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Utilizing Chemoproteomic Platforms to Elucidate Toxicological Mechanisms

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Utilizing Chemoproteomic Platforms to Elucidate Toxicological Mechanisms

By

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ABSTRACT

Utilizing Chemoproteomic Platforms to Elucidate Toxicological Mechanism

by

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Doctor of Philosophy in Endocrinology

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A large number of pharmaceuticals, endogenous metabolites, and environmental chemicals act through covalent mechanisms with protein targets. Yet, their specific interactions with the proteome still remain poorly defined for most of these reactive chemicals. Deciphering direct protein targets of reactive small-molecules is critical in understanding their biological action, off-target effects, and potential toxicological liabilities, as well as for the development of safer and more selective chemical agents. Chemoproteomic technologies have arisen as a powerful strategy that enables the assessment of proteome-wide interactions of these irreversible agents directly in complex biological systems. In Chapter one, we review several chemoproteomic strategies that have facilitated our understanding of specific protein interactions of irreversibly-acting pharmaceuticals, endogenous metabolites, and environmental electrophiles to reveal novel pharmacological, biological, and toxicological mechanisms.

The usefulness of chemoproteomic platforms in assessing the toxicity of environmental chemicals is further demonstrated in Chapter two; here, we utilize the chemoproteomic strategy termed Isotopic tandem orthogonal proteolysis-enabled activity-based protein profiling (isoTOP-ABPP) in identifying the direct protein binding, possible targets, mechanism of toxicity and target selectivity of the herbicide glyphosate. Glyphosate, the active ingredient in the commercial herbicide formulation Roundup®, is one of the most widely used pesticides in agriculture and home garden use. Whether glyphosate causes any mammalian toxicity remains highly controversial. While many studies have associated glyphosate with numerous adverse health effects, the mechanisms underlying glyphosate toxicity in mammals remain poorly understood. In chapter two, we used activity-based protein profiling to map the reactivity of glyphosate metabolites *in vivo* in mice. We show that glyphosate at high doses can be metabolized *in vivo* to reactive metabolites such as glyoxylate and react with several cysteines across many different protein targets in mouse liver. We show that glyoxylate inhibits several fatty acid oxidation enzymes and high-dose glyphosate treatment in mice increases the levels of several lipid metabolites, including triglycerides and cholesteryl esters, likely resulting from diversion of fatty acids away from oxidation and towards other lipid pathways. Our study underscores the utility of using chemoproteomic platforms to identify novel toxicological mechanisms of environmental chemicals such as glyphosate.

Understanding the many ways in which environmental chemicals, such as pesticides, or pharmaceuticals compounds interact with complex biological systems is absolutely necessary in determining the mechanism of toxicity, secondary targets, off-targets, selectivity, and therefore potential for toxicity of exogenous compounds. In this dissertation we demonstrate the versatility of chemoproteomics technologies, such as IsoTOP-ABPP, to aid in elucidating the direct targets and mechanism of action of environmental chemicals, such as the herbicide glyphosate. Furthermore, it is an additional aim of this research to demonstrate the potential of chemoproteomic platforms to be useful as part of the covalent compound discovery and development process towards developing safer chemicals.

DEDICATIONS

This dissertation is dedicated to my family and friends. Boundless appreciation to my husband Dwight for years of collaboration and keeping the big picture in view. To my children for reminding me what is most important and why we do what we do. To my mother, Cathy for always allowing me to be my crazy self and my father, Brian for a lifetime love of SciFi and exploration. To Nana for instilling in me an early love of learning and Aunt Honey for exemplifying adventure. To my dear friend Kevin for being a light in my life while you were here, and to Hiro for sharing my passion for the exquisitely toxic.

Many thanks go to my mentor and advisor Dan Nomura, for pushing me to innovate, achieve shared scientific goals and for always having our backs. To John Casida for inspiring me to see all the connections and to Dale Johnson for keeping me focused on the future. Lastly, many thanks to my wonderful lab mates who have helped me grow as a scientist and team member.

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ABBREVIATIONS

2-AG	2-Arachidonoylglycerol
ABHD12	Abhydrolase Domain Containing 12
ABPP	Activity-based protein profiling
Acaa1b	Acetyl-CoA acyltransferase 1B
Acaa2	Acetyl-CoA Acyltransferase 2
Acat2	Acetyl CoA acetyltransferase
Aldh9a1	Aldehyde Dehydrogenase 9 Family Member A1
AMPA	Aminomethylphosphonic acid
ATP	Adenosine triphosphate
BCA	Bicinchoninic acid
BTK	Bruton's tyrosine kinase
CES	Carboxylesterases
ClpP	Caseinolytic Protease, ATP-Dependent, Proteolytic Subunit
CPT1A	Carnitine Palmitoyltransferase 1A
CTN	Chlorothalonil
DAGL	Diacylglycerol lipase
DAGs	Diacylglycerols
DCTyne	Dichlorotriazine-alkyne
DTT	Dithiothreitol
EGFR	Epidermal growth factor receptor
ESI	Electrospray ionization
FAAH	Fatty acid amide hydrolase
Fabp1	Fatty Acid Binding Protein 1
FASN	Fatty acid synthase
FBS	Fetal bovine serum
FDA	Food and drug administration
GAPDH	Glyceraldehyde-3-Phosphate Dehydrogenase
HER2	Human epidermal growth factor receptor 2
HNE	4-hydroxy-2-nonenal
IA-Rh	Iodoacetamide-rhodamine

IAyne	Iodoacetamide-alkyne
ip	Intraperitoneal
IsoTOP-ABPP	Isotopic tandem orthogonal proteolysis activity-based protein profiling
JNK	c-Jun N-terminal kinase
LC-MS/MS	Liquid chromatography-mass spectrometry
MAGE	Monoalkylglycerol ether
MAGL	Monoacylglycerol lipase
MAGs	Monoacylglycerols
MMA	Monomethylarsenous acid
MudPIT	Multidimensional Protein Identification Technology
NSCLC	Non-small cell lung cancer
ONE	4-oxo-2-nonenal
OP	Organophosphorus
PBS	Phosphate-buffered saline
PHARC	Polyneuropathy, Hearing loss, Ataxia, Retinitis Pigmentosa and Cataracts
PI3K	Phosphoinositide 3-kinase
PLA2G7	Phospholipase A2, Group VII
PLK1	Polo-like kinase 1
PME	Pectinesterase
RPL7a	Ribosomal Protein L7a
RPS9	Ribosomal Protein S9
Scp2	Sterol carrier protein 2
SILAC	Stable isotope labeling of cells
SRM	Single-reaction monitoring
TAGs	Triacylglycerols
TCEP	Tris(2-carboxyethyl)phosphine
TEV	Tobacco Etch Virus
TPP	Triphenylphosphate
TPP2	Tripeptidyl Peptidase 2
ZAK	Zipper containing kinase

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Abstract and chapter 1: adapted with permission from Current Opinions in Chemical Biology, doi: https://doi.org/10.1016/j.cbpa.2015.11.007. Jessica L. Counihan, Breanna Ford, Daniel K. Nomura, "Mapping Proteome-Wide Interactions of Reactive Chemicals using Chemoproteomic Platforms." Copyright © 2015 Elsevier

Abstract and chapter 2: adapted with permission from Cell Chemical Biology, doi: https://doi.org/10.1016/j.chembiol.2016.12.013. Breanna Ford, Leslie A. Bateman, Leilani Gutierrez-Palominos, Robin Park, Daniel K. Nomura, "Mapping proteome-wide targets of glyphosate in mice." Copyright © 2016 Elsevier

Chapter One: Mapping Proteome-Wide Interactions of Reactive Chemicals Using Chemoproteomic Platforms

Introduction

We are exposed to a large number of chemicals that act through covalent mechanisms. These chemicals include pharmaceutical agents that irreversibly inhibit their respective protein targets to treat human diseases, such as Alzheimer's disease, obesity, pain, and cancer (Beck et al., 2012; Colovic et al., 2013; Hoover et al., 2008; Liu et al., 2013; Potashman and Duggan, 2009). Also included are reactive endogenous metabolites that are formed through metabolism, such as lipid aldehydes and various forms of reactive oxygen species or nitrogen stress. Many pesticides, environmental contaminants, and household chemicals also act through covalent mechanisms (Medina-Cleghorn et al., 2014, 2015; Morris et al., 2014; Nomura et al., 2008; Nomura and Casida, 2011). While most of these chemicals have undergone standard toxicological testing, the reactivity of these chemicals across the proteome still remains poorly defined. Understanding the selectivity of these reactive agents is of paramount importance in comprehending the mechanisms underlying their biological or therapeutic action, identifying off-target effects that may lead to 'idiosyncratic' toxicities, and informing the development of safer and more selective agents.

Over the past several years, there have been major advancements in the development and use of chemoproteomic platforms to determine the proteome-wide interactions of irreversible small-molecule tool compounds, therapeutics, endogenous electrophiles, and environmental chemicals. In the following sections, we will describe how chemoproteomic technologies have been used to assess both the selectivity of therapeutic agents and the toxicological mechanisms of environmental chemicals.

Chemoproteomic Profiling to Assess Selectivity of Therapeutic Irreversible Small-Molecule Inhibitors

Pharmaceutical companies have historically shied away from pursuing covalent inhibitors due to risks of haptenization and immunologic reactions that may occur through non-specific covalent modification of small-molecules with protein targets (Uetrecht, 2008). Nonetheless, many irreversible or pseudo-irreversible inhibitors have been successfully developed as well-tolerated drugs in the clinic. Examples include the anti-inflammatory drug aspirin, the broad class of antibacterial beta-lactam antibiotics such as penicillin, drugs that require metabolic bioactivation including the proton pump inhibitor omeprazole, the Alzheimer's drug rivastigmine that inhibits acetylcholinesterase, the cancer therapy bortezomib (Velcade) that targets the proteosome, and the anti-obesity drug tetrahydrolipstatin (Orlistat) that inhibits gastric lipase (Beck et al., 2012; Colovic et al., 2013; Hoover et al., 2008; Potashman and Duggan, 2009). In recent years, there has been resurgence in developing covalent and irreversible inhibitors, including several acrylamide-based inhibitors that act through Michael addition with a cysteine in the ATP binding pocket of oncogenic kinases for cancer therapy. Some examples include PCI-32765 (ibrutinib), a Bruton's tyrosine kinase (BTK) inhibitor now FDA approved for mantle cell lymphoma and chronic lymophoblastic leukemia; BIBW-2992 (afatinib) and HKI-272 (neratinib) that dually inhibit human epidermal growth factor receptor 2 (HER2) and epidermal growth factor receptor (EGFR), both of which are approved or in development for non-small cell lung cancer (NSCLC) and breast cancer, respectively; and CO1686 (Rociletinib) that specifically inhibits the mutant

T790M form of EGFR and is also currently in development for NSCLC (Liu et al., 2013) (Fig. 1-1A).
Although it may seem counterintuitive to develop selective inhibitors through reactive and covalent mechanisms, irreversible inhibitors as therapeutics in the modern era of drug discovery and chemical biology affords many benefits. First, covalent inhibitors can provide extended target engagement without the need to maintain high levels of drug. Second, the electrophilicity of the inhibitor can be fine-tuned with the affinity of the small-molecule for a particular binding pocket of a specific protein target, such that the reaction occurs selectively with minimal off-target liabilities. Third, various modern chemoproteomic approaches can be utilized to confirm target engagement and proteome-wide selectivity of covalent inhibitors *in situ* and *in vivo*, which can, in-turn, inform further medicinal chemistry efforts to optimize inhibitor properties or to confirm the safety and specificity of lead molecules. We will discuss several examples showcasing the utility of chemoproteomic platforms to define the selectivity of irreversible small-molecule inhibitors and drugs.

One chemoproteomic platform that has been successfully used to develop selective inhibitors against many protein targets is activity-based protein profiling (ABPP). ABPP uses activity-based chemical probes that directly bind to the active sites of large numbers of enzymes, thus providing a functional readout of enzyme activities *en masse* directly in complex proteomes (Medina-Cleghorn and Nomura, 2014; Roberts et al., 2016). Because these activity-based probes bind to the active-sites of enzymes, small-molecule inhibitors can be competed against probe-binding, therefore enabling the development of small-molecules for both characterized and uncharacterized enzymes. Since the activity-based probes evaluate enzyme activities across an entire enzyme class, the proteome-wide selectivity of the small-molecule inhibitor can be assessed within that particular enzyme class. While the ABPP platform has been used to develop selective reversible and irreversible inhibitors of enzymes (Adibekian et al., 2010; Bachovchin et al., 2010; Chang et al., 2015, 2011; Leung et al., 2003; Jonathan Z Long et al., 2009; J. Z. Long et al., 2009), this approach has been particularly useful for testing the efficacy and selectivity of irreversible inhibitors. Target engagement and proteome-wide selectivity can be confirmed for irreversible inhibitors by comparing *ex vivo* labeling of vehicle and inhibitor-treated proteomes (Chang et al., 2011; Jonathan Z Long et al., 2009; J. Z. Long et al., 2009). The ABPP platform has also been adapted to be compatible with modern quantitative proteomic approaches through stable isotope labeling of cells (SILAC), in which vehicle-treated "light" cells and inhibitor-treated "heavy" cells are combined after labeling with activity-based probes and, subsequently, analyzed for their selectivity by SILAC ratios (Adibekian et al., 2011) (Fig. 1-2A).

Several highly potent, selective, and *in vivo* active irreversible small-molecule inhibitors that show potential therapeutic benefit have been developed using the ABPP platform. These include monoacylglycerol lipase (MAGL) and diacylglycerol lipase (DAGL) inhibitors that hydrolyze or generate, respectively, the endocannabinoid signaling lipid 2-arachidonoylglycerol (2-AG), and also control arachidonic acid release for pro-inflammatory prostaglandin synthesis (Hsu et al., 2012; Nomura et al., 2011). The development of selective and *in vivo* efficacious irreversible MAGL inhibitors, such as JZL184, KML29, and MJN110, have led to the discovery that MAGL blockade leads to heightened 2-AG levels, cannabinoid receptor stimulation, and lower arachidonic acid and pro-inflammatory prostaglandin levels in the brain, thus providing antinociceptive, anti-inflammatory, anxiolytic, and neuroprotective effects (Chang et al., 2012;

Jonathan Z Long et al., 2009; Niphakis and Cravatt, 2014) (Fig. 1-1B, 1-3A). Hsu et al. developed DAGL inhibitors, such as KT172 and KT109, which have been used to show that DAGL blockade leads to depletion of 2-AG, arachidonic acid, and pro-inflammatory prostaglandin levels to suppress inflammatory cytokine release from macrophages (Hsu et al., 2012).

Hoover et al. used ABPP platforms to show that the obesity drug tetrahydrolipstatin inhibits multiple metabolic enzyme targets in brain, including ABHD12, TPP2, BAT5, and PLA2G7 (Hoover et al., 2008). Inloes et al. recently discovered that the previously uncharacterized enzyme DDHD2, which is linked to the genetic disorder hereditary spastic paraplegia, was the primary triacylglycerol hydrolase in brain. Using ABPP platforms, the authors developed a selective, *in vivo* efficacious and irreversible DDHD2 inhibitor, KLH45 (Inloes et al., 2014). Using this inhibitor alongside genetic DDHD2 knockout mouse models, the authors showed that DDHD2 blockade led to striking accumulations in triacylglycerol levels in the brains of these mice, potentially explaining the metabolic mechanisms underlying the associated neurological disorder (Fig. 1-3C). Using ABPP platforms, Kamat et al. developed a highly selective inhibitor, KC01, for a previously uncharacterized enzyme, ABHD16A. They then used this inhibitor to characterize ABHD16A as a phosphatidylserine hydrolase that generates lysophosphatidylserine (LPS) that, in-turn, fuels a neuroinflammatory response (Kamat et al., 2015). Previous studies showed that another formerly uncharacterized hydrolase ABHD12 is mutationally inactivated in a neurodegenerative disease known as Polyneuropathy, Hearing loss, Ataxia, Retinitis Pigmentosa, and Cataracts (PHARC), leading to accumulation of brain LPS and neuroinflammation (Lanning et al., 2014). Kamat et al. showed that KC01 lowers the high levels of LPS found in ABHD12-deficient macrophages, leading to suppression of inflammatory cytokine release, indicating that ABHD16A inhibitors may act as anti-inflammatory agents through modulating LPS signaling (Kamat et al., 2015) (Fig 1-1B, 1-3B). Thus, ABPP has been used successfully to develop irreversible small-molecule inhibitors against both characterized and uncharacterized enzymes to further our understanding of the biological and potential therapeutic functions of these enzymes.

Many studies have also developed ‘clickable’ analogs of lead small-molecule therapies or inhibitors of therapeutic targets bearing either alkyne or azide handles for chemoproteomic profiling to confirm the small-molecule’s selectivity or identify any off-targets. Lanning et al. used alkyne-bearing analogs of cysteine-reactive irreversible kinase inhibitors, ibrutinib and PF-6274484, that target BTK and EGFR, respectively, to assess their selectivity in cancer cells using click-chemistry-based chemoproteomic approaches (Lanning et al., 2014) (Fig. 1-2B). Cheng et al. developed an alkyne-bearing analog of the widely used inhibitor, C75, of the cancer therapy target fatty acid synthase (FASN), and showed that it possessed many off-targets including CPT1A, GAPDH, and 13 other enzymes beyond FASN, which may explain the high level of toxicity associated with C75 (Cheng et al., 2014). Bateman et al. developed an aspirin-alkyne probe and coupled the labeling of this probe with chemoproteomic profiling to identify 120 protein targets of aspirin, 112 of which had not been previously reported to be acetylated by aspirin in cellular or *in vivo* contexts (Bateman et al., 2013). The authors showed that aspirin-alkyne modified core histone proteins, thus implicating aspirin as a potential chemical-regulator of transcription (Bateman et al., 2013). The proteome-wide selectivity of many of the serine hydrolase inhibitors that have been developed using ABPP platforms have also been confirmed for their selectivity outside the serine hydrolase family through the development of alkyne-bearing analogs. Examples include the FAAH inhibitor PF-3845 and PF-04457845, the PME inhibitor ABL127, and the MAGL inhibitor MJN110 (Ahn et al., 2011, 2009; Bachovchin et al., 2010; Niphakis and Cravatt, 2014) (Fig. 1-1B).

Chemoproteomics has also been used to identify the targets of various natural products through the synthesis of reporter-bearing analogs. Using a Wortmannin analog bearing a tetramethylrhodamine, the conjugate AX7503 was shown to not only bind phosphoinositide 3-kinase (PI3K) and PI3K-related kinases, but also Polo-like kinase 1 (PLK1) (Liu et al., 2005). Stephan Sieber's group synthesized a series of alkyne-bearing β-lactam antibiotic analogs of penicillin, aztreonam, and cephalosporin to label diverse penicillin binding proteins (Staub and Sieber, 2008). The authors also synthesized a series of additional β-lactam probes, which labeled and inhibited a selection of penicillin-binding proteins as well as unrelated bacterial targets, including the virulence-associated enzyme ClpP and resistance-associated β-lactamase (Staub and Sieber, 2008). Yang et al. synthesized an alkyne-bearing analog of tetrahydrolipstatin (Orlistat), an FDA-approved anti-obesity drug with potential antitumor activities, and identified 8 novel targets of orlistat beyond FASN, including Hsp90AB1, GAPDH, Annexin A2, RPL7a, and RPS9 (Yang et al., 2010). In another example, Abegg et al. used an ethynyl benziodoxolones cysteine-reactive probe, JW-RF-010, to identify biological targets of the potential anti-cancer therapy curcumin. The authors identified 42 additional targets of curcumin, only one of which was previously known (Abegg et al., 2015).

Chemoproteomic Profiling of Reactive Environmental Chemicals and Endogenous Reactive Metabolites to Understand Toxicological Mechanisms

We are exposed to countless chemicals, many of which have been linked to adverse health effects, and most of which have not been characterized in terms of their toxicological potential or mechanisms. Of particular concern among chemicals in our environment are reactive electrophiles that we are directly exposed to or those metabolites that form through bioactivation, which have the potential to covalently and cumulatively react with nucleophilic amino acid hotspots within the proteome, leading to potential protein dysfunction and pathophysiological effects. Understanding the direct chemical-protein interactions of these reactive agents informs our understanding of downstream molecular, metabolic, and pathophysiological effects that may arise from chemical exposure, and provides a more direct approach towards identifying toxicological drivers of human disease. We discuss here several chemoproteomic approaches that have been successfully applied to understand unique and novel toxicological mechanisms for both environmental chemicals and endogenous reactive metabolites (Fig. 1-1C).

ABPP platforms have been used to identify off-targets of widely used organophosphorus (OP) and carbamate pesticides *in vivo*. These pesticides act as insecticides through inhibiting acetylcholinesterase, but there have been toxicological effects associated with exposure to these agents that cannot be explained by acetylcholinesterase inhibition alone, indicating possible off-targets. Using the serine hydrolase-directed activity-based probe, Nomura et al. and Medina-Cleghorn et al. identified many *in vivo* off-targets of these pesticides that are inhibited in mice, leading to downstream biochemical effects. For example, several studies have shown that OP pesticides inhibit MAGL and fatty acid amide hydrolase (FAAH) in mouse brain causing elevations in endocannabinoid signaling lipids, 2-AG, and anandamide, all of which lead to downstream cannabinoid-like behavioral effects (Medina-Cleghorn et al., 2014; Nomura et al., 2008; Nomura and Casida, 2011).

Wang et al. used an elegant quantitative chemoproteomic strategy, termed isotopic tandem orthogonal proteolysis activity-based protein profiling (isoTOP-ABPP), for mapping cysteine reactivity to investigate direct targets and site-of-modifications of lipid aldehydes generated during lipid peroxidation through competition of lipid aldehydes against the cysteine-reactive iodoacetamide-alkyne (IAyne) reactivity-based probe (Wang et al., 2014; Weerapana et al., 2010). Probe-labeled control and treated proteomes were appended to a biotin-azide analytical handle bearing a light or heavy valine and TEV protease cleavage site using click-chemistry, control and probe labeled proteomes were combined, and probe-labeled tryptic peptides were subsequently enriched and analyzed by quantitative proteomic platforms. Surprisingly, the authors showed that 4-hydroxy-2-nonenal (HNE) interacts with a select set of proteins that constitute hotspots for modifications by various lipid-derived electrophiles, rather than non-specifically reacting with cysteines. For example, they showed that HNE specifically reacts with an active-site proximal cysteine on sterile alpha motif and leucine zipper containing kinase (ZAK), leading to enzyme inhibition creating a negative feedback mechanism that can suppress the activation of c-Jun N-terminal kinase (JNK) pathways induced by oxidative stress (Wang et al., 2014). The toxic mechanisms of alkylation by lipid aldehydes were also explored with alkyne-bearing analogs of HNE and 4-oxo-2-nonenal (ONE) coupled with chemoproteomic approaches. The authors showed that HNE and ONE show particular susceptibility towards alkylating protein targets mapping to networks involved in cytoskeletal regulation with low susceptibility towards proteins involved in protein synthesis and turnover. The authors then postulated that the differential sensitivity of protein targets to lipid aldehyde alkylation may protect cells from cytotoxicity as a result of moderate levels of lipid aldehydes (Codreanu et al., 2014) (Fig. 1-2C, 1-3D).

Medina-Cleghorn et al. recently used ABPP approaches to map direct biological targets of several reactive environmental chemicals, including the fungicide chlorothalonil (CTN), the environmental contaminant monomethylarsenous acid (MMA), and a broad-spectrum insecticide chloropicrin (Medina-Cleghorn et al., 2015). The authors performed *in vitro* competition of these agents against the cysteine-reactive IAyne reactivity-based probe directly in mouse liver proteomes and found that CTN, MMA, and chloropicrin commonly inhibit several metabolic enzymes involved in fatty acid metabolism and energetic enzymes. The authors further delved into the mechanisms underlying previously reported kidney-specific toxicity associated with CTN through *in vivo* profiling of CTN targets, and subsequent *ex vivo* labeling with an alkyne-bearing CTN analog for chemoproteomic discovery of *in vivo* CTN targets in kidney. The authors showed that CTN inhibits fatty acid transport proteins, fatty acid oxidation enzymes, and glycolytic enzymes *in vivo*, leading to alterations in kidney lipid metabolism, thus revealing a novel mechanism of toxicity underlying this major fungicide (Medina-Cleghorn et al., 2015) (Fig. 1-3E).

In another study, Morris et al. used chemoproteomic profiling approaches to comprehensively identify the biological targets of the widely-used flame retardant chemical triphenylphosphate

(TPP) by using an alkyne-bearing TPP analog. The authors showed that specific liver carboxylesterases (CES), in particular CES1G, were inhibited by TPP leading to heightened DAG levels and protein kinase C stimulation in liver and serum hypertriglyceridemia (Morris et al., 2014).

Conclusion

We provide here several examples of chemoproteomic platforms and their applications to assess the selectivity or off-target profiles of tool compounds, therapeutics, and environmental chemicals that act through irreversible mechanisms. Historically, small-molecule agents that act through covalent mechanisms have been feared to cause non-specific adducts on proteins, which, in-turn, may lead to non-specific toxicities and potential haptenization or other types of idiosyncratic toxicities. Certainly, there have been historical examples of highly reactive agents or reactive metabolites that have caused these types of toxicities (Uetrecht, 2008). However, modern chemoproteomic technologies have provided a more precise and deeper understanding of how reactive chemicals interact with the proteome.

There are indeed reactive chemicals that show large numbers of off-targets. However, chemoproteomic studies have shown that even highly reactive chemicals, such as lipid aldehydes, show relatively selective interactions with specific subsets of targets over others and that these interactions occur oftentimes at hyper-reactive and functional sites on protein targets, rather than non-specific alkylation events. Chemoproteomic profiling of covalently-acting and clinically approved drugs, such as ibrutinib, have revealed potentially large numbers of off-targets at high concentrations. However, studies have shown that these off-target liabilities can be greatly minimized upon even slight chemical modifications of a drug. There have also been a substantial number of highly selective irreversibly-acting small-molecule inhibitors that have been developed in conjunction with technologies such as activity-based proteomics or click-chemistry based chemoproteomic approaches.

Thus, while many pharmaceutical and environmental electrophilic chemicals show potential off-target liabilities, a high degree of selectivity and specificity can still be achieved with irreversible compounds through medicinal chemistry efforts, especially when optimization efforts are coupled with chemoproteomic profiling. Irreversible inhibitors coupled with chemoproteomic platforms also affords substantial advantages for confirming target engagement and *in vivo* selectivity profiling, which is oftentimes difficult with reversible inhibitors. Thus, the aim of this review is not to disparage the development of irreversible inhibitors, but instead to promote the development of irreversible inhibitors coupled with the application of chemoproteomic platforms to facilitate the development of highly selective and covalent therapeutics or even agrochemicals.

Acknowledgements

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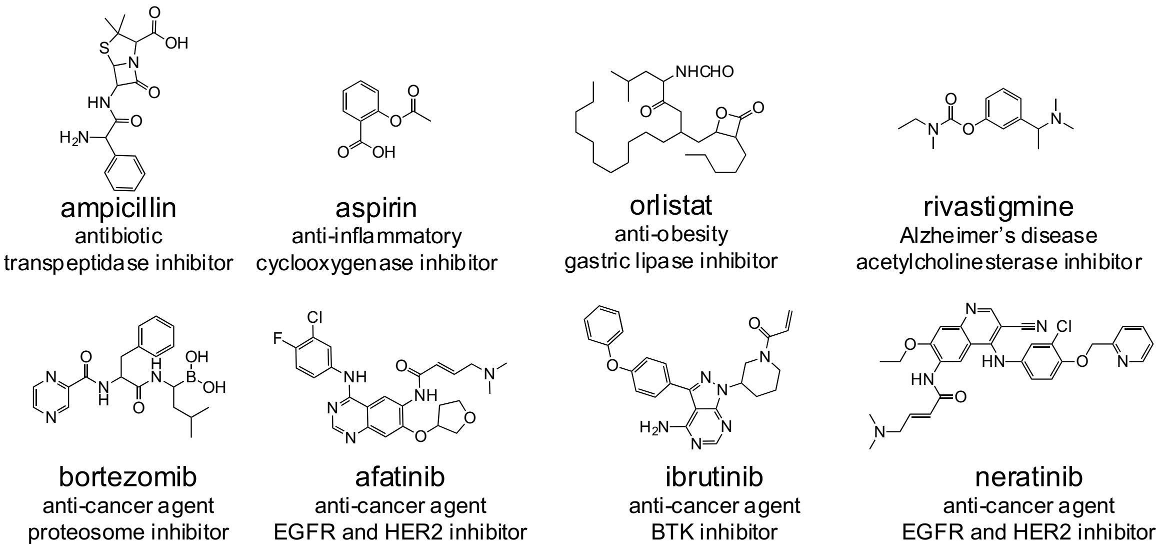
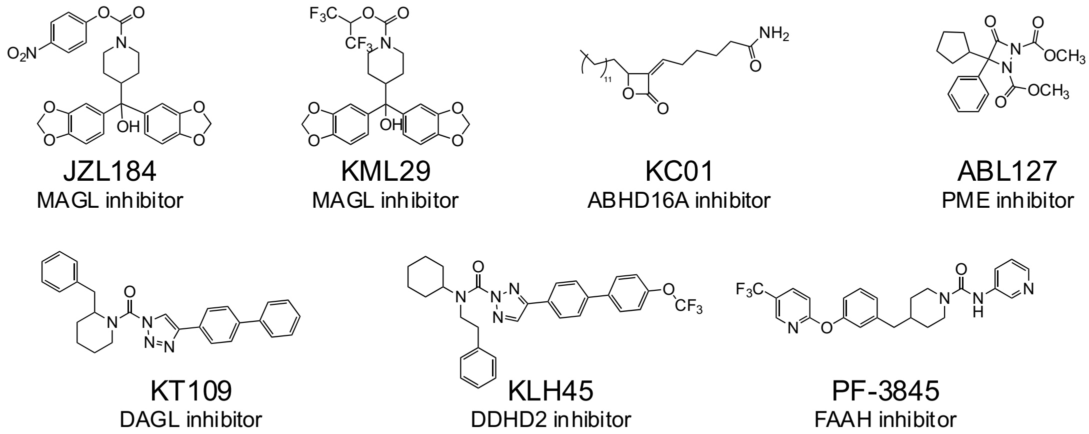
Figure 1-1.

A examples of irreversibly-acting clinically-used drugs



B examples of irreversibly-acting and selective tool compounds



C examples of reactive chemicals from environmental or endogenous sources

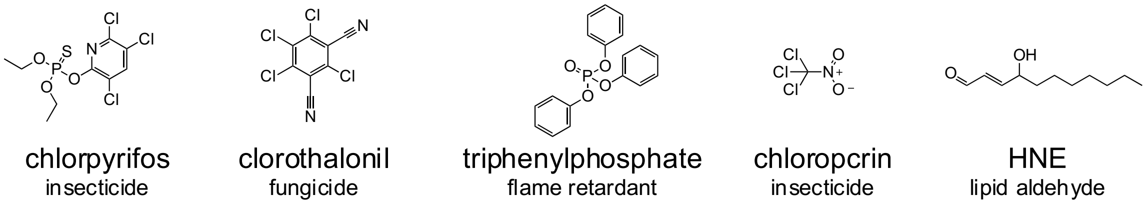


Figure 1-1. Examples of (A) irreversibly-acting drugs, (B) tool compounds, (C) environmental chemicals, and endogenous electrophiles.

Figure 1-2.

