	1.89	1.04	0.71
sp P99029 PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2	2.23	2.52	1.76	1.13	0.38
sp Q9WVK4 EHD1_MOUSE	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	2.09	-10	2.4	0.61	0.49
sp Q62433 NDRG1_MOUSE	Protein NDRG1	2.05	-10	2.05	0.82	0.4

SE	OS=Mus musculus GN=Ndrp1 PE=1 SV=1					
sp Q9JMH6 TRXR1_MOUSE SE	Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txnrd1 PE=1 SV=3	1.75	-10	1.18	0.71	0.87
sp P35700 PRDX1_MOUSE E	Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	1.52	2.5	1.6	0.11	0.78
sp P62835 RAP1A_MOUSE E	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=2 SV=1	1.47	0.46	0.47	0.38	0.03
sp Q99JI6 RAP1B_MOUSE E	Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=2 SV=2	1.47	0.46	0.47	0.38	0.03
sp P03995 GFAP_MOUSE	Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4	1.44	1.26	1.6	0.25	0.48
sp P45591 COF2_MOUSE	Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1	1.44	1.26	1.12	0.19	-0.2
sp O08807 PRDX4_MOUSE E	Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	1.43	-10	-10	0.1	0.9
sp P17809 GTR1_MOUSE	Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=4	1.43	1.03	1.16	0.91	0.86
sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus	1.36	1.27	1.11	0.42	-0.09

	GN=Actb PE=1 SV=1					
sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	1.36	1.27	1.11	0.42	-0.09
sp P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	1.35	0.67	1.05	0.46	0.06
sp P62737 ACTA_MOUSE	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	1.35	1.03	1.02	0.41	-0.1
sp P63268 ACTH_MOUSE	Actin, gamma- enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1	1.35	1.03	1.02	0.41	-0.1
sp P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	1.35	1.03	1.1	0.41	-0.1
sp P68134 ACTS_MOUSE	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	1.35	1.03	1.1	0.41	-0.1
sp Q9D1A2 CNDP2_MOUSE	Cytosolic non- specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1	1.28	0.82	0.74	0.78	0.24
sp Q91V41 RAB14_MOUSE	Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3	1.21	0.18	-0.18	0.05	-0.4
sp Q91XV3 BASP1_MOUSE	Brain acid soluble protein 1 OS=Mus musculus GN=Basp1 PE=1 SV=3	1.16	-10	0.8	1.53	0.4
sp P0C0S6 H2AZ_MOUSE	Histone H2A.Z	1.14	0.04	0.09	0.17	0.03

E	OS=Mus musculus GN=H2afz PE=1 SV=2					
sp P27661 H2AX_MOUSE	Histone H2A.x OS=Mus musculus GN=H2afx PE=1 SV=2	1.14	0.04	0.07	0.17	0.03
sp Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus musculus GN=H2afv PE=1 SV=3	1.14	0.04	0.09	0.17	0.03
sp Q64522 H2A2B_MOUSE	Histone H2A type 2-B OS=Mus musculus GN=Hist2h2ab PE=1 SV=3	1.14	0.04	0.07	0.17	0.03
sp Q8BTM8 FLNA_MOUSE	Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5	1.08	1.12	1.02	0.12	-0.02
sp Q71LX4 TLN2_MOUSE	Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	1.07	0.29	1.05	0.37	0.15
sp Q80X90 FLNB_MOUSE	Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=3	1.04	0.8	0.73	0.02	0.06
sp P05555 ITAM_MOUSE	Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=2	0.98	1.65	1.38	0.74	0.13
sp P22752 H2A1_MOUSE	Histone H2A type 1 OS=Mus musculus GN=Hist1h2ab PE=1 SV=3	0.97	-0.01	0.26	0.09	-0.15
sp Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac PE=1 SV=3	0.97	-0.01	0.26	0.09	-0.15
sp Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus musculus GN=Hist2h2aa1 PE=1 SV=3	0.97	-0.01	0.26	0.09	-0.15
sp Q8CGP5 H2A1F_MOUSE	Histone H2A type	0.97	-0.01	0.26	0.09	-0.15

SE	1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3					
sp Q8CGP6 H2A1H_MOUSE	Histone H2A type 1-H OS=Mus musculus GN=Hist1h2ah PE=1 SV=3	0.97	-0.01	0.26	0.09	-0.15
sp Q8CGP7 H2A1K_MOUSE	Histone H2A type 1-K OS=Mus musculus GN=Hist1h2ak PE=1 SV=3	0.97	-0.01	0.26	0.09	-0.15
sp Q8R1M2 H2AJ_MOUSE	Histone H2A.J OS=Mus musculus GN=H2afj PE=2 SV=1	0.97	-0.01	0.26	0.09	-0.15
sp Q69ZN7 MYOF_MOUSE	Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	0.96	0.93	0.69	1.27	1.47
sp P37040 NCPR_MOUSE	NADPH-- cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	0.9	-10	0.71	4.01	-2.98
sp P62821 RAB1A_MOUSE	Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3	0.84	0.1	-10	0.35	0.19
sp P40124 CAP1_MOUSE	Adenylyl cyclase- associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	0.8	-10	0.21	0.51	0.33
sp Q99PT1 GDIR1_MOUSE	Rho GDP- dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	0.77	-0.56	-0.13	0.7	-0.16
sp P10852 4F2_MOUSE	4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	0.74	1	1.06	0.74	0.34

sp Q9ES52 SHIP1_MOUSE	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1 OS=Musculus GN=Inpp5d PE=1 SV=2	0.74	-10	0.05	0.1	-0.31
sp P26041 MOES_MOUSE	Moesin OS=Musculus GN=Msn PE=1 SV=3	0.71	0.49	0.56	0.58	0.12
sp Q9ER72 SYCC_MOUSE	Cysteinyl-tRNA synthetase, cytoplasmic OS=Musculus GN=Cars PE=1 SV=2	0.64	0.24	0.48	0.51	0.33
sp P97429 ANXA4_MOUSE	Annexin A4 OS=Musculus GN=Anxa4 PE=2 SV=4	0.58	0.5	0.43	1.15	-10
sp P26040 EZRI_MOUSE	Ezrin OS=Musculus GN=Ezr PE=1 SV=3	0.56	0.48	0.39	0.52	0.12
sp Q3THS6 METK2_MOUSE	S-adenosylmethionine synthase isoform type-2 OS=Musculus GN=Mat2a PE=2 SV=2	0.56	0.07	0.12	0.06	0.08
sp P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=Musculus GN=P4hb PE=1 SV=2	0.55	0.46	0.41	0.81	0.26
sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Musculus GN=Ubb PE=1 SV=1	0.55	0.19	0.42	0.54	0.29
sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Musculus GN=Ubc PE=1 SV=2	0.55	0.19	0.42	0.54	0.29
sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Musculus GN=Rps27a PE=1	0.55	0.19	0.42	0.45	0.25

	SV=2					
sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Uba52 PE=1 SV=2	0.55	0.19	0.42	0.54	0.29
sp P47955 RLA1_MOUSE	60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1	0.53	-10	0.18	0.67	-0.04
sp P63101 1433Z_MOUSE	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	0.53	0.11	-0.01	0.4	0
sp Q64727 VINC_MOUSE	Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	0.52	-0.31	0.1	0.28	0.13
sp P20029 GRP78_MOUSE	78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	0.51	0.61	0.49	0.68	0.35
sp P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	0.45	0.38	0.19	0.55	0.08
sp P17156 HSP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2	0.44	0.42	0.17	0.56	0.1
sp P35278 RAB5C_MOUSE	Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	0.44	0.5	0.03	0.16	-0.34
sp P29341 PABP1_MOUSE	Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=2	0.43	0.08	-0.12	0.31	-0.08
sp P11835 ITB2_MOUSE	Integrin beta-2 OS=Mus	0.39	0.77	0.62	0.49	-0.01

	musculus GN=Itgb2 PE=1 SV=2					
sp P16627 HS71L_MOUSE E	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	0.39	0.15	0.15	0.58	0.18
sp P26043 RADI_MOUSE	Radixin OS=Mus musculus GN=Rdx PE=1 SV=3	0.39	0.48	0.39	0.56	0.01
sp P07356 ANXA2_MOUSE E	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	0.38	0.39	0.38	0.05	-0.07
sp P58771 TPM1_MOUSE	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	0.36	0.24	-0.06	0.37	-0.15
sp P21107 TPM3_MOUSE	Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2	0.35	0.31	0.05	0.35	-0.13
sp P58774 TPM2_MOUSE	Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1	0.33	0.24	-0.06	0.37	-0.15
sp O08810 U5S1_MOUSE	116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1	0.32	0.26	0.11	0.38	-0.11
sp Q6IRU2 TPM4_MOUSE E	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=3	0.32	-10	0.81	0.76	0.17
sp P14733 LMNB1_MOUSE E	Lamin-B1 OS=Mus musculus GN=Lmnb1 PE=1 SV=3	0.3	-0.11	-0.41	0.27	-0.48
sp P58252 EF2_MOUSE	Elongation factor 2	0.3	0.12	0.02	0.42	0.02

	OS=Mus musculus GN=Eef2 PE=1 SV=2					
sp Q61233 PLSL_MOUSE	Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4	0.3	-0.12	0.08	0.41	-0.08
sp Q61937 NPM_MOUSE	Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	0.3	-0.68	0.43	0.31	-0.02
sp Q99PL5 RRBP1_MOUSE	Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=2 SV=2	0.29	-10	-10	0.37	-0.16
sp P29351 PTN6_MOUSE	Tyrosine-protein phosphatase non- receptor type 6 OS=Mus musculus GN=Ptpn6 PE=1 SV=2	0.26	-10	0.19	0.16	0.24
sp Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	0.26	0.12	-0.16	0.36	0.25
sp P47915 RL29_MOUSE	60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2	0.24	-0.41	0.32	0.45	-0.06
sp Q9Z1Q5 CLIC1_MOUSE	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	0.24	0.18	0.35	0.3	-0.1
sp P61982 1433G_MOUSE	14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	0.19	0.07	0.28	0.37	0.06
sp P09411 PGK1_MOUSE	Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4	0.18	0.14	0.07	0.41	0
sp P17879 HS71B_MOUSE	Heat shock 70	0.18	-0.55	0.09	0.59	0.2

E	kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3					
sp P62492 RB11A_MOUSE E	Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a PE=1 SV=3	0.18	-10	-10	0.2	-0.59
sp Q61696 HS71A_MOUSE E	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	0.18	-0.55	0.09	0.59	0.2
sp Q8BGQ7 SYAC_MOUSE E	Alanyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1	0.18	0.02	0.34	0.23	-0.17
sp P10107 ANXA1_MOUSE E	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	0.15	-0.54	-0.13	0.26	-0.09
sp Q8VDJ3 VIGLN_MOUSE E	Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	0.15	-10	-0.5	0.38	-0.19
sp Q00612 G6PD1_MOUSE E	Glucose-6- phosphate 1- dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3	0.12	0.49	-0.04	0.28	0.32
sp P38647 GRP75_MOUSE E	Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	0.11	0.06	0.27	0.23	-0.09
sp Q9R1P4 PSA1_MOUSE E	Proteasome subunit alpha type-1 OS=Mus musculus GN=Pma1 PE=1 SV=1	0.11	-0.14	-0.09	0.38	-0.04
sp P57780 ACTN4_MOUSE E	Alpha-actinin-4 OS=Mus	0.09	0.12	-0.13	0.25	0.13

	musculus GN=Actn4 PE=1 SV=1					
sp P61027 RAB10_MOUSE	Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	0.09	-0.17	0.14	0.23	0.04
sp P17751 TPIS_MOUSE	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	0.07	-0.11	-0.15	0.47	-0.01
sp Q9CXW3 CYBP_MOUSE	Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	0.07	-10	-0.01	0.27	-10
sp P09041 PGK2_MOUSE	Phosphoglycerate kinase 2 OS=Mus musculus GN=Pgk2 PE=1 SV=4	0.05	-0.01	-0.02	0.46	0.01
sp P48036 ANXA5_MOUSE	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	0.05	0.13	0.1	0.76	0.23
sp P61089 UBE2N_MOUSE	Ubiquitin- conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1	0.04	-0.27	0.03	0.03	-0.15
sp P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1	0.04	-0.09	-0.15	0.33	-0.05
sp Q01853 TERA_MOUSE	Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4	0.04	-0.15	-0.15	0.32	0.06
sp O70456 1433S_MOUSE	14-3-3 protein sigma OS=Mus musculus GN=Sfn PE=1 SV=2	0.03	-10	-0.15	0.48	-0.02
sp P13020 GELS_MOUSE	Gelsolin OS=Mus musculus	0.03	0.43	0.19	0.41	-0.09

	GN=Gsn PE=1 SV=3					
sp P18760 COF1_MOUSE	Cofilin-1 OS=Mus musculus GN=Cf1 PE=1 SV=3	0.02	-0.09	-0.21	0.16	-0.2
sp P28656 NP1L1_MOUSE	Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap111 PE=1 SV=2	0.02	-10	-10	0.49	0.01
sp Q9CQV8 1433B_MOUSE	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	0.02	0.07	-0.14	0.31	-0.02
sp P26443 DHE3_MOUSE	Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	0.01	-0.22	-0.07	0.27	-0.47

Table 13. Effect of *Echinacea* extract 7 and alkalamide-11 a/b on LPS suppressed proteins.

Sequence Id	Sequence Name	Ips Ratio	Ips+ <i>Echinacea</i> extract 7 Ratio	alkalami de-11 a/b +Ips Ratio	Ips Ratio	Ips+ <i>Echinacea</i> extract 7 Ratio
sp O55131 SEPT7_MOUSE	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	-10	-10	0.06	-10	-10
sp O70152 DPM1_MOUSE	Dolichol-phosphate mannosyltransferase OS=Mus musculus GN=Dpm1 PE=2 SV=1	-10	-10	-10	-10	-10
sp O88844 IDHC_MOUSE	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=Idh1 PE=1 SV=2	-10	-10	-0.44	-0.89	-1.01
sp P01895 HA1Y_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus GN=H2- D1 PE=2 SV=1	-10	-10	1.07	-10	-0.14
sp P01896 HA1Z_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus PE=1	-10	-10	1.07	-10	-0.14

	SV=1					
sp P01942 HBA_MOUSE	Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2	-10	-10	-10	-10	-10
sp P03930 ATP8_MOUSE	ATP synthase protein 8 OS=Mus musculus GN=Mtstp8 PE=1 SV=1	-10	-10	-10	-10	-0.56
sp P08752 GNAI2_MOUSE	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5	-10	-10	-0.4	-0.6	-0.78
sp P24369 PPIB_MOUSE	Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=2 SV=2	-10	-10	-0.42	-10	-0.01
sp P26516 PSD7_MOUSE	26S proteasome non- ATPase regulatory subunit 7 OS=Mus musculus GN=Psmc7 PE=1 SV=2	-10	-10	-0.01	-10	-0.43
sp P28738 KIF5C_MOUSE	Kinesin heavy chain isoform 5C OS=Mus musculus GN=Kif5c PE=1 SV=3	-10	-10	-0.05	-0.1	-0.09
sp P29758 OAT_MOUSE	Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1	-10	-10	-10	-0.05	-0.15
sp P33175 KIF5A_MOUSE	Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3	-10	-10	-0.05	-0.1	-0.09
sp P49717 MCM4_MOUSE	DNA replication licensing factor MCM4 OS=Mus musculus GN=Mcm4 PE=2 SV=1	-10	-10	-10	-10	-1.4
sp P50396 GDIA_MOUSE	Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3	-10	-10	-0.42	-0.24	-0.31
sp P50516 VATA_MOUSE	V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2	-10	-10	-0.45	-10	-0.18
sp P53986 MOT1_MOUSE	Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	-10	-10	-10	-10	-0.7
sp P54071 IDHP_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	-10	-10	-0.49	-0.61	-0.68
sp P54775 PRS6B_MOUSE	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2	-10	-10	-10	-0.35	-0.19

sp P56135 ATPK_MOUSE SE	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=1 SV=3	-10	-10	-0.57	-10	-0.3
sp P57722 PCBP3_MOUSE USE	Poly(rC)-binding protein 3 OS=Mus musculus GN=Pcbp3 PE=2 SV=3	-10	-10	-0.28	-0.37	-0.38
sp P60867 RS20_MOUSE SE	40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	-10	-10	-0.55	-0.34	-0.36
sp P61161 ARP2_MOUSE SE	Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	-10	-10	0.35	-0.15	-0.44
sp P62082 RS7_MOUSE SE	40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	-10	-10	0.09	-0.39	-0.41
sp P62717 RL18A_MOUSE USE	60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	-10	-0.43	-0.77	-0.77	-0.59
sp P62806 H4_MOUSE SE	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	-10	-10	0.75	-0.06	-0.28
sp P62830 RL23_MOUSE SE	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	-10	-10	-0.26	-0.52	-0.45
sp P62855 RS26_MOUSE SE	40S ribosomal protein S26 OS=Mus musculus GN=Rps26 PE=2 SV=3	-10	-10	-10	-0.35	-0.44
sp P67984 RL22_MOUSE SE	60S ribosomal protein L22 OS=Mus musculus GN=Rpl22 PE=2 SV=2	-10	-10	-0.4	-0.42	-0.42
sp P68040 GBLP_MOUSE SE	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3	-10	-10	-10	-0.63	-0.58
sp P68433 H31_MOUSE SE	Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	-10	-10	0.71	-1.03	-0.94
sp P97310 MCM2_MOUSE SE	DNA replication licensing factor MCM2 OS=Mus musculus GN=Mcm2 PE=1 SV=3	-10	-10	-1.76	-3.13	-1.14
sp Q04646 ATNG_MOUSE SE	Sodium/potassium-transporting ATPase subunit gamma OS=Mus musculus GN=Fxyd2 PE=2 SV=2	-10	-10	-1.11	-0.13	0.04
sp Q09014 NCF1_MOUSE SE	Neutrophil cytosol factor 1 OS=Mus musculus GN=Ncf1 PE=1 SV=3	-10	-0.44	-10	-0.75	-0.39
sp Q3U9G9 LBR_MOUSE SE	Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	-10	-10	-0.09	-1.07	-0.57

sp Q501J6 DDX17_MO USE	Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	-10	-10	-0.21	- 0.22	-0.33
sp Q5SUR0 PUR4_MO USE	Phosphoribosylformylglycin amidine synthase OS=Mus musculus GN=Pfas PE=2 SV=1	-10	-0.92	-0.94	- 0.63	-0.54
sp Q5SW19 K0664_MO USE	Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 PE=2 SV=2	-10	-10	-10	- 0.29	0.4
sp Q5XJY5 COPD_MO USE	Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=2 SV=2	-10	-10	-10	-10	-10
sp Q60875 ARHG2_MO USE	Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 PE=1 SV=4	-10	-0.44	0.09	- 0.79	-0.33
sp Q60931 VDAC3_MO USE	Voltage-dependent anion- selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	-10	-10	-10	- 0.44	-10
sp Q60932 VDAC1_MO USE	Voltage-dependent anion- selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	-10	-10	-10	- 0.05	-0.2
sp Q61390 TCPW_MO USE	T-complex protein 1 subunit zeta-2 OS=Mus musculus GN=Cct6b PE=2 SV=4	-10	-10	-0.38	- 0.43	-0.42
sp Q61820 RANT_MOU SE	GTP-binding nuclear protein Ran, testis-specific isoform OS=Mus musculus GN=Rasl2-9 PE=2 SV=1	-10	-10	-10	- 0.47	-0.52
sp Q61990 PCBP2_MO USE	Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	-10	-10	-0.3	- 0.58	-0.51
sp Q62351 TFR1_MOU SE	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	-10	-10	-10	-10	-0.1
sp Q62425 NDUA4_MO USE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Mus musculus GN=Ndufa4 PE=1 SV=2	-10	-10	-0.82	-10	-0.74
sp Q641P0 ARP3B_MO USE	Actin-related protein 3B OS=Mus musculus GN=Actr3b PE=2 SV=1	-10	-10	0.37	- 0.58	-0.26
sp Q64518 AT2A3_MO USE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Mus musculus GN=Atp2a3 PE=2 SV=3	-10	-10	0.31	- 0.28	-0.29
sp Q64521 GPDM_MO USE	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus	-10	-10	-0.77	-10	0

	musculus GN=Gpd2 PE=1 SV=2					
sp Q64674 SPEE_MOUSE	Spermidine synthase OS=Mus musculus GN=Srm PE=2 SV=1	-10	-10	-0.85	-0.06	-10
sp Q6P1B1 XPP1_MOUSE	Xaa-Pro aminopeptidase 1 OS=Mus musculus GN=Xpnpep1 PE=2 SV=1	-10	-10	0.1	-10	0.11
sp Q6ZWU9 RS27_MOUSE	40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3	-10	-10	-0.3	-1.03	-1.3
sp Q6ZWW3 RL10_MOUSE	60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3	-10	-10	-10	-0.59	-0.53
sp Q6ZWY3 RS27L_MOUSE	40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=2 SV=3	-10	-10	-0.57	-1.28	-1.29
sp Q7M6Y3 PICA_MOUSE	Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus GN=Picalm PE=1 SV=1	-10	-10	-10	-10	-0.95
sp Q7TQI3 OTUB1_MOUSE	Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2	-10	-10	-10	-10	-0.53
sp Q8BG32 PSD11_MOUSE	26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psm11 PE=1 SV=3	-10	-10	-0.02	-0.03	-10
sp Q8BH04 PCKGM_MOUSE	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=2 SV=1	-10	-10	0.65	-10	-0.35
sp Q8BMJ2 SYLC_MOUSE	Leucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Lars PE=2 SV=2	-10	0.15	0.03	-0.59	-0.39
sp Q8BP47 SYNC_MOUSE	Asparaginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Nars PE=1 SV=2	-10	-10	0.48	-0.24	-0.19
sp Q8BU30 SYIC_MOUSE	Isoleucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=lars PE=2 SV=2	-10	-0.59	-0.14	-0.81	-0.49
sp Q8BWW3 ERF1_MOUSE	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Elf1 PE=1 SV=4	-10	-10	-10	-0.03	-0.29
sp Q8QZY1 EIF3L_MOUSE	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Elf3l PE=1 SV=1	-10	-10	-0.62	-0.07	-0.19
sp Q8R0W0 EPIPL_MOUSE	Epiplakin OS=Mus	-10	-10	1.41	-0.6	-0.36