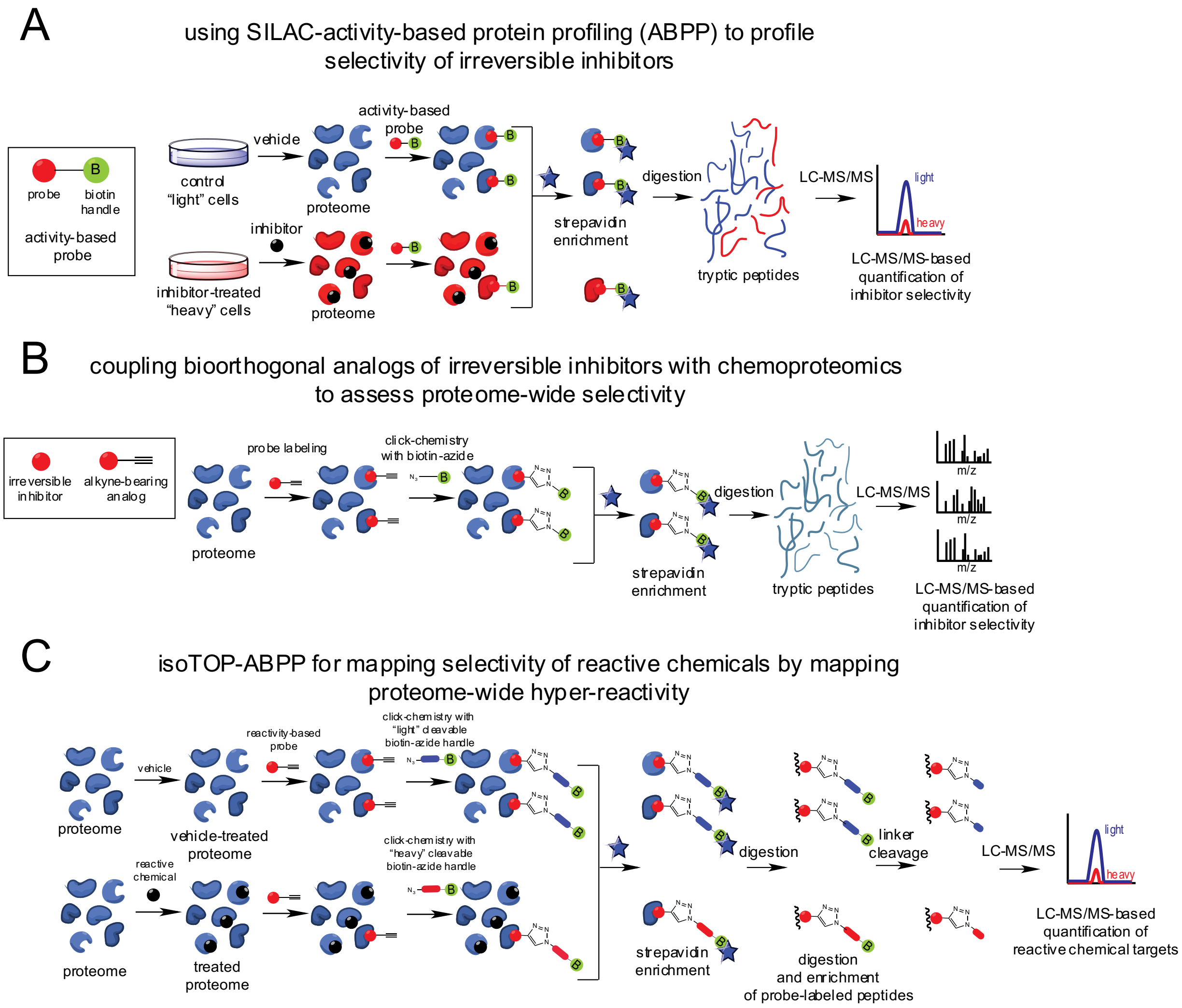


Figure 1-2. Chemoproteomic platforms for assessing proteome-wide targets of irreversibly-acting chemicals. (A) SILAC-ABPP uses active-site directed chemical probes to assess the functional state of large numbers of enzymes directly in complex proteomes. Small-molecule inhibitors can be competed against the binding of activity-based probes to enzymes to assess enzyme class-wide selectivity. Cells can be labeled with light or heavy isotopic amino acids for quantitative proteomic analysis. (B) Analogs of these inhibitors bearing a bioorthogonal handle (e.g. alkyne) can be used to assess proteome-wide selectivity of small-molecule inhibitors using chemoproteomic approaches. (C) Isotopic Tandem Orthogonal Proteolysis-ABPP (isoTOP-ABPP) can be used to map hyper-reactive and functional sites across the proteome using reactivity-based chemical probes bearing bioorthogonal handles (e.g. alkyne). Reactive electrophiles can be competed against probe binding to hyper-reactive sites to map protein targets of these reactive agents. Probe-labeled peptides can be identified through subsequent appending of a biotin-azide analytical handle bearing a TEV protease recognition sequence and

heavy or light isotopic valine tag using copper-catalyzed click chemistry. Upon mixing control and treated proteomes, probe-labeled proteins can be avidin-enriched, tryptically digested, and probe-labeled peptides can be subsequently enriched and released by TEV protease for subsequent quantitative proteomic analysis.

Figure 1-3.

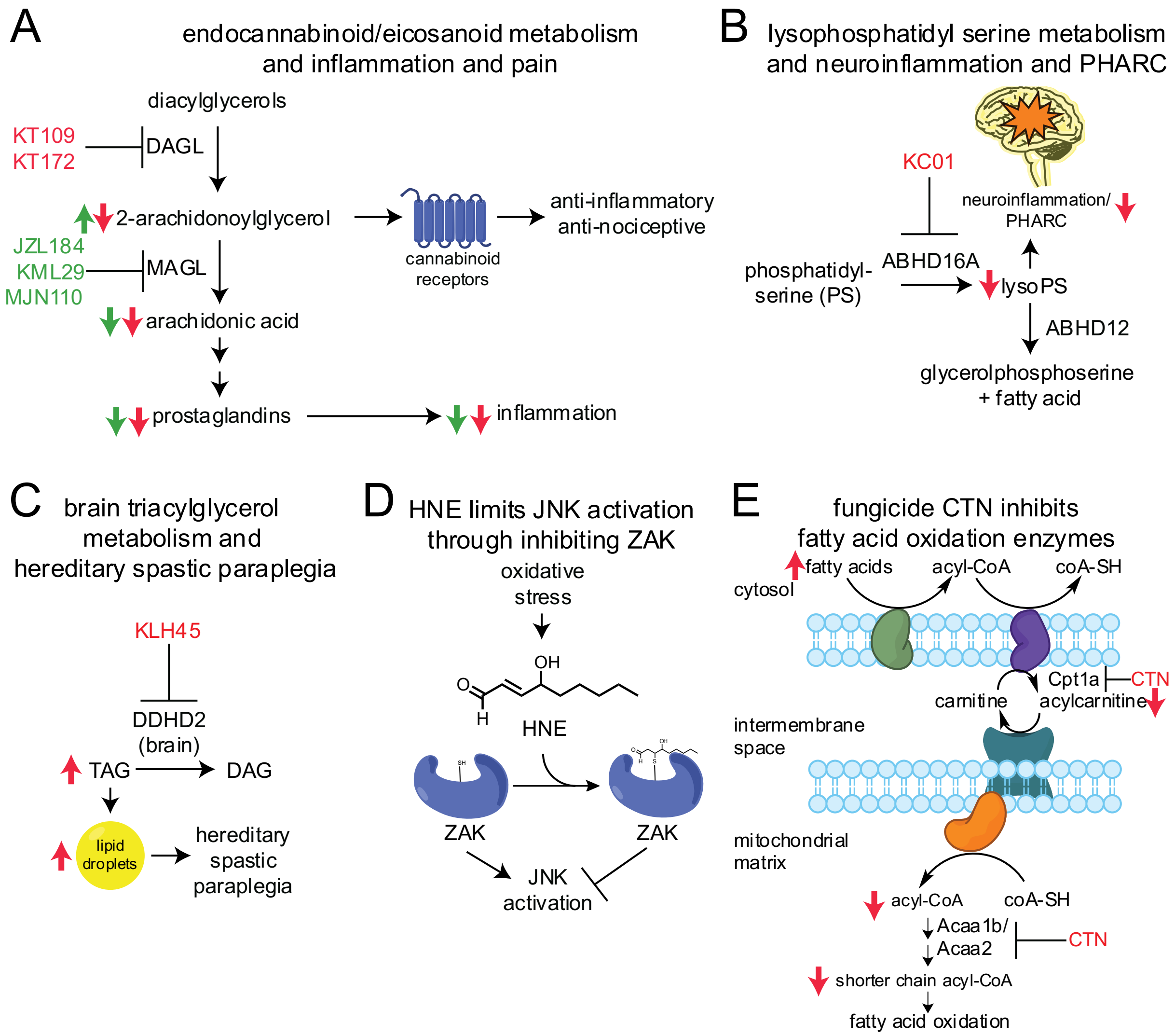


Figure 1-3. Biological insights gained from using chemoproteomic platforms. (A) ABPP has been successfully used to develop selective small-molecule inhibitors against enzymes involved the synthesis and degradation of the endocannabinoid 2-arachidonoylglycerol (2-AG). Selective DAGL inhibitors KT109 and KT172 and selective MAGL inhibitors JZL184, KML29, and MJN110 have been used to not only identify that DAGL and MAGL regulate endocannabioid metabolism and signaling, but also to show that this pathway controls arachidonic metabolism that fuels pro-inflammatory prostaglandin synthesis. (B) ABPP was used to develop the selective DDHD2 inhibitor KLH45, which was used to show that the previously uncharacterized enzyme DDHD2 was the primary triacylglycerol (TAG) hydrolase in the brain, and that inhibiting this enzyme led to accumulation in brain triacylglycerol levels and accumulation of lipid droplets. (C) ABPP was used to develop the selective ABHD16A inhibitor KC01 to determine that ABHD16A was the primary phosphatidylserine (PS) hydrolase that generates the pro-

inflammatory signaling lipid lyso-PS, which is in-turn hydrolyzed by ABHD12. Previous studies had shown that ABHD12 inactivation caused a neurodegenerative disease known as PHARC. ABHD16A inhibition protected mice from the neurotoxicological markers associated with PHARC. (D) Lipid aldehydes such as HNE were competed against the cysteine-reactive iodoacetamide-alkyne (IAyne) probe and coupled to the isoTOP-ABPP platform to map the direct protein targets of HNE. HNE showed selective interactions with certain sites such as the active-site proximal cysteine of ZAK, leading to ZAK inhibition and JAK inactivation. (E) Reactive environmental chemicals, such as the fungicide chlorothalonil (CTN) were competed against IAyne to map direct protein targets of these chemicals, leading to the discovery that CTN binds to and inhibits multiple enzymes involved in fatty acid oxidation.

Chapter Two: Mapping Proteome-Wide Targets of Glyphosate in Mice

Introduction

Glyphosate, the active ingredient in RoundUp®, is the most commonly used pesticide in the US across agricultural and home garden use, with 180-185 million pounds used in the US in 2007 (Grube et al., 2011). Glyphosate is also one of the most controversial herbicides, due to major disagreements in its safety and toxicity (Cressey, 2015). Many studies have associated glyphosate exposure with various adverse health effects (El-Shenawy, 2009; Samsel and Seneff, 2015), including cancer, liver damage, and dyslipidemia in mammals and was recently deemed a probable human carcinogen by the International Agency for Research on Cancer ("IARC Monographs on the Evaluation of Carcinogenic Risks to Humans," 2015; Portier et al., 2016). Understanding how glyphosate interacts with biological systems *in vivo* in mammals is necessary to assess the prolonged effects and mechanism of toxicity of glyphosate on human health.

There have been previous efforts to characterize the toxicological mechanisms of glyphosate including acute and long-term toxicity studies in animal models, epidemiological studies in human populations, and modern systems biology approaches to map gene expression changes (Chang and Delzell, 2016; El-Shenawy, 2009; Greim et al., 2015; Mesnage et al., 2015; Portier et al., 2016; Samsel and Seneff, 2015). However, many of these approaches have been largely correlative, and have likely still missed subtler or indirect pathological effects that may arise from long-term exposures. We believe that understanding the direct chemical-protein interactions of glyphosate or its metabolites will inform our understanding of downstream molecular, metabolic, and pathophysiological effects, providing a more direct approach towards understanding toxicological mechanisms of this widely used pesticide.

Glyphosate Can Be Metabolized to the Reactive Compound Glyoxylate *In Vivo* in Mouse Liver

Of concern is whether glyphosate may be biotransformed into electrophilic metabolites, which may in-turn react with nucleophilic amino acid hotspots on proteins such as cysteines and lysines which may cause disruption in protein biochemistry, such as enzyme catalysis, post-translational regulation, redox balance, metal binding, and protein-protein interactions. Glyphosate has been reported to be metabolized by soil microbes and possibly in mammals to aminomethylphosphonic acid (AMPA) and the reactive metabolite glyoxylate (Samsel and Seneff, 2015). Glyoxylate is an aldehyde known to react with nucleophilic amino acids on protein targets, such as cysteines, lysines, and arginines (Gohre et al., 1987; Schuette, 1998).

To determine whether glyphosate is potentially biotransformed into glyoxylate in mammals, we administered isotopic [$^{13}C/^{15}N$]glyphosate to mice at a high dose of 200 mg/kg ip, once per day over 7 days, and measured isotopically labeled [$^{13}C/^{15}N$]glyphosate, [^{15}N]AMPA, and [^{13}C]glyoxylate levels *ex vivo* in mouse liver using single-reaction monitoring (SRM)-based liquid chromatography-mass spectrometry (LC-MS/MS) derived from fragmentation and retention times of standards for each chemical. We acknowledge that these doses are much higher than exposure levels encountered by the public, but toxicological testing studies with pesticides are oftentimes performed at maximum tolerated doses. Despite previous reports claiming that glyphosate is largely not metabolized *in vivo* (Williams et al., 2000), we show significant formation of isotopic AMPA and glyoxylate in livers from [$^{13}C/^{15}N$]glyphosate-treated mice (Fig. 2-1A). The level of glyoxylate formed is approximately 4 % of glyphosate levels detected in the liver. Glyoxylate is also produced through various metabolic pathways in mammals, such as glycine degradation (Wang et al., 2013). We also treated mice with nonisotopic glyphosate (200 mg/kg ip, once per day over 7 days) and show that glyphosate treatment significantly increases endogenous glyoxylate levels by ~2-fold above endogenously generated levels at the doses used in this study (Fig. 2-1B).

Direct Protein Targets of Glyphosate and its Reactive Metabolite Glyoxylate Include Proteins Involved in Fatty Acid Metabolism

We postulated that the observed heightened levels of glyoxylate would lead to more glyoxylate reactivity with susceptible nucleophilic residues on proteins *in vivo* in mice (Fig. 2-1C). To determine whether glyphosate metabolites formed *in vivo* may affect proteome reactivity, we performed a series of chemoproteomic profiling experiments using reactivity-based probes and activity-based protein profiling (ABPP), a chemoproteomic strategy that uses active-site or reactivity-based chemical probes to map reactive, functional, and ligandable hotspots directly in complex proteomes (Fig. 2-2A) (Counihan et al., 2016; Roberts et al., 2016). When used in a competitive manner, reactive chemicals can be competed against reactivity-based probes to map their proteome-wide reactivity (Counihan et al., 2016; Roberts et al., 2016). First, we performed gel-based ABPP studies in which we determined general cysteine-reactivity from mice treated with vehicle or glyphosate by labeling mouse liver proteomes with the cysteine-reactive iodoacetamiade-alkyne (IAyne) probe, followed by appendage of rhodamine-azide by copper-catalyzed click-chemistry, and in-gel fluorescence analysis. We show that *in vivo* glyphosate treatment selectively reduced cysteine-reactivity of several protein targets in mouse liver (Fig. 2-2B). To determine the identity of these targets, we next performed an ABPP proteomic experiment, in which we enriched IAyne-labeled proteins from vehicle and glyphosate-treated mouse liver proteomes through biotin-conjugation to probe-labeled proteins, avidin-enrichment and proteomic analysis. Out of 340 IAyne-enriched proteins, we observed 51 protein targets that showed significantly less IAyne enrichment in glyphosate-treated mouse livers, compared to vehicle-treated controls, indicating that these targets possessed cysteines that were bound by reactive metabolites of glyphosate (Fig. 2-2C; Appendix 1).

To gain an in-depth understanding of which specific cysteines on proteins were particularly susceptible to *in vivo* reactive metabolites of glyphosate, we performed isotopic tandem orthogonal proteolysis-enabled activity-based protein profiling (isoTOP-ABPP) to map proteome-wide cysteine reactivity of glyphosate and its metabolites *in vivo* in mouse liver (Weerapana et al., 2010) (Fig. 2-2A). We labeled *in vivo* vehicle and glyphosate-treated mouse liver proteomes with IAyne, followed by linking an isotopically light (vehicle) or heavy (glyphosate-treated) TEV recognition site-bearing biotin handle by click chemistry, combining the vehicle and glyphosate proteomes together in a 1:1 ratio, enriching IAyne labeled proteins by biotin pull-down, tryptically digesting enriched proteins, and subsequently releasing the probe-modified tryptic peptides by TEV protease digestion. We identified >3500 peptides bearing light or heavy IAyne-modified cysteines. We only quantitatively compared and interpreted those peptides which were found in at least two of the three biological replicates. Among these resulting 320 cysteine-modified peptides, 190 of these peptides showed >1.5, 67 showed >2, and

20 showed >3 light to heavy ratios (Fig. 2-2D; Fig. 2-3A; Appendix 2). To determine whether these changes in ratios were dependent on changes in protein expression, we also performed standard proteomic profiling of vehicle and glyphosate-treated liver proteomes. While 2810007J24Rik and Selenbp2 protein expression was significantly lower in glyphosate-treated mouse livers, we show that most of the protein targets that showed >3 light to heavy ratios did not show reduced protein expression, indicating that these targets are likely direct targets of glyphosate metabolites (Fig. 2-4; Appendix 3). Among the top 21 modified peptides showing >3 light to heavy ratio, two of these cysteines corresponded to an annotated catalytic cysteine on Acaa1b (C123) and Aldh9a1 (C312) and one of these cysteines is an annotated glutathionylated site (C69) on Fabp1 (highlighted in red in Fig. 2-3A), indicating that the function of these enzymes may be impaired by glyphosate or its metabolites *in vivo* (Chevillard et al., 2004; Dörmann et al., 1993; Riveros-Rosas et al., 2013). Acaa1b is a thiolase involved in peroxisomal fatty acid oxidation (Chevillard et al., 2004; Fidaleo et al., 2011). Aldh9a1 is an aldehyde dehydrogenase involved in the dehydrogenation of gamma-aminobutyraldehyde to the neurotransmitter gamma-aminobutyric acid (Lin et al., 1996). Fabp1 is a cytosolic fatty acid binding protein involved in fatty acid transport and is a central regulator of whole-body metabolic control (Thumser et al., 2014).

We also mapped lysine reactivity using the previously described dichlorotriazine-alkyne (DCTyne) probe (Shannon et al., 2014). In mapping lysine-reactivity with isoTOP-ABPP methods, we also identified 3 additional lysines annotated as known succinylation or acetylation sites on Hsd17b10 (K222), Cps1 (K1269), and Hbb-b1 (K145) that also showed light to heavy ratios >3 (Fig. 2-5; Appendix 5).

Mining deeper into our isoTOP-ABPP data, we also noticed that the peptides bearing catalytic cysteines for several thiolase family members also showed light to heavy ratios >1.5, including C92 of the mitochondrial fatty acid oxidation enzyme Acaa2, C94 of the peroxisomal fatty acid oxidation enzyme Scp2 (Shannon et al., 2014), and C92 of the cytosolic acetyl CoA acetyltransferase (Acat2) involved in biosynthesis of ketone bodies such as acetoacetyl-CoA (Fig. 2-3B). As Acaa2, Acat2, and Scp2 protein expression were not significantly reduced upon glyphosate-treatment (Fig. 2-4; Appendix 3), we interpret these data to indicate that these cysteines are directly modified by glyphosate metabolites. We further show that glyoxylate displaces IAyne labeling of pure Acaa1b, Acaa2, and Scp2 *in vitro* and that glyoxylate also inhibits thiolase activities of Acaa1b and Acaa2 (Fig. 2-3C; Fig. 2-3D). In addition, we performed isoTOP-ABPP analysis on *in vitro* glyoxylate cysteine-reactivity in mouse liver proteomes and show that glyoxylate shows very similar reactivity signatures to those observed with *in vivo* glyphosate treatment where we show that 141 of the 190 *in vivo* targets of glyphosate (74 %) show >1.5 light to heavy ratios. This signature includes Acaa1b, Acaa2, and Scp2 which show >1.5 light to heavy ratios for nearly every probe-labeled site on these proteins for both *in vitro* glyoxylate and *in vivo* glyphosate treatments (Fig. 2-6; Appendix 4).

Interestingly, Acaa1b, Acaa2, and Scp2 are all involved in mitochondrial or peroxisomal oxidation of long-chain and branched chain fatty acids (Haapalainen et al., 2006). Genetic deficiencies in these thiolases or of peroxisomal or mitochondrial fatty acid oxidation pathways have been shown to cause liver dysfunction, lipid dysregulation in the form of elevated triacylglycerols, ceramides, and sterols, and hepatic steatosis, likely because the fatty acids that are not oxidized are diverted into other lipid metabolism pathways (Kim, 2014; Klipsic et al., 2015; Lee et al., 2016; Mizuno et al., 2013; Wanders et al., 2016).

In Vivo Subacute Exposure to Glyphosate and its Reactive Metabolites Leads to Accumulation of Fatty Acids in Mouse Liver

We hypothesized that labeling of the catalytic cysteines on several thiolases involved in fatty acid oxidation would lead to the inhibition of these targets, impaired fatty acid oxidation, and diversion of fatty acids into other lipid pathways, including triglycerides, sterols, and ceramides. We next performed a lipidomic profiling experiment in which we quantitatively measured the levels of 192 lipid and sterol species in vehicle compared to glyphosate-treated mouse livers. We identified 62 distinct lipid species whose levels were significantly altered upon glyphosate treatment (Fig. 2-3E; Appendix 6). These changes included elevations in several neutral lipids, including monoacylglycerols (MAGs), diacylglycerols (DAGs), and triacylglycerols (TAGs). We also observed increases in cholesterol and cholesteryl oleate levels as well as other lipid classes. Our data reveal that glyphosate treatment at high doses causes major lipid dysregulation, including increases in fat storage and cholesteryl esters in mouse liver (Fig. 2-3E, Appendix 6). To further confirm our hypothesis, we also treated HEPG2 hepatocytes with glyoxylate and traced the fate of exogenously added isotopically labeled [^{13}C]palmitate and show that fatty acids are incorporated more into [^{13}C]palmitoyl carnitines (C16:0 AC) and [^{13}C]triacylglycerols (C16:0/C18:1/C16:0 TAG) (Fig. 2-3F). These data are all consistent with our premise that inhibition of fatty acid oxidation enzymes by glyphosate metabolite glyoxylate is associated with diversion of fatty acids into other lipid metabolism pathways.

Conclusion

We show here using both chemoproteomic and metabolomics approaches that glyphosate may be metabolized to reactive metabolites such as glyoxylate which may react with and inhibit many cysteine-reactive protein targets *in vivo* in mouse liver, including several fatty acid oxidation enzymes, which may be associated with elevations in liver triacylglycerols, cholesteryl esters, and other lipid species (Fig. 2-3G). We caution that the doses used in this study are much higher than any exposure levels encountered by the public and that further studies using lower doses studies in more relevant exposure paradigms will be necessary to fully evaluate these findings. Our data nonetheless shows that glyphosate may be biotransformed to reactive metabolites that broadly react with key cysteines and lysines across many proteins *in vivo*, several of which are likely to cause dysfunction of those proteins, and downstream physiological effects. Since the publication of this study additional work by the Gene Expression and Therapy Group at King's College has shown that environmentally relevant exposure to glyphosate over longer periods of time may lead to hepatotoxicity and impairment of fatty acid metabolism mirroring the mechanism of toxicity and pathophysiology we propose here (Mesnage et al., 2017). Furthermore, while we identify glyoxylate as one possible metabolite of glyphosate that could be reactive, there may be additional reactive metabolites which may explain the reactivity profiles observed in this study (Gohre et al., 1987). We also do not yet understand the tissues, cell-types, and enzymes responsible for glyphosate metabolism and we cannot necessarily rule out the gut microbiome as a source for glyphosate metabolism into glyoxylate.

Our study provides much-needed mechanistic insights into the potential toxicities and toxicological mechanisms associated with glyphosate. Our data here show that *in vivo* glyphosate exposure may lead to generation of reactive metabolites such as glyoxylate which may in-turn inhibit fatty acid oxidation enzymes. We also show that glyphosate treatment at high doses is associated with heightened levels of triglycerides and cholesteryl esters, and may potentially lead to corresponding metabolic disorders. Our results underscore the utility of using chemoproteomic platforms such as ABPP to map the proteome-wide reactivity and targets of environmental chemicals, towards understanding their mechanisms of toxicity.

Materials and Methods

Mice. Male C57BL/6 mice (6-8 weeks old) were acutely (2 hours) or subacutely (7 days) exposed by intraperitoneal (ip) injection to 200 mg/kg glyphosate (Sigma #45521) in a vehicle of PBS (10 µl/g mouse weight). Following exposure, mice were sacrificed by cervical dislocation, liver and serum was immediately removed and flash frozen in liquid nitrogen. Animal experiments were conducted in accordance with the guidelines of the Institutional Animal Care and Use Committee of the University of California, Berkeley.

Processing of Mouse Liver Proteomes. Tissues were homogenized in phosphate-buffered saline (PBS), followed by a 1000 x g centrifugation of the homogenate. The resulting supernatant was collected and used for subsequent assays. Protein concentrations were determined by BCA protein assay (Pierce™).

Cell Culture and Pure Proteins. HEK293T were cultured in DMEM media containing 10% FBS and maintained at 37ºC with 5% CO2. Pure human Acaa1b, Acaa2, and Scp2 proteins were purchased from Origene.

Activity Assays. Enzymatic activity of Acaa1b and Acaa2 was performed using the Fluorometric Acetyltransferase Activity Assay Kit (ABCAM ab204536). The assay was performed per the protocol with 0.4 µg pure protein, 3 mM glyoxylate and 100 nM acetoacetyl-CoA (Sigma A1625), fluorescence was measured at 380/520 ex/em on a SpectraMax i3x detection platform.

Glyoxylate Competition, Click Chemistry and In-Gel Fluorescence Imaging. Proteome samples diluted in PBS (50 µg in 50 µl PBS) were subjected to vehicle or glyoxylate treatment for 30 min at 37ºC, (glyoxylate solution was adjusted to pH 7 prior to incubation). Then, IAyne (10 µM, CHESS Gmbh # 3187) or IA-Rhodamine (IA-Rh, Life Technologies Corporation #T6006) labeling was performed for 30 min at 37ºC. Copper-catalyzed azide-alkyne cycloaddition 'click chemistry' was performed to append rhodamine-azide onto IAyne probe-labeled proteins using previously described methods (Nomura et al., 2010). Proteomes were separated on by SDS-PAGE and scanned using a ChemiDoc MP (Bio-Rad Laboratories, Inc). Inhibition of target labeling was assessed by densitometry using ImageLab software 5.2.1 (Bio-Rad Laboratories, Inc) and regressions were calculated by Prism (GraphPad Software).

Proteomic analysis. For ABPP analysis of IAyne labeled proteins, proteome samples from control or glyphosate treated mice were diluted (1 mg diluted in 500uL PBS) then labeled with IAyne (10 µM) for 1 hour at room temperature. We added the biotin azide to IAyne labeled proteins through click chemistry by sequential addition of tris(2-carboxyethyl)phosphine (1 mM, Sigma-Aldrich), copper (II) sulfate (1 mM, Sigma-Aldrich), tris[(1-benzyl-1H-1,2,3-triazol-4-yl)methyl]amine (34 µM, Sigma-Aldrich) using previously described methods (Nomura et al., 2010; Weerapana et al., 2010). After click reactions, proteomes were precipitated by centrifugation at 6500 x g, washed twice in ice-cold methanol, then denatured and resolubilized by heating in 1.2% SDS/PBS to 85ºC for 5 minutes. Insoluble components were precipitated by centrifugation at 6500 x g and soluble proteome was diluted in 5 ml PBS, for a final concentration of 0.2% SDS. Labeled proteins were bound to avidin-agarose beads (170 µL resuspended beads/sample, Thermo Pierce) while rotating overnight at 4ºC. Bead-linked proteins were enriched by washing three times each in PBS and water, then resuspended in 6 M urea/PBS (Sigma-Aldrich) and reduced in dithiothreitol (1 mM, Sigma-Aldrich), alkylated with iodoacetamide (18 mM, Sigma-Aldrich), then washed and resuspended in 2 M urea and trypsinized overnight with 0.5 µg/µl sequencing grade trypsin (Promega). Tryptic peptides were diluted in water and acidified with final concentration of 5% formic acid (1.2 M, Spectrum).
For isoTOP-ABPP analysis, proteomes labeled with IAyne or DCTyne (100 µM) for 1 h at room temperature, and were subsequently treated with 100 µM isotopically light (control) or heavy (treated) TEV-biotin and click chemistry was performed as previously described (Nomura et al., 2010; Weerapana et al., 2010). Proteins were precipitated over one hour and pelleted by centrifugation at 6500 x g. Proteins were washed 3 times with cold methanol then denatured and resolubilized by heating in 1.2% SDS/PBS to 85ºC for 5 minutes. Insoluble components were precipitated by centrifugation at 6500 x g and soluble proteome was diluted in 5 ml PBS, for a final concentration of 0.2% SDS. Labeled proteins were bound to avidin-agarose beads (170 µL resuspended beads/sample, Thermo Pierce) while rotating overnight at 4ºC. Bead-linked proteins were enriched by washing three times each in PBS and water, then resuspended in 6 M urea/PBS (Sigma-Aldrich) and reduced in DTT (1 mM, Sigma-Aldrich), alkylated with iodoacetamide (18 mM, Sigma-Aldrich), then washed and resuspended in 2 M urea/PBS with 1mM calcium chloride and trypsinized overnight with 0.5 µg/µl sequencing grade trypsin (Promega). Tryptic pepetides were discarded and beads were washed three times each in PBS and water, then washed with one wash of TEV buffer containing 1 µM DTT. TEV-biotin tag was digested overnight in TEV buffer containing 1 µM DTT and 5 µL Ac-TEV protease at 29ºC. Peptides were diluted in water and acidified with final concentration of 5% formic acid (1.2 M, Spectrum).

Shotgun proteomic samples were prepared by precipitating proteomes using 100% trichloroacetic acid (sigma T6399), which was added to a final concentration of 20%. Samples were incubated at -80ºC overnight to precipitate proteins and then centrifuged at 4ºC for 10 min at 10,000 x g. The pellet was washed 3 times with ice cold 0.1 M HCl in 90% acetone, air-dried and then resuspended in 30 µL 8M urea in PBS. Protease max (30 µL of 0.2% in 100 mM ammonium bicarbonate) was added to samples, followed by vortexing and dilution with 40 µL ammonium bicarbonate. TCEP was added to a final concentration of 10 mM and then samples were incubated for 30 min at 60ºC, followed by addition of iodoacetamide to a final concentration of 12.5 mM, and samples were incubated in foil at room temp for 30 min. Samples were diluted with 100 µL of PBS and 1.2 µL of 1% protease max was added and vortexed well, after which 2 µg sequencing trypsin was added and samples incubated overnight at 37ºC. Trypsinized samples were acidified with 5% final concentration formic acid and centrifuged at 13200 rpm for 30min.