USE	musculus GN=Eppk1 PE=1 SV=2					
sp Q8R429 AT2A1_MOU USE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1	-10	-10	0.19	-0.28	-0.09
sp Q8VDP4 K1967_MOU USE	Protein KIAA1967 homolog OS=Mus musculus PE=1 SV=2	-10	-10	-10	-0.22	-0.46
sp Q8VIJ6 SFPQ_MOU SE	Splicing factor, proline- and glutamine-rich OS=Mus musculus GN=Sfpq PE=1 SV=1	-10	-10	-0.58	-0.51	-0.53
sp Q91VR2 ATPG_MOU USE	ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	-10	-10	-0.38	-10	-10
sp Q921F2 TADBP_MOU USE	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	-10	-0.8	-10	-10	-0.63
sp Q99JY0 ECHB_MOU SE	Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	-10	-10	-10	-0.62	-10
sp Q99JY9 ARP3_MOU SE	Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3	-10	0.25	0.37	-0.58	-0.19
sp Q99LC5 ETFA_MOU SE	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2	-10	-10	-0.41	-0.54	-0.36
sp Q99LX0 PARK7_MOU USE	Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	-10	-10	-1.35	-10	-0.67
sp Q99MR6 SRRT_MOU USE	Serrate RNA effector molecule homolog OS=Mus musculus GN=Srrt PE=1 SV=1	-10	-10	-10	-0.04	-10
sp Q9BDB7 IF44L_MOU USE	Interferon-induced protein 44-like OS=Mus musculus GN=IFI44L PE=2 SV=2	-10	-10	3.86	-0.78	-10
sp Q9CPU0 LGUL_MOU USE	Lactoylglutathione lyase OS=Mus musculus GN=Glo1 PE=1 SV=3	-10	-10	-10	-10	-10
sp Q9CQ65 MTAP_MOU USE	S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=2 SV=1	-10	-10	-10	-10	-10
sp Q9CQI6 COTL1_MOU USE	Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3	-10	-10	0.98	-0.3	-0.54
sp Q9CR16 PPID_MOU SE	Peptidyl-prolyl cis-trans isomerase D OS=Mus	-10	-10	-0.72	-10	0.11

	musculus GN=Ppid PE=1 SV=3					
sp Q9CR62 M2OM_MOUSE	Mitochondrial 2-oxoglutarate/malate carrier OS=Mus musculus GN=Slc25a11 PE=1 SV=3	-10	-10	-10	-10	-10
sp Q9CXT8 MPPB_MOUSE	Mitochondrial-processing peptidase subunit beta OS=Mus musculus GN=Pmpcb PE=2 SV=1	-10	-0.63	-10	-0.23	-0.38
sp Q9CY57 FOP_MOUSE	Friend of PRMT1 protein OS=Mus musculus GN=Fop PE=1 SV=2	-10	0.74	-10	-10	0.14
sp Q9CY64 BIEA_MOUSE	Biliverdin reductase A OS=Mus musculus GN=Blvra PE=2 SV=1	-10	-10	-0.43	-0.79	-10
sp Q9D0I9 SYRC_MOUSE	Arginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Rars PE=2 SV=2	-10	-10	-0.48	-1.37	-0.3
sp Q9D1G1 RAB1B_MOUSE	Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	-10	-10	-10	-0.18	-0.69
sp Q9DAS9 GBG12_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Mus musculus GN=Gng12 PE=1 SV=3	-10	-0.23	-0.15	-0.01	-1.52
sp Q9DCC4 P5CR3_MOUSE	Pyrroline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycr1 PE=2 SV=2	-10	-0.84	-0.69	-10	-0.47
sp Q9DCC8 TOM20_MOUSE	Mitochondrial import receptor subunit TOM20 homolog OS=Mus musculus GN=Tom20 PE=1 SV=1	-10	-10	-10	-10	-10
sp Q9DCL9 PUR6_MOUSE	Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4	-10	-10	-1.25	-0.62	-0.57
sp Q9DCX2 ATP5H_MOUSE	ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	-10	-0.93	-0.66	-10	-0.56
sp Q9EQP2 EHD4_MOUSE	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	-10	-10	0.43	-0.14	-0.5
sp Q9JJI8 RL38_MOUSE	60S ribosomal protein L38 OS=Mus musculus GN=Rpl38 PE=2 SV=3	-10	-10	-10	-10	-0.45
sp Q9JLJ5 ELOV1_MOUSE	Elongation of very long chain fatty acids protein 1 OS=Mus musculus	-10	-0.57	-10	-0.57	0.02

	GN=Elov1 PE=2 SV=1					
sp Q9JMA1 UBP14_MOUSE	Ubiquitin carboxyl-terminal hydrolase 14 OS=Mus musculus GN=Usp14 PE=1 SV=3	-10	-10	-10	-0.13	-0.42
sp Q9QXK3 COPG2_MOUSE	Coatomer subunit gamma-2 OS=Mus musculus GN=Copg2 PE=2 SV=1	-10	-10	0.09	-10	-10
sp Q9QYJ0 DNJA2_MOUSE	DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1	-10	-10	-10	-10	-0.33
sp Q9QZE5 COPG_MOUSE	Coatomer subunit gamma OS=Mus musculus GN=Copg PE=2 SV=1	-10	-10	0.03	-0.86	-0.24
sp Q9WUM4 COR1C_MOUSE	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	-10	-10	-0.33	-10	-0.9
sp Q9Z2I8 SUCB2_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Suc1g2 PE=2 SV=3	-10	-10	-10	-10	-10
sp A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn PE=1 SV=1	-7.6	-1.2	0.28	-10	4.96
sp P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus GN=Lyz2 PE=1 SV=2	-3.06	-1.96	-1.78	-0.41	-0.24
sp P17897 LYZ1_MOUSE	Lysozyme C-1 OS=Mus musculus GN=Lyz1 PE=1 SV=1	-3.06	-1.96	-1.78	-0.33	-0.29
sp P25206 MCM3_MOUSE	DNA replication licensing factor MCM3 OS=Mus musculus GN=Mcm3 PE=1 SV=2	-1.7	-10	-1.62	-1.12	-0.99
sp P43276 H15_MOUSE	Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	-1.64	-10	-1.4	-0.3	-0.62
sp Q91ZX7 LRP1_MOUSE	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	-1.55	-10	-1.71	-0.9	-0.54
sp Q91VD9 NDUS1_MOUSE	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2	-1.23	-0.99	-1.32	-10	-10
sp P49718 MCM5_MOUSE	DNA replication licensing factor MCM5 OS=Mus musculus GN=Mcm5 PE=2 SV=1	-1.22	-10	-2.65	-1.3	-0.97
sp Q922D8 C1TC_MOUSE	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus	-1.21	-0.9	-0.85	-1.81	-0.69

	GN=Mthfd1 PE=1 SV=4					
sp P57759 ERP29_MOUSE	Endoplasmic reticulum resident protein 29 OS=Mus musculus GN=Erp29 PE=1 SV=2	-1.2	-10	-0.8	-0.03	-0.19
sp P30681 HMGB2_MOUSE	High mobility group protein B2 OS=Mus musculus GN=Hmgb2 PE=1 SV=3	-1.16	-1.13	-1.41	-0.12	-0.54
sp Q9QZD8 DIC_MOUSE	Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=2 SV=2	-1.16	-10	-10	-1.01	-10
sp P43275 H11_MOUSE	Histone H1.1 OS=Mus musculus GN=Hist1h1a PE=2 SV=2	-1.1	-0.76	-0.99	-0.3	-0.73
sp Q9Z1W8 AT12A_MOUSE	Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=3	-1.1	-1.15	-0.78	-1.11	-0.58
sp Q9WV27 AT1A4_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Mus musculus GN=Atp1a4 PE=1 SV=3	-1.08	-1.15	-0.78	-0.98	-0.56
sp O54879 HMGB3_MOUSE	High mobility group protein B3 OS=Mus musculus GN=Hmgb3 PE=2 SV=3	-1.07	-10	-10	-10	-10
sp Q8BHN3 GANAB_MOUSE	Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1	-1.07	-0.57	-0.58	-0.08	-0.25
sp Q9D3B1 HACD2_MOUSE	3-hydroxyacyl-CoA dehydratase 2 OS=Mus musculus GN=Ptp1b PE=2 SV=1	-1.06	-1.31	-1.01	-0.75	-1.39
sp P10404 ENV1_MOUSE	MLV-related proviral Env polyprotein OS=Mus musculus PE=2 SV=3	-1.03	-10	-0.33	-0.47	-0.54
sp Q9D8E6 RL4_MOUSE	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	-1.03	-0.86	-0.36	-0.64	-0.54
sp P00405 COX2_MOUSE	Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1	-1.01	-0.51	-0.52	-0.4	0.07
sp Q8VDN2 AT1A1_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	-1.01	-0.99	-0.77	-0.57	-0.53
sp P17918 PCNA_MOUSE	Proliferating cell nuclear antigen OS=Mus musculus GN=Pcna PE=1 SV=2	-1	-1.32	-1.32	-0.34	-0.4
sp P50247 SAHH_MOUSE	Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	-1	-10	-1.11	-0.44	-0.49

sp Q6GQT9 NOMO1_M OUSE	Nodal modulator 1 OS=Mus musculus GN=Nomo1 PE=1 SV=1	- 0.99	-0.66	0.43	- 0.35	-0.27
sp Q9DB20 ATPO_MOU USE	ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	- 0.99	-0.38	-0.53	- 0.12	-0.46
sp P11370 ENV2_MOU SE	Retrovirus-related Env polyprotein from Fv-4 locus OS=Mus musculus GN=Fv4 PE=1 SV=2	- 0.98	-10	-0.93	- 0.47	-0.65
sp Q9DB77 QCR2_MOU USE	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	- 0.98	-1.39	-0.7	- 0.65	-0.59
sp Q6PIC6 AT1A3_MOU USE	Sodium/potassium- transporting ATPase subunit alpha-3 OS=Mus musculus GN=Atp1a3 PE=1 SV=1	- 0.97	-0.89	-0.73	- 0.86	-0.6
sp Q9CZ13 QCR1_MOU USE	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2	- 0.96	-0.63	-0.54	- 0.35	-0.52
sp Q64436 ATP4A_MOU USE	Potassium-transporting ATPase alpha chain 1 OS=Mus musculus GN=Atp4a PE=1 SV=3	- 0.95	-1.08	-0.8	- 1.17	-0.59
sp P07091 S10A4_MOU SE	Protein S100-A4 OS=Mus musculus GN=S100a4 PE=1 SV=1	- 0.92	-1.09	-1.08	- 0.22	-0.47
sp P15864 H12_MOU SE	Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	- 0.92	-0.48	-1.11	- 0.17	-0.77
sp P43277 H13_MOU SE	Histone H1.3 OS=Mus musculus GN=Hist1h1d PE=1 SV=2	- 0.92	-0.48	-1.11	- 0.15	-0.77
sp Q6PIE5 AT1A2_MOU USE	Sodium/potassium- transporting ATPase subunit alpha-2 OS=Mus musculus GN=Atp1a2 PE=1 SV=1	- 0.91	-0.89	-0.72	- 0.76	-0.57
sp Q07133 H1T_MOU SE	Histone H1t OS=Mus musculus GN=Hist1h1t PE=2 SV=4	- 0.84	-0.6	-1.56	- 0.07	-0.9
sp Q9DCT2 NDUS3_M OUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=2	- 0.84	-1.17	-0.96	- 0.86	-1.06
sp Q6ZQ38 CAND1_M OUSE	Cullin-associated NEDD8- dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	- 0.79	-1.61	-0.63	- 0.65	-0.54

sp P43274 H14_MOUSE	Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2	-0.78	-0.57	-1.2	-0.19	-0.82
sp Q9D0K2 SCOT1_MOUSE	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial OS=Mus musculus GN=Oxct1 PE=1 SV=1	-0.78	-1.33	-0.89	-0.11	-0.22
sp Q9DBG6 RPN2_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	-0.76	-10	-10	-0.26	-0.32
sp P62827 RAN_MOUSE	GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3	-0.74	-10	-0.7	-0.49	-0.47
sp O35129 PHB2_MOUSE	Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	-0.7	1.44	-0.42	-0.75	-0.66
sp P67778 PHB_MOUSE	Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	-0.68	-0.72	-0.44	-0.58	-0.52
sp Q9CQA3 DHSB_MOUSE	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=Sdhb PE=1 SV=1	-0.68	-0.48	-0.88	-0.48	-0.9
sp P51410 RL9_MOUSE	60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=2 SV=2	-0.64	0.05	-10	-0.57	-0.49
sp Q6ZWN5 RS9_MOUSE	40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	-0.61	-0.39	-0.43	-0.65	-0.53
sp Q9CQ7 AT5F1_MOUSE	ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	-0.61	-0.33	-0.42	-0.55	-0.76
sp Q68FL6 SYMC_MOUSE	Methionyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Mars PE=2 SV=1	-0.6	-10	-0.43	-10	-0.39
sp Q8VEM8 MPCP_MOUSE	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	-0.6	-0.68	-0.56	-0.39	-0.43
sp P18572 BASI_MOUSE	Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	-0.57	-10	-0.33	-10	0.02
sp Q9CR57 RL14_MOUSE	60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=2 SV=3	-0.57	-0.39	-0.23	-0.56	-0.39
sp Q9CW03 SMC3_MOUSE	Structural maintenance of chromosomes protein 3	-0.57	-10	-0.68	-0.74	-0.55

	OS=Mus musculus GN=Smc3 PE=1 SV=2					
sp Q5SWU9 ACACA_MOUSE	Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	- 0.56	-10	-10	- 1.03	-1.5
sp P19096 FAS_MOUSE	Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	- 0.55	-0.75	-0.74	- 0.76	-0.77
sp P51881 ADT2_MOUSE	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	- 0.55	-0.46	-0.32	- 0.72	-0.71
sp Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=4	- 0.55	-0.56	-0.64	- 0.96	-0.66
sp P48962 ADT1_MOUSE	ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	- 0.54	-0.54	-0.3	- 0.71	-0.74
sp Q8VDW0 DX39A_MOUSE	ATP-dependent RNA helicase DDX39A OS=Mus musculus GN=Ddx39a PE=2 SV=1	- 0.54	-0.68	-0.7	- 0.34	-0.44
sp Q61598 GDIB_MOUSE	Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	- 0.51	-10	-0.43	- 0.18	-0.37
sp Q921H8 THIKA_MOUSE	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=2 SV=1	- 0.51	-1.26	-0.44	- 0.59	-0.47
sp Q9Z1N5 DX39B_MOUSE	Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1	- 0.51	-0.68	-0.7	- 0.35	-0.36
sp Q9Z1Q9 SYVC_MOUSE	Valyl-tRNA synthetase OS=Mus musculus GN=Vars PE=2 SV=1	- 0.51	-0.73	-0.53	- 0.23	-0.42
sp Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	-0.5	-0.59	-0.27	- 0.73	-0.91
sp Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	-0.5	-10	-0.51	-10	-0.75
sp Q8K2B3 DHSA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	-0.5	-0.27	-0.39	- 0.48	-0.63
sp Q9CQ60 6PGL_MOUSE	6-phosphogluconolactonase OS=Mus musculus GN=Pgl5 PE=2 SV=1	-0.5	-10	-0.25	- 0.35	-0.52
sp Q9D1R9 RL34_MOUSE	60S ribosomal protein L34	-0.5	-0.29	-0.47	-	-0.43

SE	OS=Mus musculus GN=Rpl34 PE=3 SV=2				0.59	
sp P62264 RS14_MOU SE	40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	- 0.49	-0.13	-0.39	- 0.46	-0.31
sp Q8K1B8 URP2_MOU SE	Fermitin family homolog 3 OS=Mus musculus GN=Fermt3 PE=1 SV=1	- 0.49	0.18	-0.25	- 0.67	-0.5
sp P80317 TCPZ_MOU SE	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	- 0.48	-10	-0.47	- 0.43	-0.39
sp Q9D0E1 HNRPM_M OUSE	Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrpm PE=1 SV=3	- 0.48	-1.02	0.24	-0.3	-0.41
sp P60335 PCBP1_MO USE	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	- 0.46	-10	-0.41	-0.3	-0.35
sp Q9WUA2 SYFB_MO USE	Phenylalanyl-tRNA synthetase beta chain OS=Mus musculus GN=Farsb PE=2 SV=2	- 0.46	-10	-0.38	- 0.78	0.22
sp Q61033 LAP2A_MO USE	Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmpo PE=1 SV=4	- 0.45	-10	-10	-10	-10
sp Q6PDI5 ECM29_MO USE	Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=3	- 0.45	-10	-10	- 0.41	-0.65
sp P62281 RS11_MOU SE	40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3	- 0.43	-0.59	-0.45	- 0.81	-0.65
sp P54116 STOM_MOU SE	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	- 0.42	-0.65	-0.67	- 0.03	-0.34
sp P56480 ATPB_MOU SE	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	- 0.42	-0.65	-0.21	- 0.65	-0.69
sp Q920E5 FPPS_MOU SE	Farnesyl pyrophosphate synthase OS=Mus musculus GN=Fdps PE=2 SV=1	- 0.42	-10	-0.26	- 0.84	-0.49
sp P62245 RS15A_MO USE	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=2 SV=2	- 0.41	-10	-0.4	-10	-3.33
sp Q60930 VDAC2_MO USE	Voltage-dependent anion- selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2	- 0.41	0.06	-0.01	- 0.45	-0.39
sp Q8VCT3 AMPB_MO	Aminopeptidase B OS=Mus	-	-10	-0.33	-10	-0.18

USE	musculus GN=Rnpep PE=2 SV=2	0.41				
sp P27659 RL3_MOUSE	60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=3	-0.4	-10	-0.2	-	1.15 -0.47
sp P61255 RL26_MOUSE	60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=2 SV=1	-0.4	0.23	-10	-	0.45 -0.5
sp Q3V132 ADT4_MOUSE	ADP/ATP translocase 4 OS=Mus musculus GN=Slc25a31 PE=2 SV=1	-0.4	-0.32	-0.25	-	0.65 -0.63
sp Q922F4 TBB6_MOUSE	Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	-0.4	-0.44	-0.52	-	0.76 -0.69
sp Q9D0B0 SRSF9_MOUSE	Serine/arginine-rich splicing factor 9 OS=Mus musculus GN=Srsf9 PE=1 SV=1	-	-10	-0.53	-	0.11 -10
sp Q8C0C7 SYFA_MOUSE	Phenylalanyl-tRNA synthetase alpha chain OS=Mus musculus GN=Farsa PE=2 SV=1	-	-10	-0.24	-	10 -10
sp P62702 RS4X_MOUSE	40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	-	-0.41	-0.37	-	0.54 -0.56
sp Q9DCH4 EIF3F_MOUSE	Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Eif3f PE=1 SV=2	-	-10	-10	-	0.15 -10
sp P47962 RL5_MOUSE	60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	-	-10	-0.53	-	0.2 -0.39
sp P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	-	-0.71	-0.52	-	0.72 -0.71
sp P21550 ENOB_MOUSE	Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	-	-0.45	-0.54	-	0.1 -0.13
sp P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	-	-0.42	-0.24	-	0.22 -1.02
sp Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	-	-2.74	-0.36	-	0.17 -1.33
sp Q9ERD7 TBB3_MOUSE	Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	-	-0.65	-0.5	-	0.6 -0.65
sp Q9D6R2 IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=ldh3a PE=1 SV=1	-	-0.25	0.58	-	0.34 -0.54

sp Q1HFZ0 NSUN2_MOUSE	tRNA (cytosine(34)-C(5))-methyltransferase OS=Mus musculus GN=Nsun2 PE=1 SV=2	-0.32	-10	-10	-0.58	-0.45
sp O09167 RL21_MOUSE	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	0.31	-10	-10	0.65	-0.46
sp P61358 RL27_MOUSE	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=2 SV=2	0.31	-10	-0.46	0.07	-0.04
sp P80313 TCPH_MOUSE	T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	0.31	-0.29	-0.32	0.23	-0.4
sp Q7TMM9 TBB2A_MOUSE	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	0.31	-0.65	-0.44	0.69	-0.69
sp Q8BFR5 EFTU_MOUSE	Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	0.31	-10	0.11	0.54	-0.44
sp Q8CGK3 LONM_MOUSE	Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE=1 SV=2	0.31	-10	0.22	0.21	-0.3
sp Q9CWF2 TBB2B_MOUSE	Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1	0.31	-0.65	-0.44	0.69	-0.69
sp P41105 RL28_MOUSE	60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	-0.3	-0.13	-0.19	0.58	-0.58
sp P84104 SRSF3_MOUSE	Serine/arginine-rich splicing factor 3 OS=Mus musculus GN=Srsf3 PE=1 SV=1	-0.3	-0.5	-0.12	-0.2	-0.86
sp Q99K10 ACON_MOUSE	Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	-0.3	-0.67	-0.48	0.37	-0.37
sp Q9DBT5 AMPD2_MOUSE	AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1	-0.3	-0.34	-10	0.08	-0.37
sp Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	-0.3	-0.32	-0.21	-10	-10
sp P14115 RL27A_MOUSE	60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=5	0.29	-0.02	-0.01	0.53	-0.49
sp P14148 RL7_MOUSE	60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	0.29	-0.15	-0.35	-0.6	-0.53
sp P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	0.29	-0.49	-0.41	0.05	-0.26

sp P19253 RL13A_MOUSE	60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	- 0.29	-0.32	-0.36	- 0.47	-0.51
sp P47963 RL13_MOUSE	60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	- 0.29	-0.34	-0.38	- 0.53	-0.45
sp Q61753 SERA_MOUSE	D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	- 0.29	-0.49	-0.48	- 0.63	-0.45
sp Q6PB66 LPPRC_MOUSE	Leucine-rich PPR motif- containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	- 0.29	-0.43	1.28	- 0.25	-0.48
sp Q64514 TPP2_MOUSE	Tripeptidyl-peptidase 2 OS=Mus musculus GN=Tpp2 PE=2 SV=3	- 0.28	-10	-0.75	- 0.25	-0.31
sp P62754 RS6_MOUSE	40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	- 0.27	-0.12	-0.29	- 0.66	-0.61
sp P62918 RL8_MOUSE	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	- 0.27	-0.42	-0.3	- 0.42	-0.47
sp Q9CXW4 RL11_MOUSE	60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4	- 0.26	-0.3	-0.76	- 0.49	-0.51
sp Q61029 LAP2B_MOUSE	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4	- 0.24	-10	-0.19	- -10	-10
sp P12970 RL7A_MOUSE	60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	- 0.23	-0.34	-0.47	- 0.75	-0.54
sp P62242 RS8_MOUSE	40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	- 0.23	-0.49	-0.33	- 0.65	-0.53
sp P63323 RS12_MOUSE	40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2	- 0.23	-0.31	-0.5	- 0.03	-0.24
sp Q9CU62 SMC1A_MOUSE	Structural maintenance of chromosomes protein 1A OS=Mus musculus GN=Smc1a PE=1 SV=4	- 0.23	-0.6	-0.48	- 0.41	-0.64
sp Q9Z110 P5CS_MOUSE	Delta-1-pyrroline-5- carboxylate synthase OS=Mus musculus GN=Aldh18a1 PE=2 SV=2	- 0.23	-10	0.26	- -10	-0.68
sp P05213 TBA1B_MOUSE	Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2	- 0.21	-0.58	-0.47	- 0.71	-0.8
sp P17183 ENOG_MOUSE	Gamma-enolase OS=Mus musculus GN=Eno2 PE=1	- 0.21	-0.37	-0.27	- 0.08	-0.18

	SV=2					
sp P23116 EIF3A_MOUSE	Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=Eif3a PE=1 SV=5	- 0.21	-0.98	-0.45	- 0.27	-0.39
sp P68369 TBA1A_MOUSE	Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	- 0.21	-0.58	-0.43	-0.7	-0.8
sp P68372 TBB2C_MOUSE	Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	- 0.21	-0.62	-0.46	- 0.72	-0.69
sp P68373 TBA1C_MOUSE	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1	- 0.21	-0.58	-0.43	- 0.69	-0.79
sp Q9CZM2 RL15_MOUSE	60S ribosomal protein L15 OS=Mus musculus GN=Rpl15 PE=2 SV=4	-0.2	-0.26	-0.28	- 0.63	-0.46
sp P53657 KPYR_MOUSE	Pyruvate kinase isozymes R/L OS=Mus musculus GN=Pklr PE=2 SV=1	- 0.19	-0.2	-0.21	- 0.01	-0.27
sp Q9CQR2 RS21_MOUSE	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=2 SV=1	- 0.19	-10	-0.4	- 0.04	-0.22
sp P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	- 0.17	-0.15	-0.24	- 0.19	-0.24
sp P62301 RS13_MOUSE	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	- 0.17	-10	-10	- 0.01	-0.14
sp Q62167 DDX3X_MOUSE	ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3	- 0.17	-0.73	-0.18	- 0.34	-0.35
sp Q8BL97 SRSF7_MOUSE	Serine/arginine-rich splicing factor 7 OS=Mus musculus GN=Srsf7 PE=1 SV=1	- 0.16	0.4	-0.39	- 0.78	-10
sp Q9CRB9 CHCH3_MOUSE	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1 SV=1	- 0.16	-10	-0.12	- 0.05	-10
sp O35737 HNRH1_MOUSE	Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3	- 0.15	-1.76	-0.71	-10	-0.63
sp P25444 RS2_MOUSE	40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	- 0.15	-0.38	-0.25	- 0.44	-0.44
sp P70333 HNRH2_MOUSE	Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrnph2 PE=1 SV=1	- 0.15	-1.76	-0.71	-10	-0.7
sp Q9Z2X1 HNRPF_MOUSE	Heterogeneous nuclear	-	-10	-0.17	-10	-0.47

USE	ribonucleoprotein F OS=Mus musculus GN=Hnrnpf PE=1 SV=3	0.15				
sp O08788 DCTN1_MOUSE	Dynactin subunit 1 OS=Mus musculus GN=Dctn1 PE=1 SV=3	- 0.14	-10	-10	-10	-0.7
sp P05214 TBA3_MOUSE	Tubulin alpha-3 chain OS=Mus musculus GN=Tuba3a PE=1 SV=1	- 0.13	-0.65	-0.31	- 0.69	-0.74
sp P35980 RL18_MOUSE	60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=3	- 0.13	-0.17	-0.31	- 0.52	-0.45
sp P52480 KPYM_MOUSE	Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	- 0.13	-0.16	-0.25	- 0.15	-0.32
sp P62631 EF1A2_MOUSE	Elongation factor 1-alpha 2 OS=Mus musculus GN=Eef1a2 PE=1 SV=1	- 0.13	0	-0.27	- 0.18	-0.24
sp P80318 TCPG_MOUSE	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	- 0.13	-0.2	-0.3	- 0.28	-0.31
sp Q68FD5 CLH_MOUSE	Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	- 0.13	-10	-0.18	-0.5	-0.43
sp Q9CPR4 RL17_MOUSE	60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=2 SV=3	- 0.13	-0.45	-10	- 0.85	-0.45
sp P11983 TCPA_MOUSE	T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3	- 0.12	-10	-0.35	-0.5	-0.51
sp Q9QXX4 CMC2_MOUSE	Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1	- 0.11	-10	-0.13	-10	-0.46
sp O70133 DHX9_MOUSE	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	-0.1	-0.74	-0.73	- 0.64	-0.83
sp P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	-0.1	-0.41	0.1	- 0.22	-0.32
sp Q8VEK3 HNRPU_MOUSE	Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1	-0.1	-0.79	-0.77	- 0.34	-0.45
sp Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2	- 0.09	-0.44	1.92	- 0.65	-0.66
sp P14131 RS16_MOUSE	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV=4	- 0.08	-0.74	-10	- 0.46	-0.45
sp O08756 HCD2_MOUSE	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus	- 0.07	-10	0.01	- 0.61	-0.48

	GN=Hsd17b10 PE=1 SV=4					
sp Q9EPU0 RENT1_MOUSE	Regulator of nonsense transcripts 1 OS=Mus musculus GN=Upf1 PE=1 SV=2	-0.07	-10	-10	-0.39	-0.39
sp P60764 RAC3_MOUSE	Ras-related C3 botulinum toxin substrate 3 OS=Mus musculus GN=Rac3 PE=1 SV=1	-0.06	-0.09	-0.13	-0.21	-0.34
sp P63001 RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	-0.06	-0.09	-0.13	-0.21	-0.34
sp P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	-0.05	-0.07	-0.15	-0.28	-0.32
sp Q61879 MYH10_MOUSE	Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	-0.05	0.11	0.09	-0.66	-0.56
sp Q99NB9 SF3B1_MOUSE	Splicing factor 3B subunit 1 OS=Mus musculus GN=Sf3b1 PE=1 SV=1	-0.05	-10	-0.12	-0.27	-0.29
sp Q05144 RAC2_MOUSE	Ras-related C3 botulinum toxin substrate 2 OS=Mus musculus GN=Rac2 PE=2 SV=1	-0.04	0.02	0.02	-0.46	-0.38
sp Q7TPV4 MBB1A_MOUSE	Myb-binding protein 1A OS=Mus musculus GN=Mybbp1a PE=1 SV=2	-0.04	-0.28	-0.38	-0.17	-0.27
sp P16381 DDX3L_MOUSE	Putative ATP-dependent RNA helicase PI10 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	-0.03	-0.73	-0.18	-0.34	-0.44
sp P62267 RS23_MOUSE	40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3	-0.03	-0.15	0.22	-0.59	-0.42
sp Q6URW6 MYH14_MOUSE	Myosin-14 OS=Mus musculus GN=Myh14 PE=1 SV=1	-0.02	0.11	-0.05	-0.72	-0.57
sp Q8VDD5 MYH9_MOUSE	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	-0.01	-0.05	-0.05	-0.67	-0.55

Table 14. Effect of LPS on *Echinacea* Extract 7 induced proteins.