Peptides from all proteomic experiments were pressure-loaded onto a 250 mm i.d. fused silica capillary tubing packed with 4 cm of Aqua C18 reverse-phase resin (phenomenex # 04A-4299) which was previously equilibrated on an Agilent 600 series HPLC using gradient from 100% buffer A to 100% buffer B over 10 min, followed by a 5 min wash with 100% buffer B and a 5 min wash with 100% buffer A. The samples were then attached using a MicroTee PEEK 360 µm fitting (Thermo Fisher Scientific #p-888) to a 10 cm laser pulled column of 100 mm fused silica capillary packed with 10 cm Aqua C18 reverse-phase resin for shotgun proteomics and ABPP studies, or to a 13 cm laser pulled column packed with 10 cm Aqua C18 reverse-phase resin and 3 cm of strong-cation exchange resin (Multidimensional Protein Identification Technology (MudPIT) column) for isoTOP-ABPP studies. Samples were analyzed using an Orbitrap Q Exactive Plus mass spectrometer (Thermo Fisher Scientific). Data was collected in data-dependent acquisition mode with dynamic exclusion enabled (60 s). One full MS (MS1) scan (400-1800 m/z) was followed by 15 MS2 scans (ITMS) of the nth most abundant ions. Heated capillary temperature was set to 200ºC and the nanospray voltage was set to 2.75kV.
For 1D runs for shotgun proteomics and ABPP studies, samples were run using a two-hour gradient from 5 % to 80 % acetonitrile with 0.1 % formic acid at 100 nl/min. For MudPIT runs, samples were run with the following 5-step MudPIT program (using 0%, 10%, 25%, 80%, and 100% salt bumps). Data was extracted in the form of MS1 and MS2 files using Raw Extractor 1.9.9.2 (Scripps Research Institute) and searched against the Uniprot mouse database using ProLuCID search methodology in IP2 v.3 (Integrated Proteomics Applications, Inc) (Xu et al., 2015). Cysteine residues were searched with a static modification for carboxyaminomethylation (+57.02146) and up to two differential modifications for either the light or heavy TEV tags (+464.28596 or +470.29977, respectively). Peptides were required to have at least one tryptic end and to contain the TEV modification. ProLUCID data was filtered through DTASelect to achieve a peptide false-positive rate below 1%.

Metabolomic profiling. Nonpolar lipid metabolites from the liver or serum of *in vivo* treated mice were extracted in 3 ml of 2:1 chloroform:methanol and 1 ml of PBS with inclusion of internal standards C12:0 monoalkylglycerol ether (MAGE) (10 nmol, Santa Cruz Biotechnology) and pentadecanoic acid (10 nmol, Sigma-Aldrich). Organic and aqueous layers were separated by centrifugation at 1000 x g for 5 min and the organic layer was collected, dried under a stream of N2 and dissolved in 120 µl chloroform. An aliquot was injected onto LC/MS. Polar metabolites, such as glyphosate, AMPA, and glyoxylate, were extracted in 500 µl of 40:40:20 (acetonitrile:methanol:water) with inclusion of internal standard d3N15-serine (Cambridge Isotope Laboratories, Inc. #DNLM-6863). Samples were centrifuged at 10,000 x g for 10 min and an aliquot of the supernatant was injected onto LC/MS. Metabolites were separated by liquid chromatography as previously described (Louie et al., 2016). MS analysis was performed with an electrospray ionization (ESI) source on an Agilent 6430 QQQ LC-MS/MS (Agilent Technologies). The capillary voltage was set to 3.0 kV, and the fragmentor voltage was set to 100 V. The drying gas temperature was 350oC, the drying gas flow rate was 10 l/min, and the nebulizer pressure was 35 psi. Metabolites were identified by SRM of the transition from precursor to product ions at associated optimized collision energies and retention times as previously described (Benjamin et al., 2013; Louie et al., 2016). All metabolites measured in this paper including lipid metabolites and glyphosate and glyphosate metabolites were subjected to fragmentation analysis to yield the specific SRM targeted LC-MS/MS programs and we have confirmed that the retention times of standards matches the retention times of metabolites found in tissues. For lipidomics, SRM programs and confirmation of retention times were already performed in previous studies (Benjamin et al., 2013; Louie et al., 2016). For glyphosate and its metabolites, the SRMs and retention times used are noted in Fig. 2-1A. Metabolites were quantified by integrating the area under the curve, then normalized to internal standard values and tissue weight. Metabolite levels are expressed as relative abundances as compared to controls.

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Figure 2-1.

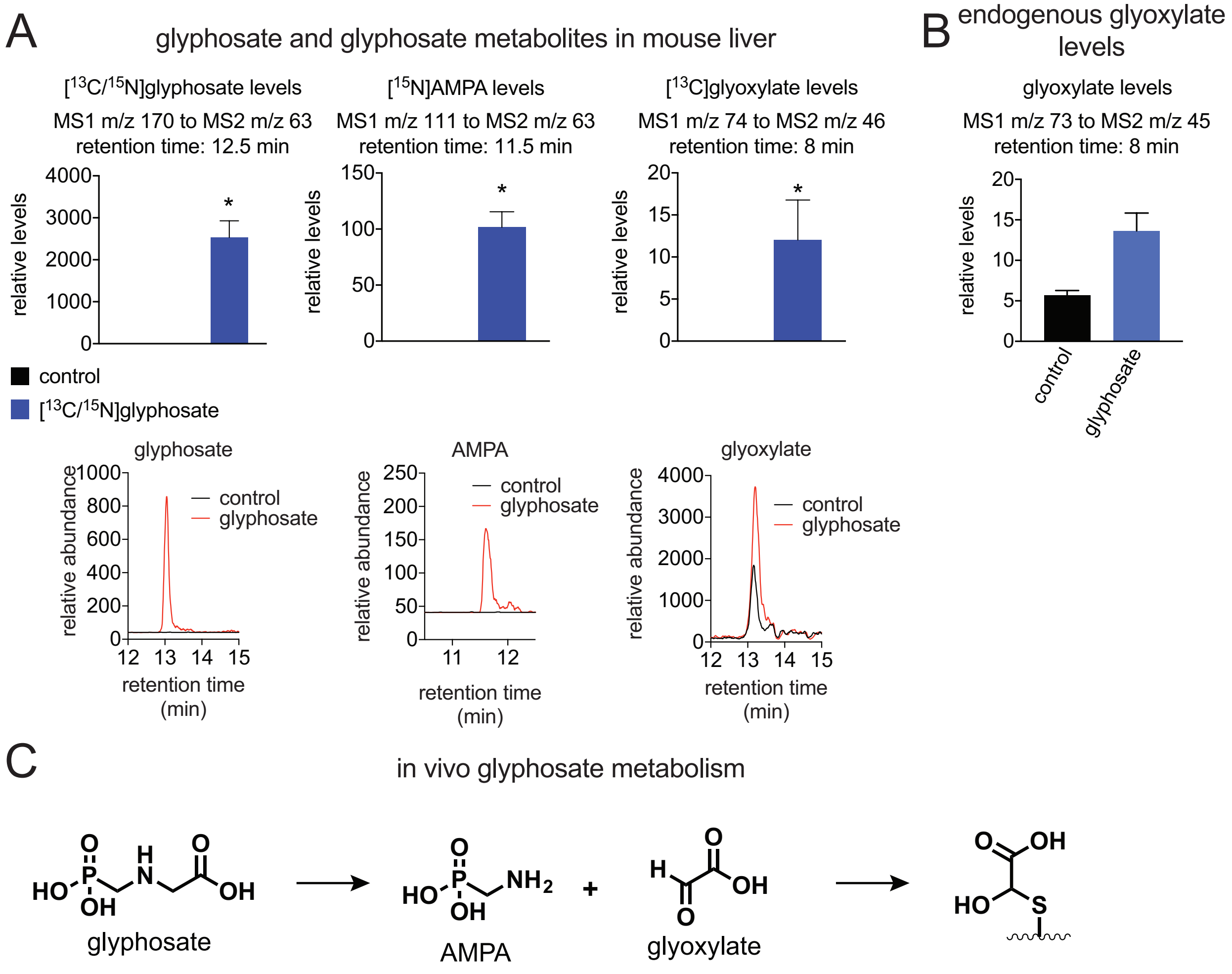

Figure 2-1. Metabolism of glyphosate in mice. (A) Mice were treated with [^{13}C/^{15}N]glyphosate (200 mg/kg ip, once per day for 7 days) after which livers were harvested and SRM-based LC-MS/MS was used to determine glyphosate, AMPA, and glyoxylate levels. Representative peaks and retention times are shown below relative levels of labelled glyphosate and proposed metabolites. (B) Mice were treated with nonisotopic glyphosate (200 mg/kg ip once per day for 7 days) after which nonisotopic total glyoxylate levels were measured by SRM-based LC-MS/MS. (C) Our data point to metabolism of glyphosate to AMPA and glyoxylate. Gloxylate can potentially react with nucleophilic amino acid hotspots such as cysteines and lysines. Data are presented as mean ± SEM, n=4-5/group. Significance is presented as *p<0.05 compared to vehicle-treated controls.

Figure 2-2.

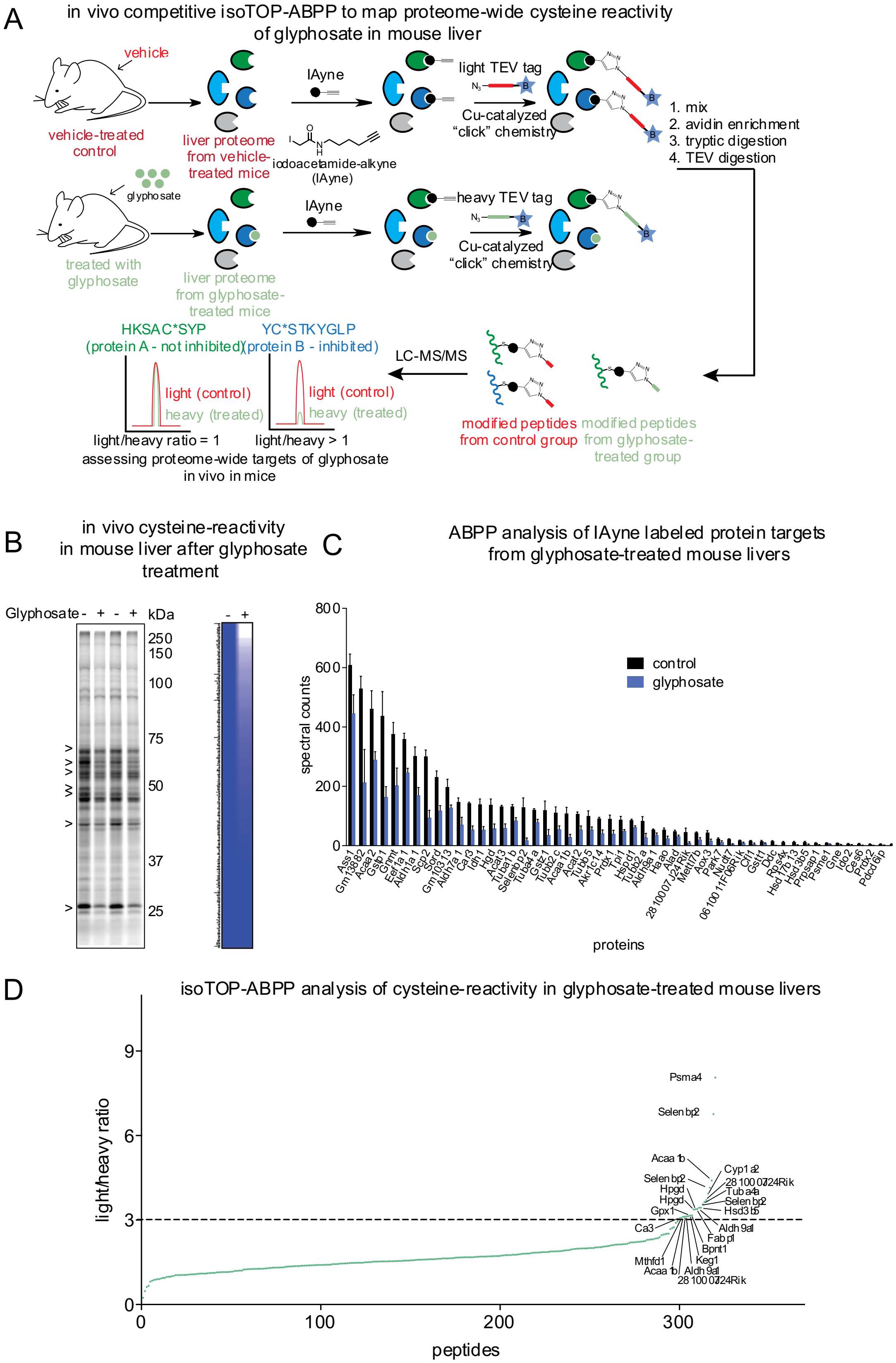
A
in vivo competitive isoTOP-ABPP to map proteome-wide cysteine reactivity of glyphosate in mouse liver
vehicle
vehicle-treated control
liver proteome from vehicle-treated mice
IAyne
iodoacetamide-alkyne (IAyne)
light TEV tag
Cu-catalyzed "click" chemistry
1. mix
2. avidin enrichment
3. tryptic digestion
4. TEV digestion
glyphosate
treated with glyphosate
liver proteome from glyphosate-treated mice
IAyne
heavy TEV tag
Cu-catalyzed "click" chemistry
HKSAC*SYP (protein A - not inhibited)
YC*STKYGLP (protein B - inhibited)
LC-MS/MS
light (control)
heavy (treated)
light (control)
heavy (treated)
light/heavy ratio = 1
light/heavy > 1
assessing proteome-wide targets of glyphosate in vivo in mice
modified peptides from control group
modified peptides from glyphosate-treated group
B
in vivo cysteine-reactivity in mouse liver after glyphosate treatment
Glyphosate - + - +
kDa
250
150
100
75
50
37
25
- +
C
ABPP analysis of IAyne labeled protein targets from glyphosate-treated mouse livers
spectral counts
800
600
400
200
0
control
glyphosate
Ass1
Gm13882
Acaa2
Gstp1
Gnmt
Eef1a1
Aldh1a1
Scp2
Sord
Gm10313
Aldh7a1
Car3
Idh1
Hgd
Acat3
Tuba1b
Selenbp2
Tuba4a
Gstz1
Tubb2c
Acaa1b
Acat2
Tubb5
Akr1c14
Prdx1
Tpi1
Hspd1
Tubb2a
Aldh9a1
Haao
Alad
2810007J24Rik
Mettl7b
Aox3
Park7
Nudt7
0610011F06Rik
Cfl1
Gstt1
Ddc
Rps4x
Hsd17b13
Hsd3b5
Prpsap1
Psme1
Gne
Ido2
Ces6
Prdx2
Pdcd6ip
proteins
D
isoTOP-ABPP analysis of cysteine-reactivity in glyphosate-treated mouse livers
light/heavy ratio
9
6
3
0
Psma4
Selenbp2
Acaa1b
Cyp1a2
Selenbp2
2810007J24Rik
Hpgd
Tuba4a
Hpgd
Selenbp2
Gpx1
Hsd3b5
Ca3
Aldh9a1
Fabp1
Bpnt1
Mthfd1
Keg1
Acaa1b
Aldh9a1
2810007J24Rik
0
100
200
300
peptides

Figure 2-2. ABPP analysis of *ex vivo* cysteine reactivity in mouse liver from *in vivo* glyphosate exposure. (A) Workflow for isoTOP-ABPP analysis. Mice were treated with glyphosate (200 mg/kg ip, once per day for 7 days), and liver proteomes were treated with IAyne (100 μM) ex vivo, followed by click-chemistry mediated appendage of a biotin tag bearing a TEV protease cleavage sequence and an isotopically light or heavy valine. Proteomes were combined, avidin enriched, tryptically digested, and modified peptides were isolated by TEV digestion followed by quantitative proteomic analysis. (B) Gel-based ABPP analysis of cysteine reactivity profiling of liver proteomes from mice treated in vivo with vehicle or glyphosate. Proteomes were labeled with IAyne followed by click-chemistry-mediated appendage of rhodamine-azide or biotin-azide, followed by in-gel fluorescence, or avidin-enrichment and proteomic analysis. Arrows are pointing to IAyne labeled bands that are lighter in glyphosate-treated groups. Shown is a representative gel and a heatmap showing IAyne-enriched protein targets, where dark blue indicates relative protein expression in control compared to that of glyphosate-treated mice. Light blue or white indicates proteins that showed reduced IAyne enrichment. (C) Proteins that showed significantly ($p<0.05$) reduced IAyne enrichment in livers from glyphosate-treated mice compared to vehicle-treated controls. (D) isoTOP-ABPP analysis of IAyne labeled peptides from vehicle-treated (light) and glyphosate-treated (heavy) mouse livers. Protein names for peptides showing light-to-heavy ratio >3 are designated. Data in (C) is presented as mean ± SEM, n=3 mice/group.

Figure 2-3.

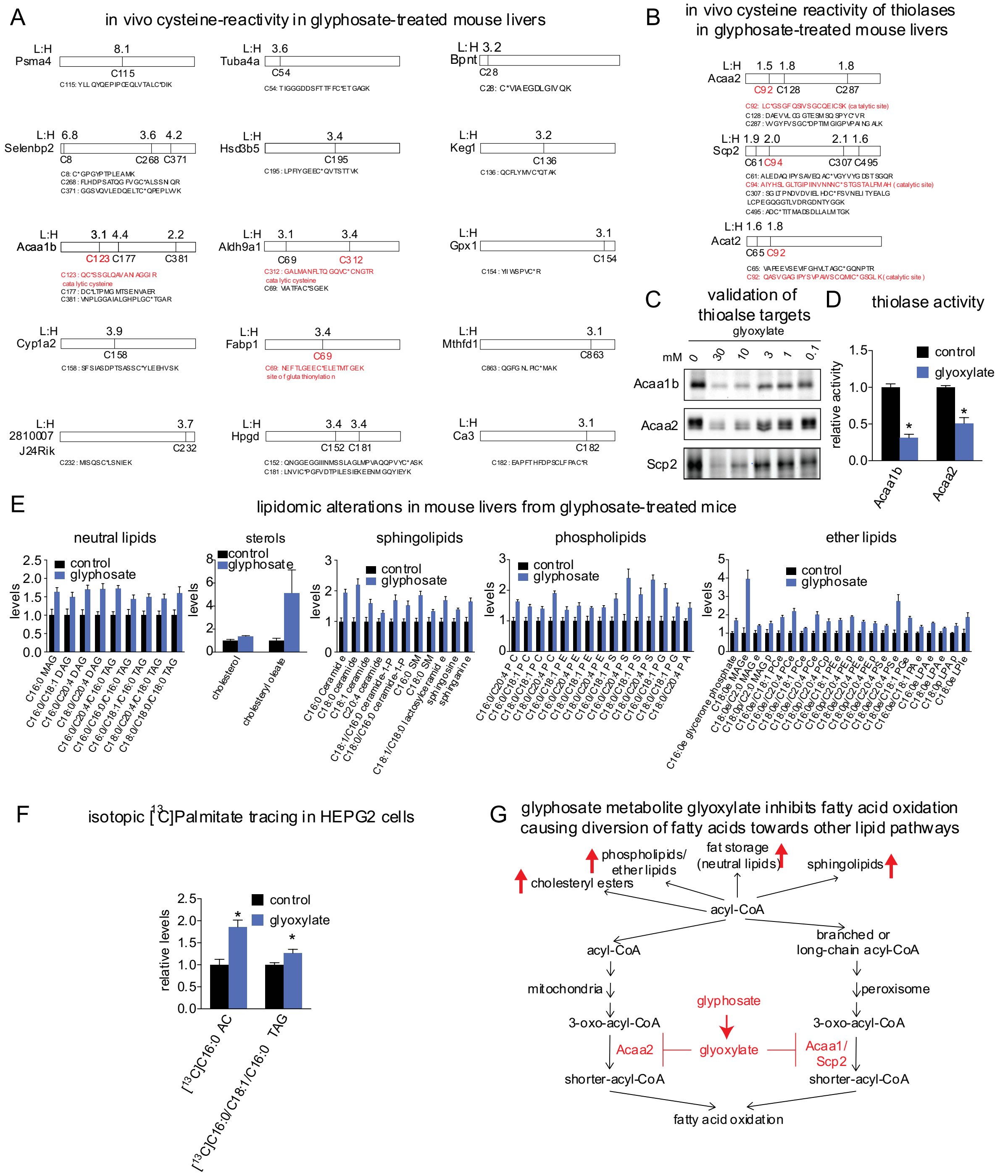

Figure 2-3. *In vivo* glyphosate targets and biochemical changes in mouse liver. (A) Proteins from specific peptides that showed >3 light to heavy ratios from isoTOP-ABPP analysis of mouse livers from vehicle (light) or glyphosate (heavy) (200 mg/kg ip, once per day over 7 days)-treated mice. Specific cysteines labeled by IAyne, their corresponding tryptic peptide sequences and sites of modification, and light to heavy ratios on each protein are shown.

Highlighted in red are catalytic cysteines (for Acaa1b and Aldh9a1) and site of cysteine glutathionylation (for Fabp1). (B) Shown is an equivalent analysis for other members of the thiolase family. (C) Glyoxylate competition study against IAyne labeling of pure human Acaa1b, Acaa2, and Scp2 analyzed by in-gel fluorescence. (D) Thiolase activity assay using pure mouse Acaa1b and Acaa2 protein showing that incubation of pure protein with gloxylate (3 mM) inhibits thiolase activity. (E) Significant changes ($p < 0.05$) in metabolites from lipidomic profiling of vehicle- versus glyphosate-treated mouse livers. (F) Isotopic [13C]C16:0 FFA tracing in HEPG2 cells. Cells were pretreated with glyoxylate (1 mM) for 1 hr prior to labeling cells with [13C]C16:0 FFA (10 mM) for 6 hr. Isotopically labeled triglycerides were measured using SRM-based LC-MS/MS. (G) Diagram showing how glyphosate metabolites inhibit thiolases involved in peroxisomal and mitochondrial fatty acid oxidation, leading to accumulation of fatty acids in other lipid and sterol species. Glyoxylate cysteine-reactivity data are shown in Figure 2-6 and Appendix 4. Data in (E and F) are presented as the mean ± SEM, n = 5/group. Significance in (F) is presented as *$p < 0.05$ compared with vehicle-treated control.

Figure 2-4.

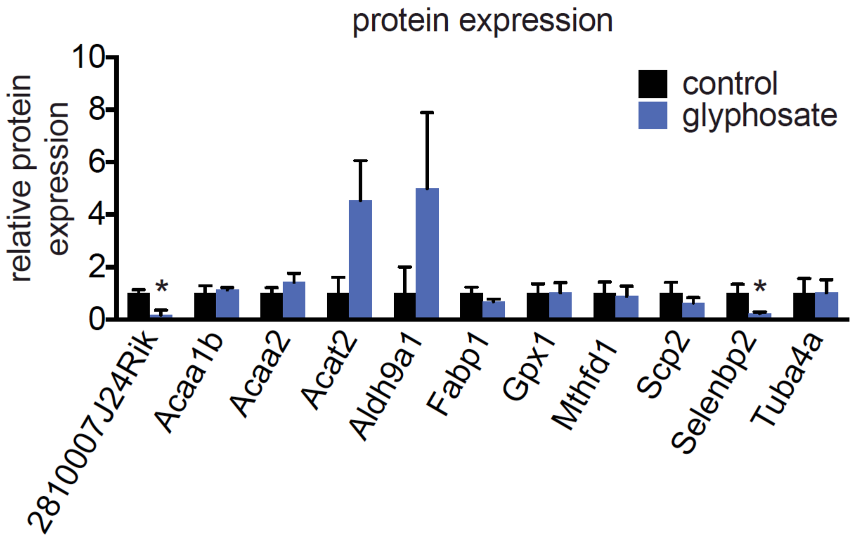

Figure 2-4. Protein expression profiling of glyphosate targets. Protein expression profiling of selected glyphosate protein targets by shotgun proteomic analysis by LC-MS/MS from mice treated with vehicle or glyphosate (200 mg/kg, ip, once per day over 7 days). Raw data is presented in Appendix 3. These selected proteins were those proteins that were detected by shotgun proteomics and showed >3 light:heavy ratio from isoTOP-ABPP analysis. Protein expression levels were determined by spectral counting. Data are presented as mean ± SEM, n=4-5 mice/group. *$p<0.05$ refers to those proteins with significantly lower protein expression in glyphosate-treated mice compared to vehicle-treated controls.

Figure 2-5.

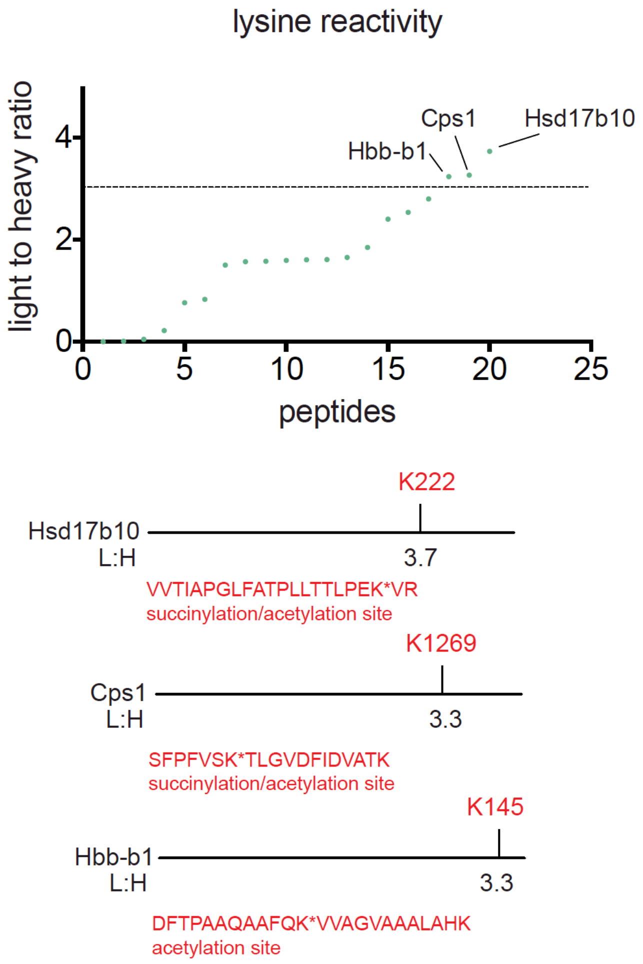

Figure 2-5. isoTOP-ABPP analysis of DCTyne lysine-reactivity in mouse livers from mice treated with vehicle or glyphosate. Proteomes were labeled with DCTyne, followed by appendage of a biotin-azide handle bearing a TEV recognition sequence and isotopically light (vehicle-treated) or heavy (glyphosate-treated) valine, combining of control and treated proteomes in a 1:1 ratio, avidin enrichment, tryptic digestion, release of modified peptides by TEV protease, and analysis by LC-MS/MS. Shown are light:heavy ratios of modified peptides and highlighted are those proteins and specific modified peptides that showed >3 light:heavy ratio. Data and ratios are from 3 mice/group. Data for this figure is presented in Appendix 5.

Figure 2-6.

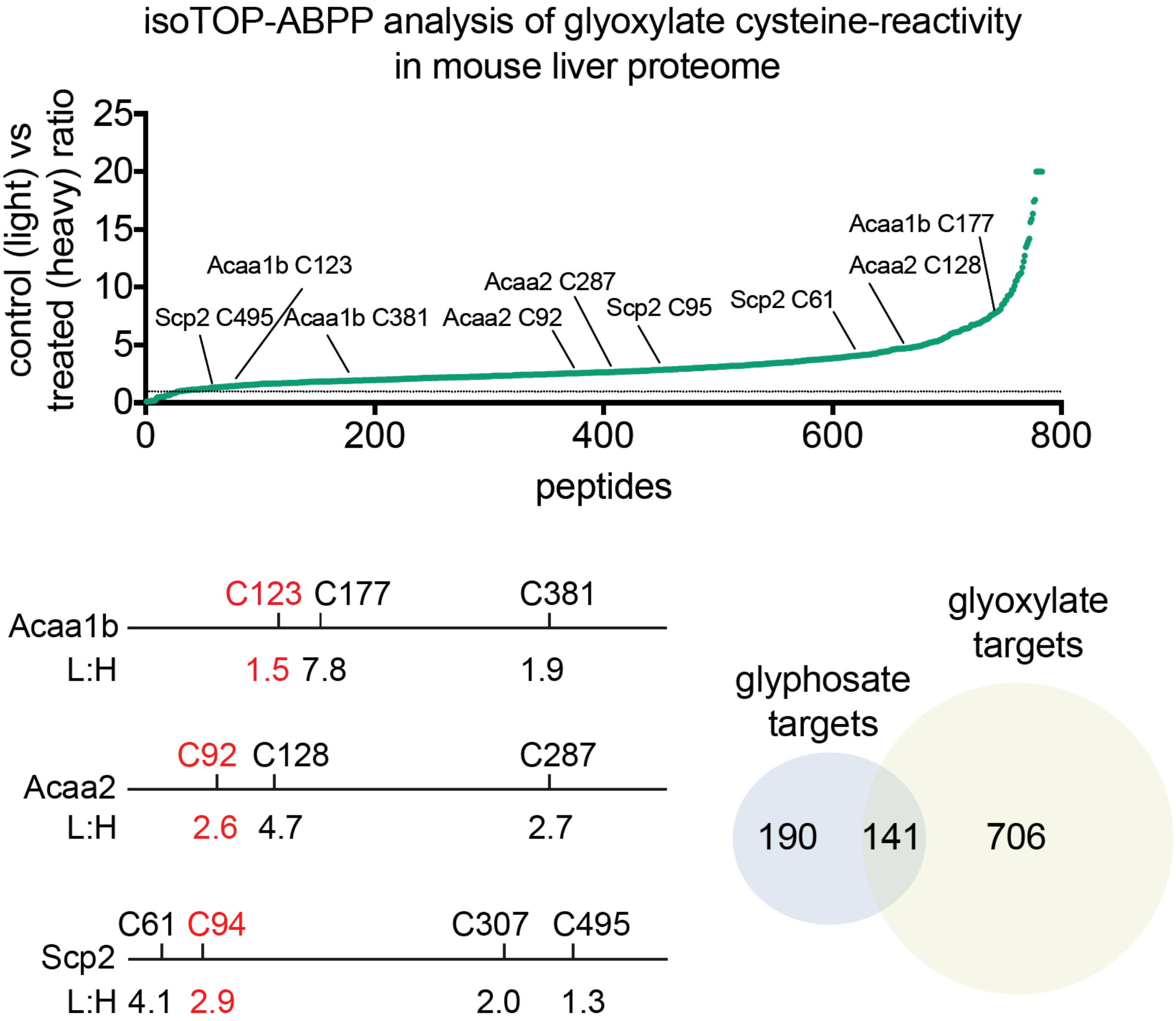

Figure 2-6. isoTOP-ABPP analysis of glyoxylate cysteine-reactivity in mouse livers. Proteomes were pretreated with glyoxylate (3 mM, 30 min) prior to labeling with IAyne, followed by appendage of a biotin-azide handle bearing a TEV recognition sequence and isotopically light (vehicle-treated) or heavy (glyphosatetreated) valine, combining of control and treated proteomes in a 1:1 ratio, avidin enrichment, tryptic digestion, release of modified peptides by TEV protease, and analysis by LC-MS/MS. Shown are average light:heavy ratios of modified peptides and modified peptides of Acaa1b, Acaa2, and Scp2 and their light to heavy ratios. Raw data is presented in Appendix 4. Highlighted in red are the catalytic cysteines of Acaa1b, Acaa2, and Scp2. Also shown graphically are the number of glyphosate *in vivo* targets (190), glyoxylate *in vitro* targets (706), and overlapping targets (141) in mouse liver that showed >1.5 light:heavy ratios. Data and average ratios are from n=3 experiments.