Sequence Id	Sequence Name	<i>Echinacea</i> Extract 7 Ratio-2	LPS+ <i>Echinacea</i> Extract 7 Ratio-2	<i>Echinacea</i> Extract 7 Ratio-1	LPS+ <i>Echinacea</i> Extract 7 Ratio-1
sp Q9WUM4 COR1C_MOUSE	Coronin-1C OS=Mus	1.65	-10	2.13	-0.9

USE	musculus GN=Coro1c PE=1 SV=2				
sp P62852 RS25_MOUSE	40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=2 SV=1	0.04	-0.3	0.87	0.26
sp P13020 GELS_MOUSE	Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	0.58	0.43	0.56	-0.09
sp Q9JMH6 TRXR1_MOUSE	Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txrd1 PE=1 SV=3	1.17	-10	0.55	0.87
sp P25444 RS2_MOUSE	40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	0.03	-0.38	0.48	-0.44
sp Q6P1B1 XPP1_MOUSE	Xaa-Pro aminopeptidase 1 OS=Mus musculus GN=Xpnpep1 PE=2 SV=1	0.57	-10	0.44	0.11
sp P97324 G6PD2_MOUSE	Glucose-6-phosphate 1- dehydrogenase 2 OS=Mus musculus GN=G6pd2 PE=2 SV=3	0.58	-10	0.39	0.18
sp Q9DBJ1 PGAM1_MOUSE	Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3	0.5	-0.31	0.38	0.04
sp Q93092 TALDO_MOUSE	Transaldolase OS=Mus musculus GN=Taldo1 PE=1 SV=2	0.37	-0.47	0.38	0.1
sp Q00612 G6PD1_MOUSE	Glucose-6-phosphate 1- dehydrogenase X OS=Mus musculus GN=G6pdx PE=1 SV=3	0.53	0.49	0.36	0.32
sp P24452 CAPG_MOUSE	Macrophage-capping protein OS=Mus musculus GN=Capg PE=1 SV=2	0.05	-0.5	0.35	0.07
sp Q9CR16 PPID_MOUSE	Peptidyl-prolyl cis-trans isomerase D OS=Mus musculus GN=Ppid PE=1 SV=3	0.03	-10	0.35	0.11
sp P16125 LDHB_MOUSE	L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2	2.94	-10	0.34	-0.21
sp Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	0.42	0.12	0.34	0.25
sp O70250 PGAM2_MOUSE	Phosphoglycerate mutase 2 OS=Mus musculus GN=Pgam2 PE=1 SV=3	0.33	-0.39	0.33	-0.1

sp P48036 ANXA5_MOUSE	Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	0.03	0.13	0.31	0.23
sp P06745 G6PI_MOUSE	Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=1 SV=4	0.51	-0.38	0.3	0.12
sp P17751 TPIS_MOUSE	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	0.23	-0.11	0.3	-0.01
sp P18572 BASI_MOUSE	Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	0.01	-10	0.3	0.02
sp P05201 AATC_MOUSE	Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Got1 PE=1 SV=3	0.12	-0.64	0.29	0.19
sp O08709 PRDX6_MOUSE	Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3	0.78	0.33	0.28	-0.12
sp P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2	0.06	0.46	0.28	0.26
sp Q60864 STIP1_MOUSE	Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1	0.23	-10	0.27	-0.21
sp P00342 LDHC_MOUSE	L-lactate dehydrogenase C chain OS=Mus musculus GN=Ldhc PE=1 SV=2	2.94	-10	0.26	-0.05
sp P09041 PGK2_MOUSE	Phosphoglycerate kinase 2 OS=Mus musculus GN=Pgk2 PE=1 SV=4	1.7	-0.01	0.26	0.01
sp P35700 PRDX1_MOUSE	Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	1.32	2.5	0.26	0.78
sp P16110 LEG3_MOUSE	Galectin-3 OS=Mus musculus GN=Lgals3 PE=1 SV=3	0.4	-0.37	0.26	0.12
sp Q9JII6 AK1A1_MOUSE	Alcohol dehydrogenase [NADP+] OS=Mus musculus GN=Akr1a1 PE=1 SV=3	0.35	-10	0.26	-0.06
sp P60122 RUVB1_MOUSE	RuvB-like 1 OS=Mus musculus GN=Ruvbl1 PE=1 SV=1	0.1	-0.27	0.26	-0.27
sp P60766 CDC42_MOUSE	Cell division control protein 42 homolog OS=Mus musculus	0.54	0.44	0.25	-0.02

	GN=Cdc42 PE=1 SV=2				
sp P17879 HS71B_MOUSE	Heat shock 70 kDa protein 1B OS=Mus musculus GN=Hspa1b PE=1 SV=3	0.52	-0.55	0.24	0.2
sp Q61696 HS71A_MOUSE	Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	0.52	-0.55	0.24	0.2
sp P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	0.42	0.12	0.24	0.13
sp P57776 EF1D_MOUSE	Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3	0.11	-0.35	0.24	-0.14
sp Q9R1P0 PSA4_MOUSE	Proteasome subunit alpha type-4 OS=Mus musculus GN=Pma4 PE=1 SV=1	0.37	-10	0.23	-0.06
sp P14152 MDHC_MOUSE	Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	0.12	-0.93	0.23	-0.32
sp P35278 RAB5C_MOUSE	Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	0.23	0.5	0.22	-0.34
sp P37040 NCPR_MOUSE	NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	0.18	-10	0.22	-2.98
sp P21550 ENOB_MOUSE	Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	1.23	-0.45	0.21	-0.13
sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=1 SV=1	0.05	0.19	0.21	0.29
sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	0.05	0.19	0.21	0.29
sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=Rps27a PE=1 SV=2	0.05	0.19	0.21	0.25
sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Uba52 PE=1 SV=2	0.05	0.19	0.21	0.29
sp P70296 PEBP1_MOUSE	Phosphatidylethanolamine-binding protein 1 OS=Mus musculus GN=Pebp1 PE=1 SV=3	0.01	-0.73	0.21	-0.24

sp P17183 ENOG_MOUSE	Gamma-enolase OS=Mus musculus GN=Eno2 PE=1 SV=2	0.42	-0.37	0.2	-0.18
sp P26883 FKB1A_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Mus musculus GN=Fkbp1a PE=2 SV=2	0.19	-0.32	0.2	0.09
sp P09411 PGK1_MOUSE	Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4	0.56	0.14	0.19	0
sp P50580 PA2G4_MOUSE	Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3	0.18	-0.45	0.19	-0.08
sp P40124 CAP1_MOUSE	Adenylyl cyclase- associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	0.53	-10	0.17	0.33
sp Q9DCD0 6PGD_MOUSE	6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=2 SV=3	0.37	0.17	0.16	-0.18
sp Q7TMK9 HNRPQ_MOUSE	Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncrip PE=1 SV=2	0.16	-10	0.16	-0.18
sp P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	0.02	0.39	0.16	-0.07
sp Q9ER72 SYCC_MOUSE	Cysteinyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2	0.32	0.24	0.15	0.33
sp P07901 HS90A_MOUSE	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	0.27	0.25	0.15	0.38
sp Q61937 NPM_MOUSE	Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	0.15	-0.68	0.15	-0.02
sp P06801 MAOX_MOUSE	NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=2	0.04	-1.11	0.15	-0.31
sp P15532 NDKA_MOUSE	Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 PE=1 SV=1	0.02	-10	0.15	0.01
sp P03995 GFAP_MOUSE	Glial fibrillary acidic	1.8	1.26	0.14	0.48

	protein OS=Mus musculus GN=Gfap PE=1 SV=4				
sp Q01768 NDKB_MOUSE	Nucleoside diphosphate kinase B OS=Mus musculus GN=Nme2 PE=1 SV=1	0.02	-10	0.13	0
sp Q9R1P4 PSA1_MOUSE	Proteasome subunit alpha type-1 OS=Mus musculus GN=Psma1 PE=1 SV=1	0.5	-0.14	0.12	-0.04
sp P63325 RS10_MOUSE	40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1	0.49	0	0.12	-0.06
sp Q922Q8 LRC59_MOUSE	Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=2 SV=1	0.26	-10	0.12	0.27
sp P40142 TKT_MOUSE	Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1	0.32	-0.62	0.11	-0.19
sp Q9EQU5 SET_MOUSE	Protein SET OS=Mus musculus GN=Set PE=1 SV=1	0.3	-1.09	0.11	-0.18
sp P05064 ALDOA_MOUSE	Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	0.47	0.01	0.1	-0.17
sp P17182 ENOA_MOUSE	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	0.24	-0.49	0.1	-0.26
sp Q9JHU9 INO1_MOUSE	Inositol-3-phosphate synthase 1 OS=Mus musculus GN=Isyna1 PE=2 SV=1	0.19	-10	0.1	-0.03
sp P50396 GDIA_MOUSE	Rab GDP dissociation inhibitor alpha OS=Mus musculus GN=Gdi1 PE=1 SV=3	0.76	-10	0.09	-0.31
sp P06151 LDHA_MOUSE	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	0.73	-0.41	0.09	-0.32
sp P62962 PROF1_MOUSE	Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	0.36	-0.05	0.09	0.39
sp P53657 KPYR_MOUSE	Pyruvate kinase isozymes R/L OS=Mus musculus GN=Pklr PE=2 SV=1	0.12	-0.2	0.09	-0.27
sp P35979 RL12_MOUSE	60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	0.32	-0.25	0.08	-0.06
sp Q78PY7 SND1_MOUSE	Staphylococcal	0.25	0.07	0.08	-0.07

	nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1				
sp P68254 1433T_MOUSE	14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1	0.24	-0.09	0.08	-0.05
sp Q9CWH6 PSA7L_MOUSE	Proteasome subunit alpha type-7-like OS=Mus musculus GN=Psm8 PE=2 SV=1	0.24	-10	0.08	0.12
sp Q9Z2U0 PSA7_MOUSE	Proteasome subunit alpha type-7 OS=Mus musculus GN=Psm7 PE=1 SV=1	0.24	-10	0.08	0.12
sp Q8QZY1 EIF3L_MOUSE	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1	0.16	-10	0.08	-0.19
sp P62270 RS18_MOUSE	40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=2 SV=3	0.11	-0.21	0.08	0.01
sp P62259 1433E_MOUSE	14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	0.22	-0.41	0.07	-0.04
sp P52480 KPYM_MOUSE	Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	0.43	-0.16	0.05	-0.32
sp P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	0.74	0.67	0.04	0.06
sp P16858 G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	0.56	-0.07	0.04	-0.32
sp P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	0.46	0.15	0.04	0.18
sp Q8BGQ7 SYAC_MOUSE	Alanyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1	0.46	0.02	0.04	-0.17
sp P17156 HSP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2	0.43	0.42	0.04	0.1
sp P58771 TPM1_MOUSE	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	0.42	0.24	0.04	-0.15
sp P58774 TPM2_MOUSE	Tropomyosin beta chain	0.42	0.24	0.04	-0.15

	OS=Mus musculus GN=Tpm2 PE=1 SV=1				
sp P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	0.4	0.38	0.04	0.08
sp Q9CQV8 1433B_MOUSE	14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	0.18	0.07	0.04	-0.02
sp P58252 EF2_MOUSE	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	0.38	0.12	0.03	0.02
sp P62274 RS29_MOUSE	40S ribosomal protein S29 OS=Mus musculus GN=Rps29 PE=2 SV=2	0.37	-10	0.03	-0.14
sp Q61598 GDIB_MOUSE	Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	0.25	-10	0.03	-0.37
sp P63001 RAC1_MOUSE	Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	0.14	-0.09	0.03	-0.34
sp O08810 U5S1_MOUSE	116 kDa U5 small nuclear ribonucleoprotein component OS=Mus musculus GN=Eftud2 PE=2 SV=1	0.37	0.26	0.02	-0.11
sp Q6ZWX6 IF2A_MOUSE	Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3	0.14	-10	0.02	-0.02
sp P63101 1433Z_MOUSE	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	0.13	0.11	0.02	0
sp P68510 1433F_MOUSE	14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	0.13	-0.09	0.02	-0.1
sp Q501J6 DDX17_MOUSE	Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	0.1	-10	0.02	-0.33
sp P26041 MOES_MOUSE	Moesin OS=Mus musculus GN=Msn PE=1 SV=3	0.49	0.49	0.01	0.12

Table 15. Effect of LPS on *Echinacea* extract 7 suppressed proteins.

Sequence Id	Sequence Name	<i>Echinacea</i> extract 7 Ratio-2	LPS+ <i>Echinacea</i> extract 7 Ratio-2	<i>Echinacea</i> extract 7 Ratio-1	LPS+ <i>Echinacea</i> extract 7 Ratio-1
sp O08528 HXK2_MOUSE	Hexokinase-2 OS=Mus musculus GN=Hk2 PE=1 SV=1	-10	-10	-0.07	-0.26
sp O08547 SC22B_MOUSE	Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3	-10	-10	-10	-0.15
sp O08756 HCD2_MOUSE	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17b10 PE=1 SV=4	-10	-10	-0.09	-0.48
sp O08788 DCTN1_MOUSE	Dynactin subunit 1 OS=Mus musculus GN=Dctn1 PE=1 SV=3	-10	-10	-0.57	-0.7
sp O09167 RL21_MOUSE	60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	-10	-10	-0.14	-0.46
sp O54879 HMGB3_MOUSE	High mobility group protein B3 OS=Mus musculus GN=Hmgb3 PE=2 SV=3	-10	-10	-10	-10
sp O55143 AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	-10	-10	-0.25	-0.23
sp O70133 DHX9_MOUSE	ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	-10	-0.74	-0.65	-0.83
sp O70152 DPM1_MOUSE	Dolichol-phosphate mannosyltransferase OS=Mus musculus GN=Dpm1 PE=2 SV=1	-10	-10	-0.14	-10
sp O88531 PPT1_MOUSE	Palmitoyl-protein thioesterase 1 OS=Mus musculus GN=Ppt1 PE=2 SV=2	-10	-10	-0.47	-10
sp P00405 COX2_MOUSE	Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1	-10	-0.51	-0.17	0.07
sp P01895 HA1Y_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus musculus GN=H2-D1 PE=2 SV=1	-10	-10	-0.11	-0.14
sp P01896 HA1Z_MOUSE	H-2 class I histocompatibility antigen, alpha chain (Fragment) OS=Mus	-10	-10	-0.11	-0.14

	musculus PE=1 SV=1				
sp P01900 HA12_MOUSE	H-2 class I histocompatibility antigen, D-D alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=1	-10	1.6	-0.11	-0.11
sp P01942 HBA_MOUSE	Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2	-10	-10	-10	-10
sp P03930 ATP8_MOUSE	ATP synthase protein 8 OS=Mus musculus GN=Mtatp8 PE=1 SV=1	-10	-10	-0.56	-0.56
sp P05555 ITAM_MOUSE	Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=2	-10	1.65	-0.17	0.13
sp P06800 PTPRC_MOUSE	Receptor-type tyrosine-protein phosphatase C OS=Mus musculus GN=Ptprc PE=1 SV=3	-10	0.55	-0.23	-0.28
sp P07724 ALBU_MOUSE	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	-10	-10	-10	-10
sp P08553 NFM_MOUSE	Neurofilament medium polypeptide OS=Mus musculus GN=Nefm PE=1 SV=4	-10	-10	-10	-10
sp P10404 ENV1_MOUSE	MLV-related proviral Env polyprotein OS=Mus musculus PE=2 SV=3	-10	-10	-0.05	-0.54
sp P11370 ENV2_MOUSE	Retrovirus-related Env polyprotein from Fv-4 locus OS=Mus musculus GN=Fv4 PE=1 SV=2	-10	-10	-0.01	-0.65
sp P15331 PERI_MOUSE	Peripherin OS=Mus musculus GN=Prph PE=1 SV=2	-10	-10	-10	0.05
sp P19246 NFH_MOUSE	Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE=1 SV=3	-10	-10	-10	-10
sp P23492 PNPH_MOUSE	Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2	-10	-10	-10	-10
sp P26516 PSD7_MOUSE	26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psm7 PE=1 SV=2	-10	-10	-0.04	-0.43
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcksl1 PE=1 SV=2	-10	3.42	-10	0.93
sp P29387 GGB4_MOUSE	Guanine nucleotide-binding protein subunit beta-4 OS=Mus musculus GN=Gnb4 PE=2 SV=4	-10	-10	-10	-10

sp P30416 FKBP4_MOUSE SE	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus GN=Fkbp4 PE=1 SV=5	-10	-10	-0.03	2.23
sp P31001 DESM_MOUSE SE	Desmin OS=Mus musculus GN=Des PE=1 SV=3	-10	-10	-10	0.05
sp P42225 STAT1_MOUSE SE	Signal transducer and activator of transcription 1 OS=Mus musculus GN=Stat1 PE=1 SV=1	-10	-10	-10	-10
sp P46638 RB11B_MOUSE SE	Ras-related protein Rab-11B OS=Mus musculus GN=Rab11b PE=1 SV=3	-10	-10	-0.55	-0.59
sp P46660 AINX_MOUSE E	Alpha-internexin OS=Mus musculus GN=Ina PE=1 SV=2	-10	-10	-10	-10
sp P47754 CAZA2_MOUSE SE	F-actin-capping protein subunit alpha-2 OS=Mus musculus GN=Capza2 PE=1 SV=3	-10	-10	-0.03	-0.25
sp P51410 RL9_MOUSE	60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=2 SV=2	-10	0.05	-0.49	-0.49
sp P53986 MOT1_MOUSE SE	Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	-10	-10	-0.33	-0.7
sp P54987 IRG1_MOUSE E	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	-10	-10	-10	4.26
sp P61358 RL27_MOUSE E	60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=2 SV=2	-10	-10	-0.15	-0.04
sp P62301 RS13_MOUSE E	40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	-10	-10	-0.1	-0.14
sp P62492 RB11A_MOUSE SE	Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a PE=1 SV=3	-10	-10	-0.55	-0.59
sp P62830 RL23_MOUSE E	60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1	-10	-10	-0.31	-0.45
sp P62849 RS24_MOUSE E	40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1	-10	-0.27	-0.38	-1.18
sp P62880 GBB2_MOUSE E	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Mus musculus GN=Gnb2 PE=1 SV=3	-10	0.26	-0.01	-10
sp P62900 RL31_MOUSE E	60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=2 SV=1	-10	-0.39	-0.25	-0.46
sp P68040 GBLP_MOUSE E	Guanine nucleotide-binding protein subunit beta-2-like 1	-10	-10	-0.28	-0.58

	OS=Mus musculus GN=Gnb2l1 PE=1 SV=3				
sp P86048 RL10L_MOUSE	60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=1	-10	-10	-0.27	-0.53
sp P97310 MCM2_MOUSE	DNA replication licensing factor MCM2 OS=Mus musculus GN=Mcm2 PE=1 SV=3	-10	-10	-0.58	-1.14
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	-10	-10	-10	-10
sp Q3THS6 METK2_MOUSE	S-adenosylmethionine synthase isoform type-2 OS=Mus musculus GN=Mat2a PE=2 SV=2	-10	0.07	-0.22	0.08
sp Q3U9G9 LBR_MOUSE	Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	-10	-10	-0.41	-0.57
sp Q3UM45 PP1R7_MOUSE	Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2	-10	-10	-0.1	-0.21
sp Q3V3R1 C1TM_MOUSE	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Mus musculus GN=Mthfd1l PE=1 SV=2	-10	0.46	-0.13	-0.46
sp Q5SW19 K0664_MOUSE	Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 PE=2 SV=2	-10	-10	-0.01	0.4
sp Q5SWU9 ACACA_MOUSE	Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	-10	-10	-0.59	-1.5
sp Q60668 HNRPD_MOUSE	Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=Hnrnpd PE=1 SV=2	-10	-10	-0.08	-0.37
sp Q60875 ARHG2_MOUSE	Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 PE=1 SV=4	-10	-0.44	-0.24	-0.33
sp Q60931 VDAC3_MOUSE	Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	-10	-10	-0.11	-10
sp Q60932 VDAC1_MOUSE	Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	-10	-10	-0.13	-0.2
sp Q61011 GBB3_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Mus musculus GN=Gnb3 PE=1	-10	-10	-10	-10

	SV=2				
sp Q61029 LAP2B_MOUSE SE	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4	-10	-10	-0.02	-10
sp Q61335 BAP31_MOUSE SE	B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=3	-10	-10	-0.02	-10
sp Q61820 RANT_MOUSE SE	GTP-binding nuclear protein Ran, testis-specific isoform OS=Mus musculus GN=Rasl2-9 PE=2 SV=1	-10	-10	-0.12	-0.52
sp Q62351 TFR1_MOUSE E	Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	-10	-10	-0.2	-0.1
sp Q62433 NDRG1_MOUSE USE	Protein NDRG1 OS=Mus musculus GN=Ndrp1 PE=1 SV=1	-10	-10	-10	0.4
sp Q64436 ATP4A_MOUSE SE	Potassium-transporting ATPase alpha chain 1 OS=Mus musculus GN=Atp4a PE=1 SV=3	-10	-1.08	-0.19	-0.59
sp Q64514 TPP2_MOUSE E	Tripeptidyl-peptidase 2 OS=Mus musculus GN=Tpp2 PE=2 SV=3	-10	-10	-0.64	-0.31
sp Q64516 GLPK_MOUSE SE	Glycerol kinase OS=Mus musculus GN=Gk PE=2 SV=2	-10	-10	-10	-10
sp Q64518 AT2A3_MOUSE SE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Mus musculus GN=Atp2a3 PE=2 SV=3	-10	-10	-0.25	-0.29
sp Q64674 SPEE_MOUSE SE	Spermidine synthase OS=Mus musculus GN=Srm PE=2 SV=1	-10	-10	-0.02	-10
sp Q68FL6 SYMC_MOUSE SE	Methionyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Mars PE=2 SV=1	-10	-10	-0.1	-0.39
sp Q69ZN7 MYOF_MOUSE SE	Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	-10	0.93	-10	1.47
sp Q6PDI5 ECM29_MOUSE USE	Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=3	-10	-10	-0.09	-0.65
sp Q6ZQ38 CAND1_MOUSE USE	Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	-10	-1.61	-0.26	-0.54
sp Q6ZWU9 RS27_MOUSE SE	40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3	-10	-10	-0.8	-1.3

sp Q6ZVV3 RL10_MOU SE	60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3	-10	-10	-0.27	-0.53
sp Q6ZWY3 RS27L_MO USE	40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=2 SV=3	-10	-10	-0.89	-1.29
sp Q76MZ3 2AAA_MOU SE	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3	-10	-10	-0.01	0.08
sp Q7M6Y3 PICA_MOU SE	Phosphatidylinositol-binding clathrin assembly protein OS=Mus musculus GN=Picalm PE=1 SV=1	-10	-10	-10	-0.95
sp Q7TQI3 OTUB1_MO USE	Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2	-10	-10	-0.24	-0.53
sp Q8BG32 PSD11_MO USE	26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psm11 PE=1 SV=3	-10	-10	-10	-10
sp Q8BH04 PCKGM_MO USE	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=2 SV=1	-10	-10	-10	-0.35
sp Q8BKC5 IPO5_MOU SE	Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	-10	-10	-0.07	-0.22
sp Q8BMJ2 SYLC_MOU SE	Leucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Lars PE=2 SV=2	-10	0.15	-0.27	-0.39
sp Q8BMK4 CKAP4_MO USE	Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=2 SV=2	-10	-10	-10	-10
sp Q8BP47 SYNC_MOU SE	Asparaginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Nars PE=1 SV=2	-10	-10	-0.22	-0.19
sp Q8BWY3 ERF1_MOU SE	Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Elf1 PE=1 SV=4	-10	-10	-0.01	-0.29
sp Q8K2Q2 GSTO2_MO USE	Glutathione S-transferase omega-2 OS=Mus musculus GN=Gsto2 PE=2 SV=1	-10	-10	-10	-10
sp Q8K4Z3 AIBP_MOUSE	Apolipoprotein A-I-binding protein OS=Mus musculus GN=Apoa1bp PE=1 SV=1	-10	-10	-0.19	-10
sp Q8R0W0 EPIPL_MO USE	Epiplakin OS=Mus musculus GN=Eppk1 PE=1 SV=2	-10	-10	-0.13	-0.36
sp Q8R429 AT2A1_MOU	Sarcoplasmic/endoplasmic	-10	-10	-0.35	-0.09

SE	reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1				
sp Q8VCT3 AMPB_MOU SE	Aminopeptidase B OS=Mus musculus GN=Rnpep PE=2 SV=2	-10	-10	-0.42	-0.18
sp Q8VDJ3 VIGLN_MOU SE	Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	-10	-10	-0.05	-0.19
sp Q8VDP4 K1967_MO USE	Protein KIAA1967 homolog OS=Mus musculus PE=1 SV=2	-10	-10	-0.05	-0.46
sp Q91V92 ACLY_MOU SE	ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	-10	-10	-0.37	-1.06
sp Q91VR2 ATPG_MOU SE	ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	-10	-10	-0.73	-10
sp Q921E2 RAB31_MO USE	Ras-related protein Rab-31 OS=Mus musculus GN=Rab31 PE=1 SV=1	-10	-10	-0.06	0.31
sp Q921F2 TADBP_MO USE	TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	-10	-0.8	-10	-0.63
sp Q921M7 FA49B_MO USE	Protein FAM49B OS=Mus musculus GN=Fam49b PE=2 SV=1	-10	-10	-0.3	-10
sp Q99JY0 ECHB_MOU SE	Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	-10	-10	-10	-10
sp Q99KC8 VMA5A_MO USE	von Willebrand factor A domain-containing protein 5A OS=Mus musculus GN=Vwa5a PE=1 SV=2	-10	-10	-0.18	-0.67
sp Q99LC5 ETFFA_MOU SE	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2	-10	-10	-0.29	-0.36
sp Q99LX0 PARK7_MO USE	Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1	-10	-10	-0.08	-0.67
sp Q9CQ65 MTAP_MOU SE	S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=2 SV=1	-10	-10	-10	-10
sp Q9CQI6 COTL1_MO USE	Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3	-10	-10	-0.22	-0.54
sp Q9CQR2 RS21_MOU SE	40S ribosomal protein S21 OS=Mus musculus GN=Rps21 PE=2 SV=1	-10	-10	-0.07	-0.22
sp Q9CR62 M2OM_MO USE	Mitochondrial 2- oxoglutarate/malate carrier	-10	-10	-0.44	-10

	protein OS=Mus musculus GN=Slc25a11 PE=1 SV=3				
sp Q9CRB9 CHCH3_MOUSE	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1 SV=1	-10	-10	-0.34	-10
sp Q9CW03 SMC3_MOUSE	Structural maintenance of chromosomes protein 3 OS=Mus musculus GN=Smc3 PE=1 SV=2	-10	-10	-0.62	-0.55
sp Q9CWY9 RIP_MOUSE	RPA-interacting protein OS=Mus musculus GN=Rpain PE=2 SV=1	-10	-1.26	-10	-0.37
sp Q9CXT8 MPPB_MOUSE	Mitochondrial-processing peptidase subunit beta OS=Mus musculus GN=Pmpcb PE=2 SV=1	-10	-0.63	-0.3	-0.38
sp Q9CXW3 CYBP_MOUSE	Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	-10	-10	-0.02	-10
sp Q9CY64 BIEA_MOUSE	Biliverdin reductase A OS=Mus musculus GN=Blvra PE=2 SV=1	-10	-10	-10	-10
sp Q9CZY3 UB2V1_MOUSE	Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=1 SV=1	-10	-10	-0.06	-10
sp Q9D0E1 HNRPM_MOUSE	Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrpm PE=1 SV=3	-10	-1.02	-0.07	-0.41
sp Q9D1R9 RL34_MOUSE	60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=3 SV=2	-10	-0.29	-0.23	-0.43
sp Q9D2M8 UB2V2_MOUSE	Ubiquitin-conjugating enzyme E2 variant 2 OS=Mus musculus GN=Ube2v2 PE=2 SV=4	-10	-10	-0.06	-10
sp Q9D3D9 ATPD_MOUSE	ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5d PE=1 SV=1	-10	-10	-0.12	-0.27
sp Q9DBG6 RPN2_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	-10	-10	-0.2	-0.32
sp Q9DCC8 TOM20_MOUSE	Mitochondrial import receptor subunit TOM20 homolog OS=Mus musculus GN=Tom20 PE=1 SV=1	-10	-10	-10	-10
sp Q9DCH4 EIF3F_MOUSE	Eukaryotic translation initiation factor 3 subunit F	-10	-10	-0.29	-10

	OS=Mus musculus GN=Eif3f PE=1 SV=2				
sp Q9EPU0 RENT1_MOUSE	Regulator of nonsense transcripts 1 OS=Mus musculus GN=Upf1 PE=1 SV=2	-10	-10	-0.11	-0.39
sp Q9EQP2 EHD4_MOUSE	EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	-10	-10	-0.74	-0.5
sp Q9ES52 SHIP1_MOUSE	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1 OS=Mus musculus GN=Inpp5d PE=1 SV=2	-10	-10	-0.26	-0.31
sp Q9JHU4 DYHC1_MOUSE	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2	-10	-0.44	-0.3	-0.66
sp Q9JIK5 DDX21_MOUSE	Nucleolar RNA helicase 2 OS=Mus musculus GN=Ddx21 PE=1 SV=3	-10	0.93	-0.29	-2.3
sp Q9JJ28 FLII_MOUSE	Protein flightless-1 homolog OS=Mus musculus GN=Flii PE=1 SV=1	-10	-10	-0.14	-0.38
sp Q9JM76 ARPC3_MOUSE	Actin-related protein 2/3 complex subunit 3 OS=Mus musculus GN=Arpc3 PE=1 SV=3	-10	-10	-0.03	-0.27
sp Q9JMA1 UBP14_MOUSE	Ubiquitin carboxyl-terminal hydrolase 14 OS=Mus musculus GN=Usp14 PE=1 SV=3	-10	-10	-0.06	-0.42
sp Q9QXX4 CMC2_MOUSE	Calcium-binding mitochondrial carrier protein Aralar2 OS=Mus musculus GN=Slc25a13 PE=1 SV=1	-10	-10	-0.21	-0.46
sp Q9QYJ0 DNJA2_MOUSE	DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1	-10	-10	-10	-0.33
sp Q9QZD8 DIC_MOUSE	Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=2 SV=2	-10	-10	-0.09	-10
sp Q9R1Q7 PLP2_MOUSE	Proteolipid protein 2 OS=Mus musculus GN=Plp2 PE=2 SV=1	-10	-10	-0.09	-0.15
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	-10	1.41	-10	0.71
sp Q9WVK4 EHD1_MOUSE	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	-10	-10	-10	0.49
sp Q9Z110 P5CS_MOUSE	Delta-1-pyrroline-5-carboxylate synthase OS=Mus musculus	-10	-10	-0.47	-0.68

	GN=Aldh18a1 PE=2 SV=2				
sp Q9Z1Q5 CLIC1_MOUSE	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	-10	0.18	-0.05	-0.1
sp Q9Z2I8 SUCB2_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Suc1g2 PE=2 SV=3	-10	-10	-10	-10
sp A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn PE=1 SV=1	-9.52	-1.2	-10	4.96
sp Q8QZT1 THIL_MOUSE	Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	-3.35	-2.74	-1.24	-1.33
sp P25206 MCM3_MOUSE	DNA replication licensing factor MCM3 OS=Mus musculus GN=Mcm3 PE=1 SV=2	-3.06	-10	-0.41	-0.99
sp Q8CGK3 LONM_MOUSE	Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE=1 SV=2	-2.3	-10	-0.12	-0.3
sp P80317 TCPZ_MOUSE	T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	-2.04	-10	-0.18	-0.39
sp P63038 CH60_MOUSE	60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	-2	-0.92	-0.12	-0.06
sp Q8VCH0 THIKB_MOUSE	3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1	-1.96	-1.14	-0.06	0.31
sp Q8BMS1 ECHA_MOUSE	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	-1.91	-10	-0.21	-0.75
sp Q91VD9 NDUS1_MOUSE	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2	-1.79	-0.99	-0.05	-10
sp Q9WV27 AT1A4_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-4 OS=Mus musculus GN=Atp1a4 PE=1 SV=3	-1.74	-1.15	-0.21	-0.56
sp Q9DB77 QCR2_MOUSE	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	-1.66	-1.39	-0.35	-0.59
sp Q9D0K2 SCOT1_MOUSE	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1,	-1.59	-1.33	-0.18	-0.22

	mitochondrial OS=Mus musculus GN=Oxct1 PE=1 SV=1				
sp Q9DCW4 ETFB_MOUSE	Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	-1.55	-0.32	-0.28	-10
sp Q9CZ13 QCR1_MOUSE	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2	-1.48	-0.63	-0.3	-0.52
sp Q6PIE5 AT1A2_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Mus musculus GN=Atp1a2 PE=1 SV=1	-1.44	-0.89	-0.19	-0.57
sp Q8VDN2 AT1A1_MOUSE	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	-1.34	-0.99	-0.2	-0.53
sp Q9DCX2 ATP5H_MOUSE	ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	-1.32	-0.93	-0.34	-0.56
sp P62806 H4_MOUSE	Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	-1.3	-10	-0.08	-0.28
sp P54071 IDHP_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	-1.27	-10	-0.23	-0.68
sp P56480 ATPB_MOUSE	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	-1.26	-0.65	-0.34	-0.69
sp Q922D8 C1TC_MOUSE	C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4	-1.2	-0.9	-0.93	-0.69
sp P68433 H31_MOUSE	Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	-1.17	-10	-10	-0.94
sp P84228 H32_MOUSE	Histone H3.2 OS=Mus musculus GN=Hist1h3b PE=1 SV=2	-1.17	-10	-10	-0.94
sp P84244 H33_MOUSE	Histone H3.3 OS=Mus musculus GN=H3f3a PE=1 SV=2	-1.17	-10	-10	-0.94
sp Q99MN1 SYK_MOUSE	Lysyl-tRNA synthetase OS=Mus musculus GN=Kars PE=1 SV=1	-1.17	-10	-10	-0.08
sp Q9JKR6 HYOU1_MOUSE	Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1	-1.17	1.07	-0.18	-0.04
sp Q6PIC6 AT1A3_MOUSE	Sodium/potassium-	-1.16	-0.89	-0.22	-0.6

SE	transporting ATPase subunit alpha-3 OS=Mus musculus GN=Atp1a3 PE=1 SV=1				
sp P67778 PHB_MOUSE	Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	-1.15	-0.72	-0.36	-0.52
sp Q9D3B1 HACD2_MOUSE	3-hydroxyacyl-CoA dehydratase 2 OS=Mus musculus GN=Ptp1b PE=2 SV=1	-1.14	-1.31	-10	-1.39
sp Q8CGP0 H2B3B_MOUSE	Histone H2B type 3-B OS=Mus musculus GN=Hist3h2bb PE=1 SV=3	-1.13	-0.25	-0.35	-10
sp Q9D2U9 H2B3A_MOUSE	Histone H2B type 3-A OS=Mus musculus GN=Hist3h2ba PE=1 SV=3	-1.13	-0.25	-0.35	-10
sp P97807 FUMH_MOUSE	Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=3	-1.12	-0.81	-10	-10
sp Q9Z1W8 AT12A_MOUSE	Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=3	-1.12	-1.15	-0.21	-0.58
sp Q03265 ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	-1.09	-0.59	-0.39	-0.91
sp P10853 H2B1F_MOUSE	Histone H2B type 1-F/J/L OS=Mus musculus GN=Hist1h2bf PE=1 SV=2	-1.08	-0.21	-0.37	-0.53
sp P10854 H2B1M_MOUSE	Histone H2B type 1-M OS=Mus musculus GN=Hist1h2bm PE=1 SV=2	-1.08	-0.21	-0.37	-0.53
sp P70696 H2B1A_MOUSE	Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba PE=2 SV=3	-1.08	-0.21	-0.29	-10
sp Q64475 H2B1B_MOUSE	Histone H2B type 1-B OS=Mus musculus GN=Hist1h2bb PE=1 SV=3	-1.08	-0.21	-0.37	-0.53
sp Q64478 H2B1H_MOUSE	Histone H2B type 1-H OS=Mus musculus GN=Hist1h2bh PE=1 SV=3	-1.08	-0.21	-0.37	-0.53
sp Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac PE=1 SV=3	-1.08	-0.01	-0.17	-0.15
sp Q64525 H2B2B_MOUSE	Histone H2B type 2-B OS=Mus musculus GN=Hist2h2bb PE=1 SV=3	-1.08	-0.21	-0.37	-0.53
sp Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus musculus GN=Hist2h2aa1 PE=1 SV=3	-1.08	-0.01	-0.17	-0.15
sp Q6ZWY9 H2B1C_MOUSE	Histone H2B type 1-C/E/G OS=Mus musculus GN=Hist1h2bc PE=1 SV=3	-1.08	-0.21	-0.37	-0.53

sp Q8CGP2 H2B1P_MOUSE	Histone H2B type 1-P OS=Mus musculus GN=Hist1h2bp PE=1 SV=3	-1.08	-0.21	-0.37	-0.53
sp O08749 DLDH_MOUSE	Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2	-1.07	-0.13	-0.25	-0.12
sp P22752 H2A1_MOUSE	Histone H2A type 1 OS=Mus musculus GN=Hist1h2ab PE=1 SV=3	-1.06	-0.01	-0.17	-0.15
sp Q8BFU2 H2A3_MOUSE	Histone H2A type 3 OS=Mus musculus GN=Hist3h2a PE=1 SV=3	-1.06	-0.01	-0.17	-0.15
sp Q8CGP5 H2A1F_MOUSE	Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	-1.06	-0.01	-0.17	-0.15
sp Q8CGP6 H2A1H_MOUSE	Histone H2A type 1-H OS=Mus musculus GN=Hist1h2ah PE=1 SV=3	-1.06	-0.01	-0.17	-0.15
sp Q8CGP7 H2A1K_MOUSE	Histone H2A type 1-K OS=Mus musculus GN=Hist1h2ak PE=1 SV=3	-1.06	-0.01	-0.17	-0.15
sp Q8R1M2 H2AJ_MOUSE	Histone H2A.J OS=Mus musculus GN=H2afj PE=2 SV=1	-1.06	-0.01	-0.17	-0.15
sp Q9DBT5 AMPD2_MOUSE	AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1	-1.06	-0.34	-0.03	-0.37
sp P20491 FCERG_MOUSE	High affinity immunoglobulin epsilon receptor subunit gamma OS=Mus musculus GN=Fcer1g PE=1 SV=1	-1.05	-10	-0.08	0.09
sp Q9DCT2 NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=2	-1.03	-1.17	-0.08	-1.06
sp Q64524 H2B2E_MOUSE	Histone H2B type 2-E OS=Mus musculus GN=Hist2h2be PE=1 SV=3	-1.01	-0.25	-0.35	-10
sp P50518 VATE1_MOUSE	V-type proton ATPase subunit E 1 OS=Mus musculus GN=Atp6v1e1 PE=1 SV=2	-1	-10	-0.27	0.14
sp Q8CGP1 H2B1K_MOUSE	Histone H2B type 1-K OS=Mus musculus GN=Hist1h2bk PE=1 SV=3	-1	-0.21	-0.37	-0.53
sp Q64522 H2A2B_MOUSE	Histone H2A type 2-B OS=Mus musculus GN=Hist2h2ab PE=1 SV=3	-0.95	0.04	-0.15	0.03
sp P27661 H2AX_MOUSE	Histone H2A.x OS=Mus musculus GN=H2afx PE=1 SV=2	-0.91	0.04	-0.15	0.03

sp Q9D1G1 RAB1B_MOUSE	Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	-0.9	-10	-0.04	-0.69
sp Q64433 CH10_MOUSE	10 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspe1 PE=1 SV=2	-0.87	-0.26	-0.09	-0.09
sp Q8BFR5 EFTU_MOUSE	Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	-0.86	-10	-0.28	-0.44
sp P0C0S6 H2AZ_MOUSE	Histone H2A.Z OS=Mus musculus GN=H2afz PE=1 SV=2	-0.82	0.04	-0.15	0.03
sp Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus musculus GN=H2afv PE=1 SV=3	-0.82	0.04	-0.15	0.03
sp P54116 STOM_MOUSE	Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	-0.81	-0.65	-0.42	-0.34
sp Q3TW96 UAP1L_MOUSE	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Mus musculus GN=Uap111 PE=2 SV=1	-0.79	-10	-10	0.07
sp Q6PB66 LPPRC_MOUSE	Leucine-rich PPR motif- containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	-0.75	-0.43	-0.29	-0.48
sp P12787 COX5A_MOUSE	Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2	-0.74	-10	-0.04	-0.05
sp Q9ERK4 XPO2_MOUSE	Exportin-2 OS=Mus musculus GN=Cse11 PE=2 SV=1	-0.73	-0.14	-0.23	-0.24
sp Q8VEM8 MPCP_MOUSE	Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	-0.72	-0.68	-0.34	-0.43
sp Q91ZX7 LRP1_MOUSE	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	-0.72	-10	-0.11	-0.54
sp Q99KI0 ACON_MOUSE	Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	-0.72	-0.67	-0.2	-0.37
sp Q07133 H1T_MOUSE	Histone H1t OS=Mus musculus GN=Hist1h1t PE=2 SV=4	-0.69	-0.6	-0.72	-0.9
sp O35129 PHB2_MOUSE	Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1	-0.68	1.44	-0.32	-0.66

	SV=1				
sp Q5SUR0 PUR4_MOUSE SE	Phosphoribosylformylglycine midine synthase OS=Mus musculus GN=Pfas PE=2 SV=1	-0.68	-0.92	-0.21	-0.54
sp P80315 TCPD_MOUSE SE	T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	-0.67	-0.57	-0.03	-0.3
sp Q06185 ATP5I_MOUSE SE	ATP synthase subunit e, mitochondrial OS=Mus musculus GN=Atp5i PE=1 SV=2	-0.67	-10	-0.07	-0.19
sp P43276 H15_MOUSE	Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	-0.66	-10	-0.46	-0.62
sp P43274 H14_MOUSE	Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2	-0.64	-0.57	-0.67	-0.82
sp Q9Z2X1 HNRPF_MOUSE	Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnrnpf PE=1 SV=3	-0.64	-10	-0.4	-0.47
sp P15864 H12_MOUSE	Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	-0.63	-0.48	-0.57	-0.77
sp P63276 RS17_MOUSE E	40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	-0.63	-10	-0.19	-0.34
sp P43277 H13_MOUSE	Histone H1.3 OS=Mus musculus GN=Hist1h1d PE=1 SV=2	-0.62	-0.48	-0.57	-0.77
sp P48962 ADT1_MOUSE E	ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	-0.61	-0.54	-0.42	-0.74
sp Q9CQ7 AT5F1_MOUSE USE	ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	-0.61	-0.33	-0.41	-0.76
sp P56135 ATPK_MOUSE E	ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=1 SV=3	-0.6	-10	-0.12	-0.3
sp Q921H8 THIKA_MOUSE SE	3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=2 SV=1	-0.6	-1.26	-0.1	-0.47
sp Q99LP6 GRPE1_MOUSE USE	GrpE protein homolog 1, mitochondrial OS=Mus musculus GN=Grpel1 PE=1 SV=1	-0.6	-10	-10	-10
sp Q61753 SERA_MOUSE SE	D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	-0.59	-0.49	-0.23	-0.45

sp P08113 ENPL_MOUSE	Endoplasmic reticulum protein OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	-0.58	-0.08	-0.07	0
sp Q8K2B3 DHSA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	-0.58	-0.27	-0.09	-0.63
sp Q9CQA3 DHSB_MOUSE	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=Sdhb PE=1 SV=1	-0.58	-0.48	-0.36	-0.9
sp Q62095 DDX3Y_MOUSE	ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2	-0.56	-0.97	-0.14	-0.44
sp Q9DB20 ATPO_MOUSE	ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	-0.56	-0.38	-0.25	-0.46
sp P43275 H11_MOUSE	Histone H1.1 OS=Mus musculus GN=Hist1h1a PE=2 SV=2	-0.55	-0.76	-0.84	-0.73
sp Q99K51 PLST_MOUSE	Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	-0.54	-1.06	-0.1	-0.01
sp Q99NB9 SF3B1_MOUSE	Splicing factor 3B subunit 1 OS=Mus musculus GN=Sf3b1 PE=1 SV=1	-0.54	-10	-0.2	-0.29
sp P51881 ADT2_MOUSE	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	-0.53	-0.46	-0.41	-0.71
sp Q9D6R2 LDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Ldh3a PE=1 SV=1	-0.52	-0.25	-0.18	-0.54
sp P17710 HXK1_MOUSE	Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=3	-0.51	-0.14	-0.32	-0.45
sp P16381 DDX3L_MOUSE	Putative ATP-dependent RNA helicase P10 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	-0.5	-0.73	-0.34	-0.44
sp P42208 SEPT2_MOUSE	Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2	-0.5	-10	-0.16	-0.2
sp Q62167 DDX3X_MOUSE	ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3	-0.5	-0.73	-0.31	-0.35
sp Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=4	-0.49	-0.56	-0.3	-0.66

sp Q8VC28 AK1CD_MOUSE	Aldo-keto reductase family 1 member C13 OS=Mus musculus GN=Akr1c13 PE=1 SV=2	-0.49	-1.43	-1.3	-1.13
sp P10107 ANXA1_MOUSE	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	-0.48	-0.54	-0.03	-0.09
sp P80316 TCPE_MOUSE	T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	-0.47	-0.33	-0.02	-0.35
sp Q9DAS9 GBG12_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Mus musculus GN=Gng12 PE=1 SV=3	-0.47	-0.23	-0.35	-1.52
sp P30681 HMGB2_MOUSE	High mobility group protein B2 OS=Mus musculus GN=Hmgb2 PE=1 SV=3	-0.46	-1.13	-0.07	-0.54
sp P47738 ALDH2_MOUSE	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	-0.46	-0.42	-0.13	-1.02
sp P38647 GRP75_MOUSE	Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	-0.45	0.06	-0.07	-0.09
sp P60335 PCBP1_MOUSE	Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	-0.45	-10	-0.02	-0.35
sp P97351 RS3A_MOUSE	40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	-0.45	0.01	-0.24	-0.59
sp Q62425 NDUA4_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Mus musculus GN=Ndufa4 PE=1 SV=2	-0.45	-10	-0.36	-0.74
sp P54775 PRS6B_MOUSE	26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2	-0.43	-10	-0.29	-0.19
sp P26443 DHE3_MOUSE	Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	-0.41	-0.22	-10	-0.47
sp Q3V132 ADT4_MOUSE	ADP/ATP translocase 4 OS=Mus musculus GN=Slc25a31 PE=2 SV=1	-0.38	-0.32	-0.38	-0.63
sp Q8JZQ9 EIF3B_MOUSE	Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1	-0.36	-10	-0.06	-0.35
sp Q9D8E6 RL4_MOUSE	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4	-0.36	-0.86	-0.3	-0.54