Chapter Three: Conclusions

The aim of this dissertation work has been to contribute new perspectives on the potential applications of chemoproteomics platforms and strategies for assessing toxicity of environmental chemicals, pharmaceuticals and endogenous metabolites. The rise of omics-based tools, including chemoproteomics, has allowed for greater understanding of the complexity of interactions that small molecules have within biological systems. These new technologies provide a promise of faster and better analysis of these complex interactions and a more complete picture of how the many exogenous compounds, both environmental chemicals and pharmaceutics, we are exposed to are affecting biological systems and human health outcomes. In this dissertation we have looked at the use of chemoproteomic platforms, as well as complementary omics technologies, to map toxicological mechanism, find off targets and assess selectivity of environmental chemicals with a focus on the herbicide glyphosate.

In chapter one we discussed the diverse uses of chemoproteomics platforms for understanding the potential toxicity of pharmaceuticals and environmental chemicals. The intrinsic and perceived risks associated with covalently acting therapeutics, combined with the growth of this pharmaceutical area, requires new efforts to better assess the selectivity of these compounds. The use of ‘clickable’ drug analogs, such as those developed to profile selectivity of covalently acting kinase or FAAH inhibitors showcase how these technologies could be used as part of the drug development pipeline. These examples, along with others discussed in chapter one, demonstrate the usefulness of chemoproteomic platforms as part of covalent drug design and discovery.

The use of chemoproteomics platforms to assess the off-targets of environmental chemicals was a second area of interest for chapter one. In reviewing activity-based protein profiling efforts for pesticides, including organophosphates, carbamates and the fungicide chlorthalonil, it was illustrated that direct targets of environmental electrophiles could be identified through these novel technologies. Through these and other projects presented in chapters one and two we show that chemoproteomic platforms, including ABPP, provide an innovative tool in examining the proteome wide reactivity of electrophilic chemicals to covalently modify proteins. Additionally, the works reviewed in chapter one provide important examples of innovative strategies for toxicity assessment using technologies such as ABPP, for both assessing and improving the selectivity of covalently acting exogenous compounds towards the development of safer environmental chemicals and pharmaceutics in the future.

With a perspective of the benefits of incorporating chemoproteomic tools into toxicological analysis we demonstrate this approach as applied to the herbicide glyphosate. Utilizing integrated omics technologies, including lipidomic and chemoproteomic profiling, we first showed that glyphosate is metabolized *in vivo* in mouse liver to AMPA and glyoxylate. Having identified a reactive, electrophilic metabolite of glyphosate we used quantitative chemoproteomic analysis to map cysteine-reactivity of glyphosate and its reactive metabolites in mouse liver proteome. Ultimately using these tools to identify the protein targets Acaa1b, Acaa2, and Scp2, all of which are involved in mitochondrial or peroxisomal fatty acid oxidation. By pairing chemoproteomics with lipidomic platforms we were able to both identify the direct targets of glyphosate and its reactive metabolite glyoxylate, as well as the downstream pathophysiological effects of dysregulation of fatty acid metabolism caused by subacute treatment with glyphosate *in vivo* in mice. Our studies into the direct protein targets of glyphosate and its bioactive metabolites *in vivo* provide much needed mechanistic insights into the toxicity of glyphosate as it relates to fatty acid metabolism and reinforced the utility of chemoproteomic platforms for the study of toxicology.

Establishing new approaches to assessing toxicity of environmental chemicals, pharmaceuticals and endogenous metabolites will continue to be a crucial area of research as the number of exogenous compounds we are exposed to increases. We have shown in the research presented in chapters one and two that chemoproteomic platforms, including IsoTOP-ABPP, provide a useful way to identify covalent binding of small molecules in and assess the selectivity and off-targets, and aid in determining the mechanism of toxicity of environmental chemicals and pharmaceuticals in complex proteomes. We expect that future areas of interest in the application of chemoproteomics to toxicology research will include studies looking at known or predicted covalently acting metabolites formed during phase I and phase II detoxification, as well as assessing the selectivity of environmental electrophiles in a larger variety of biological systems and applications including agrochemical development.

In conclusion, chemoproteomics can be a useful tool in mapping the mechanism of action, identifying off-targets, in addition to assessing the selectivity and direct protein binding of covalently acting environmental chemicals and pharmaceuticals. Our research with the herbicide glyphosate has a shown that the chemoproteomic approach isoTOP-ABPP can be used to establish the direct targets of reactive metabolites *in vivo* and when paired with complementary omics approaches can help determine potential mechanisms of toxicity. This research, along with the many other research efforts discussed in chapter one show that these approaches can provide useful tools in future practical toxicology applications.

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Appendices

Appendix 1. ABPP chemoproteomic profiling of *in vivo* glyphosate reactivity in mouse liver

Enrichment of IAyne-labeled proteins from livers from mice treated with vehicle or glyphosate. Proteomes were labeled with IAyne, followed by appendage of biotin-azide by click-chemistry, avidin enrichment, tryptic digestion, and analysis by LC-MS/MS. Table 1 shows enriched IAyne-labeled proteins that show >3 spectral counts, and Table 2 shows those proteins that showed significantly less IAyne labeling in glyphosate-treated mouse livers compared to their control counterparts. These tables relate to Figure 2-2C.

Table 1. Enriched IAyne-labeled Proteins That Show >3 Spectral Counts

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
0610011F06Rik UPF0585 protein C16orf13 homolog	0610011F06Rik	18.3	0.3	9.0	2.9	0.0163
1190003J15Rik 5-hydroxyisourate hydrolase	1190003J15Rik	12.0	3.5	5.0	3.6	0.1183
2810007J24Rik Sulfotransferase-like protein 1	2810007J24Rik	45.3	13.9	8.7	4.7	0.0332
3110049J23Rik Phenazine biosynthesis-like domain-containing protein 2	3110049J23Rik	4.3	4.3	10.7	6.4	0.2284
4931406C07Rik Ester hydrolase C11orf54 homolog	4931406C07Rik	8.3	2.3	3.3	2.4	0.1049
Aars Alanyl-tRNA synthetase, cytoplasmic	Aars	8.3	0.3	7.7	3.7	0.4334
Abat Isoform 1 of 4-aminobutyrate aminotransferase, mitochondrial	Abat	5.0	1.0	6.7	4.7	0.3723
Abcd3 ATP-binding cassette sub-family D member 3	Abcd3	16.7	5.2	5.7	5.7	0.1136
Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase B, peroxisomal	Acaa1b	108.7	20.7	28.7	9.4	0.0123
Acaa2 Putative uncharacterized protein	Acaa2	461.7	60.7	290.3	26.6	0.0305
Acadm Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadm	8.0	0.6	11.0	1.5	0.0700
Acads Putative uncharacterized protein	Acads	11.7	4.3	15.0	0.6	0.2441
Acadvl Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadvl	11.3	2.7	18.3	2.4	0.0633
Acat1 Acetyl-CoA acetyltransferase, mitochondrial	Acat1	123.3	12.1	97.7	20.3	0.1693
Acat2 Acetyl-CoA acetyltransferase, cytosolic	Acat2	107.3	6.3	53.0	13.5	0.0110
Acat3 acetyl-Coenzyme A acetyltransferase 3	Acat3	132.3	3.7	60.0	13.6	0.0034
Acly Putative uncharacterized protein	Acly	49.3	9.8	42.0	12.7	0.3361
Aco1 Cytoplasmic aconitase	Aco1	13.3	2.2	11.0	4.0	0.3178
Acox1 Putative uncharacterized protein	Acox1	28.3	14.7	46.7	17.7	0.2347
Acox2 peroxisomal acyl-coenzyme A oxidase 2	Acox2	14.3	4.2	12.7	7.0	0.4237
Acsf2 Acyl-CoA synthetase family member 2, mitochondrial	Acsf2	25.3	6.4	22.0	4.6	0.3463
Acsl1 long-chain-fatty-acid--CoA ligase 1	Acsl1	28.0	12.4	27.0	3.0	0.4707
Acsl5 Long-chain-fatty-acid--CoA ligase 5	Acsl5	3.7	2.0	5.0	3.6	0.3817
Acsm1 Isoform 1 of Acyl-coenzyme A synthetase ACSM1, mitochondrial	Acsm1	28.7	3.8	31.3	5.9	0.3620
Acta1 Actin, alpha skeletal muscle	Acta1	11.7	11.7	0.0	0.0	0.1870
Actb Actin, cytoplasmic 1	Actb	72.3	40.7	76.0	40.3	0.4760

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Actc1 Putative uncharacterized protein	Actc1	14.3	14.3	24.0	12.2	0.3174
Actg1 Putative uncharacterized protein	Actg1	34.7	34.7	19.0	19.0	0.3561
Adh1 Alcohol dehydrogenase 1	Adh1	299.3	37.8	286.0	4.6	0.3718
Adh5 Alcohol dehydrogenase class-3	Adh5	42.3	8.4	41.3	10.5	0.4720
Adk Isoform Long of Adenosine kinase	Adk	92.7	12.0	65.0	17.4	0.1306
Adsl Adenylosuccinate lyase	Adsl	5.0	1.2	0.0	0.0	0.0062
Agl amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Agl	15.0	5.7	14.3	5.5	0.4684
Ahcy Adenosylhomocysteinase	Ahcy	72.7	9.3	62.7	15.5	0.3050
Akr1c12 aldo-keto reductase family 1, member C12	Akr1c12	7.7	3.9	8.0	4.4	0.4787
Akr1c13 Aldo-keto reductase family 1 member C13	Akr1c13	3.7	3.7	3.0	3.0	0.4474
Akr1c14 Putative uncharacterized protein	Akr1c14	91.7	4.1	41.7	11.6	0.0076
Akr1c19 aldo-keto reductase family 1, member C19	Akr1c19	5.3	2.7	4.7	2.9	0.4370
Akr1c6 Estradiol 17 beta-dehydrogenase 5	Akr1c6	76.0	4.0	89.3	11.1	0.1617
Akr1d1 3-oxo-5-beta-steroid 4-dehydrogenase	Akr1d1	12.0	3.6	10.7	2.6	0.3896
Akr7a5 aflatoxin B1 aldehyde reductase member 2	Akr7a5	11.7	4.1	7.7	3.9	0.2599
Alad Delta-aminolevulinic acid dehydratase	Alad	49.0	3.2	31.7	3.7	0.0118
Aldh1a1 Retinal dehydrogenase 1	Aldh1a1	301.7	31.1	170.0	26.0	0.0157
Aldh1a7 Aldehyde dehydrogenase, cytosolic 1	Aldh1a7	86.3	11.8	53.3	10.7	0.0531
Aldh1b1 Aldehyde dehydrogenase X, mitochondrial	Aldh1b1	6.3	1.5	7.7	2.4	0.3299
Aldh1l1 10-formyltetrahydrofolate dehydrogenase	Aldh1l1	160.3	27.0	123.7	16.9	0.1568
Aldh2 Aldehyde dehydrogenase, mitochondrial	Aldh2	111.0	24.2	148.3	3.8	0.1011
Aldh4a1 delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor	Aldh4a1	39.3	8.6	37.0	11.6	0.4398
Aldh6a1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Aldh6a1	71.3	9.7	63.0	3.5	0.2316
Aldh7a1 Isoform 1 of Alpha-aminoadipic semialdehyde dehydrogenase	Aldh7a1	147.0	14.1	71.0	24.9	0.0283
Aldh8a1 Aldehyde dehydrogenase family 8 member A1	Aldh8a1	43.0	6.6	41.7	7.6	0.4505
Aldh9a1 4-trimethylaminobutyraldehyde dehydrogenase	Aldh9a1	53.3	2.8	36.0	7.0	0.0418
Aldob Fructose-bisphosphate aldolase B	Aldob	109.0	23.6	148.0	18.6	0.1323
Amdhd1 Probable imidazolonepropionase	Amdhd1	11.0	0.0	11.3	2.3	0.4467
Aox3 Aldehyde oxidase 1	Aox3	43.7	7.0	16.0	6.2	0.0208
Arf4 20 kDa protein	Arf4	13.0	3.8	11.0	4.5	0.3756
Asl Argininosuccinate lyase	Asl	6.3	2.0	6.7	2.0	0.4565
Aspg 60 kDa lysophospholipase	Aspg	4.3	2.2	4.0	2.0	0.4579
Ass1 Argininosuccinate synthase	Ass1	608.7	37.4	446.7	61.7	0.0441
Atl3 Isoform 1 of Atlastin-3	Atl3	6.7	1.2	5.7	3.0	0.3850
Atp5a1 ATP synthase subunit alpha, mitochondrial	Atp5a1	35.0	16.3	34.0	4.6	0.4779

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Atp5g2 ATP synthase lipid-binding protein, mitochondrial	Atp5g2	9.0	9.0	0.0	0.0	0.1870
Baat Bile acid-CoA:amino acid N-acyltransferase	Baat	25.7	3.7	23.7	11.6	0.4388
LOC100048676;Bckdhb Isoform 1 of 2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	Bckdhb	20.3	6.2	17.7	5.6	0.3826
Bdh1 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	Bdh1	65.3	19.3	34.7	12.7	0.1276
Bhmt Betaine--homocysteine S-methyltransferase 1	Bhmt	297.0	25.5	165.3	85.7	0.1074
Bhmt2 Betaine--homocysteine S-methyltransferase 2	Bhmt2	10.0	10.0	0.0	0.0	0.1870
Car3 Carbonic anhydrase 3	Car3	143.7	3.2	53.3	13.4	0.0014
Cat catalase	Cat	39.3	25.8	10.0	5.0	0.1637
Cbs Isoform 1 of Cystathionine beta-synthase	Cbs	9.3	3.7	4.7	2.6	0.1808
Cct2 T-complex protein 1 subunit beta	Cct2	5.7	1.2	4.0	2.0	0.2573
Cct4 T-complex protein 1 subunit delta	Cct4	3.3	1.7	1.7	0.9	0.2133
Cct5 T-complex protein 1 subunit epsilon	Cct5	7.7	2.0	6.0	3.1	0.3365
Ces6 Putative uncharacterized protein	Ces6	6.3	1.7	1.0	1.0	0.0258
Cfl1 Putative uncharacterized protein	Cfl1	16.7	1.2	4.3	4.3	0.0259
Clic4 Chloride intracellular channel protein 4	Clic4	5.0	1.2	3.7	1.9	0.2874
Cmbl Carboxymethylenebutenolidase homolog	Cmbl	16.7	3.4	4.7	4.7	0.0529
Cndp2 Cytosolic non-specific dipeptidase	Cndp2	5.7	1.5	3.3	1.8	0.1825
Comt1 catechol O-methyltransferase	Comt1	18.0	5.9	9.0	1.5	0.1057
Cps1 Carbamoyl-phosphate synthase [ammonia], mitochondrial	Cps1	492.0	130.8	501.3	16.6	0.4735
Crot Peroxisomal carnitine O-octanoyltransferase	Crot	4.7	0.7	6.3	1.9	0.2228
Csad Cysteine sulfinic acid decarboxylase	Csad	56.0	7.5	36.7	7.2	0.0685
Cth Cystathionine gamma-lyase	Cth	4.3	1.2	5.0	2.6	0.4149
Cyb5b Cytochrome b5 type B	Cyb5b	10.0	5.1	6.7	2.4	0.2940
Cyp1a2 Cytochrome P450 1A2	Cyp1a2	18.3	6.2	9.7	4.8	0.1656
Cyp2a12 MCG133379, isoform CRA_a	Cyp2a12	9.7	5.2	0.0	0.0	0.0694
Cyp2c29 Cytochrome P450 2C29	Cyp2c29	43.3	23.2	19.0	7.0	0.1860
Cyp2c37 cytochrome P450 2C37	Cyp2c37	17.3	4.1	7.3	4.1	0.0781
Cyp2c37 Cytochrome P450 2C37	Cyp2c37	6.7	6.7	3.7	3.7	0.3567
Cyp2c39 Cytochrome P450 2C39	Cyp2c39	5.0	1.2	2.3	2.3	0.1818
Cyp2c40 cytochrome P450 2C40	Cyp2c40	9.7	3.5	5.3	3.2	0.2066
Cyp2c44 cytochrome P450, family 2, subfamily c, polypeptide 44 isoform 1	Cyp2c44	5.0	2.6	2.3	1.2	0.2054
Cyp2c50 Isoform 1 of Cytochrome P450 2C50	Cyp2c50	16.3	8.3	11.3	3.3	0.3029
Cyp2c54 Cytochrome P450 2C54	Cyp2c54	11.3	5.7	9.7	3.8	0.4095
Cyp2c67 Putative uncharacterized protein	Cyp2c67	8.0	4.0	5.7	3.2	0.3358
Cyp2c68 cytochrome P450, family 2, subfamily c, polypeptide 68	Cyp2c68	5.0	5.0	5.7	3.2	0.4579

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Cyp2c70 Cytochrome P450 2C70	Cyp2c70	7.0	4.0	5.3	3.2	0.3811
Cyp2d10 Cytochrome P450 2D10	Cyp2d10	25.3	5.5	18.0	2.0	0.1378
Cyp2d22 cytochrome P450, family 2, subfamily d, polypeptide 22	Cyp2d22	5.3	3.2	5.0	2.6	0.4698
Cyp2d26 Cytochrome P450 2D26	Cyp2d26	9.7	3.9	12.0	4.2	0.3522
Cyp2d9 cytochrome P450 2D9	Cyp2d9	13.0	2.6	13.7	0.9	0.4114
Cyp2e1 Cytochrome P450 2E1	Cyp2e1	8.0	4.2	16.7	5.0	0.1279
Cyp2f2 Cytochrome P450 2F2	Cyp2f2	7.7	4.1	3.0	1.5	0.1729
Cyp2j5 Cytochrome P450 2J5	Cyp2j5	4.7	2.4	4.0	2.3	0.4256
Cyp3a11 Cytochrome P450 3A11	Cyp3a11	7.0	3.8	3.3	2.4	0.2297
Dak Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	Dak	122.0	9.6	119.0	10.5	0.4218
Dcxr L-xylulose reductase	Dcxr	12.3	3.4	6.7	1.8	0.1058
Ddc Aromatic-L-amino-acid decarboxylase	Ddc	14.3	2.8	0.7	0.7	0.0048
Ddt D-dopachrome decarboxylase	Ddt	8.7	4.4	7.3	1.7	0.3949
Decr2 Peroxisomal 2,4-dienoyl-CoA reductase	Decr2	6.0	3.1	3.0	2.1	0.2313
Dhdpsl Dihydrodipicolinate synthase-like, mitochondrial	Dhdpsl	5.7	2.8	5.0	1.2	0.4194
Dpyd Dihydropyrimidine dehydrogenase [NADP+]	Dpyd	6.0	3.1	14.3	5.4	0.1242
Dpys Dihydropyrimidinase	Dpys	24.0	7.1	25.0	3.8	0.4535
Dstn Destrin	Dstn	15.0	1.5	7.7	3.9	0.0785
Echs1 Enoyl-CoA hydratase, mitochondrial	Echs1	27.3	14.4	21.0	2.5	0.3441
Eef1a1 Elongation factor 1-alpha 1	Eef1a1	359.0	20.0	246.7	14.0	0.0050
Eef1a2 Elongation factor 1-alpha 2	Eef1a2	86.3	86.3	0.0	0.0	0.1870
Eef1g Elongation factor 1-gamma	Eef1g	8.3	1.3	9.0	2.6	0.4165
Eef2 Elongation factor 2	Eef2	99.7	9.9	91.0	15.2	0.3289
Ehhadh peroxisomal bifunctional enzyme	Ehhadh	11.0	4.0	7.0	3.5	0.2483
Eif4a1 Eukaryotic initiation factor 4A-I	Eif4a1	14.0	3.5	17.0	5.3	0.3306
Gm5506;Eno1;LOC100044223 Alpha-enolase	Eno1	34.7	6.4	30.7	6.4	0.3407
Ephx2 Isoform 1 of Epoxide hydrolase 2	Ephx2	43.7	18.8	25.0	1.0	0.1890
Eprs Bifunctional aminoacyl-tRNA synthetase	Eprs	5.7	1.5	3.3	1.8	0.1825
Es31 Isoform 1 of Liver carboxylesterase 31	Es31	9.0	3.2	5.0	2.9	0.2035
Esd S-formylglutathione hydrolase	Esd	35.0	1.0	24.7	6.2	0.0869
Etfa Electron transfer flavoprotein subunit alpha, mitochondrial	Etfa	15.0	2.5	11.0	1.5	0.1229
Ethe1 Protein ETHE1, mitochondrial	Ethe1	5.0	1.5	3.7	1.9	0.3043
Fah fumarylacetoacetase	Fah	26.7	6.0	22.0	5.7	0.3014
Fasn Fatty acid synthase	Fasn	117.0	20.5	79.7	5.4	0.0766
Fbp1 Fructose-1,6-bisphosphatase 1	Fbp1	225.7	53.7	211.3	18.6	0.4067
Fdps Farnesyl pyrophosphate synthase	Fdps	6.3	2.3	6.3	2.2	0.5000

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Fh1 fumarate hydratase, mitochondrial precursor	Fh1	6.3	1.9	8.0	1.5	0.2631
Fmo1 Dimethylaniline monooxygenase [N-oxide-forming] 1	Fmo1	4.3	2.2	4.7	1.5	0.4525
LOC100046051;Fmo5 dimethylaniline monooxygenase [N-oxide-forming] 5	Fmo5	4.3	2.3	1.7	1.7	0.2025
Ftcd Formimidoyltransferase-cyclodeaminase	Ftcd	34.7	5.0	24.7	8.5	0.1828
Gamt Isoform 2 of Guanidinoacetate N-methyltransferase	Gamt	22.7	2.4	15.3	9.0	0.2365
Gcat 2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial	Gcat	11.7	2.8	3.7	2.7	0.0562
Gcdh glutaryl-CoA dehydrogenase, mitochondrial precursor	Gcdh	6.3	0.9	5.0	2.9	0.3408
Gckr Glucokinase regulatory protein	Gckr	6.3	1.2	8.7	4.4	0.3170
Gclc Glutamate--cysteine ligase catalytic subunit	Gclc	12.7	4.5	7.7	4.1	0.2283
Gclm Glutamate--cysteine ligase regulatory subunit	Gclm	6.7	2.7	2.7	1.5	0.1327
Gcn1l1 GCN1 general control of amino-acid synthesis 1-like 1	Gcn1l1	3.3	2.4	0.0	0.0	0.1189
Glud1 Glutamate dehydrogenase 1, mitochondrial	Glud1	16.7	6.8	27.7	9.5	0.2002
Glul Glutamine synthetase	Glul	53.3	15.3	31.0	10.1	0.1454
Gm10035 UbiE3 protein	Gm10035	5.3	4.4	1.0	1.0	0.1943
Gm10119 Putative uncharacterized protein Gm10119	Gm10119	5.3	0.9	6.3	3.3	0.3916
Gm10169 similar to macrophage migration inhibitory factor isoform 1	Gm10169	8.7	1.2	4.0	2.3	0.0738
Gm10313 similar to LOC654472 protein	Gm10313	198.0	26.0	127.7	9.4	0.0318
Gm10362 similar to Rpl17 protein	Gm10362	6.7	1.3	7.3	3.8	0.4389
Gm11353 Ribosomal protein S8	Gm11353	6.0	6.0	13.3	9.2	0.2706
Gm13882 hypothetical protein	Gm13882	529.3	41.7	212.7	111.3	0.0281
Gm13910 similar to Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	Gm13910	42.7	21.3	33.3	17.0	0.3748
Gm14438;Gm14289 similar to ribosomal protein S8	Gm14438	9.7	5.2	13.7	9.1	0.3617
Gm5424 Argininosuccinate synthase	Gm5424	348.0	177.6	219.0	112.2	0.2862
Gm7251 hypothetical protein	Gm7251	22.3	11.5	0.0	0.0	0.0616
Gm9755 Elongation factor Tu	Gm9755	6.0	3.2	0.0	0.0	0.0677
Gne bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	Gne	8.7	0.3	4.0	0.6	0.0011
Gnmt Glycine N-methyltransferase	Gnmt	376.7	39.0	202.7	58.9	0.0347
Got2 Aspartate aminotransferase, mitochondrial	Got2	19.0	8.7	32.3	14.4	0.2365
Gpd1 Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	Gpd1	24.3	1.2	19.3	3.7	0.1324
Gpt Alanine aminotransferase 1	Gpt	16.3	5.9	18.7	6.2	0.3993
Gpx1 Glutathione peroxidase 1	Gpx1	22.3	7.9	9.0	4.6	0.1087
Grhpr Glyoxylate reductase/hydroxypyruvate reductase	Grhpr	69.7	9.3	41.0	12.1	0.0663

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Gsta3 Glutathione S-transferase A3	Gsta3	64.7	13.7	47.0	5.9	0.1506
Gstm1 Glutathione S-transferase Mu 1	Gstm1	49.7	19.7	50.0	11.4	0.4945
Gstm2 Glutathione S-transferase Mu 2	Gstm2	15.7	9.2	11.7	5.8	0.3665
Gstm3 Glutathione S-transferase Mu 3	Gstm3	24.0	13.3	7.0	7.0	0.1608
Gstm5 Glutathione S-transferase Mu 5	Gstm5	6.0	4.6	6.0	1.7	0.5000
Gstm6 Glutathione S-transferase Mu 6	Gstm6	15.3	5.8	10.3	5.2	0.2778
Gstm7 Glutathione S-transferase Mu 7	Gstm7	18.0	10.1	15.0	2.0	0.3928
Gsto1 Glutathione S-transferase omega-1	Gsto1	7.3	2.0	7.0	2.3	0.4594
Gstp1 Glutathione S-transferase P 1	Gstp1	437.7	81.7	164.0	35.2	0.0185
Gstt1 glutathione S-transferase theta-1	Gstt1	15.3	2.6	7.7	2.2	0.0436
Gstt2 glutathione S-transferase theta-2	Gstt2	4.3	2.6	0.0	0.0	0.0857
Gstt3 Glutathione S-transferase, theta 3	Gstt3	11.0	1.7	9.0	2.1	0.2506
Gstz1 Maleylacetoacetate isomerase	Gstz1	119.0	31.4	35.0	19.4	0.0427
Gulo Putative uncharacterized protein	Gulo	15.0	7.9	16.3	8.4	0.4569
Gys2 Glycogen [starch] synthase, liver	Gys2	6.3	1.5	3.0	3.0	0.1870
Haao 3-hydroxyanthranilate 3,4-dioxygenase	Haao	53.0	6.8	24.7	7.3	0.0233
Hacl1 2-hydroxyacyl-CoA lyase 1	Hacl1	19.7	4.9	21.0	4.4	0.4245
Hadh Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Hadh	5.3	2.7	7.0	1.0	0.2949
Hadha Trifunctional enzyme subunit alpha, mitochondrial	Hadha	26.3	5.9	28.7	4.1	0.3807
Hadhb Trifunctional enzyme subunit beta, mitochondrial	Hadhb	10.7	10.7	16.0	16.0	0.3976
Hal Histidine ammonia-lyase	Hal	9.0	3.2	13.3	3.2	0.1961
Hao1 Hydroxyacid oxidase 1	Hao1	6.0	3.2	3.3	1.8	0.2537
Hba-a2;Hba-a1 hemoglobin alpha, adult chain 2	Hba-a1	12.7	1.2	27.0	4.0	0.0136
Hbb-b1 Beta-globin	Hbb-b1	260.0	40.6	209.7	57.8	0.2577
Hgd homogentisate 1,2-dioxygenase	Hgd	138.0	19.3	57.7	15.2	0.0153
Hmgcl hydroxymethylglutaryl-CoA lyase, mitochondrial precursor	Hmgcl	53.7	9.1	36.7	11.3	0.1534
LOC100040592;Hmgcs1 Hydroxymethylglutaryl-CoA synthase, cytoplasmic	Hmgcs1	48.0	3.0	51.7	11.9	0.3897
Hmgcs2 Hydroxymethylglutaryl-CoA synthase, mitochondrial	Hmgcs2	694.0	57.4	686.3	50.2	0.4624
Hnrnpk Isoform 2 of Heterogeneous nuclear ribonucleoprotein K	Hnrnpk	9.3	1.2	11.3	3.2	0.2940
Hpd 4-hydroxyphenylpyruvate dioxygenase	Hpd	12.7	6.4	12.3	6.7	0.4865
Hsd17b10 3-hydroxyacyl-CoA dehydrogenase type-2	Hsd17b10	14.3	3.0	9.7	5.5	0.2479
Hsd17b13 Isoform 1 of 17-beta-hydroxysteroid dehydrogenase 13	Hsd17b13	12.0	2.6	1.7	1.7	0.0149
Hsd17b2 Estradiol 17-beta-dehydrogenase 2	Hsd17b2	4.7	3.3	3.7	1.9	0.4020
Hsd3b3 3 beta-hydroxysteroid dehydrogenase/Delta 5-- 4-isomerase type 3	Hsd3b3	7.3	3.7	2.7	2.7	0.1808
Hsd3b5 3 beta-hydroxysteroid dehydrogenase type 5	Hsd3b5	12.0	3.0	4.0	2.0	0.0454

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Hsp90ab1 Heat shock protein HSP 90-beta	Hsp90ab1	20.7	5.5	22.3	11.2	0.4501
Hspa9 stress-70 protein, mitochondrial	Hspa9	33.3	14.9	29.7	13.5	0.4320
Hspd1 Isoform 1 of 60 kDa heat shock protein, mitochondrial	Hspd1	86.0	3.5	61.7	5.2	0.0088
Iah1 Isoamyl acetate-hydrolyzing esterase 1 homolog	Iah1	33.3	3.8	23.0	10.4	0.2022
Idh1 Putative uncharacterized protein	Idh1	138.7	18.7	54.7	9.6	0.0081
Ido2 RIKEN cDNA C230043N17	Ido2	6.7	0.9	2.7	1.5	0.0391
Iigp1 Interferon-inducible GTPase 1	Iigp1	8.0	2.1	5.0	1.0	0.1319
Inmt Indolethylamine N-methyltransferase	Inmt	31.7	13.0	14.0	3.5	0.1299
Isoc2a Isochorismatase domain-containing protein 2A, mitochondrial	Isoc2a	8.3	3.2	7.7	2.9	0.4423
Keg1 Glycine N-acyltransferase-like protein Keg1	Keg1	6.3	3.5	2.0	1.0	0.1487
Khk 38 kDa protein	Khk	17.3	2.3	13.7	3.9	0.2337
Lap3 Isoform 1 of Cytosol aminopeptidase	Lap3	20.7	3.2	15.3	4.1	0.1796
Ldha L-lactate dehydrogenase A chain isoform 2	Ldha	63.3	10.3	77.3	15.9	0.2503
LOC100045982 similar to MOSC domain-containing protein 1, mitochondrial isoform 1	LOC100045982	10.0	5.5	6.0	3.8	0.2909
Mat1a S-adenosylmethionine synthase isoform type-1	Mat1a	165.7	25.7	235.0	41.5	0.1142
Mdh1 Malate dehydrogenase, cytoplasmic	Mdh1	13.0	2.9	14.3	4.6	0.4095
Me1 NADP-dependent malic enzyme	Me1	26.0	7.9	20.3	5.2	0.2910
Mettl7b Methyltransferase-like protein 7B	Mettl7b	44.0	2.3	21.0	6.0	0.0118
Mgst1 26 kDa protein	Mgst1	149.7	29.4	81.0	23.2	0.0703
Mosc2 MOSC domain-containing protein 2, mitochondrial	Mosc2	8.0	2.1	7.0	4.0	0.4183
mt-Co2 Cytochrome c oxidase subunit 2	mt-Co2	4.3	2.3	4.7	2.6	0.4643
Mtch2 Mitochondrial carrier homolog 2	Mtch2	6.0	6.0	7.3	3.8	0.4303
Mthfd1 C-1-tetrahydrofolate synthase, cytoplasmic	Mthfd1	38.0	2.6	29.3	8.7	0.1969
Mug1 Murinoglobulin-1	Mug1	4.0	2.3	13.3	3.0	0.0339
Naprt1 Nicotinate phosphoribosyltransferase	Naprt1	20.7	0.3	16.0	4.6	0.1853
Nars Asparaginyl-tRNA synthetase, cytoplasmic	Nars	4.3	2.3	0.7	0.7	0.1027
Ndrg2 Isoform 1 of Protein NDRG2	Ndrg2	19.0	1.5	13.7	4.4	0.1584
Nit1 Nitrilase 1	Nit1	11.0	1.2	9.0	4.7	0.3510
Nudt7 Isoform 2 of Peroxisomal coenzyme A diphosphatase NUDT7	Nudt7	21.7	1.9	4.3	2.2	0.0019
P4hb Protein disulfide-isomerase	P4hb	189.3	12.6	259.0	14.0	0.0105
Pah phenylalanine-4-hydroxylase	Pah	14.7	5.8	12.0	6.0	0.3833
Park7 Protein DJ-1	Park7	23.7	2.7	12.7	3.9	0.0415
Pbld Phenazine biosynthesis-like domain-containing protein 1	Pbld	25.7	5.9	17.0	3.2	0.1340
Pcbp1 Poly(rC)-binding protein 1	Pcbp1	16.3	4.1	10.0	4.0	0.1664
Pccb Propionyl Coenzyme A carboxylase, beta polypeptide, isoform CRA_a	Pccb	5.7	2.8	6.7	3.4	0.4161

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Pck1 Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	Pck1	19.7	5.5	31.7	4.5	0.0823
Pcx pyruvate carboxylase isoform 1	Pcx	98.7	22.4	148.3	22.7	0.0972
Pdcd6ip Isoform 3 of Programmed cell death 6-interacting protein	Pdcd6ip	5.3	1.3	1.7	0.9	0.0418
Pdia3 Protein disulfide-isomerase A3	Pdia3	79.0	28.8	66.3	22.4	0.3729
Pdia4 protein disulfide-isomerase A4	Pdia4	26.0	10.5	21.7	11.6	0.3980
Pdia5 Protein disulfide-isomerase A5	Pdia5	8.0	4.9	13.0	5.3	0.2637
Pdia6 Putative uncharacterized protein	Pdia6	36.0	5.7	42.7	18.4	0.3734
Pgk1 Phosphoglycerate kinase 1	Pgk1	8.0	4.0	12.0	6.0	0.3054
Pgrmc1 Membrane-associated progesterone receptor component 1	Pgrmc1	6.7	3.2	2.7	1.5	0.1582
Pipox Peroxisomal sarcosine oxidase	Pipox	11.3	6.6	4.7	2.6	0.2015
Pklr pyruvate kinase isozymes R/L isoform 2	Pklr	23.3	8.7	22.3	4.1	0.4610
Pls3 Plastin 3	Pls3	9.7	4.7	10.3	3.3	0.4565
Pnp purine nucleoside phosphorylase	Pnp	6.7	3.4	9.7	5.2	0.3278
Ppa1 Inorganic pyrophosphatase	Ppa1	10.0	2.6	8.0	4.4	0.3574
Prdx1 Peroxiredoxin-1	Prdx1	90.3	12.9	40.0	11.8	0.0227
Prdx2 Peroxiredoxin-2	Prdx2	5.3	0.9	0.7	0.7	0.0067
Prodh2 Probable proline dehydrogenase 2	Prodh2	5.7	1.2	3.0	1.7	0.1373
Prpsap1 phosphoribosyl pyrophosphate synthetase-associated protein 1	Prpsap1	9.3	0.9	2.3	1.5	0.0073
Psmc4 26S protease regulatory subunit 6B	Psmc4	10.3	4.9	6.0	1.2	0.2194
Psmd2 26S proteasome non-ATPase regulatory subunit 2	Psmd2	3.7	1.9	6.0	3.0	0.2722
Psme1 Proteasome activator complex subunit 1	Psme1	9.0	1.0	4.7	1.2	0.0251
Psme2 proteasome activator complex subunit 2 isoform 2	Psme2	12.3	2.8	4.3	3.0	0.0617
Pter Isoform 1 of Phosphotriesterase-related protein	Pter	4.7	0.7	5.3	1.5	0.3490
Ptgr2 Isoform 1 of Prostaglandin reductase 2	Ptgr2	9.7	1.2	6.0	1.5	0.0661
Pygl glycogen phosphorylase, liver form	Pygl	23.3	7.7	30.3	8.2	0.2830
Qdpr Dihydropteridine reductase	Qdpr	5.7	5.7	3.3	2.0	0.3590
Qprt Nicotinate-nucleotide pyrophosphorylase [carboxylating]	Qprt	4.0	1.2	3.7	1.2	0.4256
Rdh1 36 kDa protein	Rdh1	43.0	11.6	17.0	9.5	0.0792
Rdh19 retinol dehydrogenase similar protein 2	Rdh19	13.0	13.0	22.3	3.5	0.2633
Rdh7 Retinol dehydrogenase 7	Rdh7	55.3	17.9	19.0	10.4	0.0775
Rgn Regucalcin	Rgn	32.3	7.7	29.7	11.3	0.4272
Rpl10;LOC100048462;Gm13891;Gm10041;LOC100048223 60S ribosomal protein L10	Rpl10	5.0	2.6	4.7	2.3	0.4646
Rpl23 60S ribosomal protein L23	Rpl23	8.7	4.4	3.3	2.4	0.1726
Rpl3 60S ribosomal protein L3	Rpl3	30.0	17.0	21.3	11.5	0.3474
Rpl4 60S ribosomal protein L4	Rpl4	5.0	2.6	4.7	1.5	0.4587
Rplp0 60S acidic ribosomal protein P0	Rplp0	6.3	1.2	4.3	2.6	0.2620

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Rpn1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Rpn1	7.7	4.1	11.7	4.5	0.2731
Rps11 Putative uncharacterized protein	Rps11	5.0	5.0	0.7	0.7	0.2194
Rps2 Putative uncharacterized protein Rps2	Rps2	13.3	1.2	11.0	5.7	0.3543
Rps23;LOC100046668;Gm15450 Putative uncharacterized protein	Rps23	9.0	5.9	3.3	3.3	0.2239
Rps3 40S ribosomal protein S3	Rps3	40.7	10.7	26.0	5.6	0.1447
Rps4x 40S ribosomal protein S4, X isoform	Rps4x	12.0	2.5	0.0	0.0	0.0044
Rps5 40S ribosomal protein S5	Rps5	9.7	5.8	8.0	4.6	0.4164
Sardh Sarcosine dehydrogenase, mitochondrial	Sardh	25.3	5.9	28.0	7.2	0.3948
Scp2 Isoform SCPx of Non-specific lipid-transfer protein	Scp2	300.3	22.0	94.3	24.9	0.0017
Sdha Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Sdha	8.0	1.5	12.3	2.3	0.0976
Sds L-serine dehydratase/L-threonine deaminase	Sds	34.0	4.0	51.7	10.2	0.0909
Selenbp1;LOC100044204 Selenium-binding protein 1	Selenbp1	35.0	18.3	6.7	6.7	0.1101
Selenbp2 Selenium-binding protein 2	Selenbp2	128.7	32.2	18.3	7.7	0.0145
Sephs2 Selenide, water dikinase 2	Sephs2	18.0	1.5	13.3	3.3	0.1335
Serpina1d Alpha-1-antitrypsin 1-4	Serpina1d	4.0	0.6	8.7	4.7	0.1886
Serpina1e Alpha-1-antitrypsin 1-5	Serpina1e	3.0	1.5	7.0	4.7	0.2329
Shmt1 serine hydroxymethyltransferase, cytosolic	Shmt1	9.3	4.8	7.7	4.3	0.4047
Slc25a13 Calcium-binding mitochondrial carrier protein Aralar2	Slc25a13	8.3	4.2	12.7	3.8	0.2418
Slc25a15 Mitochondrial ornithine transporter 1	Slc25a15	4.3	2.2	6.3	1.8	0.2579
Slc25a20 Mitochondrial carnitine/acylcarnitine carrier protein	Slc25a20	7.3	2.3	7.7	5.2	0.4780
Slc25a4 ADP/ATP translocase 1	Slc25a4	5.3	5.3	0.0	0.0	0.1870
Slc25a5 ADP/ATP translocase 2	Slc25a5	33.7	18.8	27.7	3.7	0.3850
Slc27a2 very long-chain acyl-CoA synthetase	Slc27a2	13.0	3.5	16.0	3.6	0.2904
Slc27a5 Bile acyl-CoA synthetase	Slc27a5	32.3	6.7	24.7	9.0	0.2652
Snd1 Staphylococcal nuclease domain-containing protein 1	Snd1	5.7	2.7	7.7	2.3	0.3036
Sord 40 kDa protein	Sord	230.7	21.0	118.0	16.9	0.0069
Spr sepiapterin reductase	Spr	9.3	3.2	6.0	3.0	0.2441
Sqrdl sulfide:quinone oxidoreductase, mitochondrial precursor	Sqrdl	5.0	1.2	3.3	2.0	0.2573
Stard10 PCTP-like protein	Stard10	24.0	11.4	20.0	6.0	0.3857
Sult1a1 Sulfotransferase family 1A, phenol-preferring, member 1, isoform CRA_a	Sult1a1	30.7	5.4	27.0	4.5	0.3142
Sult1d1 Tyrosine-ester sulfotransferase	Sult1d1	5.7	1.2	4.0	2.3	0.2784
Tcp1 Isoform 1 of T-complex protein 1 subunit alpha	Tcp1	8.3	1.8	6.7	2.3	0.2996
Tdo2 Tryptophan 2,3-dioxygenase	Tdo2	6.3	3.5	8.3	3.8	0.3580
Tkt Transketolase	Tkt	11.7	1.5	11.3	3.7	0.4684
Tpi1 triosephosphate isomerase	Tpi1	86.7	12.0	49.7	4.8	0.0229

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	p-value
Ttpa Alpha-tocopherol transfer protein	Ttpa	6.7	3.4	11.0	2.9	0.1925
Tuba1a Tubulin alpha-1A chain	Tuba1a	64.0	32.7	59.0	4.0	0.4434
Tuba1b Tubulin alpha-1B chain	Tuba1b	131.7	6.7	84.7	9.8	0.0085
Tuba1c Tubulin alpha-1C chain	Tuba1c	85.3	43.5	83.3	10.7	0.4833
Tuba4a Tubulin alpha-4A chain	Tuba4a	121.3	3.2	79.3	9.5	0.0070
Tuba8 Tubulin alpha-8 chain	Tuba8	35.3	35.3	0.0	0.0	0.1870
Tubb2a Tubulin beta-2A chain	Tubb2a	83.3	14.7	27.0	14.4	0.0260
Tubb2b Tubulin beta-2B chain	Tubb2b	68.0	35.4	39.3	19.8	0.2593
Tubb2c Tubulin beta-2C chain	Tubb2c	111.3	19.2	56.0	11.0	0.0334
Tubb3 Tubulin beta-3 chain	Tubb3	41.0	21.9	30.7	4.3	0.3340
Tubb4 Tubulin beta-4 chain	Tubb4	46.7	24.5	17.0	17.0	0.1881
Tubb5 Tubulin beta-5 chain	Tubb5	99.3	17.9	53.3	9.7	0.0436
Tubb6 Tubulin beta-6 chain	Tubb6	25.0	25.0	12.7	12.7	0.3413
Txn1 Thioredoxin	Txn1	21.0	11.8	12.3	7.5	0.2852
Txndc5 Thioredoxin domain-containing protein 5	Txndc5	8.3	3.5	9.0	5.2	0.4601
Txnrd1 Isoform 1 of Thioredoxin reductase 1, cytoplasmic	Txnrd1	11.7	0.9	12.0	2.5	0.4533
Uba1 Ubiquitin-like modifier-activating enzyme 1	Uba1	9.3	2.7	12.0	6.0	0.3538
Ugdh UDP-glucose 6-dehydrogenase	Ugdh	9.0	4.7	11.3	2.3	0.3404
Ugp2 Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	Ugp2	27.0	7.0	21.0	8.9	0.3122
Ugt1a6b;LOC632297;Ugt1a2;Ugt1a10;Ugt1a9;Ugt1a7c;Ugt1a1;Ugt1a5 UDP-glucuronosyltransferase 1-1	Ugt1a1	14.0	7.4	19.0	5.0	0.3023
Ugt2a3 UDP-glucuronosyltransferase 2A3	Ugt2a3	3.0	1.7	1.3	1.3	0.2441
Ugt2b1 UDP glucuronosyltransferase 2 family, polypeptide B1	Ugt2b1	9.3	4.7	2.3	1.5	0.1140
Ugt2b5 UDP-glucuronosyltransferase 2B5 precursor	Ugt2b5	10.7	4.6	5.0	1.7	0.1578
Uqcrc1 cytochrome b-c1 complex subunit 1, mitochondrial precursor	Uqcrc1	6.0	1.5	5.3	2.7	0.4194
Uroc1 Putative uncharacterized protein	Uroc1	15.0	1.0	14.7	3.2	0.4626
Vdac2 Voltage-dependent anion-selective channel protein 2	Vdac2	11.3	3.8	10.3	5.8	0.4462
Vdac3 Voltage-dependent anion channel 3	Vdac3	13.0	5.0	7.3	5.9	0.2527
Xdh xanthine dehydrogenase/oxidase	Xdh	4.3	2.2	6.0	3.0	0.3383
Xylb Xylulose kinase	Xylb	13.0	4.6	10.7	4.1	0.3618
Ywhae 14-3-3 protein epsilon	Ywhae	5.7	1.8	3.0	1.5	0.1584
Ywhag 14-3-3 protein gamma	Ywhag	3.7	0.7	1.7	0.9	0.0724
Ywhaq 34 kDa protein	Ywhaq	4.7	2.6	3.3	1.8	0.3467

Table 2. Proteins that Showed Significantly Less IAyne Labeling in Glyphosate-Treated Mouse Livers Compared to their Control Counterparts

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Ass1 Argininosuccinate synthase	Ass1	608.7	37.4	446.7	61.7	0.0441
Gm13882 hypothetical protein	Gm13882	529.3	41.7	212.7	111.3	0.0281
Acaa2 Putative uncharacterized protein	Acaa2	461.7	60.7	290.3	26.6	0.0305
Gstp1 Glutathione S-transferase P 1	Gstp1	437.7	81.7	164.0	35.2	0.0185
Gnmt Glycine N-methyltransferase	Gnmt	376.7	39.0	202.7	58.9	0.0347
Eef1a1 Elongation factor 1-alpha 1	Eef1a1	359.0	20.0	246.7	14.0	0.0050
Aldh1a1 Retinal dehydrogenase 1	Aldh1a1	301.7	31.1	170.0	26.0	0.0157
Scp2 Isoform SCPx of Non-specific lipid-transfer protein	Scp2	300.3	22.0	94.3	24.9	0.0017
Sord 40 kDa protein	Sord	230.7	21.0	118.0	16.9	0.0069
Gm10313 similar to LOC654472 protein	Gm10313	198.0	26.0	127.7	9.4	0.0318
Aldh7a1 Isoform 1 of Alpha-aminoadipic semialdehyde dehydrogenase	Aldh7a1	147.0	14.1	71.0	24.9	0.0283
Car3 Carbonic anhydrase 3	Car3	143.7	3.2	53.3	13.4	0.0014
Idh1 Putative uncharacterized protein	Idh1	138.7	18.7	54.7	9.6	0.0081
Hgd homogentisate 1,2-dioxygenase	Hgd	138.0	19.3	57.7	15.2	0.0153
Acat3 acetyl-Coenzyme A acetyltransferase 3	Acat3	132.3	3.7	60.0	13.6	0.0034
Tuba1b Tubulin alpha-1B chain	Tuba1b	131.7	6.7	84.7	9.8	0.0085
Selenbp2 Selenium-binding protein 2	Selenbp2	128.7	32.2	18.3	7.7	0.0145
Tuba4a Tubulin alpha-4A chain	Tuba4a	121.3	3.2	79.3	9.5	0.0070
Gstz1 Maleylacetoacetate isomerase	Gstz1	119.0	31.4	35.0	19.4	0.0427
Tubb2c Tubulin beta-2C chain	Tubb2c	111.3	19.2	56.0	11.0	0.0334
Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase B, peroxisomal	Acaa1b	108.7	20.7	28.7	9.4	0.0123
Acat2 Acetyl-CoA acetyltransferase, cytosolic	Acat2	107.3	6.3	53.0	13.5	0.0110
Tubb5 Tubulin beta-5 chain	Tubb5	99.3	17.9	53.3	9.7	0.0436
Akr1c14 Putative uncharacterized protein	Akr1c14	91.7	4.1	41.7	11.6	0.0076
Prdx1 Peroxiredoxin-1	Prdx1	90.3	12.9	40.0	11.8	0.0227
Tpi1 triosephosphate isomerase	Tpi1	86.7	12.0	49.7	4.8	0.0229
Hspd1 Isoform 1 of 60 kDa heat shock protein, mitochondrial	Hspd1	86.0	3.5	61.7	5.2	0.0088
Tubb2a Tubulin beta-2A chain	Tubb2a	83.3	14.7	27.0	14.4	0.0260
Aldh9a1 4-trimethylaminobutyraldehyde dehydrogenase	Aldh9a1	53.3	2.8	36.0	7.0	0.0418
Haao 3-hydroxyanthranilate 3,4-dioxygenase	Haao	53.0	6.8	24.7	7.3	0.0233
Alad Delta-aminolevulinic acid dehydratase	Alad	49.0	3.2	31.7	3.7	0.0118
2810007J24Rik Sulfotransferase-like protein 1	2810007J24Rik	45.3	13.9	8.7	4.7	0.0332
Mettl7b Methyltransferase-like protein 7B	Mettl7b	44.0	2.3	21.0	6.0	0.0118
Aox3 Aldehyde oxidase 1	Aox3	43.7	7.0	16.0	6.2	0.0208
Park7 Protein DJ-1	Park7	23.7	2.7	12.7	3.9	0.0415

Protein	Protein ID	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Nudt7 Isoform 2 of Peroxisomal coenzyme A diphosphatase NUDT7	Nudt7	21.7	1.9	4.3	2.2	0.0019
0610011F06Rik UPF0585 protein C16orf13 homolog	0610011F06Rik	18.3	0.3	9.0	2.9	0.0163
Cfl1 Putative uncharacterized protein	Cfl1	16.7	1.2	4.3	4.3	0.0259
Gstt1 glutathione S-transferase theta-1	Gstt1	15.3	2.6	7.7	2.2	0.0436
Ddc Aromatic-L-amino-acid decarboxylase	Ddc	14.3	2.8	0.7	0.7	0.0048
Rps4x 40S ribosomal protein S4, X isoform	Rps4x	12.0	2.5	0.0	0.0	0.0044
Hsd17b13 Isoform 1 of 17-beta-hydroxysteroid dehydrogenase 13	Hsd17b13	12.0	2.6	1.7	1.7	0.0149
Hsd3b5 3 beta-hydroxysteroid dehydrogenase type 5	Hsd3b5	12.0	3.0	4.0	2.0	0.0454
Prpsap1 phosphoribosyl pyrophosphate synthetase-associated protein 1	Prpsap1	9.3	0.9	2.3	1.5	0.0073
Psme1 Proteasome activator complex subunit 1	Psme1	9.0	1.0	4.7	1.2	0.0251
Gne bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase	Gne	8.7	0.3	4.0	0.6	0.0011
Ido2 RIKEN cDNA C230043N17	Ido2	6.7	0.9	2.7	1.5	0.0391
Ces6 Putative uncharacterized protein	Ces6	6.3	1.7	1.0	1.0	0.0258
Prdx2 Peroxiredoxin-2	Prdx2	5.3	0.9	0.7	0.7	0.0067
Pdcd6ip Isoform 3 of Programmed cell death 6-interacting protein	Pdcd6ip	5.3	1.3	1.7	0.9	0.0418
Adsl Adenylosuccinate lyase	Adsl	5.0	1.2	0.0	0.0	0.0062

Appendix 2. IsoTOP-ABPP analysis of IAyne cysteine-reactivity in mouse livers from mice treated with vehicle or glyphosate

Table 3 shows proteomes which were labeled with IAyne, followed by appendage of a biotin-azide handle bearing a TEV recognition sequence and isotopically light (vehicle-treated) or heavy (glyphosate-treated) valine, combining of control and treated proteomes in a 1:1 ratio, avidin enrichment, tryptic digestion, release of modified peptides by TEV protease, and analysis by LC-MS/MS. Shown are modified peptides and their corresponding protein IDs that were quantified by measuring the light to heavy ratios of peptides. Specific modified cysteines are presented as C(464.28596) or C(470.29977) or C*. This table relates to Figure 2-3D.

Table 3. Final Ratios for Modified Peptides of IsoTOP-ABPP Analysis with IAyne

Peptide	L/H Ratio	Protein	Protein ID
YLLQYQEPIPCEQLVTALC*DIK	8.0577	E9PW69 Proteasome subunit alpha type OS=Mus musculus GN=Psma4 PE=3 SV=1 , Q9R1P0 Proteasome subunit alpha type-4 OS=Mus musculus GN=Psma4 PE=1 SV=1 ,	Psma4
C*GPGYPTPLEAMK	6.7644	Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 ,	Selenbp2
DC*LIPMGITSENVAER	4.4071	Q3UKM0 MCG21883, isoform CRA_e OS=Mus musculus GN=Acaa1b PE=2 SV=1 , Q8VCH0 3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1 ,	Acaa1b
MISQSC*LSNIEK	4.2894	Q8BGL3 RIKEN cDNA 2810007J24, isoform CRA_a OS=Mus musculus GN=2810007J24Rik PE=2 SV=1 ,	2810007J24Rik
GGSVQVLEDQELTC*QPEPLVVK	4.1520	P17563 Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2 , Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 ,	Selenbp1
SFSIASDPTSASSC*YLEEHVSK	3.9389	P00186 Cytochrome P450 1A2 OS=Mus musculus GN=Cyp1a2 PE=1 SV=1 , B6VGH4 Cytochrome P450 family 1 subfamily a polypeptide 2 OS=Mus musculus GN=Cyp1a2 PE=3 SV=1 ,	Cyp1a2
TIGGGDDSFTTFFC*ETGAGK	3.6399	P68368 Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 ,	Tuba4a
FLHDPSATQGFVGC*ALSSNIQR	3.5596	P17563 Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2 , Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 ,	Selenbp1
LPFIYGEEC*QVTSTTVK	3.4415	Q61694 3 beta-hydroxysteroid dehydrogenase type 5 OS=Mus musculus GN=Hsd3b5 PE=1 SV=4 ,	Hsd3b5
GALMANFLTQGQVC*CNGTR	3.4413	Q3U367 Putative uncharacterized protein OS=Mus musculus GN=Aldh9a1 PE=2 SV=1 , Q9JLJ2 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 ,	Aldh9a1
NEFTLGEEC*ELETMTGEK	3.3904	P12710 Fatty acid-binding protein, liver OS=Mus musculus GN=Fabp1 PE=1 SV=2 , Q3V2F7 Fatty acid binding protein 1, liver OS=Mus musculus GN=Fabp1 PE=2 SV=1 ,	Fabp1
LNVIC*PGFVDTPILESIEKEENMGQYIEYK	3.3847	Q8VCC1 15-hydroxyprostaglandin dehydrogenase [NAD+] OS=Mus musculus GN=Hpgd PE=2 SV=1 ,	Hpgd
QNGGEGGIIINMSSLAGLMPVAQQPVYC*ASK	3.3755	Q8VCC1 15-hydroxyprostaglandin dehydrogenase [NAD+] OS=Mus musculus GN=Hpgd PE=2 SV=1 ,	Hpgd
C*VIAEGDLGIVQK	3.1650	Q9Z0S1 3'(2'),5'-bisphosphate nucleotidase 1 OS=Mus musculus GN=Bpnt1 PE=1 SV=2 ,	Bpnt1
QCFLYMVC*QTAK	3.1577	Q9DCY0 Glycine N-acyltransferase-like protein Keg1 OS=Mus musculus GN=Keg1 PE=1 SV=1 ,	Keg1
YIIWSPVC*R	3.1361	P11352 Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2 ,	Gpx1
VIATFAC*SGEK	3.1282	Q3U367 Putative uncharacterized protein OS=Mus musculus GN=Aldh9a1 PE=2 SV=1 , Q9JLJ2 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 ,	Aldh9a1

Peptide	L/H Ratio	Protein	Protein ID
MISQSC*LSNIEK	3.1217	Q8BGL3 RIKEN cDNA 2810007J24, isoform CRA_a OS=Mus musculus GN=2810007J24Rik PE=2 SV=1 ,	2810007J24Rik
QC*SSGLQAVANIAGGIR	3.1143	Q3UKM0 MCG21883, isoform CRA_e OS=Mus musculus GN=Acaa1b PE=2 SV=1 , Q8VCH0 3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1 ,	Acaa1b
QGFGNLPIC*MAK	3.0792	F6YW06 Uncharacterized protein (Fragment) OS=Mus musculus GN=Mthfd1 PE=4 SV=1 , Q922D8 C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=4 ,	Mthfd1
EAPFTHFDPSCLFPAC*R	3.0570	P16015 Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3 ,	Ca3
SGANVLICGPNGC*GK	2.9558	P55096 ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=2 ,	Abcd3
AVC*MLSNTTAIAEAWAR	2.8982	P68368 Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 , P68369 Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 , Q52L87 Tubulin, alpha 1C OS=Mus musculus GN=Tuba1c PE=2 SV=1 , P68373 Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1 , P05213 Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2 ,	Tuba4a
LC*DFGVSGQLIDSMANSFVGTR	2.7443	P31938 Dual specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2 , Q3TMJ8 Mitogen activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=2 SV=1 ,	Map2k1
EEVVTIDTWMQGLLKPTC*LYGQLPK	2.7169	P19157 Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2 ,	Gstp1
AC*GANLPENFSISQIFSQAMAAR	2.6822	P34914 Epoxide hydrolase 2 OS=Mus musculus GN=Ephx2 PE=1 SV=2 ,	Ephx2
EWVDQNSPVLLNDPVLC*DVAK	2.5143	Q8VC28 Aldo-keto reductase family 1 member C13 OS=Mus musculus GN=Akr1c13 PE=1 SV=2 , Q571M4 MKIAA4014 protein (Fragment) OS=Mus musculus GN=Akr1c13 PE=2 SV=1 , Q9JLI0 Aldo-keto reductase a OS=Mus musculus GN=Akr1c12 PE=2 SV=1 ,	Akr1c13
GAALVSAVAC*K	2.5125	P52792-2 Isoform 2 of Glucokinase OS=Mus musculus GN=Gck , Q5SVI5 Glucokinase OS=Mus musculus GN=Gck PE=2 SV=1 , Q5SVI6 Glucokinase OS=Mus musculus GN=Gck PE=2 SV=1 , P52792 Glucokinase OS=Mus musculus GN=Gck PE=2 SV=1 ,	Gck
NGGTLQTCALRPMC*IYGER	2.4970	P26150 3 beta-hydroxysteroid dehydrogenase/Delta 5-- 4-isomerase type 3 OS=Mus musculus GN=Hsd3b3 PE=2 SV=3 , B1ARN8 Hydroxysteroid dehydrogenase-2, delta<5 -3-beta OS=Mus musculus GN=Hsd3b3 PE=3 SV=1 ,	Hsd3b3
INILINCAAGNFLC*PASALSFNAFK	2.4832	Q9WV68 Peroxisomal 2,4-dienoyl-CoA reductase OS=Mus musculus GN=Decr2 PE=1 SV=1 , Q3UVJ7 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal OS=Mus musculus GN=Decr2 PE=2 SV=1 ,	Decr2
STLTDSLVC*K	2.4585	P58252 Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2 ,	Eef2
DIILVSYC*TLGSSR	2.3926	Q91WT7 3-alpha-hydroxysteroid dehydrogenase type 1 OS=Mus musculus GN=Akr1c14 PE=2 SV=1 ,	Akr1c14
HLNEIDLFHC*IDPNDSK	2.3548	Q9R0Q7 Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1 , E9PXA6 Uncharacterized protein OS=Mus musculus GN=Ptges3 PE=4 SV=1 , D3Z7C6 Uncharacterized protein OS=Mus musculus GN=Ptges3 PE=4 SV=1 ,	Ptges3
YKPVCNQVEC*HLYLNQSQMLDYCK	2.3482	Q91WT7 3-alpha-hydroxysteroid dehydrogenase type 1 OS=Mus musculus GN=Akr1c14 PE=2 SV=1 ,	Akr1c14
PSCLFPAC*R	2.3318	P16015 Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3 ,	Ca3
LGESC*IFAPANVTSEK	2.3107	Q99N15 17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase OS=Mus musculus GN=Hsd17b10 PE=2 SV=1 , A2AFQ2 Hydroxysteroid (17-beta) dehydrogenase 10 OS=Mus musculus GN=Hsd17b10 PE=3 SV=1 ,	Hsd17b10
VFSANSTAAC*TELAK	2.3103	Q9D0M1 Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Mus musculus GN=Prpsap1 PE=1 SV=1 , B1AT82 MCG6846, isoform CRA_c OS=Mus musculus GN=Prpsap1 PE=4 SV=1 ,	Prpsap1