	PE=1 SV=3				
sp O54734 OST48_MOUSE SE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddost PE=1 SV=2	-0.35	-10	-0.13	-10
sp P62245 RS15A_MOUSE SE	40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=2 SV=2	-0.35	-10	-1.68	-3.33
sp O35326 SRSF5_MOUSE SE	Serine/arginine-rich splicing factor 5 OS=Mus musculus GN=Srsf5 PE=1 SV=1	-0.34	-0.7	-0.12	-0.15
sp Q8VE97 SRSF4_MOUSE USE	Serine/arginine-rich splicing factor 4 OS=Mus musculus GN=Srsf4 PE=2 SV=1	-0.34	-0.7	-0.12	-0.15
sp P34022 RANG_MOUSE SE	Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	-0.33	-10	-0.08	-0.28
sp Q8C0C7 SYFA_MOUSE SE	Phenylalanyl-tRNA synthetase alpha chain OS=Mus musculus GN=Farsa PE=2 SV=1	-0.33	-10	-0.19	-10
sp P84104 SRSF3_MOUSE SE	Serine/arginine-rich splicing factor 3 OS=Mus musculus GN=Srsf3 PE=1 SV=1	-0.31	-0.5	-0.55	-0.86
sp P29341 PABP1_MOUSE SE	Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=2	-0.3	0.08	-0.1	-0.08
sp P97311 MCM6_MOUSE SE	DNA replication licensing factor MCM6 OS=Mus musculus GN=Mcm6 PE=1 SV=1	-0.29	-10	-10	-0.85
sp Q9DCC4 P5CR3_MOUSE USE	Pyrroline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycr1 PE=2 SV=2	-0.29	-0.84	-0.05	-0.47
sp O35737 HNRH1_MOUSE USE	Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3	-0.28	-1.76	-0.4	-0.63
sp P70333 HNRH2_MOUSE USE	Heterogeneous nuclear ribonucleoprotein H2 OS=Mus musculus GN=Hnrnph2 PE=1 SV=1	-0.28	-1.76	-10	-0.7
sp Q04447 KCRB_MOUSE SE	Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1	-0.27	-10	-10	-0.26
sp Q8VEK3 HNRPU_MOUSE USE	Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1	-0.26	-0.79	-0.27	-0.45

sp Q9ERD7 TBB3_MOUSE SE	Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	-0.25	-0.65	-0.24	-0.65
sp P14206 RSSA_MOUSE SE	40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	-0.23	-0.5	-0.15	-0.17
sp P68372 TBB2C_MOUSE SE	Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	-0.23	-0.62	-0.23	-0.69
sp Q9CZU6 CISY_MOUSE SE	Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	-0.21	0.12	-0.97	-0.37
sp Q9D1Q4 DPM3_MOUSE SE	Dolichol-phosphate mannosyltransferase subunit 3 OS=Mus musculus GN=Dpm3 PE=2 SV=1	-0.21	-0.14	-0.32	-0.98
sp P11983 TCPA_MOUSE SE	T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3	-0.2	-10	-0.2	-0.51
sp P80318 TCPG_MOUSE SE	T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	-0.19	-0.2	-0.15	-0.31
sp Q922F4 TBB6_MOUSE SE	Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	-0.19	-0.44	-0.24	-0.69
sp P62082 RS7_MOUSE SE	40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	-0.17	-10	-0.22	-0.41
sp P70168 IMB1_MOUSE SE	Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2	-0.17	-0.53	-0.01	-0.17
sp Q7TMM9 TBB2A_MOUSE SE	Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	-0.17	-0.65	-0.23	-0.69
sp Q9CWF2 TBB2B_MOUSE SE	Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1	-0.17	-0.65	-0.23	-0.69
sp Q9WUU7 CATZ_MOUSE SE	Cathepsin Z OS=Mus musculus GN=Ctsz PE=2 SV=1	-0.17	0.56	-0.08	-0.44
sp P14131 RS16_MOUSE SE	40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=2 SV=4	-0.16	-0.74	-0.19	-0.45
sp O88569 ROA2_MOUSE SE	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	-0.15	-0.7	-0.11	-0.07
sp P08752 GNAI2_MOUSE SE	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Mus musculus GN=Gnai2 PE=1 SV=5	-0.14	-10	-0.07	-0.78
sp P53026 RL10A_MOUSE SE	60S ribosomal protein L10a OS=Mus musculus	-0.14	-10	-0.08	-0.1

	GN=Rpl10a PE=1 SV=3				
sp P62918 RL8_MOUSE	60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	-0.14	-0.42	-0.25	-0.47
sp P27659 RL3_MOUSE	60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=3	-0.12	-10	-0.05	-0.47
sp P31254 UBA1Y_MOUSE	Ubiquitin-like modifier- activating enzyme 1 Y OS=Mus musculus GN=Ube1ay PE=2 SV=2	-0.1	-0.61	-0.16	0.1
sp P99024 TBB5_MOUSE	Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	-0.09	-0.71	-0.28	-0.71
sp Q9D6F9 TBB4_MOUSE	Tubulin beta-4 chain OS=Mus musculus GN=Tubb4 PE=1 SV=3	-0.09	-0.63	-0.21	-0.67
sp Q8C166 CPNE1_MOUSE	Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1	-0.05	-10	-10	-10
sp P50247 SAHH_MOUSE	Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	-0.04	-10	-0.09	-0.49
sp Q8VDM4 PSMD2_MOUSE	26S proteasome non- ATPase regulatory subunit 2 OS=Mus musculus GN=Psm2 PE=1 SV=1	-0.04	0.1	-0.28	-0.11
sp P08003 PDIA4_MOUSE	Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=3	-0.03	-10	-10	0.01
sp P70372 ELAV1_MOUSE	ELAV-like protein 1 OS=Mus musculus GN=Elav1 PE=1 SV=2	-0.03	-0.17	-0.5	-0.39
sp Q14C59 TM11B_MOUSE	Transmembrane protease serine 11B OS=Mus musculus GN=Tmprss11b PE=2 SV=2	-0.03	-0.1	-10	-0.22
sp Q80UM7 MOGS_MOUSE	Mannosyl-oligosaccharide glucosidase OS=Mus musculus GN=Mogs PE=2 SV=1	-0.02	-0.6	-0.37	0.07
sp P10126 EF1A1_MOUSE	Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	-0.01	-0.15	-0.09	-0.24

Table 16. List of LPS induced proteins (Log₂ value > 1) consistently in experiment 2 and 1.

Sequence ID	Proteins	Experiment -2	Experiment -1
		Ips Ratio	Ips Ratio

sp P54987 IRG1_MOUSE	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	3.1	3.58
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	3.6	4.89
sp Q9CQS8 SC61B_MOUSE	Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3	1.02	3
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcksl1 PE=1 SV=2	1.63	4.15
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	1.04	2.49
sp Q91XV3 BASP1_MOUSE	Brain acid soluble protein 1	1.16	1.53

Table 17. List of *Echinacea* extract 7 induced proteins (Log_2 value > 1) consistently in experiment 2 and 1.

Sequence Id	Proteins Sequence Name	Experiment-2 <i>Echinacea</i> extract 7 Ratio	Experiment-1 <i>Echinacea</i> extract 7 Ratio
sp Q9WUM4 COR1C_MOUSE	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	1.65	2.13

Table 18. List of alkylamide-11a/b induced proteins (Log_2 value > 1) in experiment 2.

Table 15. List of alkylamide-11a/b induced proteins (Log_2 value > 1) in experiment 2		
Sequence ID	Proteins	Experiment -2 alkylamide-11 a/b Ratio
sp A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn PE=1 SV=1	5.96
sp P19246 NFH_MOUSE	Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE=1 SV=3	2.18
sp P29387 GBB4_MOUSE	Guanine nucleotide-binding protein subunit beta-4	1.61

	OS=Mus musculus GN=Gnb4 PE=2 SV=4	
sp Q61011 GBB3_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Mus musculus GN=Gnb3 PE=1 SV=2	1.61
sp Q6ZWX6 IF2A_MOUSE	Eukaryotic translation initiation factor 2	1.89

Table 19. Effect of *Echinacea* Extract 7 on LPS induced proteins (Log₂ value > 1) in experiment 2 and 1.

Sequence ID	Proteins	Experiment-3		Experiment -2		Experiment -1	
		LPS Ratio	LPS+ <i>Echinacea</i> Extract 7 Ratio	LPS Ratio	LPS+ <i>Echinacea</i> Extract 7 Ratio	LPS Ratio	LPS+ <i>Echinacea</i> Extract 7 Ratio
sp P54987 IRG1_MOUSE	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	6.33	5.3	3.1	4.26	3.58	-10
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	5.09	-10	3.6	-10	4.89	-10
sp Q9CQS8 SC61B_MOUSE	Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3	0.58	-10	1.02	0.63	3	-10
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcks1 PE=1 SV=2	3.34	3.14	1.63	0.93	4.15	3.42
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	1.56	1.8	1.04	0.71	2.49	1.41

Table 20. Effect of *Echinacea* Extract 7 on LPS induced proteins in experiment 2 and 1.

Sequence Id	Sequence Name	LPS Ratio -2	LPS+ <i>Echinacea</i> Extract 7 Ratio-2	LPS Ratio-1	LPS+ <i>Echinacea</i> Extract 7 Ratio-1
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	4.89	-10	3.6	-10
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcks1 PE=1 SV=2	4.15	3.42	1.63	0.93
sp P54987 IRG1_MOUSE	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	3.58	-10	3.1	4.26
sp P61957 SUMO2_MOUSE	Small ubiquitin-related modifier 2 OS=Mus musculus GN=Sumo2 PE=2 SV=1	3.1	1.97	0.17	-0.12
sp Q9Z172 SUMO3_MOUSE	Small ubiquitin-related modifier 3 OS=Mus musculus GN=Sumo3 PE=2 SV=1	3.1	1.97	0.17	-0.12
sp Q9CQS8 SC61B_MOUSE	Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3	3	-10	1.02	0.63
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	2.49	1.41	1.04	0.71
sp Q9WVK4 EHD1_MOUSE	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	2.09	-10	0.61	0.49
sp Q62433 NDRG1_MOUSE	Protein NDRG1 OS=Mus musculus GN=Ndrp1 PE=1 SV=1	2.05	-10	0.82	0.4
sp Q8BFZ3 ACTBL_MOUSE	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=1 SV=1	1.54	0.99	0.64	-0.13
sp P62835 RAP1A_MOUSE	Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=2 SV=1	1.47	0.46	0.38	0.03
sp Q99J16 RAP1B_MOUSE	Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=2 SV=2	1.47	0.46	0.38	0.03
sp P45591 COF2_MOUSE	Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1	1.44	1.26	0.19	-0.2
sp P17809 GTR1_MOUSE	Solute carrier family 2,	1.43	1.03	0.91	0.86

	facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=4				
sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	1.36	1.27	0.42	-0.09
sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	1.36	1.27	0.42	-0.09
sp P26039 TLN1_MOUSE	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2	1.35	0.67	0.46	0.06
sp P62737 ACTA_MOUSE	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	1.35	1.03	0.41	-0.1
sp P63268 ACTH_MOUSE	Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1	1.35	1.03	0.41	-0.1
sp P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	1.35	1.03	0.41	-0.1
sp P68134 ACTS_MOUSE	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	1.35	1.03	0.41	-0.1
sp Q9D1A2 CNDP2_MOUSE	Cytosolic non-specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1	1.28	0.82	0.78	0.24
sp Q91V41 RAB14_MOUSE	Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3	1.21	0.18	0.05	-0.4
sp Q91XV3 BASP1_MOUSE	Brain acid soluble protein 1 OS=Mus musculus GN=Basp1 PE=1 SV=3	1.16	-10	1.53	0.4
sp P0C0S6 H2AZ_MOUSE	Histone H2A.Z OS=Mus musculus GN=H2afz PE=1 SV=2	1.14	0.04	0.17	0.03
sp P27661 H2AX_MOUSE	Histone H2A.x OS=Mus musculus GN=H2afx PE=1 SV=2	1.14	0.04	0.17	0.03
sp Q3THW5 H2AV_MOUSE	Histone H2A.V OS=Mus musculus GN=H2afv PE=1 SV=3	1.14	0.04	0.17	0.03
sp Q64522 H2A2B_MOUSE	Histone H2A type 2-B OS=Mus musculus GN=Hist2h2ab PE=1 SV=3	1.14	0.04	0.17	0.03
sp Q8BTM8 FLNA_MOUSE	Filamin-A OS=Mus musculus GN=Flna PE=1 SV=5	1.08	1.12	0.12	-0.02
sp Q71LX4 TLN2_MOUSE	Talin-2 OS=Mus musculus GN=Tln2 PE=1 SV=3	1.07	0.29	0.37	0.15
sp Q80X90 FLNB_MOUSE	Filamin-B OS=Mus musculus GN=Flnb PE=1	1.04	0.8	0.02	0.06

	SV=3				
sp P05555 ITAM_MOUSE	Integrin alpha-M OS=Mus musculus GN=Itgam PE=1 SV=2	0.98	1.65	0.74	0.13
sp P22752 H2A1_MOUSE	Histone H2A type 1 OS=Mus musculus GN=Hist1h2ab PE=1 SV=3	0.97	-0.01	0.09	-0.15
sp Q64523 H2A2C_MOUSE	Histone H2A type 2-C OS=Mus musculus GN=Hist2h2ac PE=1 SV=3	0.97	-0.01	0.09	-0.15
sp Q6GSS7 H2A2A_MOUSE	Histone H2A type 2-A OS=Mus musculus GN=Hist2h2aa1 PE=1 SV=3	0.97	-0.01	0.09	-0.15
sp Q8BFU2 H2A3_MOUSE	Histone H2A type 3 OS=Mus musculus GN=Hist3h2a PE=1 SV=3	0.97	-0.01	0.09	-0.15
sp Q8CGP5 H2A1F_MOUSE	Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	0.97	-0.01	0.09	-0.15
sp Q8CGP6 H2A1H_MOUSE	Histone H2A type 1-H OS=Mus musculus GN=Hist1h2ah PE=1 SV=3	0.97	-0.01	0.09	-0.15
sp Q8CGP7 H2A1K_MOUSE	Histone H2A type 1-K OS=Mus musculus GN=Hist1h2ak PE=1 SV=3	0.97	-0.01	0.09	-0.15
sp Q8R1M2 H2AJ_MOUSE	Histone H2A.J OS=Mus musculus GN=H2afj PE=2 SV=1	0.97	-0.01	0.09	-0.15
sp P37040 NCPR_MOUSE	NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	0.9	-10	4.01	-2.98
sp P62821 RAB1A_MOUSE	Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3	0.84	0.1	0.35	0.19
sp P40124 CAP1_MOUSE	Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4	0.8	-10	0.51	0.33
sp Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	0.77	-0.56	0.7	-0.16
sp P10852 4F2_MOUSE	4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	0.74	1	0.74	0.34
sp Q9ES52 SHIP1_MOUSE	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1 OS=Mus musculus GN=Inpp5d PE=1 SV=2	0.74	-10	0.1	-0.31

sp P26041 MOES_MOUSE	Moesin OS=Mus musculus GN=Msn PE=1 SV=3	0.71	0.49	0.58	0.12
sp Q9ER72 SYCC_MOUSE	Cysteinyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Cars PE=1 SV=2	0.64	0.24	0.51	0.33
sp P97429 ANXA4_MOUSE	Annexin A4 OS=Mus musculus GN=Anxa4 PE=2 SV=4	0.58	0.5	1.15	-10
sp P26040 EZRI_MOUSE	Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	0.56	0.48	0.52	0.12
sp P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2	0.55	0.46	0.81	0.26
sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=1 SV=1	0.55	0.19	0.54	0.29
sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	0.55	0.19	0.54	0.29
sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Uba52 PE=1 SV=2	0.55	0.19	0.54	0.29
sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=Rps27a PE=1 SV=2	0.55	0.19	0.45	0.25
sp P47955 RLA1_MOUSE	60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1	0.53	-10	0.67	-0.04
sp Q64727 VINC_MOUSE	Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	0.52	-0.31	0.28	0.13
sp P07901 HS90A_MOUSE	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	0.47	0.25	0.45	0.38
sp P63017 HSP7C_MOUSE	Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	0.45	0.38	0.55	0.08
sp P17156 HSP72_MOUSE	Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=2	0.44	0.42	0.56	0.1
sp P29341 PABP1_MOUSE	Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=2	0.43	0.08	0.31	-0.08
sp P06800 PTPRC_MOUSE	Receptor-type tyrosine- protein phosphatase C OS=Mus musculus GN=Ptprc PE=1 SV=3	0.42	0.55	0.3	-0.28

sp P16627 HS71L_MOUSE	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa1l PE=2 SV=4	0.39	0.15	0.58	0.18
sp P26043 RADI_MOUSE	Radixin OS=Mus musculus GN=Rdx PE=1 SV=3	0.39	0.48	0.56	0.01
sp P11835 ITB2_MOUSE	Integrin beta-2 OS=Mus musculus GN=Itgb2 PE=1 SV=2	0.39	0.77	0.49	-0.01
sp P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	0.38	0.39	0.05	-0.07
sp P58771 TPM1_MOUSE	Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	0.36	0.24	0.37	-0.15

Table 21. Effect of *Echinacea* extract 7 on LPS induced proteins in experiment 3, 2 and 1.

Sequence Id	Sequence Name	LPS Ratio -1	LPS+ <i>Echinacea</i> extract 7 Ratio-1	LPS Ratio -2	LPS+ <i>Echinacea</i> extract 7 Ratio-2	LPS Ratio -3	LPS+ <i>Echinacea</i> extract 7 Ratio-3
sp P09103 PDIA1_MOUSE	Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2	4.01	-2.98	0.9	-10	1.17	1.46
sp P10107 ANXA1_MOUSE	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	3.6	-10	4.89	-10	5.09	-10
sp P17809 GTR1_MOUSE	Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=4	3.1	4.26	3.58	-10	6.33	5.3
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Mus musculus GN=Marcksl1 PE=1	1.63	0.93	4.15	3.42	3.34	3.14

	SV=2						
sp P37040 NCPR_MOUSE	NADPH-- cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	1.04	0.71	2.49	1.41	1.56	1.8
sp P46638 RB11B_MOUSE	Ras-related protein Rab- 11B OS=Mus musculus GN=Rab11 b PE=1 SV=3	1.02	0.63	3	-10	0.58	-10
sp P47915 RL29_MOUSE	60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2	0.91	0.86	1.43	1.03	2.19	1.65
sp P54987 IRG1_MOUSE	Immune- responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	0.81	0.26	0.55	0.46	0.17	-0.05
sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	0.7	-0.16	0.77	-0.56	0.22	0.19
sp P62492 RB11A_MOUSE	Ras-related protein Rab- 11A OS=Mus musculus GN=Rab11 a PE=1 SV=3	0.64	-0.13	1.54	0.99	0.9	0.95
sp P62737 ACTA_MOUSE	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	0.61	0.49	2.09	-10	1.83	-10

sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	0.45	-0.06	0.24	-0.41	0.09	-0.41
sp P63268 ACTH_MOUSE	Actin, gamma-enteric smooth muscle OS=Mus musculus GN=Actg2 PE=2 SV=1	0.42	-0.09	1.36	1.27	0.99	0.78
sp P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1	0.42	-0.09	1.36	1.27	0.99	0.78
sp P68134 ACTS_MOUSE	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	0.41	-0.1	1.35	1.03	0.93	0.74
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	0.41	-0.1	1.35	1.03	0.93	0.74
sp Q8BFZ3 ACTBL_MOUSE	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=1 SV=1	0.41	-0.1	1.35	1.03	0.93	0.74
sp Q99PT1 GDIR1_MOUSE	Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	0.41	-0.1	1.35	1.03	0.93	0.74
sp Q9CQS8 SC61B_MOUSE	Protein transport protein Sec61 subunit beta	0.3	-0.1	0.24	0.18	1.52	0.45

	OS=Mus musculus GN=Sec61b PE=1 SV=3						
sp Q9WTK5 NFKB2_MOUSE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	0.26	-0.09	0.15	-0.54	0.54	0.47
sp Q9WVK4 EHD1_MOUSE	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	0.2	-0.59	0.18	-10	0.83	0.63
sp Q9Z1Q5 CLIC1_MOUSE	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	0.2	-0.59	0.18	-10	0.83	0.63

Table 22. Effect of LPS on alkylamide-11 a/b induced proteins.

Sequence ID	Proteins	Experiment -2	
		alkylamide-11 a/b Ratio	alkylamide-11 a/b +LPS ratio
sp A2ASS6 TITIN_MOUSE	Titin OS=Mus musculus GN=Ttn PE=1 SV=1	5.96	0.28
sp P19246 NFH_MOUSE	Neurofilament heavy polypeptide OS=Mus musculus GN=Nefh PE=1 SV=3	2.18	-10
sp P29387 GGB4_MOUSE	Guanine nucleotide-binding protein subunit beta-4 OS=Mus musculus GN=Gnb4 PE=2 SV=4	1.61	-10
sp Q61011 GGB3_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Mus musculus GN=Gnb3 PE=1 SV=2	1.61	-10
sp Q6ZWX6 IF2A_MOUSE	Eukaryotic translation initiation factor 2	1.89	-0.24

Table 23. Effect of LPS and alkylamide-11a/b together induced proteins.

Sequence ID	Protein	LPS + alkylamide-11 a/b ratio
sp P01895 HA1Y_MOUSE	H-2 class I histocompatibility antigen, alpha chain	1.07
sp Q6R5P0 TLR11_MOUSE	Toll-like receptor 11	2.77

Table 24. Effect of alkylamides 11a/b and 15 on LPS induced proteins.