Peptide	L/H Ratio	Protein	Protein ID
ECVEPEETTSTFC*GTPEYLAPEVLR	2.3022	A2A5N9 Serum/glucocorticoid regulated kinase 2 OS=Mus musculus GN=Sgk2 PE=4 SV=1 , Q9QZS5 Serine/threonine-protein kinase Sgk2 OS=Mus musculus GN=Sgk2 PE=2 SV=1 , E9Q4F0 Uncharacterized protein OS=Mus musculus GN=Sgk2 PE=4 SV=1 ,	Sgk2
AVQMGMSSVFFNKGENC*IAAGR	2.2977	Q8R0Y6 Aldehyde dehydrogenase family 1 member L1 OS=Mus musculus GN=Aldh1l1 PE=2 SV=1 ,	Aldh1l1
GVSVC*ETECTDMGLR	2.2554	Q922Q1 MOSC domain-containing protein 2, mitochondrial OS=Mus musculus GN=Mosc2 PE=1 SV=1 ,	Mosc2
GLVVLGFPC*NQFGHQENGKNEEILNSLK	2.2486	P11352 Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2 ,	Gpx1
LGPNYLQIPVNC*PYR	2.2340	P24270 Catalase OS=Mus musculus GN=Cat PE=1 SV=4 ,	Cat
C*MPTFQFYK	2.2288	P10639 Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3 , A2AV97 Thioredoxin OS=Mus musculus GN=Txn1 PE=3 SV=1 ,	Txn
LVVPATQC*GSLIGK	2.2271	P60335 Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 ,	Pcbp1
C*LTQQAVALQR	2.2174	Q5SW19-3 Isoform 3 of Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 , Q5SW19 Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 PE=2 SV=2 ,	Kiaa0664
C*LQTDMVDITK	2.2111	Q9JIZ0 Probable N-acetyltransferase CML1 OS=Mus musculus GN=Cml1 PE=1 SV=1 , E9PUL7 Uncharacterized protein OS=Mus musculus GN=Cml1 PE=4 SV=1 ,	Cml1
INISEGNC*PER	2.2085	Q61990 Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1 , P60335 Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 , Q61990-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 ,	Pcbp2
LEAPC*QQWMELR	2.2068	Q9CRB3 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1 SV=1 ,	Urah
GYWASLDASTQTTHELTIPNNLIGC*IIGR	2.1907	P60335 Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 ,	Pcbp1
VGGIC*TVIQTK	2.1579	Q8VCB3 Glycogen [starch] synthase, liver OS=Mus musculus GN=Gys2 PE=1 SV=2 ,	Gys2
VNPLGGAIALGHPLGC*TGAR	2.1491	Q921H8 3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=2 SV=1 , Q3UKM0 MCG21883, isoform CRA_e OS=Mus musculus GN=Acaa1b PE=2 SV=1 , Q8VCH0 3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1 ,	Acaa1a
YQALGAELNVLPFC*SQFIPMEVINAPR	2.1482	Q8R0Y6 Aldehyde dehydrogenase family 1 member L1 OS=Mus musculus GN=Aldh1l1 PE=2 SV=1 ,	Aldh1l1
SSFANQGEIC*LCTSR	2.1338	Q8BH00 Aldehyde dehydrogenase family 8 member A1 OS=Mus musculus GN=Aldh8a1 PE=1 SV=1 ,	Aldh8a1
EPGAYDWSSIVQHAC*ELEGDR	2.1326	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=2 SV=1 ,	Inmt
KLGESC*IFAPANVTSEK	2.1315	Q99N15 17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase OS=Mus musculus GN=Hsd17b10 PE=2 SV=1 , A2AFQ2 Hydroxysteroid (17-beta) dehydrogenase 10 OS=Mus musculus GN=Hsd17b10 PE=3 SV=1 ,	Hsd17b10
GLATFC*LDK	2.1294	Q80UU9 Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2 , Q3TFP8 Uncharacterized protein OS=Mus musculus GN=Pgrmc1 PE=2 SV=1 , Q3TXU8 Progesterone receptor membrane component 1 OS=Mus musculus GN=Pgrmc1 PE=2 SV=1 , O55022 Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4 ,	Pgrmc2
EEVVTIDTWMQGLLKPTC*LYGQLPK	2.1217	P19157 Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2 ,	Gstp1

Peptide	L/H Ratio	Protein	Protein ID
SGLTPNDVDVIELHDC*FSVNELITYEALGLCPEGQGGTLVDRGDNTYGGK	2.1073	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 ,	Scp2
GSEVNVIGIGTSVVTC*PK	2.1059	Q8CC86 Nicotinate phosphoribosyltransferase OS=Mus musculus GN=Naprt1 PE=2 SV=1 ,	Naprt1
TVYTFVGQPEC*VVEGALHAAR	2.0849	Q91XD4 Formimidoyltransferase-cyclodeaminase OS=Mus musculus GN=Ftcd PE=1 SV=1 ,	Ftcd
GHSELDTAFMYC*DGQSENILGGLGLGLGSGDCTVK	2.0789	Q8CG76 Aflatoxin B1 aldehyde reductase member 2 OS=Mus musculus GN=Akr7a2 PE=1 SV=3 ,	Akr7a2
IVSNASC*TTNCLAPLAK	2.0668	E9Q9E5 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10481 PE=3 SV=1 , E9QP42 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdhs PE=3 SV=1 , D3Z0Z9 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm5069 PE=3 SV=1 , F6QXU4 Uncharacterized protein (Fragment) OS=Mus musculus PE=4 SV=1 , Q64467 Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Mus musculus GN=Gapdhs PE=1 SV=1 , E9Q1F8 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm8055 PE=3 SV=1 , E9PZH9 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10566 PE=3 SV=1 , D3YV03 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10290 PE=3 SV=1 , E9PZP4 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10313 PE=3 SV=1 , D3YU05 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm6316 PE=3 SV=1 ,	Gm10481
IQEEAGC*LIK	2.0561	P56593 Cytochrome P450 2A12 OS=Mus musculus GN=Cyp2a12 PE=1 SV=2 ,	Cyp2a12
VFIMDSC*DELIPEYLNFIR	2.0446	P11499 Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3 , Q71LX8 Heat shock protein 84b OS=Mus musculus GN=Hsp90ab1 PE=2 SV=1 ,	Hsp90ab1
NINNDTTYC*IK	2.0332	Q99KR3 Beta-lactamase-like protein 2 OS=Mus musculus GN=Lactb2 PE=1 SV=1 ,	Lactb2
TAC*QEYTVTEFQPLYYVAESFNDAK	2.0332	P16331 Phenylalanine-4-hydroxylase OS=Mus musculus GN=Pah PE=1 SV=4 ,	Pah
QVADEGDALVAGGVSQTPSYLSC*K	2.0269	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1 ,	Bhmt
SAGAC*TAAAFLR	2.0215	Q9CPY7-2 Isoform 2 of Cytosol aminopeptidase OS=Mus musculus GN=Lap3 , Q9CPY7 Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3 ,	Lap3
LILADALC*YAHTFNPK	2.0063	Q9CPY7-2 Isoform 2 of Cytosol aminopeptidase OS=Mus musculus GN=Lap3 , Q9CPY7 Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3 ,	Lap3
LTTPTYGDLNHLVSATMSGVTTC*LR	2.0039	Q9D6F9 Tubulin beta-4 chain OS=Mus musculus GN=Tubb4 PE=1 SV=3 , P68372 Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1 , Q9CWF2 Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1 , B2RSN3 MCG1395 OS=Mus musculus GN=Tubb2b PE=2 SV=1 ,	Tubb4
LC*NPPVNAISPTVITEVR	2.0035	Q9DBM2 Peroxisomal bifunctional enzyme OS=Mus musculus GN=Ehhadh PE=1 SV=4 ,	Ehhadh
AIYHSLGLTGIPIINVNNNC*STGSTALFMAH	1.9974	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 ,	Scp2
EDNIPQLEDVSQFLQTC*TGFR	1.9940	P16331 Phenylalanine-4-hydroxylase OS=Mus musculus GN=Pah PE=1 SV=4 ,	Pah
GTNTGVWVGVSGSEASEALSRDP	1.9939	P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 ,	Fasn

Peptide	L/H Ratio	Protein	Protein ID
ETLLGYSMVGC*QR			
LVVPASQC*GSLIGK	1.9931	Q61990 Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1 , Q61990-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 ,	Pcbp2
DNSIIAQATSAAEAFC*AVK	1.9863	Q61635 GTP-binding protein OS=Mus musculus GN=Ifi47 PE=2 SV=1 ,	Ifi47
TWYVQATC*ATQGTGLYEGLDWLSNELSK	1.9847	P61750 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=2 SV=2 , Q14BR4 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=2 SV=1 ,	Arf4
LQDAFSSIGQSC*HLDLPQIAVVGGQSAGK	1.9805	E9Q5S0 Uncharacterized protein OS=Mus musculus GN=Dnm2 PE=3 SV=1 , P39054 Dynamin-2 OS=Mus musculus GN=Dnm2 PE=1 SV=2 , P39054-2 Isoform 2 of Dynamin-2 OS=Mus musculus GN=Dnm2 , Q3T9X3 Uncharacterized protein OS=Mus musculus GN=Dnm2 PE=2 SV=1 ,	Dnm2
VSLCGGGYC*ISK	1.9774	O88451 Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=2 SV=1 ,	Rdh7
TPPLGSAQVPLADC*VLTFLAMECACPDIDTYR	1.9697	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=2 SV=1 ,	Inmt
SVFPEVDIVVPGIC*IANTDTR	1.9566	Q8C165 Probable carboxypeptidase PM20D1 OS=Mus musculus GN=Pm20d1 PE=2 SV=1 ,	Pm20d1
TCSC*LDENYYK	1.9403	O09173 Homogentisate 1,2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2 ,	Hgd
SDFNLENLAIC*GSNLFTAGTETTSTTLR	1.9271	E9Q5K4 Uncharacterized protein OS=Mus musculus GN=Cyp2c44 PE=3 SV=1 ,	Cyp2c44
VIEINPYLLGTMSGC*AADCQYWER	1.9259	P28063 Proteasome subunit beta type-8 OS=Mus musculus GN=Psmb8 PE=1 SV=2 ,	Psmb8
VIEINPYLLGTMAGGAADC*SFWER	1.9143	O55234 Proteasome subunit beta type-5 OS=Mus musculus GN=Psmb5 PE=1 SV=3 , D3Z2T2 Proteasome subunit beta type OS=Mus musculus GN=Psmb5 PE=3 SV=1 ,	Psmb5
ILQACGGNSLGSYSASQGVNC*IR	1.9081	Q8BGT5 Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=2 SV=1 ,	Gpt2
NWYVQPSC*ATSGDGLYEGLTWLTSNYK	1.9014	Q3U0D7 Putative uncharacterized protein OS=Mus musculus GN=Arf6 PE=2 SV=1 , P62331 ADP-ribosylation factor 6 OS=Mus musculus GN=Arf6 PE=1 SV=2 ,	Arf6
ALTNHTVYC*STK	1.8954	Q91X52 L-xylulose reductase OS=Mus musculus GN=Dcxr PE=2 SV=2 , A2AC15 Dicarbonyl L-xylulose reductase OS=Mus musculus GN=Dcxr PE=3 SV=1 ,	Dcxr
AATMSAVEAATC*R	1.8943	Q9DCC4 Pyrroline-5-carboxylate reductase 3 OS=Mus musculus GN=Pycrl PE=2 SV=2 ,	Pycrl
AAVEEGIVLGGGC*ALLR	1.8876	P63038 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 ,	Hspd1
LSTPLQTNC*TASESVVQSPSVATTASPATK	1.8863	P31230 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus GN=Aimp1 PE=1 SV=2 , Q3UZG4 Putative uncharacterized protein OS=Mus musculus GN=Aimp1 PE=2 SV=1 ,	Aimp1
TPPLGSAQVPLADCVLTFLAMEC*ACPDIDTYR	1.8857	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=2 SV=1 ,	Inmt
C*GYDLDGCPVWYDIIGPLDAK	1.8778	Q99J08 SEC14-like protein 2 OS=Mus musculus GN=Sec14l2 PE=2 SV=1 , Q5SQ25 SEC14-like 2 (S. cerevisiae) OS=Mus musculus GN=Sec14l2 PE=2 SV=1 ,	Sec14l2
TIYAGNALC*TVK	1.8688	Q99LC5 Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2 , B1B1B4 Electron transferring flavoprotein, alpha polypeptide OS=Mus musculus GN=Etfa PE=4 SV=1 ,	Etfa
ALEDAQIPYSAVEQAC*VGYVYGDSTSGQR	1.8657	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 ,	Scp2

Peptide	L/H Ratio	Protein	Protein ID
WFTPVSEVPLC*GHATLASAAVLFHK	1.8636	Q9DCG6 Phenazine biosynthesis-like domain-containing protein 1 OS=Mus musculus GN=Pbld1 PE=2 SV=2 ,	Pbld1
IFSYEC*R	1.8625	P58710 L-gulonolactone oxidase OS=Mus musculus GN=Gulo PE=1 SV=3 ,	Gulo
VIVVGNPANTNC*LTASK	1.8596	P14152 Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3 ,	Mdh1
LLEETGIC*VVPGSGFGQR	1.8479	Q8BGT5 Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=2 SV=1 ,	Gpt2
VC*FGIQLLNAVAR	1.8470	E9Q3B9 Uncharacterized protein OS=Mus musculus GN=Mgll PE=4 SV=1 , O35678 Monoglyceride lipase OS=Mus musculus GN=Mgll PE=1 SV=1 , D3YYS6 Uncharacterized protein OS=Mus musculus GN=Mgll PE=4 SV=1 ,	Mgll
ELLTEFGYKGEETPVIVGSALC*ALEQR	1.8444	Q8BFR5-2 Isoform 2 of Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm , Q8BFR5 Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1 ,	Tufm
ISLGLPVGAVINC*ADNTGAK	1.8389	A2A6F9 Ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=3 SV=1 , P62830 60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1 ,	Rpl23
SGQGAFGNMC*R	1.8375	Q564E8 Ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=2 SV=1 , Q9D8E6 60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3 ,	Rpl4
DIGQC*LTNFSK	1.8228	E9Q7C8 Uncharacterized protein OS=Mus musculus GN=Cyp2c40 PE=3 SV=1 , Q569X9 Cytochrome P450, family 2, subfamily c, polypeptide 67 OS=Mus musculus GN=Cyp2c67 PE=2 SV=1 , P56657 Cytochrome P450 2C40 OS=Mus musculus GN=Cyp2c40 PE=2 SV=2 , E9PXC3 Uncharacterized protein OS=Mus musculus GN=Cyp2c69 PE=3 SV=1 , E9QAE5 Uncharacterized protein OS=Mus musculus GN=Cyp2c68 PE=3 SV=1 ,	Cyp2c40
VCLIGC*GFSTGYGSAVK	1.8111	Q3UKA4 Alcohol dehydrogenase 1 (Class I), isoform CRA_c OS=Mus musculus GN=Adh1 PE=2 SV=1 , P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2 ,	Adh1
VVGYFVSGC*DPTIMGIGPVPAINGALK	1.8071	Q8BWT1 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 ,	Acaa2
AQGTGELTQLLNSLC*TAIK	1.8044	Q9QXD6 Fructose-1,6-bisphosphatase 1 OS=Mus musculus GN=Fbp1 PE=2 SV=3 ,	Fbp1
DAEVVLC*GGTESMSQSPYCVR	1.8012	Q8BWT1 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 ,	Acaa2
VALVC*TGSEGSSITNSQLDAR	1.7992	Q4LDG0 Bile acyl-CoA synthetase OS=Mus musculus GN=Slc27a5 PE=2 SV=2 ,	Slc27a5
AAAPAPEEEMDEC*EQALAAEPK	1.7885	Q4FZK2 Eukaryotic translation elongation factor 1 gamma OS=Mus musculus GN=Eef1g PE=2 SV=1 , Q9D8N0 Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3 ,	Eef1g
VDEFPLC*GHMVSDEYEQLSSEALEAAR	1.7802	P86048 60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=1 , Q6ZWV3 60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3 ,	Rpl10l
EAELLC*WEDSAGHWLYE	1.7705	Q9WV85 Nucleoside diphosphate kinase 3 OS=Mus musculus GN=Nme3 PE=2 SV=3 ,	Nme3
FC*CVDVLEILPYLSCLTASDQDR	1.7702	A2ANC9 Novel protein (D430028G21Rik) OS=Mus musculus GN=Mavs PE=4 SV=1 , Q8VCF0 Mitochondrial antiviral-signaling protein OS=Mus musculus GN=Mavs PE=1 SV=1 ,	Mavs
YCVGDEVSMADVC*LVPQVANAER	1.7667	Q9WVL0 Maleylacetoacetate isomerase OS=Mus musculus GN=Gstz1 PE=1 SV=1 ,	Gstz1
MEC*CDVPAETLYDVLHDIEYR	1.7576	Q66JR2 Stard10 protein (Fragment) OS=Mus musculus GN=Stard10 PE=2 SV=1 , E9PVP0 Uncharacterized protein OS=Mus musculus GN=Stard10 PE=4 SV=1 , Q0VG22 START domain containing 10 OS=Mus musculus GN=Stard10 PE=2 SV=1 , Q9JMD3 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 , E9PVT5 Uncharacterized protein OS=Mus musculus GN=Stard10 PE=4 SV=1 ,	Stard10

Peptide	L/H Ratio	Protein	Protein ID
QASVGAGIPYSVPAWSCQMIC*GSGLK	1.7576	Q8CAY6 Acetyl-CoA acetyltransferase, cytosolic OS=Mus musculus GN=Acat2 PE=1 SV=2 , Q80X81 Acetyl-Coenzyme A acetyltransferase 3 OS=Mus musculus GN=Acat3 PE=2 SV=1 ,	Acat2
VLTLDTMNPC*VR	1.7562	Q8QZR5 Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=2 SV=3 , Q566C3 Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=2 SV=1 ,	Gpt
VFANPEDC*AGFGK	1.7548	Q53ZD4 Microsomal glutathione S-transferase 1 OS=Mus musculus GN=Mgst1 PE=2 SV=1 , Q91VS7 Microsomal glutathione S-transferase 1 OS=Mus musculus GN=Mgst1 PE=1 SV=3 , E9QJW0 Uncharacterized protein OS=Mus musculus GN=Mgst1 PE=4 SV=1 ,	Mgst1
C*PGLLTPSQIKPGTYK	1.7466	Q9CRB3 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1 SV=1 ,	Urah
GEGILC*GTPEEVWDCIKPVASGLR	1.7389	D3YU00 StAR-related lipid transfer (START) domain containing 5, isoform CRA_a OS=Mus musculus GN=Stard5 PE=4 SV=1 , Q9EPQ7 StAR-related lipid transfer protein 5 OS=Mus musculus GN=Stard5 PE=2 SV=2 ,	Stard5
VILSSSSSC*LLPSK	1.7287	A7VMV2 Crystallin, lamda 1, isoform CRA_a OS=Mus musculus GN=Cryl1 PE=2 SV=1 , Q99KP3 Lambda-crystallin homolog OS=Mus musculus GN=Cryl1 PE=2 SV=3 ,	Cryl1
C*MALSTAILVGEAK	1.7227	Q9EQ20 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1 , Q8K0L1 Aldh6a1 protein OS=Mus musculus GN=Aldh6a1 PE=2 SV=1 ,	Aldh6a1
VVMALGDYMGASCHAC*IGGTNVR	1.7198	Q5F2A7 Eukaryotic translation initiation factor 4A1 OS=Mus musculus GN=Eif4a1 PE=2 SV=1 , P60843 Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=2 SV=1 ,	Eif4a1
VSHALAEGLGVIAC*IGEK	1.7193	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3 ,	Tpi1
ILATAVC*HTDAYTLSGADPEGCFPVILGHEGAGIVESVGEGVTK	1.7139	Q6P5I3 Alcohol dehydrogenase 5 (Class III), chi polypeptide OS=Mus musculus GN=Adh5 PE=2 SV=2 , P28474 Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3 ,	Adh5
VNEAAC*DIAR	1.7127	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1 ,	Bhmt
IIYGGSVTGATC*K	1.7092	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3 ,	Tpi1
ASVGFGGSC*FQK	1.7067	D3Z3F7 Uncharacterized protein OS=Mus musculus GN=Ugdh PE=4 SV=1 , O70475 UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1 , Q3TS38 UDP-glucose dehydrogenase OS=Mus musculus GN=Ugdh PE=2 SV=1 ,	Ugdh
NIC*FTVWDVGGQDK	1.7052	P84084 ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=2 SV=2 , P61750 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=2 SV=2 , Q14BR4 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=2 SV=1 ,	Arf5
GLIAAIC*AGPTALLAHEVGFGCK	1.7040	Q99LX0 Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1 , A2A813 Parkinson disease (Autosomal recessive, early onset) 7 OS=Mus musculus GN=Park7 PE=4 SV=1 , A2A815 Parkinson disease (Autosomal recessive, early onset) 7 (Fragment) OS=Mus musculus GN=Park7 PE=4 SV=1 ,	Park7
SGDAAIVDMVPGKPMC*VESFSDYPPLGR	1.7036	P10126 Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 , Q58E64 Elongation factor 1-alpha OS=Mus musculus GN=Eef1a1 PE=2 SV=1 ,	Eef1a1
IYHPNINSNGSIC*LDILR	1.7012	P62838 Ubiquitin-conjugating enzyme E2 D2 OS=Mus musculus GN=Ube2d2 PE=1 SV=1 , Q3UT95 Ubiquitin carrier protein OS=Mus musculus GN=Ube2d2 PE=2 SV=1 , P61079 Ubiquitin-conjugating enzyme E2 D3 OS=Mus musculus GN=Ube2d3 PE=1 SV=1 , Q4QQL2 Ubiquitin carrier protein OS=Mus musculus GN=Ube2d3 PE=2 SV=1 ,	Ube2d2
GC*LLYGPPGTGK	1.6950	P62334 26S protease regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1 , Q14AQ1 Proteasome (Prosome, macropain) 26S subunit, ATPase, 6 OS=Mus musculus GN=Psmc6 PE=2 SV=1 ,	Psmc6
VLVC*GAGPVGMVTLLVAK	1.6928	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 ,	Sord

Peptide	L/H Ratio	Protein	Protein ID
NMSVHLSPC*FR	1.6894	D3Z3M6 MCG49907 OS=Mus musculus GN=Gm9808 PE=3 SV=1 , P62281 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3 , Q3UC02 MCG23457 OS=Mus musculus GN=Rps11 PE=2 SV=1 , E9PXE7 Uncharacterized protein OS=Mus musculus GN=Rps11 PE=3 SV=1 ,	Gm9808
GHISAGSNQTMVVSGAAGAC*GSLAGQIGHLLGCSR	1.6819	Q3TXN1 Uncharacterized protein OS=Mus musculus GN=Ptgr2 PE=2 SV=1 , Q8VDQ1 Prostaglandin reductase 2 OS=Mus musculus GN=Ptgr2 PE=1 SV=2 , Q8VDQ1-2 Isoform 2 of Prostaglandin reductase 2 OS=Mus musculus GN=Ptgr2 ,	Ptgr2
GVLFGVPGAFTPGC*SK	1.6810	E9Q9H9 Uncharacterized protein OS=Mus musculus GN=Prdx5 PE=4 SV=1 , P99029 Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2 , P99029-2 Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 ,	Prdx5
IGPALSC*GNTVVVKPAEQTPLTALHLASLIK	1.6801	P24549 Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5 ,	Aldh1a1
AVLEALGSC*LNNK	1.6795	P50431 Serine hydroxymethyltransferase, cytosolic OS=Mus musculus GN=Shmt1 PE=1 SV=3 ,	Shmt1
CPALYWLSGLTC*TEQNFISK	1.6790	Q9R0P3 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=2 SV=1 ,	Esd
TFPSLLVACDVCLC*PYTSHGHCGLLSENGAFLAEESR	1.6786	P10518 Delta-aminolevulinic acid dehydratase OS=Mus musculus GN=Alad PE=1 SV=1 ,	Alad
ITAFVPNDGC*LNFIEENDEVLVAGFGR	1.6734	Q9CZI5 Uncharacterized protein OS=Mus musculus GN=Rps23 PE=2 SV=1 , P62267 40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3 ,	Rps23
FYDVALDTGDKVVQC*GR	1.6723	Q9DBE0 Cysteine sulfinic acid decarboxylase OS=Mus musculus GN=Csad PE=2 SV=1 ,	Csad
VLSMTETC*R	1.6696	Q3TXS7 26S proteasome non-ATPase regulatory subunit 1 OS=Mus musculus GN=Psmd1 PE=1 SV=1 ,	Psmd1
AERPDGLILGMGGQTALNC*GVELFK	1.6685	Q8C196 Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 ,	Cps1
AIQSLTDTC*SDDLSVVTDCMEHALTACHPR	1.6606	O88451 Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=2 SV=1 ,	Rdh7
NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDC*HTAHIACK	1.6507	P10126 Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 , Q58E64 Elongation factor 1-alpha OS=Mus musculus GN=Eef1a1 PE=2 SV=1 ,	Eef1a1
AIVDALPPPCESAC*SLPTDVDKWFHQQK	1.6462	Q4FK49 Pyp protein OS=Mus musculus GN=Ppa1 PE=2 SV=1 , Q9D819 Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1 ,	Ppa1
DAEVVLCGGTESMSQSPYC*VR	1.6436	Q8BWT1 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 ,	Acaa2
GVLLYGPPGC*GK	1.6380	Q9D5T0 ATPase family AAA domain-containing protein 1 OS=Mus musculus GN=Atad1 PE=1 SV=1 ,	Atad1
C*VEELPEWNFDGSSTFQSEGSNSDMYLHPVAMFR	1.6367	P15105 Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6 ,	Glul
SGEEDFESLASQFSDC*SSAK	1.6365	Q9QUR7 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Mus musculus GN=Pin1 PE=1 SV=1 ,	Pin1
LC*YVALDFEQEMATAASSSSLEK	1.6357	P60710 Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 , P63260 Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 , B2RRX1 Actin, beta OS=Mus musculus GN=Actb PE=2 SV=1 , Q4KL81 Actin, gamma, cytoplasmic 1 OS=Mus musculus GN=Actg1 PE=2 SV=1 ,	Actb
FELTC*YSLAPQIK	1.6268	P16460 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1 , Q3UJ34 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=2 SV=1 ,	Ass1

Peptide	L/H Ratio	Protein	Protein ID
NQSFC*PTVNLDKLWTLVSEQTR	1.6240	P14115 60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=5 , D3Z6J9 Uncharacterized protein OS=Mus musculus GN=Gm5908 PE=3 SV=1 ,	Rpl27a
DVLSGDGFDAVICLGNSFAHLPDC*K	1.6214	A9C489 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=3 SV=1 , Q9QXF8 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=1 SV=3 ,	Gnmt
ADC*TITMADSDLLALMTGK	1.6155	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 ,	Scp2
QQIACIGGPPNIC*LDRLENWITSLAESQLQTR	1.6108	Q6GU23 Signal transducer and activator of transcription 3 OS=Mus musculus GN=Stat3 PE=2 SV=1 , P42227-3 Isoform Del-701 of Signal transducer and activator of transcription 3 OS=Mus musculus GN=Stat3 , P42227-2 Isoform Stat3B of Signal transducer and activator of transcription 3 OS=Mus musculus GN=Stat3 , P42227 Signal transducer and activator of transcription 3 OS=Mus musculus GN=Stat3 PE=1 SV=2 ,	Stat3
ELDLSNNC*MGGPGVLQLLESLK	1.6075	Q91VI7 Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1 ,	Rnh1
GQNNPQVC*PYNLYAEQLSGSAFTCPR	1.6064	O09173 Homogentisate 1,2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2 ,	Hgd
AYLMSQPLAYHTPDC*GK	1.6018	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1 ,	Bhmt
AIVDALPPPC*ESACSLPTDVDK	1.5994	Q9D819 Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1 , Q4FK49 Pyp protein OS=Mus musculus GN=Ppa1 PE=2 SV=1 , E9Q5Z3 Uncharacterized protein OS=Mus musculus GN=Ppa1 PE=4 SV=1 ,	Ppa1
C*LLTTVDPDTGISDR	1.5986	Q9CW42 MOSC domain-containing protein 1, mitochondrial OS=Mus musculus GN=Mosc1 PE=1 SV=2 , D3YZZ3 Uncharacterized protein OS=Mus musculus GN=Mosc1 PE=4 SV=1 ,	Mosc1
CPEALFQPSFLGMESC*GIHETTFNSIMK	1.5958	P60710 Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 , P63260 Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 , B2RRX1 Actin, beta OS=Mus musculus GN=Actb PE=2 SV=1 , Q4KL81 Actin, gamma, cytoplasmic 1 OS=Mus musculus GN=Actg1 PE=2 SV=1 ,	Actb
C*GESPVWEEASQSLLFVDIPSK	1.5910	Q64374 Regucalcin OS=Mus musculus GN=Rgn PE=1 SV=1 ,	Rgn
AWVWNTHADFADEC*PKPELLAIR	1.5885	P34022 Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2 ,	Ranbp1
LTLLEVGC*GTGANFK	1.5884	Q8C6B0 MCG20149, isoform CRA_a OS=Mus musculus GN=Mettl7a1 PE=2 SV=1 , Q5K4Q9 AAM-B protein OS=Mus musculus GN=Mettl7a1 PE=2 SV=1 ,	Mettl7a1
ASATGMIIMDSVEVPEENVLPNVSSLAGPFGC*LNTAR	1.5845	Q60759 Glutaryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Gcdh PE=2 SV=2 ,	Gcdh
CLGELIC*TLNAANVPAGTEVVCAPPTAYIDFAR	1.5749	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3 ,	Tpi1
TC*GFDFSGALEDISK	1.5729	P05202 Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1 ,	Got2
LTEGC*SFR	1.5650	Q6ZWU9 40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3 , Q6ZWY3 40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=2 SV=3 , E9QAB4 Uncharacterized protein OS=Mus musculus GN=Gm17241 PE=3 SV=1 ,	Rps27
VAPEEVSEVIFGHVLTAGC*GQNPTR	1.5613	Q8CAY6 Acetyl-CoA acetyltransferase, cytosolic OS=Mus musculus GN=Acat2 PE=1 SV=2 , Q80X81 Acetyl-Coenzyme A acetyltransferase 3 OS=Mus musculus GN=Acat3 PE=2 SV=1 ,	Acat2
C*MTEEIFGPVTCVVPFDSEEEVITR	1.5610	Q8BH00 Aldehyde dehydrogenase family 8 member A1 OS=Mus musculus GN=Aldh8a1 PE=1 SV=1 ,	Aldh8a1
VPTPNVSVVDLTC*R	1.5584	E9Q9E5 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10481 PE=3 SV=1 , E9QP42 Glyceraldehyde-3-phosphate	Gm10481

Peptide	L/H Ratio	Protein	Protein ID
		dehydrogenase OS=Mus musculus GN=Gapdhs PE=3 SV=1 , Q64467 Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Mus musculus GN=Gapdhs PE=1 SV=1 , E9PZH9 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10566 PE=3 SV=1 ,	
EQGVTFPSGEVQEQLIC*SLYQPAGLAPESLEYIEAHGTGTK	1.5529	P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 ,	Fasn
SWC*PDCVEAEPVIR	1.5513	Q9CQM5 Thioredoxin domain-containing protein 17 OS=Mus musculus GN=Txndc17 PE=1 SV=1 ,	Txndc17
GYVSC*ALGCPYEGK	1.5468	P38060 Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Mus musculus GN=Hmgcl PE=1 SV=2 ,	Hmgcl
VQQEIDEVIGQVQC*PEMADQAR	1.5427	Q9JKY7 Cytochrome P450 CYP2D22 OS=Mus musculus GN=Cyp2d22 PE=2 SV=1 ,	Cyp2d22
IDGASPLDKVCLIGC*GFSTGYGSAVK	1.5419	Q3UKA4 Alcohol dehydrogenase 1 (Class I), isoform CRA_c OS=Mus musculus GN=Adh1 PE=2 SV=1 , P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2 ,	Adh1
EGIC*ALGGTSELSSEGTQHSYSEEEKYAFVNWINK	1.5402	B1AX58 Plastin 3 (T-isoform) OS=Mus musculus GN=Pls3 PE=4 SV=1 , Q99K51 Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3 ,	Pls3
TYITDPVSAPC*APPLQPK	1.5388	Q8BFW7 Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp PE=1 SV=1 , Q8BFW7-4 Isoform 4 of Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp ,	Lpp
ALANVNIGSLIC*NVGAGGPAPAAGAAPAGGAAPSTAAAPAEEK	1.5381	Q58E35 MCG10168 OS=Mus musculus GN=Rplp1 PE=4 SV=1 , P47955 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1 ,	Rplp1
EVESVTPEHC*IFASNTSALPINQIAAVSK	1.5354	Q8BMS1 Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 ,	Hadha
TGIQTSC*LCPVFVNTGFTK	1.5338	A8Y5N6 Hydroxysteroid (17-beta) dehydrogenase 13 OS=Mus musculus GN=Hsd17b13 PE=3 SV=1 , A8Y5N5 Hydroxysteroid (17-beta) dehydrogenase 13 OS=Mus musculus GN=Hsd17b13 PE=3 SV=1 ,	Hsd17b13
VILITPPPLC*EAAWEK	1.5314	Q9DB29 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Mus musculus GN=Iah1 PE=2 SV=1 ,	Iah1
QVCQLPGLFC*YAQHIASIDGR	1.5298	A2AFW7 MCG13498, isoform CRA_d OS=Mus musculus GN=Mtch2 PE=3 SV=1 , Q791V5 Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtch2 PE=1 SV=1 ,	Mtch2
VPTPNVSVVDLTC*R	1.5296	E9PZH9 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10566 PE=3 SV=1 , E9PX42 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm2606 PE=3 SV=1 ,	Gm10566
AFVFDVLHEGC*LITPPELLR	1.5284	Q9DC50 Peroxisomal carnitine O-octanoyltransferase OS=Mus musculus GN=Crot PE=1 SV=1 ,	Crot
IIPGFMC*QGGDFTR	1.5263	P17742 Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2 , Q5SVY2 Peptidyl-prolyl cis-trans isomerase OS=Mus musculus GN=Ppia PE=2 SV=1 ,	Ppia
LNISFPATGC*QK	1.5241	P62754 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1 , Q5BLK1 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=2 SV=1 ,	Rps6
GVILTSEC*PGIFSAGLDLLEMYGR	1.5233	Q8QZV3 Dci protein OS=Mus musculus GN=Eci1 PE=2 SV=1 ,	Eci1
IPFLEFSC*PGVPPGLETLK	1.5218	D3Z3G5 Uncharacterized protein OS=Mus musculus GN=Sult1a1 PE=4 SV=1 , Q91W19 Sulfotransferase family 1A, phenol-preferring, member 1 OS=Mus musculus GN=Sult1a1 PE=2 SV=1 , E9QNL5 Uncharacterized protein OS=Mus musculus GN=Sult1a1 PE=4 SV=1 , P52840 Sulfotransferase 1A1 OS=Mus musculus GN=Sult1a1 PE=2 SV=1 ,	Sult1a1
GTPEQPQC*GFSNAVVQILR	1.5088	Q80Y14 Glutaredoxin-related protein 5, mitochondrial OS=Mus musculus GN=Glrx5 PE=2 SV=2 ,	Glrx5

Peptide	L/H Ratio	Protein	Protein ID
LLACIASRPGQC*GR	1.5051	Q497E9 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=2 SV=1 , P62242 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2 , Q5SZV3 40S ribosomal protein S8 OS=Mus musculus GN=Gm11353 PE=3 SV=1 ,	Rps8
LAAASSVC*EVVR	1.5045	Q91X44 Glucokinase regulatory protein OS=Mus musculus GN=Gckr PE=2 SV=3 ,	Gckr
VDLNSNGFIC*DYELHELFK	1.5042	B1AX58 Plastin 3 (T-isoform) OS=Mus musculus GN=Pls3 PE=4 SV=1 , Q99K51 Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3 ,	Pls3
IVLAAAGGVC*HNELLELAK	1.4918	Q9CXT8 Mitochondrial-processing peptidase subunit beta OS=Mus musculus GN=Pmpcb PE=2 SV=1 ,	Pmpcb
LC*GSGFQSIVSGCQEICSK	1.4862	Q8BWT1 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 ,	Acaa2
VC*NYGLTFTQK	1.4845	Q3TX38 Putative uncharacterized protein OS=Mus musculus GN=Vdac3 PE=2 SV=1 , Q60931 Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1 ,	Vdac3
DAFEHIVTQFSSVPVSVVSDSYDIYNAC*EK	1.4825	Q99KQ4 Nicotinamide phosphoribosyltransferase OS=Mus musculus GN=Nampt PE=1 SV=1 ,	Nampt
YLLGTSLARPC*IAR	1.4821	P16460 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1 , Q3UJ34 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=2 SV=1 ,	Ass1
VAC*IGAWHPAR	1.4787	P27659 60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=3 ,	Rpl3
MTPGC*EAEAEAEALCFFIK	1.4783	P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 ,	Fasn
TC*FSMVPALQK	1.4781	P85094 Isochorismatase domain-containing protein 2A, mitochondrial OS=Mus musculus GN=Isoc2a PE=2 SV=1 ,	Isoc2a
WSSC*NIFSTQDHAAAAIAK	1.4691	P50247 Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3 , Q3TF14 Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=2 SV=1 ,	Ahcy
LPDSVTFEEGALIEPLSVGIYAC*R	1.4645	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 ,	Sord
C*LGELICTLNAANVPAGTEVVCAPPTAYIDFAR	1.4582	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3 ,	Tpi1
SAYALGGLGSGIC*PNK	1.4578	Q8C196 Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 ,	Cps1
LLLGPC*TPVQYR	1.4568	P97872 Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Mus musculus GN=Fmo5 PE=2 SV=4 ,	Fmo5
VAASDWTFLHC*LPR	1.4527	P11725 Ornithine carbamoyltransferase, mitochondrial OS=Mus musculus GN=Otc PE=1 SV=1 , Q8R1A8 Ornithine transcarbamylase OS=Mus musculus GN=Otc PE=2 SV=1 , Q543H3 Ornithine transcarbamylase OS=Mus musculus GN=Otc PE=2 SV=1 ,	Otc
GYVSCALGC*PYEGK	1.4438	P38060 Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Mus musculus GN=Hmgcl PE=1 SV=2 ,	Hmgcl
C*EFQDAYVLLSEK	1.4384	P63038 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 ,	Hspd1
GPSIALDTAC*SSSLLALQNAYQAIR	1.4377	P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 ,	Fasn
VPAFEGDDGFC*VFESNAIAYYVSNEELR	1.4359	Q4FZK2 Eukaryotic translation elongation factor 1 gamma OS=Mus musculus GN=Eef1g PE=2 SV=1 , Q9D8N0 Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3 ,	Eef1g
TGC*TFPEKPDFH	1.4229	P55264 Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2 , P55264-2 Isoform Short of Adenosine kinase OS=Mus musculus GN=Adk ,	Adk
DYPLELFMSQC*YGNVNDPGK	1.4123	Q3U3J1 Branched chain ketoacid dehydrogenase E1, alpha polypeptide OS=Mus musculus GN=Bckdha PE=2 SV=1 ,	Bckdha
ILLAGC*PSYDK	1.4121	Q3TCI8 Glucosamine OS=Mus musculus GN=Gne PE=2 SV=1 , Q91WG8 Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Mus musculus GN=Gne PE=1 SV=1 , Q3UW64 UDP-N-	Gne

Peptide	L/H Ratio	Protein	Protein ID
		acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Mus musculus GN=Gne PE=2 SV=1 ,	
METYC*NSGSTDTSSVINAVTHALTAATPYTR	1.4118	Q80XN0 D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Mus musculus GN=Bdh1 PE=1 SV=2 ,	Bdh1
VC*IDSEHSSDTLLATLNK	1.4092	O08997 Copper transport protein ATOX1 OS=Mus musculus GN=Atox1 PE=2 SV=1 ,	Atox1
YIC*TTSAIQNR	1.4088	Q3V117 ATP citrate lyase OS=Mus musculus GN=Acly PE=2 SV=1 , A2A4H2 ATP citrate lyase OS=Mus musculus GN=Acly PE=4 SV=1 , Q91V92 ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1 ,	Acly
SVSAFAPICNPVLC*SWGK	1.4084	Q9R0P3 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=2 SV=1 ,	Esd
LSYYPHC*LASFTELVR	1.4058	A9C489 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=3 SV=1 , Q9QXF8 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=1 SV=3 ,	Gnmt
ANPYEC*GFDPTSSAR	1.4032	P03899 NADH-ubiquinone oxidoreductase chain 3 OS=Mus musculus GN=Mtnd3 PE=3 SV=3 , F6TR71 Uncharacterized protein (Fragment) OS=Mus musculus GN=mt-Nd3 PE=4 SV=1 ,	Mtnd3
SC*SGVEFSTSGSSNTDTGK	1.4031	Q60930 Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2 ,	Vdac2
MECC*DVPAETLYDVLHDIEYR	1.3961	Q66JR2 Stard10 protein (Fragment) OS=Mus musculus GN=Stard10 PE=2 SV=1 , E9PVP0 Uncharacterized protein OS=Mus musculus GN=Stard10 PE=4 SV=1 , Q0VG22 START domain containing 10 OS=Mus musculus GN=Stard10 PE=2 SV=1 , Q9JMD3 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 , E9PVT5 Uncharacterized protein OS=Mus musculus GN=Stard10 PE=4 SV=1 ,	Stard10
C*PFTGNVSIR	1.3950	D3Z3M6 MCG49907 OS=Mus musculus GN=Gm9808 PE=3 SV=1 , P62281 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3 , Q3UC02 MCG23457 OS=Mus musculus GN=Rps11 PE=2 SV=1 , E9PXE7 Uncharacterized protein OS=Mus musculus GN=Rps11 PE=3 SV=1 ,	Gm9808
FCCVDVLEILPYLSC*LTASDQDR	1.3907	A2ANC9 Novel protein (D430028G21Rik) OS=Mus musculus GN=Mavs PE=4 SV=1 , Q8VCF0 Mitochondrial antiviral-signaling protein OS=Mus musculus GN=Mavs PE=1 SV=1 ,	Mavs
QATLGAGLPISTPC*TTVNK	1.3903	Q8QZT1 Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1 ,	Acat1
TCSLTAASCPYFC*SVLTK	1.3849	Q91VI7 Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1 ,	Rnh1
SDDHVVSGTLVTPLPAVLGHEGAGIVESVGEGVTC*VKPGDK	1.3804	Q3UKA4 Alcohol dehydrogenase 1 (Class I), isoform CRA_c OS=Mus musculus GN=Adh1 PE=2 SV=1 , P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2 ,	Adh1
VGEVPLADSILC*DGLTDAFHNYHMGITAENVAK	1.3764	Q80X81 Acetyl-Coenzyme A acetyltransferase 3 OS=Mus musculus GN=Acat3 PE=2 SV=1 ,	Acat3
AFAFVTFADDKVAQSLC*GEDLIIK	1.3761	Q6VYI4 TAR DNA binding protein OS=Mus musculus GN=Tardbp PE=2 SV=1 , Q544R5 MCG16669, isoform CRA_b OS=Mus musculus GN=Tardbp PE=2 SV=1 , Q921F2 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 , Q8R0B4 MCG16669, isoform CRA_a OS=Mus musculus GN=Tardbp PE=2 SV=1 , Q8BLD4 MCG16669, isoform CRA_f OS=Mus musculus GN=Tardbp PE=2 SV=1 , Q6VYI5 TAR DNA binding protein OS=Mus musculus GN=Tardbp PE=2 SV=1 ,	Tardbp
TDDYLDQPCC*ETINR	1.3660	Q61598-2 Isoform 2 of Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 , Q61598 Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1 ,	Gdi2
FAELVYTGFWHSPEC*EFVR	1.3655	P16460 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1 , Q3UJ34 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=2 SV=1 ,	Ass1
IGIASQALGIAQASLDC*AVK	1.3642	Q07417 Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acads PE=2 SV=2 ,	Acads

Peptide	L/H Ratio	Protein	Protein ID
SLC*LGPTLIYSAK	1.3583	Q9CZB0 Succinate dehydrogenase cytochrome b560 subunit, mitochondrial OS=Mus musculus GN=Sdhc PE=2 SV=1 ,	Sdhc
NELFTDSEC*QEISAVTGNPVHESLK	1.3522	Q99J39 Malonyl-CoA decarboxylase, mitochondrial OS=Mus musculus GN=Mlycd PE=2 SV=1 , F6ZUJ0 Uncharacterized protein (Fragment) OS=Mus musculus GN=Mlycd PE=4 SV=1 , Q99J39-2 Isoform Cytoplasmic+peroxisomal of Malonyl-CoA decarboxylase, mitochondrial OS=Mus musculus GN=Mlycd ,	Mlycd
NVLVIGTTGSQTTFLPEGELPEC*AR	1.3521	A2ADY9 Protein DDI1 homolog 2 OS=Mus musculus GN=Ddi2 PE=1 SV=1 ,	Ddi2
MQLIMLC*YNPDFEK	1.3463	P10649 Glutathione S-transferase Mu 1 OS=Mus musculus GN=Gstm1 PE=1 SV=2 ,	Gstm1
IVFVLC*SALNPWNK	1.3417	P49429 4-hydroxyphenylpyruvate dioxygenase OS=Mus musculus GN=Hpd PE=1 SV=3 ,	Hpd
GC*TATLGNFAK	1.3337	D3YWA0 Uncharacterized protein OS=Mus musculus GN=Gm6139 PE=3 SV=1 ,	Gm6139
NYDYILSTGC*APPGK	1.3192	A9C489 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=3 SV=1 , Q9QXF8 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=1 SV=3 ,	Gnmt
VQQAPIEEHWIIEC*NDGVFQR	1.3172	O35969 Guanidinoacetate N-methyltransferase OS=Mus musculus GN=Gamt PE=1 SV=1 , O35969-2 Isoform 2 of Guanidinoacetate N-methyltransferase OS=Mus musculus GN=Gamt ,	Gamt
IAVNIC*YGR	1.3142	Q3UEK4 Ureidopropionase, beta, isoform CRA_a OS=Mus musculus GN=Upb1 PE=2 SV=1 , Q8VC97 Beta-ureidopropionase OS=Mus musculus GN=Upb1 PE=2 SV=1 ,	Upb1
DGGQYALVAAC*AAGGQGH	1.3128	Q99JY0 Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1 ,	Hadhb
IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK	1.3128	P61979 Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1 , Q5FWJ5 Hnrpk protein OS=Mus musculus GN=Hnrnpk PE=2 SV=1 , D3YWG1 Uncharacterized protein OS=Mus musculus GN=Gm7964 PE=4 SV=1 , P61979-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk ,	Hnrnpk
GENVSTGEVEC*VLSSLDFLEEVNVYGVPVPGCEGK	1.3128	Q4LDG0 Bile acyl-CoA synthetase OS=Mus musculus GN=Slc27a5 PE=2 SV=2 ,	Slc27a5
LGTLHGGLTATLVDSISTMALMC*TER	1.3080	Q4VA32 Thioesterase superfamily member 2 OS=Mus musculus GN=Acot13 PE=2 SV=1 , Q9CQR4 Acyl-coenzyme A thioesterase 13 OS=Mus musculus GN=Acot13 PE=1 SV=1 ,	Acot13
MECC*DVPAETLYDVLHDIEYR	1.3018	Q66JR2 Stard10 protein (Fragment) OS=Mus musculus GN=Stard10 PE=2 SV=1 , E9PVP0 Uncharacterized protein OS=Mus musculus GN=Stard10 PE=4 SV=1 , Q0VG22 START domain containing 10 OS=Mus musculus GN=Stard10 PE=2 SV=1 , Q9JMD3 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 , E9PVT5 Uncharacterized protein OS=Mus musculus GN=Stard10 PE=4 SV=1 ,	Stard10
TMLQNC*LPR	1.2925	Q9QXE0 2-hydroxyacyl-CoA lyase 1 OS=Mus musculus GN=Hacl1 PE=1 SV=2 , D3YZ54 Uncharacterized protein OS=Mus musculus GN=Hacl1 PE=3 SV=2 ,	Hacl1
AAC*LESAQEPAGAWSNK	1.2806	Q8VDJ3 Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1 , Q3U4Z7 High density lipoprotein (HDL) binding protein, isoform CRA_d OS=Mus musculus GN=Hdlbp PE=2 SV=1 ,	Hdlbp
SSFATPGVNVGLFC*STPAVALGR	1.2798	Q9D7J9 Enoyl-CoA hydratase domain-containing protein 3, mitochondrial OS=Mus musculus GN=Echdc3 PE=2 SV=1 ,	Echdc3
CEMASTGEVAC*FGEGIHTAFLK	1.2735	Q8C196 Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 ,	Cps1
GILGYTEDQVVSC*DFNINSHTSTFDAGAGIALNDNFVK	1.2717	F6UT49 Uncharacterized protein (Fragment) OS=Mus musculus PE=4 SV=1 ,	4 SV

Peptide	L/H Ratio	Protein	Protein ID
SLVANLAAANC*YK	1.2717	P55264 Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2 , P55264-2 Isoform Short of Adenosine kinase OS=Mus musculus GN=Adk ,	Adk
DVQIGDIVTVGEC*RPLSK	1.2703	D3Z3M6 MCG49907 OS=Mus musculus GN=Gm9808 PE=3 SV=1 , P62281 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3 , Q3UC02 MCG23457 OS=Mus musculus GN=Rps11 PE=2 SV=1 , E9PXE7 Uncharacterized protein OS=Mus musculus GN=Rps11 PE=3 SV=1 ,	Gm9808
LVEEAIQC*AEK	1.2672	Q8BH95 Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Echs1 PE=1 SV=1 ,	Echs1
TIAEC*LADELINAAK	1.2664	D3YYM6 Uncharacterized protein OS=Mus musculus GN=Rps5 PE=3 SV=1 , Q91V55 Ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=2 SV=1 ,	Rps5
LVIVGDGAC*GK	1.2640	Q62159 Rho-related GTP-binding protein RhoC OS=Mus musculus GN=Rhoc PE=1 SV=2 ,	Rhoc
GLC*AIAQAESLR	1.2569	Q5YLW3 Ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1 , P62908 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1 ,	Rps3
NANC*SIEESFQR	1.2568	P38060 Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Mus musculus GN=Hmgcl PE=1 SV=2 ,	Hmgcl
VTPGSTCAVFGLGGVGLSVIIGC*K	1.2545	Q3UKA4 Alcohol dehydrogenase 1 (Class I), isoform CRA_c OS=Mus musculus GN=Adh1 PE=2 SV=1 , P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2 ,	Adh1
METYC*NSGSTDTSSVINAVTHALTAATPYTR	1.2469	Q80XN0 D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Mus musculus GN=Bdh1 PE=1 SV=2 ,	Bdh1
AGDTVIPLYIPQCGEC*K	1.2381	Q6P5I3 Alcohol dehydrogenase 5 (Class III), chi polypeptide OS=Mus musculus GN=Adh5 PE=2 SV=2 , P28474 Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3 ,	Adh5
LDVGNFSWGSEC*CTR	1.2060	Q497E9 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=2 SV=1 , P62242 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2 , Q5SZV3 40S ribosomal protein S8 OS=Mus musculus GN=Gm11353 PE=3 SV=1 ,	Rps8
YTIVVSATASDAAPLQYLAPYSGC*SMGEYFR	1.2036	D3Z6F5 ATP synthase subunit alpha OS=Mus musculus GN=Atp5a1 PE=3 SV=1 , Q03265 ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1 ,	Atp5a1
VIGSGC*NLDSAR	1.1996	P06151 L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3 , Q564E2 L-lactate dehydrogenase OS=Mus musculus GN=Ldha PE=2 SV=1 ,	Ldha
TSAC*FEPSLDYMVTK	1.1960	Q8C196 Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 ,	Cps1
VAC*ITEQVLTLVNK	1.1950	Q91YQ5 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=2 SV=1 ,	Rpn1
VTDGALVVVDCVSGVC*VQTETVLR	1.1697	P58252 Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2 ,	Eef2
TGPC*PQGPAPEVVIYQQLR	1.1660	Q91YR9 Prostaglandin reductase 1 OS=Mus musculus GN=Ptgr1 PE=2 SV=2 , A2ALW3 Leukotriene B4 12-hydroxydehydrogenase OS=Mus musculus GN=Ptgr1 PE=4 SV=1 ,	Ptgr1
YFAGNLASGGAAGATSLC*FVYPLDFAR	1.1579	P51881 ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3 , Q545A2 MCG11560 OS=Mus musculus GN=Slc25a5 PE=2 SV=1 ,	Slc25a5
VDIDEFDENKFVDEHEEAAAAAGEPGPDPC*EVDGLLR	1.1520	Q9D898 Actin-related protein 2/3 complex subunit 5-like protein OS=Mus musculus GN=Arpc5l PE=1 SV=1 , A3KGQ6 Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5l PE=3 SV=1 ,	Arpc5l
KYESAYGTQFTPC*QLLLDHANNSSK	1.1506	Q8BMS1 Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 ,	Hadha
VQELSLSAPLTVLPTVTC*EDTIAILR	1.1506	Q91WT9 Cystathionine beta-synthase OS=Mus musculus GN=Cbs PE=2 SV=3 ,	Cbs
VTC*VDPNPNFEK	1.1505	Q9DD20 Methyltransferase-like protein 7B OS=Mus musculus GN=Mettl7b PE=2 SV=2 ,	Mettl7b

Peptide	L/H Ratio	Protein	Protein ID
ATFHTPFSQLGQSPEAC*SSYTFPK	1.1467	Q3TCD4 Putative uncharacterized protein OS=Mus musculus GN=Eci2 PE=2 SV=1 , Q9WUR2-2 Isoform 2 of Enoyl-CoA delta isomerase 2, mitochondrial OS=Mus musculus GN=Eci2 , Q9WUR2 Enoyl-CoA delta isomerase 2, mitochondrial OS=Mus musculus GN=Eci2 PE=1 SV=2 ,	Eci2
ASFENNC*EVGCFAK	1.1455	O55135 Eukaryotic translation initiation factor 6 OS=Mus musculus GN=Eif6 PE=1 SV=2 , Q545K4 Eukaryotic translation initiation factor 6 OS=Mus musculus GN=Eif6 PE=2 SV=1 ,	Eif6
NYLPAINGIVFLVDC*ADHER	1.1415	Q9CQC9 GTP-binding protein SAR1b OS=Mus musculus GN=Sar1b PE=1 SV=1 , Q0VGU0 SAR1 gene homolog B (S. cerevisiae) OS=Mus musculus GN=Sar1b PE=2 SV=1 ,	Sar1b
C*IVVEEGKEILVGDVGATITDPFK	1.1217	Q4FK36 Destrin OS=Mus musculus GN=Dstn PE=2 SV=1 , Q9R0P5 Destrin OS=Mus musculus GN=Dstn PE=1 SV=3 ,	Dstn
VVNSETPVVVDFHAQWC*GPCK	1.1216	A2A439 Thioredoxin 2 OS=Mus musculus GN=Txn2 PE=4 SV=1 , P97493 Thioredoxin, mitochondrial OS=Mus musculus GN=Txn2 PE=2 SV=1 ,	Txn2
TFQDC*YSSK	1.1197	Q8BH95 Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Echs1 PE=1 SV=1 ,	Echs1
SYIEGYVPSQADVAVFEAVSGPPPADLC*HALR	1.1175	O70251 Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5 ,	Eef1b
LEVDAIVNAANSSLLGGGGVDGC*IHR	1.1079	Q922B1 MACRO domain-containing protein 1 OS=Mus musculus GN=Macrod1 PE=2 SV=2 ,	Macrod1
LQTPLASLVVIVC*GGSNISLAQLQALK	1.0993	Q8VBT2 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=3 , Q3UEN6 Serine dehydratase OS=Mus musculus GN=Sds PE=2 SV=1 ,	Sds
ADFAQAC*QDAGVR	1.0986	E9QPD7 Uncharacterized protein OS=Mus musculus GN=Pcx PE=4 SV=1 , Q05920 Pyruvate carboxylase, mitochondrial OS=Mus musculus GN=Pc PE=1 SV=1 ,	Pcx
YLAAAFPSAC*GK	1.0971	Q9Z2V4 Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Mus musculus GN=Pck1 PE=2 SV=1 , A2APF6 Phosphoenolpyruvate carboxykinase 1, cytosolic OS=Mus musculus GN=Pck1 PE=3 SV=1 ,	Pck1
C*ELSSSVQTDINLPYLTMDASGPK	1.0959	Q7TSZ0 Heat shock protein 9 OS=Mus musculus GN=Hspa9 PE=2 SV=1 , P38647 Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2 ,	Hspa9
FLYEC*PWR	1.0955	E9QPD7 Uncharacterized protein OS=Mus musculus GN=Pcx PE=4 SV=1 , Q05920 Pyruvate carboxylase, mitochondrial OS=Mus musculus GN=Pc PE=1 SV=1 ,	Pcx
FCTPASQC*PIIDPAWESPEGVPIEGIIFGGR	1.0856	Q9Z2V4 Phosphoenolpyruvate carboxykinase, cytosolic [GTP] OS=Mus musculus GN=Pck1 PE=2 SV=1 , A2APF6 Phosphoenolpyruvate carboxykinase 1, cytosolic OS=Mus musculus GN=Pck1 PE=3 SV=1 ,	Pck1
GLYGINEDVFLSVPC*ILGQNGISDVVK	1.0761	P06151 L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3 , Q564E2 L-lactate dehydrogenase OS=Mus musculus GN=Ldha PE=2 SV=1 ,	Ldha
LSDLQNAAAGSFASAFAALVLC*PTELVK	1.0737	Q9WVD5 Mitochondrial ornithine transporter 1 OS=Mus musculus GN=Slc25a15 PE=2 SV=1 , Q543E2 Solute carrier family 25 (Mitochondrial carrier ornithine transporter), member 15, isoform CRA_b OS=Mus musculus GN=Slc25a15 PE=2 SV=1 ,	Slc25a15
VWNLANC*K	1.0717	P68040 Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3 ,	Gnb2l1
ETLSAKPGAIVLSVGGGGLLC*GVVQGLR	1.0669	Q8VBT2 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=3 , Q3UEN6 Serine dehydratase OS=Mus musculus GN=Sds PE=2 SV=1 ,	Sds
LPQGC*AEQTMIYLAPTLTASNYLDR	1.0578	P01029 Complement C4-B OS=Mus musculus GN=C4b PE=1 SV=3 ,	C4b
ILVEPAC*GAALAAVYSR	1.0536	Q8VBT2 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=3 , Q3UEN6 Serine dehydratase OS=Mus musculus GN=Sds PE=2 SV=1 ,	Sds

Peptide	L/H Ratio	Protein	Protein ID
MQLIMLC*YNPDFTR	1.0523	F6WHQ7 Uncharacterized protein (Fragment) OS=Mus musculus GN=Gstm1 PE=4 SV=1 ,	Gstm1
IC*DPYSWLEDPDSEQTK	1.0506	Q9QUR6 Prolyl endopeptidase OS=Mus musculus GN=Prep PE=2 SV=1 , E9Q0H7 Uncharacterized protein OS=Mus musculus GN=Prep PE=4 SV=1 , Q543B9 Prolyl endopeptidase OS=Mus musculus GN=Prep PE=2 SV=1 ,	Prep
VGC*DESPSPSEQQVAQDTEEVFR	1.0482	E9Q2G9 Uncharacterized protein OS=Mus musculus GN=Bak1 PE=4 SV=1 , O08734 Bcl-2 homologous antagonist/killer OS=Mus musculus GN=Bak1 PE=1 SV=1 , E9QM21 Uncharacterized protein OS=Mus musculus GN=Bak1 PE=4 SV=1 , Q91WX5 N-BAK1 OS=Mus musculus GN=Bak1 PE=2 SV=1 ,	Bak1
QAIDDDC*NQTGQMTAGLLDWPQGTFASQVTLEGDKVK	1.0481	Q9DCW4 Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3 ,	Etfb
GEC*YGLHAFVVPIR	1.0434	Q9R0H0 Peroxisomal acyl-coenzyme A oxidase 1 OS=Mus musculus GN=Acox1 PE=1 SV=5 ,	Acox1
GFVPVAPIC*TDK	1.0431	Q8VCR7 Abhydrolase domain-containing protein 14B OS=Mus musculus GN=Abhd14b PE=2 SV=1 , E9QN99 Uncharacterized protein OS=Mus musculus GN=Abhd14b PE=4 SV=1 ,	Abhd14b
ALLATASQC*QQPAGNK	1.0182	B1ARS0 Adenylyl cyclase-associated protein (Fragment) OS=Mus musculus GN=Cap1 PE=3 SV=1 , P40124 Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=4 ,	Cap1
TAC*YGHFGR	1.0020	Q91X83 S-adenosylmethionine synthase isoform type-1 OS=Mus musculus GN=Mat1a PE=2 SV=1 ,	Mat1a
C*LLQIQASSGENK	0.9883	Q9Z2Z6 Mitochondrial carnitine/acylcarnitine carrier protein OS=Mus musculus GN=Slc25a20 PE=1 SV=1 ,	Slc25a20
LPACVVDC*GTGYTK	0.9855	Q3ULF7 Actr3 protein OS=Mus musculus GN=Actr3 PE=2 SV=1 , Q99JY9 Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3 ,	Actr3
AGAIAPC*EVTVPAQNTGLGPEK	0.9772	P14869 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3 , Q5M8R8 Ribosomal protein, large, P0 OS=Mus musculus GN=Rplp0 PE=2 SV=1 , E9Q070 Uncharacterized protein OS=Mus musculus GN=Gm8730 PE=3 SV=1 ,	Rplp0
VNQAIWLLC*TGAR	0.9450	D3YYM6 Uncharacterized protein OS=Mus musculus GN=Rps5 PE=3 SV=1 , Q91V55 Ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=2 SV=1 ,	Rps5
QAGNNQPFTLDDVQYMIFHTPFC*K	0.9446	P54869 Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2 ,	Hmgcs2
TVPAAVPGIC*FLSGGMSEEDATLNLNAINR	0.9290	Q3UER1 Fructose-bisphosphate aldolase OS=Mus musculus GN=Aldob PE=2 SV=1 , Q91Y97 Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3 ,	Aldob
NQESCGSC*YSFASMGMLEAR	0.9055	E9Q2Q0 Uncharacterized protein OS=Mus musculus GN=Ctsc PE=3 SV=1 , P97821 Dipeptidyl peptidase 1 OS=Mus musculus GN=Ctsc PE=2 SV=1 , Q3UBY5 Cathepsin C, isoform CRA_b OS=Mus musculus GN=Ctsc PE=2 SV=1 ,	Ctsc
TFPTVNPSTGEVIC*QVAEGNKEDVDK	0.9038	Q544B1 Aldehyde dehydrogenase 2, mitochondrial, isoform CRA_b OS=Mus musculus GN=Aldh2 PE=2 SV=1 , P47738 Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1 ,	Aldh2
QAGNNQPFTLDDVQYMIFHTPFC*K	0.8845	P54869 Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2 ,	Hmgcs2
MVNSVEGC*ADDALAGLVASNPDLQLLQGHR	0.8726	Q3UTZ4 Uncharacterized protein OS=Mus musculus GN=Dak PE=2 SV=1 , Q8VC30 Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Mus musculus GN=Dak PE=2 SV=1 ,	Dak
TLTQC*SWLLDGFPR	0.8427	Q9WTP7 GTP:AMP phosphotransferase, mitochondrial OS=Mus musculus GN=Ak3 PE=1 SV=3 ,	Ak3
MGFC*SVQEDINSLCLTVVQR	0.8125	P54869 Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2 ,	Hmgcs2
TCNVLVALEQQSPDIAQC*VHLDR	0.6639	Q91X83 S-adenosylmethionine synthase isoform type-1 OS=Mus musculus GN=Mat1a PE=2 SV=1 ,	Mat1a

Peptide	L/H Ratio	Protein	Protein ID
NEEDVGAGDQGLMFGYATDETEEC*MPLTIVLAHK	0.6272	Q91X83 S-adenosylmethionine synthase isoform type-1 OS=Mus musculus GN=Mat1a PE=2 SV=1 ,	Mat1a
VVVFIKPTC*PYCR	0.4772	Q9QUH0 Glutaredoxin-1 OS=Mus musculus GN=Glrx PE=1 SV=3 , Q3U6L3 Glutaredoxin OS=Mus musculus GN=Glrx PE=2 SV=1 ,	Glrx
CDVTQSQPLGGVSLPPADCLLSTLC*LDAACPDLPAYR	0.2426	O55239 Nicotinamide N-methyltransferase OS=Mus musculus GN=Nnmt PE=1 SV=1 ,	Nnmt

Appendix 3. Shotgun proteomics data showing protein expression of proteins in mouse liver proteomes from mice treated with vehicle or glyphosate

Table 4 shows those proteins that had an average of 3 spectral counts, in Table 5 are the relative expression of proteins that were identified as having >3 light:heavy ratios from the isoTOP-ABPP analysis or proteins in the thiolase family that were also detected by shotgun proteomics. These tables relate to Figure 2-4.