Sequence Id	Sequence Name	LPS Ratio	LPS+ Echinacea extract 7 Ratio	Alkylamide 11 a/b + LPS Ratio	Alkylamide 15 + LPS Ratio
sp P07724 ALBU_MOUSE	Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	6.66	-10	-10	-10
sp P54987 IRG1_MOUSE	Immune-responsive gene 1 protein OS=Mus musculus GN=Irg1 PE=2 SV=2	6.33	5.3	4.34	2.92
sp O55131 SEPT7_MOUSE	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	6.08	-10	-10	-10
sp Q64282 IFIT1_MOUSE	Interferon-induced protein with tetratricopeptide repeats 1 OS=Mus musculus GN=Ifit1 PE=2 SV=2	6	2.12	4.51	-10
sp Q05769 PGH2_MOUSE	Prostaglandin G/H synthase 2 OS=Mus musculus GN=Ptgs2 PE=1 SV=1	5.09	-10	-10	-10
sp P29387 GGB4_MOUSE	Guanine nucleotide-binding protein subunit beta-4 OS=Mus musculus GN=Gnb4 PE=2 SV=4	4.54	-10	-10	-10
sp Q64337 SQSTM_MOUSE	Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1	4.43	5.63	3.33	-10
sp P29477 NOS2_MOUSE	Nitric oxide synthase, inducible OS=Mus musculus GN=Nos2 PE=1 SV=1	4.03	-10	-10	-10
sp O55143 AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2	4.01	0.11	-0.04	0.35

	PE=1 SV=2				
sp Q8R429 AT2A1_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Musculus GN=Atp2a1 PE=2 SV=1	4.01	-10	-10	0.35
sp Q61081 CDC37_MOUSE	Hsp90 co-chaperone Cdc37 OS=Musculus GN=Cdc37 PE=2 SV=1	3.79	-0.11	-10	-10
sp Q64339 ISG15_MOUSE	Ubiquitin-like protein ISG15 OS=Musculus GN=Isg15 PE=1 SV=4	3.49	2.77	4.14	-10
sp P28667 MRP_MOUSE	MARCKS-related protein OS=Musculus GN=Marcks1 PE=1 SV=2	3.34	3.14	2.02	-10
sp P14901 HMOX1_MOUSE	Heme oxygenase 1 OS=Musculus GN=Hmx1 PE=1 SV=1	3.11	3.54	4.67	3.85
sp P62880 GGB2_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Musculus GN=Gnb2 PE=1 SV=3	3.06	0.27	-0.05	0.2
sp P62874 GGB1_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Musculus GN=Gnb1 PE=1 SV=3	3.06	0.27	-0.05	0.2
sp Q61011 GGB3_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3 OS=Musculus GN=Gnb3 PE=1 SV=2	3.06	0.27	-10	-10
sp Q60766 IRGM1_MOUSE	Immunity-related GTPase family M protein 1 OS=Musculus GN=Irgm1 PE=1 SV=1	2.93	2.65	1.55	-10
sp Q91XB0 TREX1_MOUSE	Three prime repair exonuclease 1 OS=Musculus GN=Trex1 PE=1 SV=2	2.63	2.74	-10	-10
sp P11928 OAS1A_MOUSE	2'-5'-oligoadenylate synthase 1A OS=Musculus GN=Oas1a PE=2 SV=2	2.29	-10	-10	-10
sp Q9CWJ9 PUR9_MOUSE	Bifunctional purine biosynthesis protein PURH OS=Mus	2.22	-0.29	-0.48	-10

	musculus GN=Atic PE=1 SV=2				
sp P17809 GTR1_MOUSE	Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=4	2.19	1.65	0.61	-10
sp Q9WVK4 EHD1_MOUSE E	EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	1.83	-10	-10	-10
sp P09671 SODM_MOUSE	Superoxide dismutase [Mn], mitochondrial OS=Mus musculus GN=Sod2 PE=1 SV=3	1.69	1.54	0.55	1.31
sp Q9R233 TPSN_MOUSE	Tapasin OS=Mus musculus GN=Tapbp PE=2 SV=2	1.69	1.88	-10	0.93
sp P70460 VASP_MOUSE	Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=Vasp PE=1 SV=4	1.69	0.53	1.26	-10
sp P61161 ARP2_MOUSE	Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	1.66	0.46	-0.17	-0.37
sp Q9QUH0 GLRX1_MOUSE SE	Glutaredoxin-1 OS=Mus musculus GN=Glrx PE=1 SV=3	1.65	2.25	-10	0.81
sp Q9JHK5 PLEK_MOUSE	Pleckstrin OS=Mus musculus GN=Plek PE=1 SV=1	1.63	2.32	0.78	1.02
sp P35700 PRDX1_MOUSE E	Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	1.57	2.21	1.71	2.44
sp Q9WTK5 NFKB2_MOUSE SE	Nuclear factor NF-kappa-B p100 subunit OS=Mus musculus GN=Nfkb2 PE=1 SV=1	1.56	1.8	-10	-10
sp Q61792 LASP1_MOUSE E	LIM and SH3 domain protein 1 OS=Mus musculus GN=Lasp1 PE=1 SV=1	1.55	1.55	1.19	0.82
sp Q9Z1Q5 CLIC1_MOUSE E	Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	1.52	0.45	0.25	0.32
sp P20491 FCERG_MOUSE E	High affinity immunoglobulin epsilon receptor subunit gamma OS=Mus musculus GN=Fcer1g PE=1 SV=1	1.47	1.28	-10	0.35
sp Q9CQW9 IFM3_MOUSE E	Interferon-induced transmembrane protein 3 OS=Mus musculus	1.36	-10	-0.71	0.23

	GN=Ifitm3 PE=1 SV=1				
sp Q8R1F1 NIBL1_MOUSE	Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=1 SV=2	1.36	-10	-0.05	-10
sp P42225 STAT1_MOUSE	Signal transducer and activator of transcription 1 OS=Mus musculus GN=Stat1 PE=1 SV=1	1.34	2.09	-10	-10
sp P99029 PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2	1.33	-10	0.39	0.56
sp P04223 HA1K_MOUSE	H-2 class I histocompatibility antigen, K-K alpha chain OS=Mus musculus GN=H2-K1 PE=1 SV=1	1.26	0.95	1	-10
sp P01901 HA1B_MOUSE	H-2 class I histocompatibility antigen, K-B alpha chain OS=Mus musculus GN=H2-K1 PE=1 SV=1	1.26	0.95	1	-10
sp P06339 HA15_MOUSE	H-2 class I histocompatibility antigen, D-37 alpha chain OS=Mus musculus GN=H2-T23 PE=1 SV=1	1.26	0.95	1	-10
sp P14426 HA13_MOUSE	H-2 class I histocompatibility antigen, D-K alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=1	1.26	0.95	1	-10
sp P14427 HA14_MOUSE	H-2 class I histocompatibility antigen, D-P alpha chain OS=Mus musculus GN=H2-D1 PE=2 SV=1	1.26	0.95	1	-10
sp P14428 HA1Q_MOUSE	H-2 class I histocompatibility antigen, K-Q alpha chain (Fragment) OS=Mus musculus GN=H2-K1 PE=2 SV=1	1.26	0.95	1	-10
sp P14431 HA19_MOUSE	H-2 class I histocompatibility antigen, Q9 alpha chain (Fragment) OS=Mus musculus GN=H2-Q9 PE=2 SV=1	1.26	0.95	1	-10
sp P14429 HA17_MOUSE	H-2 class I histocompatibility antigen, Q7 alpha chain OS=Mus musculus	1.26	0.95	1	-10

	GN=H2-Q7 PE=1 SV=1				
sp P14430 HA18_MOUSE	H-2 class I histocompatibility antigen, Q8 alpha chain OS=Mus musculus GN=H2-Q8 PE=2 SV=1	1.26	0.95	1	-10
sp P03991 HA1W_MOUSE	H-2 class I histocompatibility antigen, K-W28 alpha chain OS=Mus musculus GN=H2-K1 PE=1 SV=2	1.26	0.95	1	-10
sp P23492 PNPH_MOUSE	Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2	1.26	1.11	0.46	-10
sp P01897 HA1L_MOUSE	H-2 class I histocompatibility antigen, L-D alpha chain OS=Mus musculus GN=H2-L PE=1 SV=2	1.21	1.25	1.04	0.84
sp P01899 HA11_MOUSE	H-2 class I histocompatibility antigen, D-B alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=2	1.2	1.16	0.99	0.99
sp Q8R180 ERO1A_MOUSE	ERO1-like protein alpha OS=Mus musculus GN=Ero1l PE=1 SV=2	1.19	1.34	0.26	-10
sp Q8CGC7 SYEP_MOUSE	Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=4	1.17	-0.13	0.19	-10
sp P37040 NCPR_MOUSE	NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	1.17	1.46	0.7	-10
sp Q8BV66 IFI44_MOUSE	Interferon-induced protein 44 OS=Mus musculus GN=Ifi44 PE=2 SV=1	1.13	1.52	-10	-10

CHAPTER IV
METHOD DEVELOPMENT FOR ANALYSIS OF COMPLEX PROTEIN
SAMPLES USING OFFLINE LC-MALDI MS/MS

4.1 Introduction

In this research project, we attempted to use a proteomics approach employing mass spectrometry to study changes in protein expression by cultured macrophage cells in response to treatment with *Echinacea* extracts. In the preliminary studies, we used bovine serum albumin (BSA) as a standard to optimize the methods. These methods were ultimately employed for analysis of complex protein samples.

4.2 Identification Without Prior Separation

The first step in optimizing the methods for protein identification was to attempt to analyze bovine serum albumin without prior separation. A pure sample of protein (Sigma) was digested in trypsin and the resulting peptides were mixed with a matrix (alpha-cyano-4-hydroxycinnamic acid or CHCA) and spotted on a single spot on a stainless steel MALDI plate. This MALDI plate was then analyzed using a MALDI-TOF-TOF mass spectrometer (4700, Applied

Biosystems). The resulting MALDI mass spectrum for the peptide mixture is shown in Figure 11, while Figure 12 shows the MS-MS spectrum for one of the more abundant of these peptides at m/z 1479. Based on the MS and MS-MS data, a MASCOT search (GPS Explorer TM V 3.6, Matrix Science) was performed, which accurately identified the peptide as bovine serum albumin (Table-1).

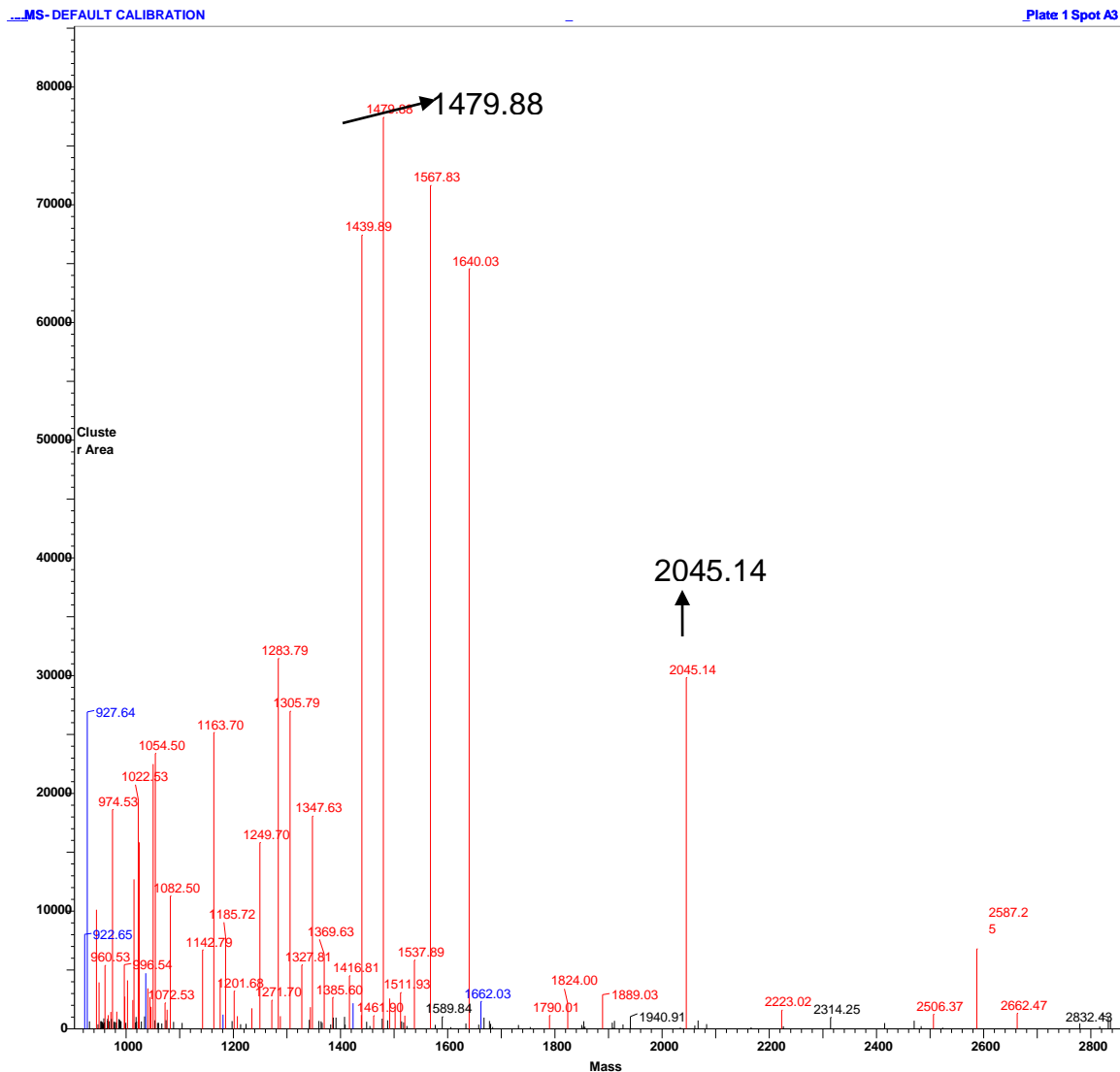


Figure 11. MALDI mass spectrum of digested bovine serum albumin (BSA) without prior separation. Trypsin digestion was done on 50µg Bovine serum albumin (BSA). Trypsin was used for digestion and sample mixture was incubated at 37°C over night. Peptides of BSA were mixed with CHCA 10 mg/mL concentration and spotted on MALDI plate and ionized by MALDI-TOF.

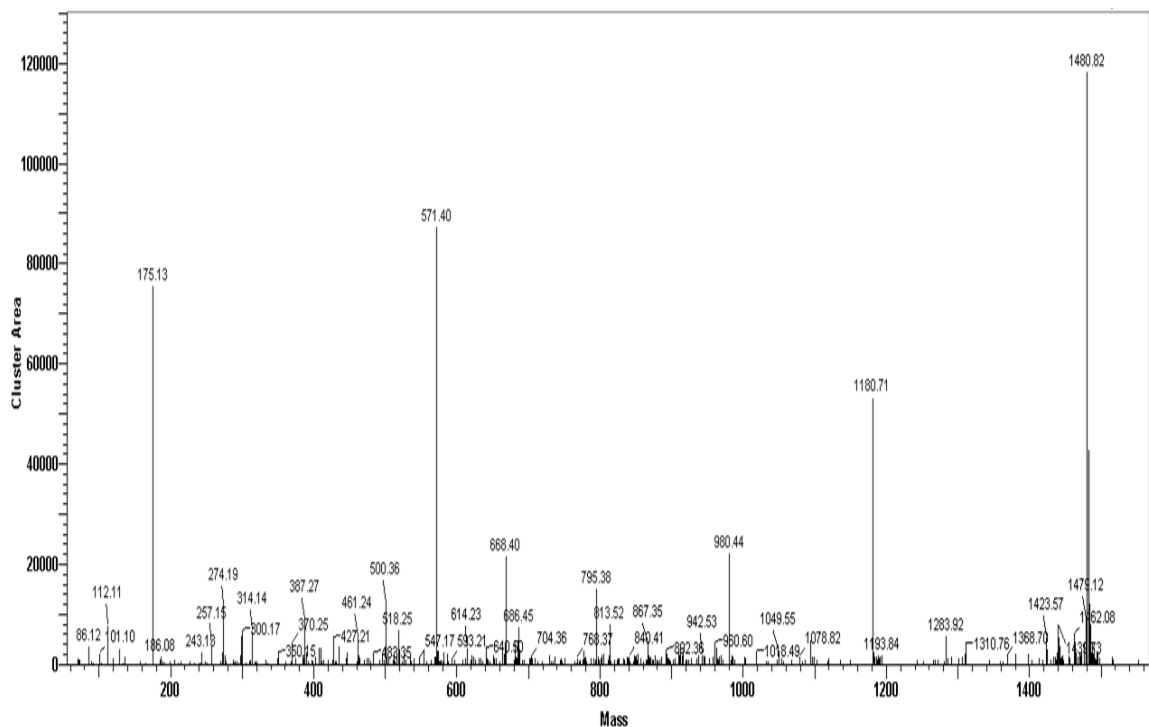


Figure 12. MALDI MS-MS spectrum of peptide m/z 1479.

Table 25. Mascot Search Results for Identification without prior separation.

Rank	Protein Name	Accession No	Protein Score	Protein Score C.I %
1	(P02769) Serum albumin precursor	ALBU_BOVIN	126	100

4.3 Reduction and Alkylation of Protein

The presence of disulfide bonds in a protein can hamper the digestion process, resulting in incomplete sequence coverage. Reduction using DL-Dithiothreitol solution (DTT) followed by alkylation (using iodoacetamide) is typically performed prior to the digestion step when proteins are to be analyzed

by MALDI. This disrupts the disulfide bonds and prevents them from reforming, and should therefore increase the number of peptides produced in the digestion step and improve sequence coverage. We investigated the effectiveness of reduction and alkylation prior to digestion of BSA. The final concentration of DTT and iodoacetamide was adjusted to 5mM and 15 mM, respectively. Figure 13 shows an increase in the number of peptides in the mass range of 1650-2050 m/z that is observed when reduction and alkylation is performed, as compared to the results for protein that is not reduced or alkylated (Figure 12).

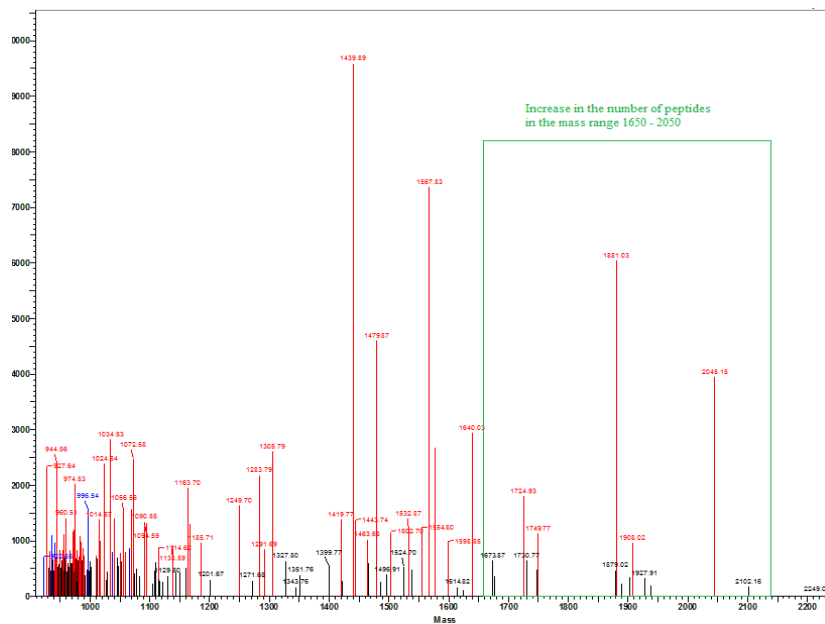


Figure 13. Mass spectrum of BSA after reduction and alkylation: Reduction of 50 μg of BSA was accomplished by incubating the BSA with 5mM final concentration of DTT at 60°C for 30 min. The reduction step was followed by alkylation with 15mM final concentration.

4.4 LC-MALDI of Bovine Serum Albumin

Successful identification of pure BSA could be accomplished without any prior separation (Table 1). However, for a mixture of proteins such as that which will be obtained by extracting cells, it will be necessary to accomplish some additional separation prior to analysis with MALDI. We sought to employ HPLC as a separation step prior to MALDI analysis, a technique referred to as LC-MALDI. In the LC-MALDI technique, digested peptides are separated by liquid chromatography and peptides eluting from column are mixed with matrix (CHCA) and spotted on the MALDI plate using a robotic spotter (Probot, Dionex/LC Packings). The peptides are thereby separated across the MALDI plate, and can then be analyzed in with MALDI mass spectrometry as described in the previous section. The same sample was analyzed via LC-ESI-MS to see how digested peptides are eluted throughout the HPLC run (Figure 15). Table 2 shows the MASCOT search results for digested BSA samples run by LC-MALDI Technique. The BSA (ALBU_BOVIN) was successfully identified by this technique with a good protein score (80), with the first hit being BSA. The proteins scores were selected based on probability-based MOWSE score from mascot search results. Mascot is a software used to estimate protein sequences from MS and MS/MS data of MALDI-TOF. The probability based MOWSE algorithm is employed by Mascot to predict the correctness of the match. The advantages of this method are 1) It tells about significance of match, 2) peptide masses (MS data) and

fragment ions (MS/MS data) can be searched together, 3) search results can be compared with different databases and 4) choice of search parameters is possible. The total ion score represents the absolute probability that the resulting match can be a random event. The score is reported as $-10 \cdot \text{LOG}_{10}(P)$, here P is the absolute probability. If the probability is low, the score is high. The higher the score, the more significant the match.

4.5 Mascot Score Histogram

Protein score is $-10 \cdot \text{Log}(P)$, where P is the absolute probability that the resulting match can be a random event. Protein scores greater than 67 are considered significant ($p < 0.05$)

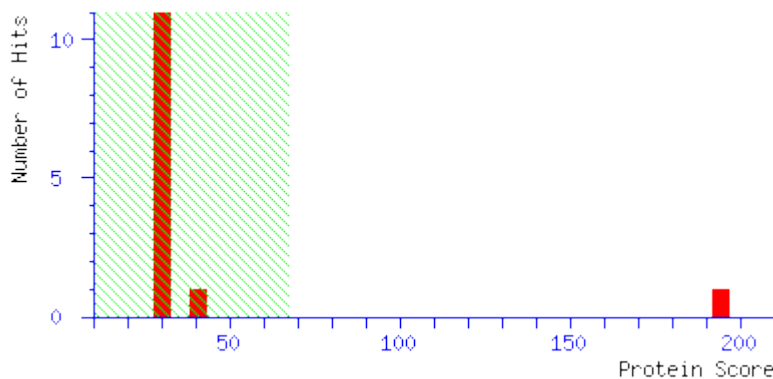


Figure 14. Probability Based MOWSE Score.

At each scoring position the Number of protein matches is indicated in red. The green shaded region indicates non-significant area. Usually most matches

are non-significant. In this example, there is only one significant match (www.matrixscience.com).

Table 26. Mascot Search Results for LC-MALDI of BSA.

Rank	Protein Name	Accession #	Protein Score	Protein Score C.I.%
1	(PO2769) Serum Albumin Precursor	ALBU_BOVIN	80	99.9

4.6 LC-MALDI of a Standard Protein Mixture

After successful identification of BSA by MALDI without prior to separation and LC-MALDI technique, The LC-MALDI technique was applied on sample mixture containing peptides of BSA and lysozyme. The sample mixture was successfully identified with the MASCOT search engine. Table 3 shows the top two proteins identified by the MASCOT search engine. Our ultimate goal with this project is to accomplish identification on complex biological sample which might have hundreds of different proteins. The results in Table 3 show the first step towards accomplishing this goal, analysis of a mixture of proteins.

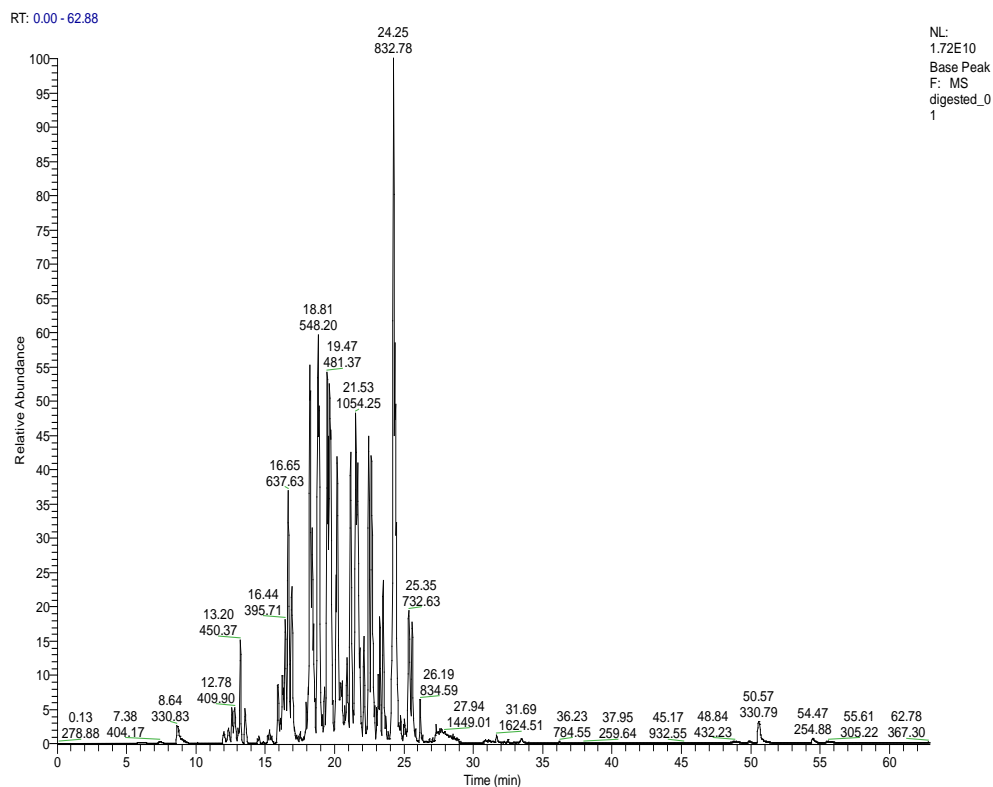


Figure 15. Chromatogram of digested BSA. BSA (50 μ g) was digested with 1 μ g of trypsin. The digested sample (5 μ g) was injected onto the column and eluted with mobile phase with flow rate of 2 μ L per min. The mobile phase gradient used was 0-5 min 1% acetic acid and 5-32min 100% acetonitrile. An HP1100 HPLC system (Agilent, Palo Alto, CA, USA) was used with a narrow bore C18 column. This HPLC was coupled to an ion trap mass spectrometer with electrospray ionization (ESI) source (LCQ Advantage, Thermo Scientific, San Jose, CA, USA). The positive ionization mode was used for the analysis and the mass range was 50-2000 m/z.

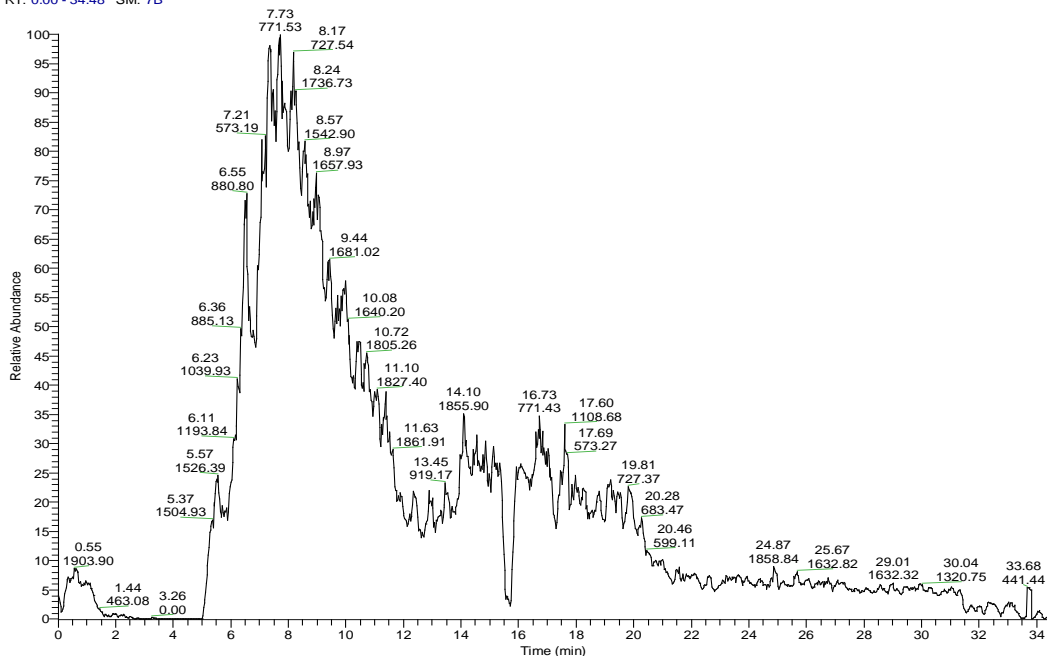
Table 27. Mascot Search Results for LC-MALDI of a protein mixture.

Rank	Protein Name	Accession No	Protein Score	Protein Score C.I %
1	(P02769) Serum albumin precursor	ALBU_BOVIN	277	100
2	P00698) Lysozyme C precursor (EC 3.2.1.17)	LYSC_CHICK	264	100

4.7 LC-MALDI of Jurkat Cell Proteins

Cultured Jurkat T-lymphocyte cells were used as a model system to optimize the conditions and method. The reason for the choosing Jurkat cells, because they serve as an good example for proteomics on cultured immune cells. The LC-MALDI technique was applied to peptides obtained from digesting soluble proteins extracted from Jurkat cells. Several proteins were identified based on probability based MOWSE score from the MASCOT search engine. Figure-6 shows the chromatogram (obtained with LC-MS) of peptides obtained from digesting proteins extracted from the cells. Table 4 shows the list of proteins identified from the Jurkat proteome with protein scores >67.

RT: 0.00 - 34.48 SM: 7B



NL:
1.78E6
Base Peak
F: MS
jurkat-2-2-
mix

Figure 16. Chromatogram of peptides obtained from In-solution digestion of proteins from Jurkat T cells. RIPA buffer (1 mL) along with protease inhibitor cocktail (100 μ L) was used extract protein from the 1 million cells. Proteins were subjected to reduction with DTT (5mM), alkylation with iodoacetamide (15mM) and digested using 20 μ g of trypsin. All the conditions were similar to those described for Figure 15.

Table 28. List of proteins identified from Jurkat T cells by MALDI MASCOT search engine.

Rank	Protein Name	Accession No	Protein Score	Protein Score C.I %
1	Myosin XV	MYO15_HUMAN	110	100
2	Alu subfamily SB1 sequence contamination warning entry	ALU3_HUMAN	73	100
3	Ciliary dynein heavy chain 11	DYH11_HUMAN	72	100

4	Putative pre-mRNA splicing factor RNA helicase	DHX16_HUMAN	71	100
5	Dynein heavy chain, cytosolic (DYHC)	DYHC_HUMAN	70	100
6	Alu subfamily sb sequence contamination warning entry	ALU2_HUMAN	68	100

4.8 Conclusion

We have successfully developed off-line LC-MALDI-MS/MS method for identification of single protein and simple mixture of proteins, However we couldn't not get enough reproducibility of proteins when complex protein sample (example: cell lysate) was used. Reasons: 1) one dimensional Chromatographic separation was not sufficient enough to separate thousands of peptides resulting from digestion of cell lysate. 2) Inefficient Ionization: Several peptides on single MALDI spot competing with each other to ionize by MALDI.

CHAPTER V
ELECTROSPRAY IONIZATION-HIGH RESOLUTION MASS
SPECTROMETRY METHOD WITH ACCURATE MASS MEASUREMENTS TO
DETECT BACTERIAL LIPOPROTEINS

5.1 Abstract

Rationale: The aim of this study was to develop a simple and quick liquid chromatography electrospray ionization high resolution mass spectrometry (LC-ESI-HRMS) method that would enable the detection of bacterial lipoproteins from bacterial cultures with minimal sample preparation.

Methods: Using an ultra-performance liquid chromatography (UPLC) hybrid linear Ion Trap-Orbitrap (LTQ-Orbitrap) Mass Spectrometer (LTQ Orbitrap XL) system, an electrospray ionization (ESI) method was developed for the detection of $[M + H]^+$ ions of the derivatized product of acid hydrolyzed lipoproteins and lipopeptides. The optimized method employed acetonitrile and water as mobile phase solvents for separation of derivatized products on a reversed phase C18 column. Liquid chromatography electrospray ionization high resolution

massspectra (LC-ESI-HRMS) were acquired in both the positive and negative ionization modes.

Results: An LC-ESI-HRMS method has been developed for determination of three different derivatized product of acid hydrolyzed lipoprotein. All the three derivatized products were detected using full scan MS in the positive ion mode. However, one of them was detected in both the positive and negative ion mode with better sensitivity. Derivatization of hydrolyzed product of lipoprotein 2,3-Dihydroxypropyl cysteine, with hydrophobic molecules altered its structural characteristics, which significantly improved the sensitivity of detection by LC-ESI-HRMS. Mass accuracy of less than 5ppm was obtained in all the LC-ESI-HRMS runs.

Conclusions: The LC-ESI-HRMS method developed here is quicker and simpler than existing methods, and enables effective identification of bacterial lipoproteins from *Echinacea* and other bacterial cultures with very little sample clean up.

5.2 Introduction

The bacterial lipoprotein is a component of the cell membrane of both Gram positive and Gram negative bacteria. It is a potent activator of the innate immune response (Hashimoto 2006). Lipoproteins are postulated to be present in

Echinacea preparations, and could be introduced by bacterial contamination or by the presence of bacteria that live in the plant as endophytes (Pugh 2008, Tamta 2008). As mentioned previously, other constituents of *Echinacea* such as alkylamides possess anti-inflammatory activity (consistent with suppression of the innate immune response). Thus, *Echinacea* extracts may contain a mixture of constituents with opposing (immunosuppressive and immunostimulatory) activity. This complicates the issue of how best to use *Echinacea* extracts therapeutically, and it may be desirable in some cases to prepare extracts with either one class of constituents or the other, but not both. For example, an extract with high lipoprotein content *may* be useful as an immune stimulant, but would likely be contraindicated in the treatment of inflammation, while optimal preparations for treatment of inflammation might contain high levels of alkylamides but not lipoproteins. Thus, it would be very useful to be able to screen extracts for the presence of lipoprotein contamination. In order to do that, our goal was to develop a new LC-MS analytical method to analyze immunostimulatory lipoproteins from bacteria that are present in *Echinacea*.

Braun-type lipoproteins consist of a diacylglycerol moiety, which is linked to a peptide chain at the N-terminal cysteine by a thioester bond (Rezwan 2007). All bacterial lipoproteins do not have the same sequence homology, but they all can be characterized by the presence of an N-terminal amino acid 2,3-Dihydroxypropyl cysteine (**1**) (Spohn, 2004). All the lipoproteins have a lipid part

and a peptide part. The peptide part acylated at the N-terminal cysteine is responsible for the pro-inflammatory properties of lipoproteins. Lipoproteins from different bacteria differ in their structure. It is very hard to find a single method that can detect all of them. However, acid hydrolysis of all types of lipoproteins give a common residue called 2,3-Dihydroxypropyl cysteine. Lipoprotein of bacterial origin can be confirmed by detecting this 2,3-dihydroxypropyl cysteine, which is a unique structural component of lipoproteins of prokaryotic bacteria (Pugh 2008).

The Muhlradt group were one of the first to identify 2, 3 dihydroxypropyl cysteine using a mass spectrometer. Their approach employed fast atom bombardment (FAB) as an ionization source. In FAB ionization, the analyte is dissolved in a liquid matrix such as glycerol or thioglycerol, and is spotted on the target plate and bombarded with a beam of inert gas such as xenon or argon. This causes desorption and ionization of analyte. One of the limitations of this technique is high chemical background generated by cluster ions that are formed from the liquid matrix, which impacts the detection limits. Other limitations include that selection of the liquid matrix to solubilize the analyte is also a challenge, that the FAB ionization technique is not good for multiply charged compounds, and that online coupling of FAB ionization to separation techniques like liquid chromatography is difficult. Another drawback of the approach employed by the

Muhlradt group was that the mass spectrometer used did not provide accurate mass measurements.

In this project, a novel LC-ESI-HRMS method, which is selective and sensitive, and with very less chemical noise than FAB, has been used. ESI can be easily coupled online to a mass spectrometer, and employs common organic solvents in which analyte solubility is typically less of a problem. Using a high resolution mass spectrometer can also provide accurate mass measurements, which increases confidence in identification of an analyte. The goal of this project was to develop a LC-ESI-HRMS method for analysis of 2, 3 dihydroxypropyl cysteine. We sought to employ dansyl chloride, fluorenylmethyloxycarbonyl chloride (Fmoc-Cl), and dabsyl chloride as derivatizing agents to modify the structural properties of 2, 3 dihydroxypropyl cysteine and improve its detection.

This project employed a synthetic lipoprotein, Pam3CSK4, as a control. Structurally, Pam3CSK4 contains three lipid chains. Two of the lipid chains are attached to the glycerol backbone by an ester bond, which in turn is connected to the N-terminal cysteine at the sulfur atom. The third lipid chain is connected by an amide bond to the amino terminus. The reason for using Pam3CSK4 is that it behaves the same way as natural lipoproteins (targeting toll like receptors on immune cells) and is commercially available.

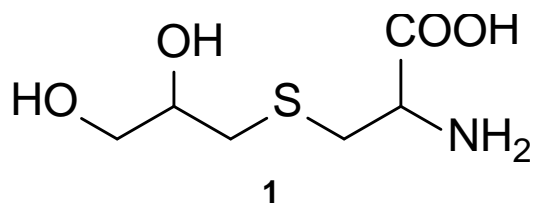


Figure 17. Structure of 2,3-Dihydroxypropyl cysteine.

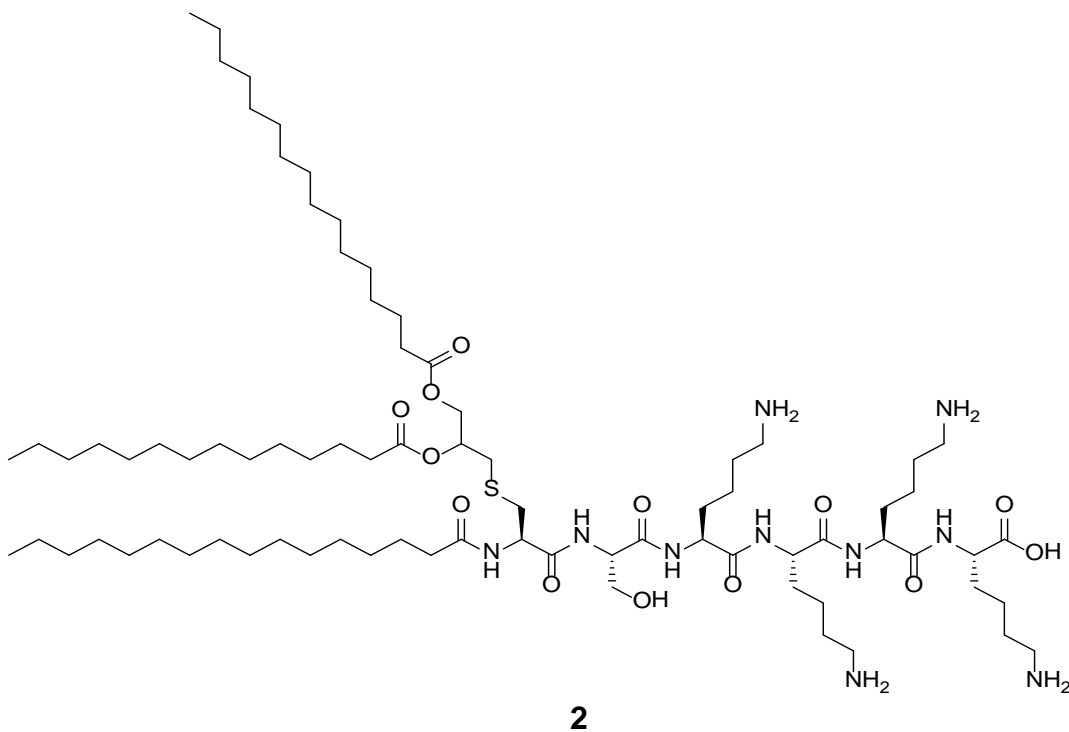


Figure 18. Structure of Pam3CSK4 Lipopeptide.

5.3 Experimental

5.3.1 Chemical and reagents

Pam3CSK4 was obtained from Invivogen (San Diego, CA, USA). Dansyl chloride, Fmoc-chloride and methane sulfonic acid solution were purchased from Fluka (St. Louis, MO, USA), dabsyl chloride was obtained from Supelco

Analytical (Bellefonte, PA, USA). All solvents, water and acetonitrile, used were LC-MS grade (Fisher Scientific, NJ, USA).

5.3.2 Acid hydrolysis method

Pam3csk4 (150 µg) and lipoprotein isolated from *Escherichia coli* (*E.coli*) and an *Echinacea* endophyte were acid hydrolyzed with 250 µL of 4N methanesulfonic acid at 1100 °C for 18 hours. The acid layer was neutralized with 200 µL of 5N NaOH and extracted 3 times with cyclohexane. The derivatizing agents dansyl chloride, fluorenylmethyloxycarbonyl chloride (FMOC-chloride), or dabsyl chloride (Figure 19) (400 µL of 20%w/v in acetone) were added to the aqueous layer and stirred overnight in the dark at room temperature. The solution was then filtered through a 0.2 µm filter and analyzed by LC-MS.

5.3.3 Lipoprotein extraction

Escherichia coli and bacteria isolated from *Echinacea purpurea* were grown in one liter of tryptic soy broth and centrifuged at 10000 rpm for 45 min. The resulting pellet was suspended in 45 mL of saline and subjected to 5 freeze-thaw cycles, resulting in a suspension that was centrifuged for 30 min at 3,500 rpm. The pellet was then suspended in 10 mL of PBS and extracted with 10 mL of chloroform-methanol mixture (2:1, vol/vol). The water phase was freeze dried, and the resulting material was dissolved in 10 mL of 50mM octylglucoside in

phosphate buffered saline (PBS) and treated with boiling water for 5 min. The insoluble material was removed by centrifugation at 3,500 rpm for 30 min and the soluble material was lyophilized and stored. This protocol was based on a previous publication (Muhlradt 1996).

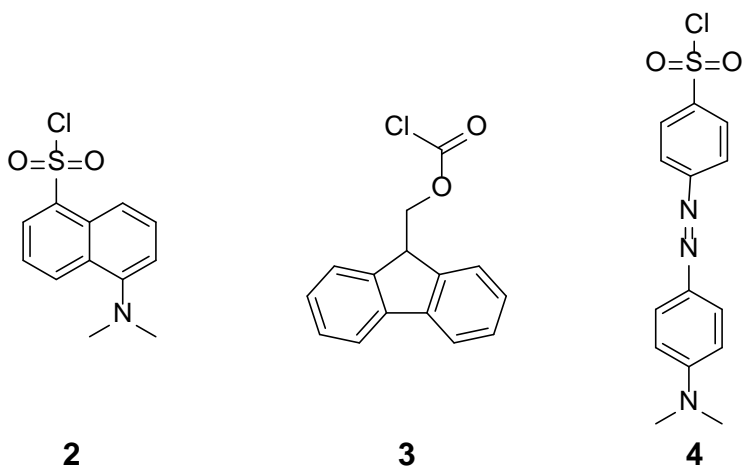


Figure 19. Structures of different derivatizing agents used, dansyl chloride (2), Fmoc chloride (3), and dabsyl chloride (4).

5.3.4 Isolation of bacteria from *Echinacea purpurea*

Peeled *E. purpurea* seeds were surface sterilized for 1 min in 95% ethanol, 1 min in 3% of sodium hypochlorite, and 1 min in 95% ethanol. Surface-sterilized seeds were plated on tryptic soy agar (TSA) dishes. Single colony isolations were performed from bacterial cultures. Each bacterial culture was incubated in tryptic soy broth (TSB) at 37°C for 28 hr. This culture was mixed 1:1 with glycerol (total volume 2 mL) and stored at -80°C.

5.3.5 LC-MS method

All LC-MS experiments were conducted using an Acquity UPLC system (Waters Corporation, Milford, MA, USA) coupled online to a LTQ-orbitrap mass spectrometer (LTQ XLThermo Fisher Scientific, San Jose, CA). Compounds were separated using an Acquity BEH C18 reverse phase column (Waters, Milford, MA, 50mm X 2.1 mm i.d, 1.7 μ m particle size) at a flow rate of 250 μ L/min and column temperature was maintained at 40 $^{\circ}$ C. Full scan MS analysis was performed using the Orbitrap mass analyzer in high resolution mode using 60,000 resolving power. Electrospray ionization in positive and negative ion modes was used (in two separate analyses for each sample). The source voltage was set at 4 KV and the temperature of the heated metal capillary was set at 300 $^{\circ}$ C. The compounds were eluted from with a linear gradient as follows: 5% solvent A from 0 to 5 mins, 5 to 90% from 5-30 mins, 90% A from 30 to 32 mins, 5% A from 32 to 35 mins. Here solvent A is acetonitrile with 0.1% formic acid and solvent B is water with 0.1% formic acid.

5.4 Results and Discussion

Figure 20 shows the schematic representation of acid hydrolysis of the Pam3CSK4 lipopeptide and derivatization of 2,3-Dihydroxypropyl cysteine. Compound 1 (2,3-Dihydroxypropyl cysteine) is very polar and of low molecular weight, and is therefore not a very good candidate for reverse phase LC-MS analysis. To increase the sensitivity of detection of this compound, we have

derivatized compound 1 with various derivatizing agents. We have selected three compounds with different hydrophobicity as derivatizing agents for our study, dansyl chloride, FMOCl and dabsyl chloride. Molecular weights of these compounds are 269.0773, 258.04476, 323.04953, and LogP values are 3.05, 4.09, and 4.49, respectively.

2,3-Dihydroxypropyl cysteine was not detected as a product of the acid hydrolysis when no derivatization was conducted. However, the derivatization increased its hydrophobicity, thereby increasing retention on the HPLC column and improving the signal in the mass spectrometer. Analytes with more hydrophobic portions will have greater electrospray response in comparison to polar analytes (Okamoto 1995). Hydrophobic analytes tend to accumulate more on the surface of electrospray droplet and has greater chance of getting charged. The analytes which accumulate on the surface of ESI droplet have higher ESI response (Iribane 1983). Also, derivatization increases the mass of the analyte and shifts the analyte to higher mass region in mass spectrum where the noise from solvents and other contaminants is less and in turn improves the signal to noise ratio (Cech 2001). Hydrophobic analytes also have higher affinity for reverse phase stationary phase in liquid chromatography and elute later in the run where the percentage of organic solvent is more, which helps in ionization (Cech 2001).

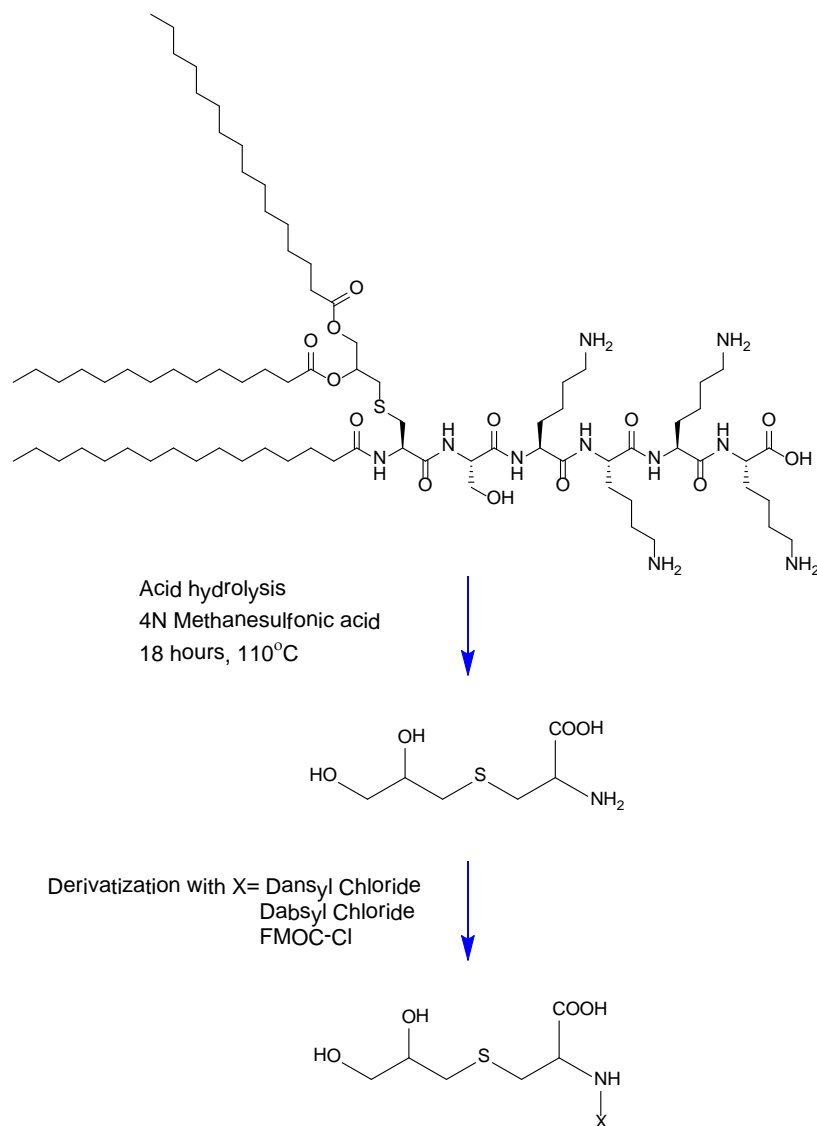


Figure 20. Steps involved in acid hydrolysis of Pam3csk4 and derivatization of 2,3-Dihydroxypropyl cysteine.

The synthetic analog of lipoprotein, Pam3csk4 lipopeptide, was acid hydrolyzed with methane sulfonic acid to compound 1, which in turn were derivatized using three different derivatizing agents. The resulting compounds were analyzed by LC-ESI-MS. Figure 21 shows chromatographic peaks of the

derivatized products of compound 1. Panel A shows the dansylated product eluting at the retention time 10 mins. Chromatograms B and C represent FMOC-chloride derivatives of compound 1 at the retention time 14.7 mins. Chromatogram D represents the dansyl chloride derivative of compound 1 at the retention time 9.3 mins. The FMOC-chloride derivative of compound 1 is more hydrophobic than the others and elutes at a later retention time. As expected, this derivative also shows higher sensitivity when compared to the other derivatives. There was approximately 100 fold increase in chromatographic peak area when FMOC-chloride was used as a derivatizing agent (figure 21 panel B, C) compared to other derivatizing agents like dansyl chloride (Figure 21 panel A), and dansyl chloride (Figure 21 panel D).

The mass accuracies of the pseudomolecular ions detected for all the derivatized products of compound 1 were all less than 4 ppm (Table 1), confirming correct assignment of the molecular formula. The mass spectra of derivatized products of compound after reaction with dansyl chloride derivative (A), FMOC-chloride (B, C), and dansyl chloride derivative (D) are shown in Figure 22.

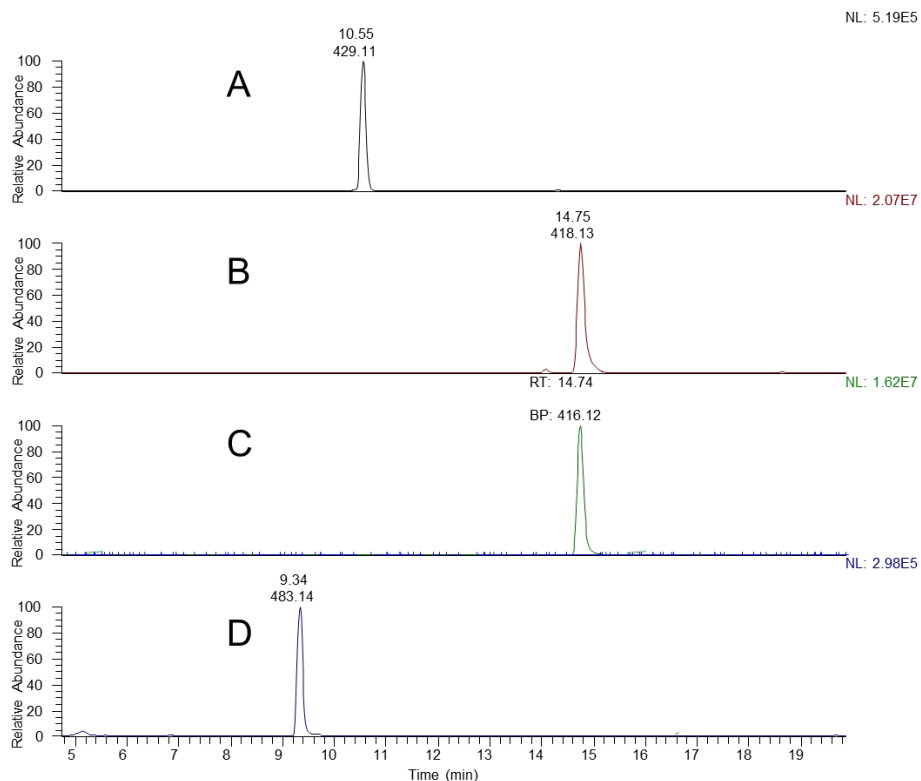
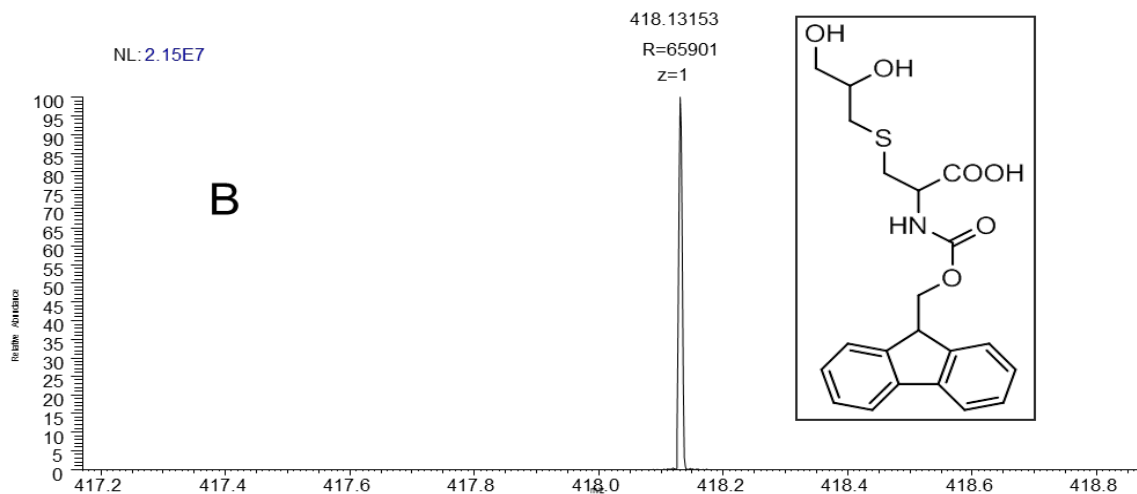
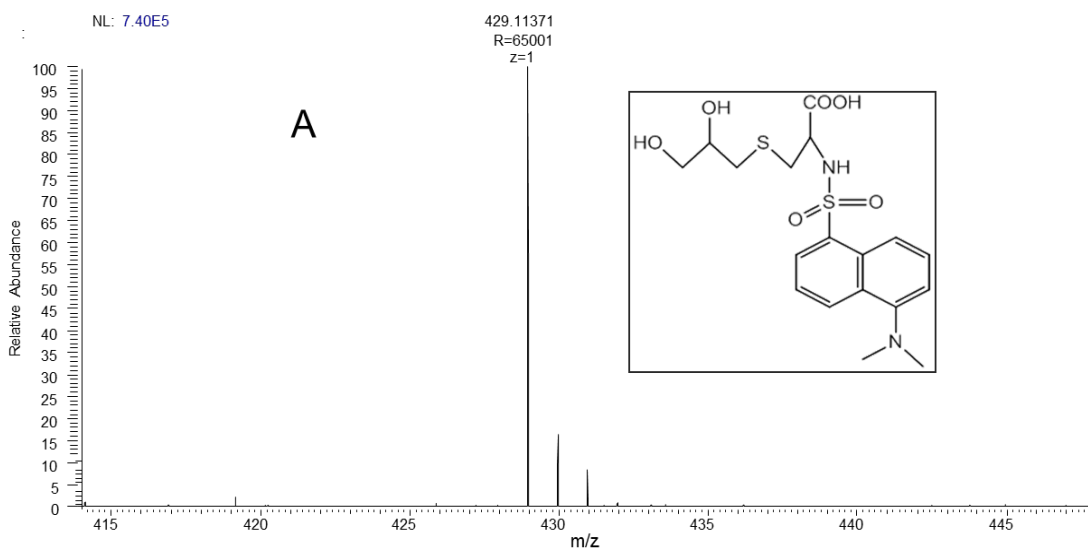


Figure 21. LC-ESI-MS selected ion chromatograms at of derivatized product of compound 1 with different derivatizing agents A) dansyl chloride in (+) Ion mode B) Fmoc-chloride in (+) Ion mode C) Fmoc-chloride in (-) Ion mode D) dansyl chloride in (+) Ion mode.

Table 29. Calculated and measured masses of the products of reactions of 2,3-Dihydroxypropyl cysteine with various derivatizing agents.

Derivatizing Agent	Molecular formula of product	Theoretical Mass [M+H] ⁺	Experimental Mass [M+H] ⁺	Mass Accuracy in ppm
Dansyl chloride	$C_{18}H_{24}N_2O_6S_2$	429.11538	429.11371	3.5
Dabsyl chloride	$C_{20}H_{26}N_4O_6S_2$	483.13718	483.13651	1.3
Fluorenylmethoxycarbonyl chloride (FMOC-chloride)	$C_{21}H_{23}NO_6S$	418.13241	429.13135	2.1

	Molecular formula	Theoretical Mass [M-H] ⁻	Experimental Mass [M-H] ⁻	Mass Accuracy in ppm
Fluorenylmethyloxycarbonyl chloride (Fmoc-chloride)	C ₂₁ H ₂₃ NO ₆ S	416.11661	416.11682	0.7



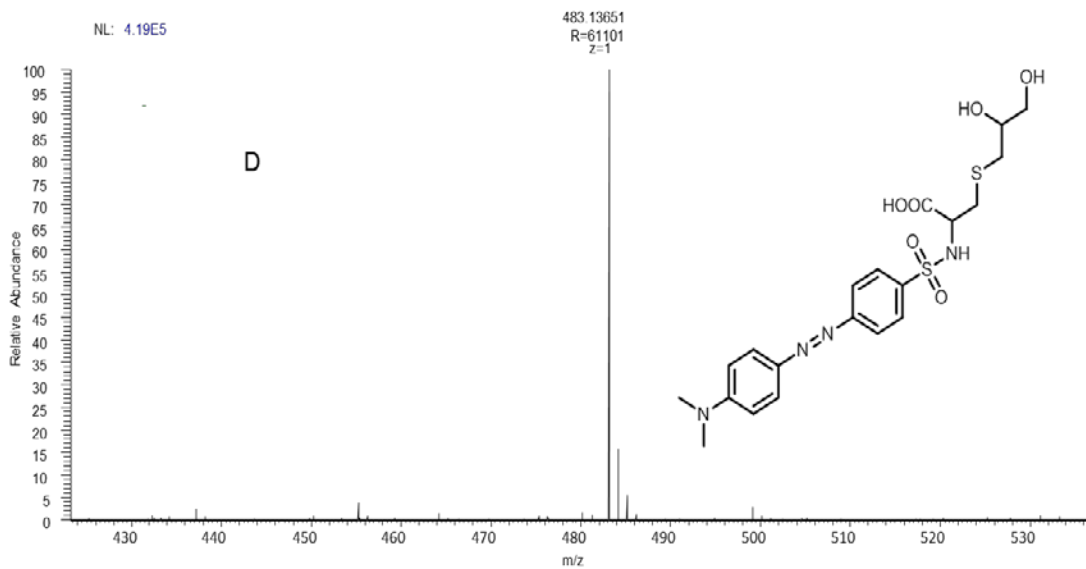
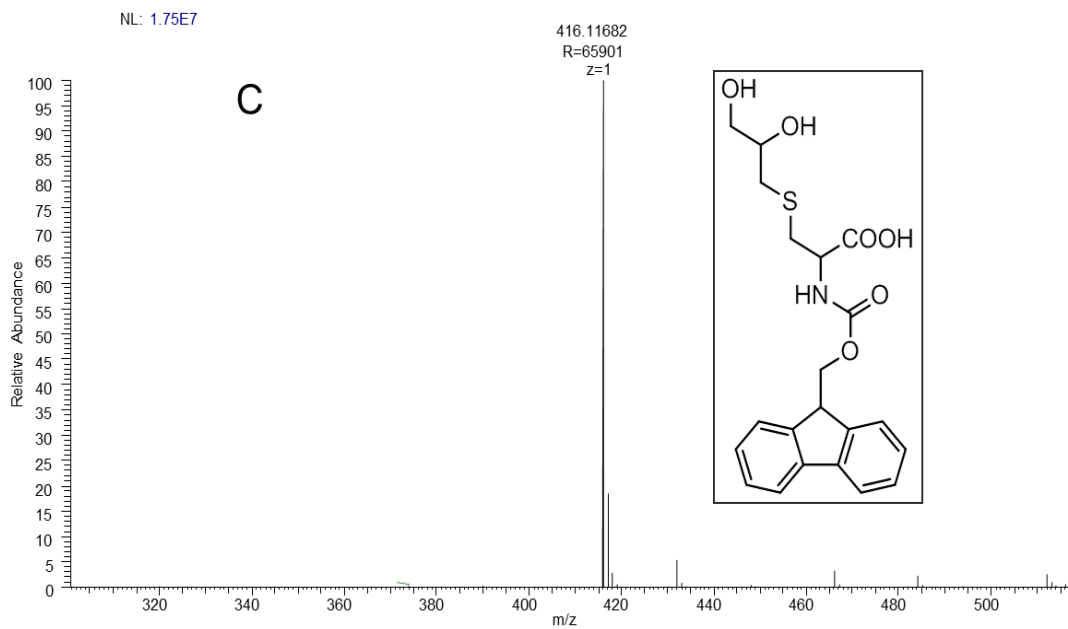


Figure 22. Mass spectrum of derivatized products of compound 1 with different derivatizing agents A) dansyl chloride in (+) Ion mode B) FMOc-chloride in (+) ion mode C) FMOc-chloride in (-) Ion mode D) dansyl Chloride in (+) Ion mode.

After successful identification of 2,3-Dihydroxypropyl cysteine from Pam3CSK4, this same technique was applied to lipoprotein isolated from *E. Coli* and bacteria isolated from *Echinacea*. The predicted products of reaction of the derivatizing agents with the 2,3-Dihydroxypropyl cysteine were indeed detected (Figures 7,8,9,10). The mass accuracies of the molecular ions detected were less than 4 ppm (Table 2) for all of the derivatized products of compound 1. Selected ion chromatograms of the dansyl chloride derivatives of compound 1 from both types of bacteria, *E. Coli* (A) and the *Echinacea* endophyte (B), are shown in Figure 23. Similar data for FMOC-chloride derivatives are shown in figures 10 and 11. The ability to detect derivatives at the predicted accurate masses for both types of bacteria using the two different derivatizing agents supports the conclusion that the derivatization reaction was, indeed, successful.

The advantage of our method is, we use ESI which doesn't require any liquid matrix so there is less chemical noise, which in turn, increases detection limits. Also, our derivatized products of compound 1 were readily soluble in organic solvents. Since our mass spectrometer is connected online to liquid chromatography system, it doesn't require lot of sample clean up steps, which reduces time of analysis. Muhlradt group did the sample cleanup of derivatized product of compound 1, by extracting with cyclohexane and chloroform and then purifying the compound by HPLC. Since the mass spectrometer we used was coupled online with reverse phase liquid chromatography system the sample

clean up steps were avoided. David Pasco group identified compound 1 derivatized with o-phthalaldehyde using reverse phase liquid chromatography coupled to a fluorescence detector (Pugh 2008). This group isolated compound 1 by extracting a large batch of *Echinacea* roots. They have identified compound based on retention time. The disadvantage of this method is the mixture was so complex that there was no base peak resolution in the chromatogram. There is a chance that many peaks co elute with each other and it is unknown whether the peak is a single compound or group of compounds. Furthermore, matching retention times doesn't always guarantee correct identification. The advantage of our method is we have identified three different derivatives of compound 1 based both on retention time and accurate mass. Altogether, the new LC-ESI-HRMS method developed in this study to identify compound 1 is more sensitive and selective and doesn't need sample clean up steps in comparison to previously developed methods.

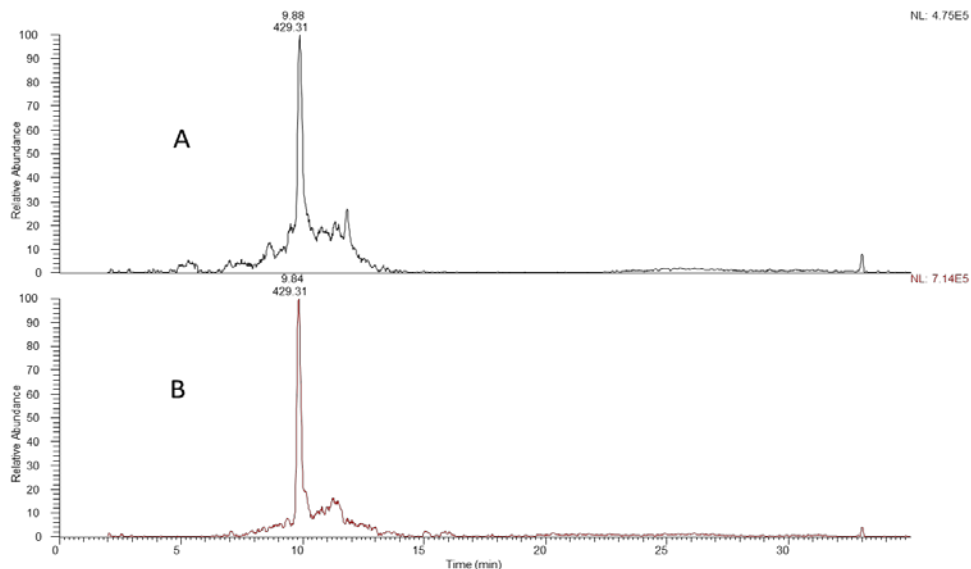


Figure 23. LC-ESI-MS selected ion chromatograms at 429.1 m/z (Isolation window 428.61-429.61 m/z) of derivatized product of compound 1 isolated from A) *E. Coli* and B) bacteria isolated from *Echinacea purpurea* seeds, with dansyl chloride as derivatizing agent.

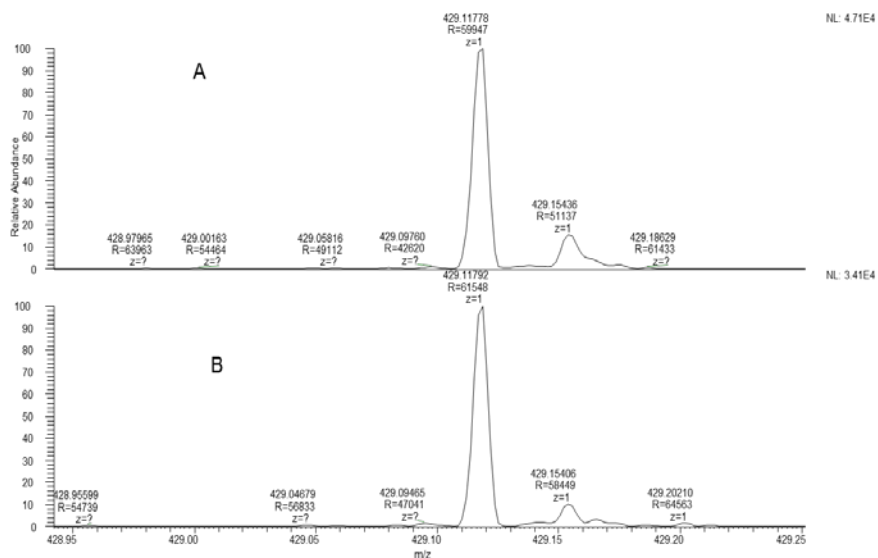


Figure 24. Mass spectra of derivatized product of compound 1 isolated from A) *E.Coli* and B) bacteria isolated from *Echinacea*, with dansyl chloride as derivatizing agent.

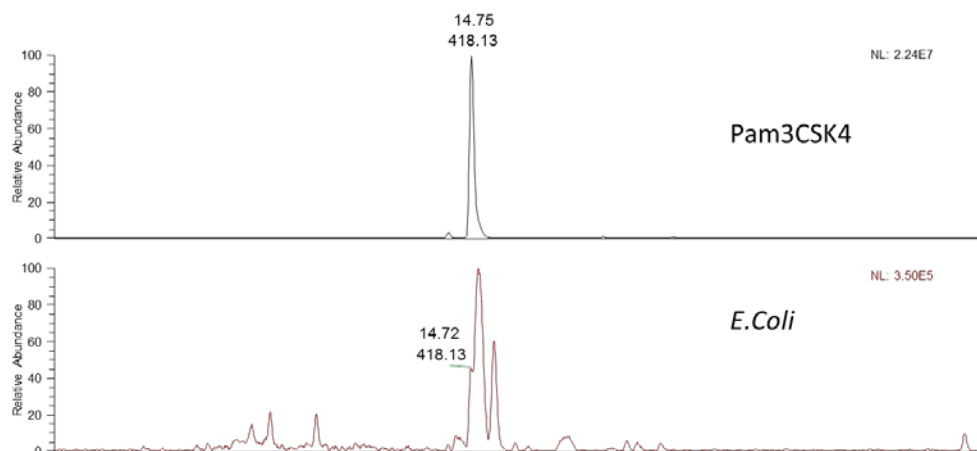


Figure 25. LC-ESI-MS selected ion chromatogram at 418.1 m/z (Isolation window 428.61-429.61 m/z) chromatograms of derivatized product of compound 1, isolated from A) Pam3CSK4, B) *E. Coli* with FMOCl as derivatizing agent.

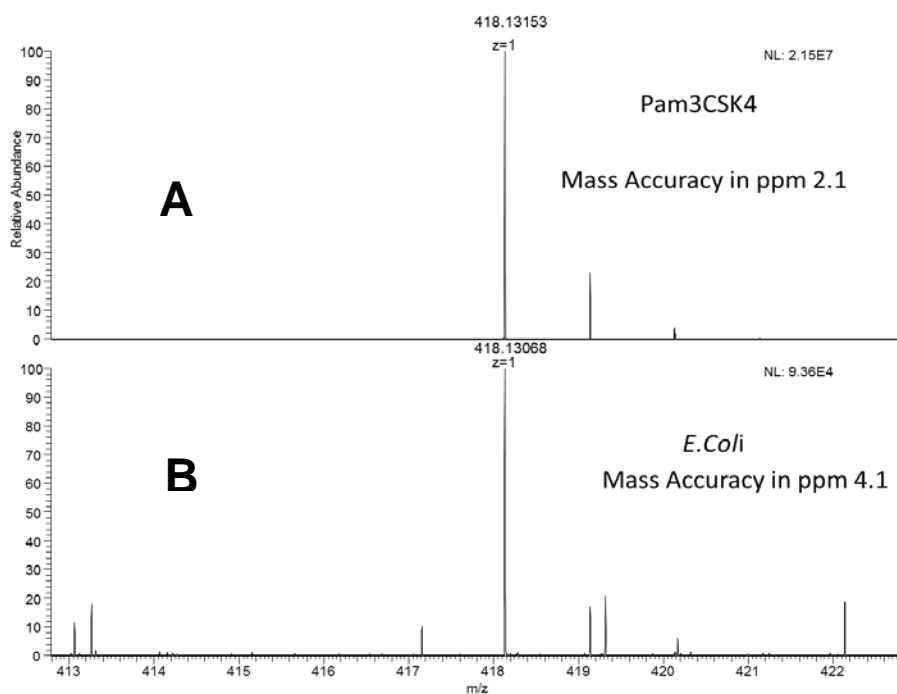


Figure 26. Mass spectrum of derivatized product of compound 1 isolated from A) Pam3CSK4, B) *E. Coli* with FMOCl as derivatizing agent. The reason this mass spectrum looks different from other is that it is zoomed out more.

Table 30. Masses and associated accuracies of the derivatized products of compound 1 from *E. Coli* and the bacteria Isolated from *Echinacea purpurea* seeds.

Derivative of compound 1 isolated from <i>E.Coli</i>	Molecular formula	Theoretical Mass [M+H] ⁺	Experimental Mass [M+H] ⁺	Mass Accuracy (ppm)
Fluorenylmethyloxy carbonyl chloride (FMOC-chloride)	C ₂₁ H ₂₃ NO ₆ S	418.13241	418.13068	4.1
Dansyl chloride	C ₁₈ H ₂₄ N ₂ O ₆ S ₂	429.11538	429.11722	4.2
Derivative of compound 1 from bacteria isolated from <i>Echinacea</i>	Molecular formula	Theoretical Mass [M+H] ⁺	Experimental Mass [M+H] ⁺	Mass Accuracy (ppm)
C ₁₈ H ₂₄ N ₂ O ₆ S ₂	C ₁₈ H ₂₄ N ₂ O ₆ S ₂	429.11538	429.11734	4.5

5.5 Conclusion

An LC-ESI-HRMS method for identification of lipoprotein was successfully developed. This method includes sample preparation, acid hydrolysis, derivatization and chromatographic and mass spectrometric analysis. The LC-ESI-HRMS method developed is more rapid and simple in comparison to existing methods and can identify the compound with both retention time and accurate mass. We are the first to report online LC-ESI-HRMS method for identification of bacterial lipoproteins from bacterial cultures with very little sample clean up (Muhlradt 1996).

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