Table 4. Proteins with an Average of >3 Spectral Counts

Protein	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Rpn1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	2.0	0.95	11.3	1.38	0.0007
Hnrnpa3 Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	0.4	0.40	5.8	1.03	0.0011
Ech1 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	0.8	0.80	8.3	1.31	0.0014
S100a9 Protein S100-A9	0.6	0.60	6.5	1.19	0.0021
LOC100045191 similar to heterogeneous nuclear ribonucleoprotein A2/B1	0.0	0.00	5.8	1.44	0.0026
Oat Ornithine aminotransferase, mitochondrial	0.4	0.40	5.0	1.08	0.0033
Ncl Nucleolin	2.2	0.97	6.3	0.25	0.0086
Mug1 Murinoglobulin-1	2.8	1.71	10.0	0.71	0.0096
Hdlbp Vigilin	2.8	1.32	10.3	1.80	0.0110
Atp2a2 Isoform SERCA2B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	0.8	0.80	6.3	1.49	0.0112
Aifm1 Apoptosis-inducing factor 1, mitochondrial	2.8	0.80	7.3	1.18	0.0145
Ubc Polyubiquitin-C	2.0	0.89	6.0	0.82	0.0146
Pcx pyruvate carboxylase isoform 1	30.4	6.86	73.8	12.85	0.0159
Gcdh glutaryl-CoA dehydrogenase, mitochondrial precursor	3.6	1.17	8.5	0.96	0.0167
Rps6;Gm13654 40S ribosomal protein S6	2.6	1.08	6.5	0.29	0.0167
Mat1a S-adenosylmethionine synthase isoform type-1	8.4	1.29	42.5	12.60	0.0185
Sephs2 Selenide, water dikinase 2	2.0	1.26	6.8	0.85	0.0219
Pdia4 protein disulfide-isomerase A4	8.0	2.19	15.3	1.11	0.0299
Actn4 Alpha-actinin-4	2.6	1.17	10.3	2.87	0.0312
LOC100045699 similar to Electron transferring flavoprotein, beta polypeptide isoform 2	15.6	2.96	28.0	3.63	0.0316
Myh9 Myosin-9	11.2	2.06	22.0	3.76	0.0321
Rpl4 60S ribosomal protein L4	4.8	0.73	9.3	1.65	0.0325
Acadm Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	5.2	1.24	9.5	0.96	0.0343
Gstm2 Glutathione S-transferase Mu 2	0.0	0.00	12.5	5.84	0.0449
Rrbp1 Isoform 3 of Ribosome-binding protein 1	10.6	2.29	18.8	2.50	0.0477
Acat2 Acetyl-CoA acetyltransferase, cytosolic	2.2	1.36	10.0	3.34	0.0508
Suclg1 Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial	3.6	0.51	5.8	0.85	0.0574
Hba-a2;Hba-a1 hemoglobin alpha, adult chain 2	150.4	35.96	288.5	51.56	0.0578

Protein	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Pnp purine nucleoside phosphorylase	1.2	0.80	5.0	1.68	0.0646
Pck1 Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	1.8	0.80	5.3	1.49	0.0672
Cltc Clathrin, heavy polypeptide	2.4	1.12	7.3	2.17	0.0725
Sult1a1 Sulfotransferase family 1A, phenol-preferring, member 1, isoform CRA_a	0.0	0.00	5.5	3.01	0.0763
LOC100046684;D10Jhu81e ES1 protein homolog, mitochondrial	2.6	1.17	5.8	0.85	0.0770
Gm9755 Elongation factor Tu	1.6	1.03	6.0	2.04	0.0788
Ugt2b1 UDP glucuronosyltransferase 2 family, polypeptide B1	16.4	6.36	1.5	0.96	0.0793
Hbb-b1 Beta-globin	95.8	35.38	208.8	43.97	0.0821
Hspa9 stress-70 protein, mitochondrial	24.0	5.96	46.0	9.72	0.0831
Mup-ps19 similar to Predicted gene, OTTMUSG00000007485	7.6	2.56	1.5	0.96	0.0834
Gstp1 Glutathione S-transferase P 1	113.0	24.70	56.0	4.49	0.0837
Acadvl Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	2.2	1.43	8.5	3.07	0.0852
Aass Alpha-aminoadipic semialdehyde synthase, mitochondrial	0.0	0.00	6.5	3.71	0.0862
Uba1 Ubiquitin-like modifier-activating enzyme 1	1.2	1.20	6.0	2.27	0.0873
Glud1 Glutamate dehydrogenase 1, mitochondrial	39.4	6.47	60.5	8.85	0.0889
Hsd17b10 Hydroxysteroid (17-beta) dehydrogenase 10	2.4	1.03	8.0	2.94	0.0890
Selenbp2 Selenium-binding protein 2	120.0	41.44	28.8	5.66	0.0947
Acat1 Acetyl-CoA acetyltransferase, mitochondrial	14.0	1.84	23.0	4.81	0.0980
Selenbp1;LOC100044204 Selenium-binding protein 1	78.0	21.69	29.8	7.03	0.0988
Fh1 fumarate hydratase, mitochondrial precursor	15.0	2.72	24.0	4.14	0.1012
Por NADPH--cytochrome P450 reductase	5.2	1.98	14.8	5.27	0.1057
Dpys Dihydropyrimidinase	5.4	0.75	8.0	1.29	0.1090
Es31 Isoform 1 of Liver carboxylesterase 31	40.0	10.64	17.8	1.49	0.1094
Calr Calreticulin	9.6	2.58	16.0	2.31	0.1153
Mettl7b Methyltransferase-like protein 7B	2.8	1.16	5.5	0.87	0.1183
Actc1 Putative uncharacterized protein	26.0	4.53	54.5	17.33	0.1193
Echs1 Enoyl-CoA hydratase, mitochondrial	5.2	1.98	9.3	0.63	0.1240
Sult1a1 Arylsulfotransferase ST1A4	1.2	0.80	5.0	2.27	0.1267
Aox3 Aldehyde oxidase 1	14.4	5.12	4.3	0.85	0.1268
Uqcrc1 cytochrome b-c1 complex subunit 1, mitochondrial precursor	9.0	2.35	14.0	1.47	0.1347
Aldob Fructose-bisphosphate aldolase B	86.8	21.43	164.3	44.98	0.1389
Dmgdh Dimethylglycine dehydrogenase, mitochondrial	7.6	2.58	15.0	3.92	0.1453
Csad Cysteine sulfinic acid decarboxylase	5.8	2.11	11.0	2.38	0.1455
Hyou1 Hypoxia up-regulated protein 1	6.8	2.50	13.0	2.97	0.1515
Acsf2 Acyl-CoA synthetase family member 2, mitochondrial	5.4	1.72	8.8	0.85	0.1530
Pdia3 Protein disulfide-isomerase A3	17.8	3.87	27.0	4.49	0.1627

Protein	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Hpd 4-hydroxyphenylpyruvate dioxygenase	25.2	6.29	41.3	8.50	0.1639
Mup2;Mup11 major urinary protein 11	55.6	30.33	2.5	2.50	0.1672
Gm4738 liver carboxylesterase 31-like isoform 1	27.8	11.33	8.0	0.82	0.1678
Cyb5 Cytochrome b5	14.6	2.01	18.5	1.26	0.1683
Mup1 Major urinary protein 1	41.4	23.83	0.0	0.00	0.1693
Hbb-b2 Hemoglobin subunit beta-2	11.4	7.28	35.3	15.21	0.1725
Suclg2 Isoform 1 of Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	5.4	1.36	8.8	1.80	0.1733
Got1 Aspartate aminotransferase, cytoplasmic	5.4	1.50	12.3	4.87	0.1805
Ppa1 Inorganic pyrophosphatase	3.2	1.32	6.8	2.14	0.1825
Acly Putative uncharacterized protein	5.4	1.60	13.3	5.81	0.1904
Ftl1 Ferritin light chain 1	7.4	2.56	13.5	3.52	0.1938
Hacl1 2-hydroxyacyl-CoA lyase 1	3.6	1.60	8.8	3.52	0.1940
Car3 Carbonic anhydrase 3	61.6	13.83	37.0	7.84	0.1941
Hint1 Histidine triad nucleotide-binding protein 1	6.6	1.69	9.8	1.25	0.1970
Eif4a1 Eukaryotic initiation factor 4A-I	8.2	2.33	12.5	1.66	0.1974
Fdps Farnesyl pyrophosphate synthase	1.8	1.11	6.5	3.48	0.1979
Mut methylmalonyl-CoA mutase, mitochondrial precursor	4.6	2.14	12.5	5.78	0.2030
Gm3934;LOC100046536 similar to glutathione S-transferase pi class A	28.8	15.85	3.3	3.25	0.2030
Snd1 Staphylococcal nuclease domain-containing protein 1	5.6	1.50	9.0	1.96	0.2030
Rplp2 60S acidic ribosomal protein P2	6.8	3.68	13.0	1.87	0.2093
Amdhd1 Probable imidazolonepropionase	6.4	1.33	4.3	0.48	0.2111
Pbld Phenazine biosynthesis-like domain-containing protein 1	13.4	2.66	8.0	2.92	0.2143
Serpina3k Serine protease inhibitor A3K	15.4	5.95	26.5	5.25	0.2168
LOC100040592;Hmgcs1 Hydroxymethylglutaryl-CoA synthase, cytoplasmic	2.2	1.56	5.8	2.32	0.2303
Ugt2a3 UDP-glucuronosyltransferase 2A3	5.6	3.78	0.0	0.00	0.2322
Cfl1 Putative uncharacterized protein	2.8	1.16	5.0	1.22	0.2359
Serpina1e Alpha-1-antitrypsin 1-5	8.4	4.66	1.5	0.87	0.2376
Tubb2c Tubulin beta-2C chain	24.2	4.91	32.3	3.68	0.2516
Rpl14 Putative uncharacterized protein	3.4	1.66	7.0	2.48	0.2518
Adk Isoform Long of Adenosine kinase	5.2	1.59	14.3	8.02	0.2536
Cyp2d9 cytochrome P450 2D9	11.2	1.98	7.8	1.89	0.2570
Cyp2e1 Cytochrome P450 2E1	3.0	1.26	6.0	2.27	0.2618
Dak Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	28.2	8.39	53.0	20.57	0.2639
Tubb2a Tubulin beta-2A chain	18.4	4.58	26.8	5.20	0.2665
LOC635091 similar to Predicted gene, OTTMUSG00000007485	15.4	11.40	0.0	0.00	0.2723
Hmgcs2 Hydroxymethylglutaryl-CoA synthase, mitochondrial	23.8	10.37	45.0	15.40	0.2754
Actb Actin, cytoplasmic 1	14.4	8.82	44.3	26.46	0.2766

Protein	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Gm9819 Putative uncharacterized protein Gm9819	3.4	1.03	5.3	1.25	0.2862
Ces6 Putative uncharacterized protein	8.6	2.11	5.8	0.75	0.2889
Ugt1a6b;LOC632297;Ugt1a2;Ugt1a10;Ugt1a9;Ugt1a7c;Ugt1a1;Ugt1a5 UDP glucuronosyltransferase 1 family, polypeptide A6B	0.0	0.00	5.3	5.25	0.2924
Eef1g Elongation factor 1-gamma	4.4	0.87	5.8	0.75	0.2932
Acaa2 Putative uncharacterized protein	88.2	18.45	125.8	29.69	0.2983
Fabp1 Fatty acid-binding protein, liver	111.8	26.45	77.0	10.28	0.3032
Glyat Isoform 1 of Glycine N-acyltransferase	4.2	1.96	8.3	3.33	0.3063
Hsp90aa1 Heat shock protein HSP 90-alpha	14.8	5.49	7.5	2.60	0.3073
Ddt D-dopachrome decarboxylase	11.6	2.16	8.3	2.14	0.3134
Slc25a13 Calcium-binding mitochondrial carrier protein Aralar2	3.8	1.24	7.0	2.97	0.3163
Ywhaz 14-3-3 protein zeta/delta	4.0	1.52	6.0	0.91	0.3269
Esd S-formylglutathione hydrolase	3.6	1.60	6.5	2.47	0.3389
Tubb5 Tubulin beta-5 chain	18.2	4.16	24.0	3.56	0.3398
Asl Argininosuccinate lyase	21.2	1.83	30.5	10.19	0.3449
Phb Prohibitin	9.6	2.42	13.3	2.72	0.3492
LOC100048885 18 kDa protein	37.4	31.74	1.8	1.75	0.3553
Cyp2f2 Cytochrome P450 2F2	15.0	8.02	6.3	0.85	0.3695
Atp5d ATP synthase subunit delta, mitochondrial	5.8	2.76	2.5	1.66	0.3715
Pgam1 Phosphoglycerate mutase 1	4.0	0.77	5.3	1.11	0.3722
Arg1 Arginase-1	60.8	17.08	83.3	15.80	0.3775
Gdi2 Isoform 1 of Rab GDP dissociation inhibitor beta	3.4	1.08	5.0	1.35	0.3792
Acox1 Acyl-Coenzyme A oxidase 1, palmitoyl, isoform CRA_a	9.2	2.58	12.5	2.25	0.3809
Pygl glycogen phosphorylase, liver form	45.8	18.53	25.5	6.25	0.3810
Gm9824 Putative uncharacterized protein ENSMUSP00000082571	8.0	4.24	3.5	0.65	0.3838
Ces3 Carboxylesterase 3	18.4	4.63	13.0	2.86	0.3845
Ugp2 Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	4.6	1.78	7.5	2.72	0.3847
Gm13910 similar to Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	3.2	2.33	7.5	4.35	0.3855
Gm10362 similar to Rpl17 protein	6.2	2.63	9.0	0.71	0.3893
Adh5 Alcohol dehydrogenase class-3	7.8	3.20	12.0	3.24	0.3927
Aldh6a1 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	12.4	1.57	17.0	5.46	0.3985
Hspa5 78 kDa glucose-regulated protein	30.8	30.80	0.0	0.00	0.4071
Gm5069 Glyceraldehyde-3-phosphate dehydrogenase	19.2	19.20	0.0	0.00	0.4071
LOC100047129 similar to Glyceraldehyde-3-phosphate dehydrogenase	8.0	8.00	0.0	0.00	0.4071
Gm5863 similar to glyceraldehyde-3-phosphate-dehydrogenase isoform 1	5.6	5.60	0.0	0.00	0.4071
Fasn Fatty acid synthase	32.4	10.92	58.5	31.38	0.4164

Protein	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Cct5 T-complex protein 1 subunit epsilon	3.4	1.54	5.5	1.94	0.4169
Alb Serum albumin	45.4	12.02	61.5	15.09	0.4252
Prdx6 Putative uncharacterized protein	53.2	16.81	34.3	13.37	0.4252
Aldh1a1 Retinal dehydrogenase 1	37.6	10.46	27.0	4.85	0.4281
Rgn Regucalcin	22.4	4.27	17.5	3.88	0.4356
Glul Glutamine synthetase	21.4	4.68	26.0	2.16	0.4409
Mgst1 26 kDa protein	18.0	7.85	10.0	4.76	0.4427
AU018778 Putative uncharacterized protein	15.2	3.38	11.8	2.10	0.4441
LOC100047352 similar to Glyceraldehyde-3-phosphate dehydrogenase	45.2	20.22	64.3	6.14	0.4453
Akr1a4 Alcohol dehydrogenase [NADP+]	6.2	1.43	8.0	1.78	0.4501
Ywhag 14-3-3 protein gamma	3.8	1.11	5.3	1.49	0.4519
Pdia6 Putative uncharacterized protein	6.0	2.28	8.3	1.31	0.4530
Dbi acyl-CoA-binding protein isoform 1	44.0	13.88	31.3	5.15	0.4617
Ugt1a6b;LOC632297;Ugt1a2;Ugt1a10;Ugt1a9;Ugt1a7c;Ugt1a1;Ugt1a5 UDP-glucuronosyltransferase 1-1	15.0	4.02	10.8	3.73	0.4739
Acsm1 Isoform 1 of Acyl-coenzyme A synthetase ACSM1, mitochondrial	10.0	3.21	13.8	3.88	0.4765
Scp2 Isoform SCPx of Non-specific lipid-transfer protein	54.0	22.79	34.3	11.05	0.4975
Hsp90b1 Endoplasmin	32.2	13.73	45.0	10.11	0.4982
Khk 38 kDa protein	10.8	6.71	20.0	12.24	0.5074
Bhmt2 Betaine--homocysteine S-methyltransferase 2	8.6	5.48	14.3	5.94	0.5086
Acat3 acetyl-Coenzyme A acetyltransferase 3	8.2	1.69	10.5	3.07	0.5088
Ptms Ptms protein	5.2	3.20	8.5	3.57	0.5136
Aco1 Cytoplasmic aconitase	21.2	9.71	12.5	7.18	0.5151
Gnmt Glycine N-methyltransferase	18.4	5.73	24.3	6.37	0.5171
Tpi1 triosephosphate isomerase	13.0	3.61	17.5	6.24	0.5314
Aldh8a1 Aldehyde dehydrogenase family 8 member A1	8.2	2.22	10.0	1.22	0.5322
Tubb6 Tubulin beta-6 chain	7.4	4.56	3.5	3.50	0.5372
Atp5a1 ATP synthase subunit alpha, mitochondrial	72.6	15.17	87.0	15.99	0.5375
Lap3 Isoform 1 of Cytosol aminopeptidase	14.4	4.23	18.5	4.97	0.5473
Aldh2 Aldehyde dehydrogenase, mitochondrial	25.2	6.70	31.8	8.08	0.5487
Cat catalase	58.0	16.50	45.3	9.37	0.5525
Otc Ornithine carbamoyltransferase, mitochondrial	16.0	2.88	19.5	5.20	0.5530
Acsl1 long-chain-fatty-acid--CoA ligase 1	12.8	4.43	9.0	4.02	0.5557
Atp5b ATP synthase subunit beta, mitochondrial	163.0	23.44	183.8	23.47	0.5568
Uox Uricase	11.2	2.80	9.0	2.04	0.5653
Sod2 Superoxide dismutase [Mn], mitochondrial	4.4	2.64	6.5	2.25	0.5767
Etfa Electron transfer flavoprotein subunit alpha, mitochondrial	47.8	16.54	36.0	8.51	0.5773
Ephx2 Isoform 1 of Epoxide hydrolase 2	29.8	9.17	22.8	7.00	0.5779

Protein	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Rps21 40S ribosomal protein S21	3.0	3.00	5.3	2.29	0.5868
Tst Thiosulfate sulfurtransferase	8.0	4.17	5.3	1.11	0.5868
Ehhadh Peroxisomal bifunctional enzyme	3.8	1.62	5.5	2.72	0.5910
Hadh Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	4.2	1.96	5.8	1.89	0.5935
Atp5c1 ATP synthase subunit gamma, mitochondrial	8.0	3.70	11.8	6.42	0.6102
Eef2 Elongation factor 2	20.2	6.03	24.5	5.78	0.6291
Hmgcl hydroxymethylglutaryl-CoA lyase, mitochondrial precursor	4.2	1.74	5.5	1.89	0.6302
Ldha L-lactate dehydrogenase A chain isoform 2	9.4	3.99	12.8	5.79	0.6379
Got2 Aspartate aminotransferase, mitochondrial	16.0	2.32	17.5	1.94	0.6470
Sod1 Superoxide dismutase [Cu-Zn]	94.6	38.87	72.8	13.83	0.6473
Ak2 Isoform 1 of Adenylate kinase 2, mitochondrial	15.0	9.54	9.5	4.56	0.6480
Aldh7a1 Isoform 1 of Alpha-aminoadipic semialdehyde dehydrogenase	5.6	2.50	7.5	3.20	0.6488
Pklr pyruvate kinase isozymes R/L isoform 2	29.4	15.63	20.5	8.01	0.6549
Sardh Sarcosine dehydrogenase, mitochondrial	22.6	8.23	17.8	5.25	0.6555
Slc25a5 ADP/ATP translocase 2	11.6	6.76	16.5	8.51	0.6612
Tkt Transketolase	29.0	5.84	33.3	7.65	0.6660
Gsta3 Glutathione S-transferase A3	143.4	25.14	126.8	27.17	0.6678
P4hb Protein disulfide-isomerase	69.4	27.62	86.8	27.23	0.6730
Ppia Peptidyl-prolyl cis-trans isomerase	22.4	4.50	24.8	2.50	0.6849
Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase A, peroxisomal	11.2	3.22	12.8	0.95	0.6909
Vcp Transitional endoplasmic reticulum ATPase	15.0	3.73	17.3	3.90	0.6917
Park7 Protein DJ-1	7.8	3.81	6.0	0.71	0.6926
Grhpr Glyoxylate reductase/hydroxypyruvate reductase	4.6	1.66	5.5	1.32	0.6964
Hsp90ab1 Putative uncharacterized protein	34.0	10.93	27.8	10.71	0.6999
Hsd17b4 Peroxisomal multifunctional enzyme type 2	5.4	2.82	6.8	1.18	0.7001
Fbp1 Fructose-1,6-bisphosphatase 1	90.8	26.38	107.5	32.93	0.7001
Gm10313 similar to LOC654472 protein	7.2	7.20	11.0	6.56	0.7150
Gpd1 Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	4.6	1.17	5.5	2.25	0.7167
Hadha Trifunctional enzyme subunit alpha, mitochondrial	34.6	15.44	42.8	15.25	0.7225
Dci 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	6.2	1.39	7.0	1.73	0.7260
Gstm1 Glutathione S-transferase, mu 1	39.2	11.61	46.0	15.09	0.7266
Haao 3-hydroxyanthranilate 3,4-dioxygenase	15.4	3.43	17.0	2.55	0.7319
Aldh4a1 delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial precursor	17.2	6.52	20.5	6.98	0.7413
Gstm3 Glutathione S-transferase Mu 3	3.8	3.80	5.5	2.78	0.7416
Cyp2d26 Cytochrome P450 2D26	4.0	1.92	5.0	2.35	0.7486
Serpina1a Alpha-1-antitrypsin 1-1	8.2	4.96	6.3	2.02	0.7507
Gstz1 Maleylacetoacetate isomerase	16.4	8.32	13.0	4.74	0.7513

Protein	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
Mdh1 Malate dehydrogenase, cytoplasmic	24.0	5.87	21.3	5.88	0.7535
Adh1 Alcohol dehydrogenase 1	54.8	19.82	46.3	17.47	0.7625
Ftcd Formimidoyltransferase-cyclodeaminase	13.6	2.73	12.3	3.64	0.7704
Hspa8 Heat shock cognate 71 kDa protein	31.6	8.94	35.8	10.55	0.7712
Serpina1b Alpha-1-antitrypsin 1-2	7.2	4.80	5.5	1.85	0.7734
Ahcy Adenosylhomocysteinase	30.4	8.08	34.3	10.37	0.7744
Sord 40 kDa protein	39.2	16.54	46.5	18.43	0.7768
Gpi1 Glucose-6-phosphate isomerase	10.4	2.91	11.8	3.75	0.7805
Cps1 Carbamoyl-phosphate synthase [ammonia], mitochondrial	411.8	85.63	448.0	96.27	0.7867
Acads Putative uncharacterized protein	7.2	2.97	8.3	2.02	0.7907
Mdh2 Malate dehydrogenase, mitochondrial	12.6	1.40	12.0	1.78	0.7954
Actg1 Actin, cytoplasmic 2	14.2	7.17	18.8	18.75	0.8114
Apoa1 apolipoprotein A-I preproprotein	7.8	2.03	8.5	1.94	0.8141
Pah phenylalanine-4-hydroxylase	10.0	2.35	9.3	2.29	0.8284
Fah fumarylacetoacetase	49.4	13.83	45.3	11.34	0.8296
Tuba1b Tubulin alpha-1B chain	16.0	4.37	17.3	3.82	0.8404
Apoa2 apolipoprotein A-II precursor	5.2	2.85	4.5	1.04	0.8410
Aco2 Aconitate hydratase, mitochondrial	9.2	3.25	10.3	4.17	0.8455
Atp5h ATP synthase subunit d, mitochondrial	4.6	2.04	5.3	2.56	0.8461
Cth Cystathionine gamma-lyase	8.8	0.97	8.3	3.17	0.8595
Mthfd1 C-1-tetrahydrofolate synthase, cytoplasmic	15.4	6.56	13.8	5.85	0.8604
Gm6316 Glyceraldehyde-3-phosphate dehydrogenase	6.2	4.32	5.0	5.00	0.8604
Hspd1 Isoform 1 of 60 kDa heat shock protein, mitochondrial	139.2	44.54	129.3	31.00	0.8672
Pgm1;Pgm2 Phosphoglucomutase 2	11.0	3.44	10.3	2.69	0.8739
Aldh1l1 10-formyltetrahydrofolate dehydrogenase	49.6	8.26	52.0	12.89	0.8749
Cyp2d10 Cytochrome P450 2D10	6.4	1.47	6.8	1.60	0.8770
LOC100048117 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1	34.0	21.58	38.8	23.25	0.8857
Gm10327;LOC100046806 similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) isoform 1	63.8	30.39	57.5	34.19	0.8943
Rpl12 60S ribosomal protein L12	8.6	2.42	9.0	1.47	0.8988
Pgk1 Phosphoglycerate kinase 1	16.6	4.01	17.3	3.17	0.9064
Hspe1 10 kDa heat shock protein, mitochondrial	22.6	5.78	21.8	3.15	0.9082
Bhmt Betaine--homocysteine S-methyltransferase 1	211.0	46.21	218.3	39.98	0.9117
Idh1 Putative uncharacterized protein	45.2	12.63	43.3	13.09	0.9184
Prdx1 Peroxiredoxin-1	25.2	7.10	24.3	6.85	0.9273
Akr1c6 Estradiol 17 beta-dehydrogenase 5	35.8	6.72	36.5	2.47	0.9320
Sds L-serine dehydratase/L-threonine deaminase	10.8	2.99	10.5	2.25	0.9412
Hal Histidine ammonia-lyase	13.2	4.14	12.8	5.79	0.9500

Protein	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
mt-Co2 Cytochrome c oxidase subunit 2	6.6	1.57	6.8	1.75	0.9509
Ass1 Argininosuccinate synthase	181.8	63.26	176.5	54.11	0.9526
Hnrnpk Isoform 2 of Heterogeneous nuclear ribonucleoprotein K	11.8	5.46	12.3	4.59	0.9531
Cct2 T-complex protein 1 subunit beta	4.8	2.44	5.0	2.20	0.9544
3110049J23Rik Phenazine biosynthesis-like domain-containing protein 2	10.0	4.52	9.8	1.31	0.9633
Uroc1 Putative uncharacterized protein	7.4	1.36	7.5	2.18	0.9687
Eef1a1 Elongation factor 1-alpha 1	90.6	34.63	92.3	23.23	0.9713
Gpx1 Glutathione peroxidase 1	5.4	1.94	5.5	2.06	0.9730
Gm5506;Eno1;LOC100044223 Alpha-enolase	74.6	33.03	76.0	27.41	0.9758
Tuba4a Tubulin alpha-4A chain	8.8	4.93	9.0	4.38	0.9773
Hadhb Trifunctional enzyme subunit beta, mitochondrial	8.0	6.60	7.8	7.75	0.9810
Hrsp12 Ribonuclease UK114	19.8	6.13	20.0	5.52	0.9818
Aldh1a7 Aldehyde dehydrogenase, cytosolic 1	9.4	4.26	9.5	2.36	0.9854

Table 5. Relative Expression of Proteins Identified Ratios from the IsoTOP-ABPP Analysis

Protein	ID	Control Avg	Control SEM	Glyphosate Avg	Glyphosate SEM	P-value
2810007J24Rik 2810007J24Rik protein	2810007J24Rik	1	0.13	0.18	0.18	0.0035
Acaa1b;Acaa1a 3-ketoacyl-CoA thiolase A, peroxisomal	Acaa1b	1	0.29	1.14	0.08	0.3455
Acaa2 Putative uncharacterized protein	Acaa2	1	0.21	1.43	0.34	0.1492
Acat2 Acetyl-CoA acetyltransferase, cytosolic	Acat2	1	0.62	4.55	1.52	0.0254
Aldh9a1 4-trimethylaminobutyraldehyde dehydrogenase	Aldh9a1	1	1.00	5.00	2.89	0.0965
Fabp1 Fatty acid-binding protein, liver	Fabp1	1	0.24	0.69	0.09	0.1516
Gpx1 Glutathione peroxidase 1	Gpx1	1	0.36	1.02	0.38	0.4865
Mthfd1 C-1-tetrahydrofolate synthase, cytoplasmic	Mthfd1	1	0.43	0.89	0.38	0.4302
Scp2 Isoform SCPx of Non-specific lipid-transfer protein	Scp2 Isoform	1	0.42	0.63	0.20	0.2488
Selenbp2 Selenium-binding protein 2	Selenbp2	1	0.35	0.24	0.05	0.0474
Tuba4a Tubulin alpha-4A chain	Tuba4a	1	0.56	1.02	0.50	0.4887

Appendix 4. IsoTOP-ABPP analysis of glyoxylate cysteine reactivity from *in vitro* pre-treatment with glyoxylate

Table 6 shows IsoTOP-ABPP analysis of glyoxylate cysteine reactivity from *in vitro* pre-treatment with glyoxylate (3 mM, 30 min) prior to labeling with IAyne followed by appendage of a biotin-azide handle bearing a TEV recognition sequence and isotopically light (vehicle-treated) or heavy (glyphosate-treated) valine, combining of control and treated proteomes in a 1:1 ratio, avidin enrichment, tryptic digestion, release of modified peptides by TEV protease, and analysis by LC-MS/MS. Shown are modified peptides and their corresponding protein IDs that were quantified by measuring the light to heavy ratios of peptides. Table 7 shows the target list for glyphosate (>1.5 L:H ratio) and those peptides that also showed >1.5 L:H ratios with glyoxylate isoTOP-ABPP analysis. These tables are related to Figure 2-6.

Table 6. IsoTOP-ABPP Analysis of Glyoxylate Cysteine Reactivity *in vitro*

Peptide	L/H Ratio	Protein
VCEDFGVIATFDPKPIPGNWNGAGC*HTN	177.1245	P15105 Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6 #
GDILDAQC*LK	54.6483	Q3UIU9 3 beta-hydroxysteroid dehydrogenase type 4 OS=Mus musculus GN=Gm10681 PE=2 SV=1 # Q61767 3 beta-hydroxysteroid dehydrogenase type 4 OS=Mus musculus GN=Hsd3b4 PE=2 SV=3 # Q61694 3 beta-hydroxysteroid dehydrogenase type 5 OS=Mus musculus GN=Hsd3b5 PE=1 SV=4 # E9Q007 Protein Gm4450 OS=Mus musculus GN=Gm4450 PE=1 SV=1 #
DCSCAPDC*CQAK	28.4429	Q3UEG6 Alanine--glyoxylate aminotransferase 2# mitochondrial OS=Mus musculus GN=Agxt2 PE=1 SV=1 #
SAAPLIIC*PMSGIDGFSGHVGNHGHSMETSP	26.9292	Q62158 Zinc finger protein RFP OS=Mus musculus GN=Trim27 PE=1 SV=2 #
NWTLLSYPGAGHLIEPPYTPLC*QASR	23.7081	Q91X34 Bile acid-CoA:amino acid N-acyltransferase OS=Mus musculus GN=Baat PE=1 SV=1 #
SPLIIFADC*DLNK	20.9156	Q8R0Y6 Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1l1 PE=1 SV=1 #
VETAEVC*SRPQELPQSPR	17.5519	Q76LS9-2 Isoform 2 of Protein FAM63A OS=Mus musculus GN=Fam63a # Q76LS9 Protein FAM63A OS=Mus musculus GN=Fam63a PE=1 SV=1 #
IYC*TDLLNNDLKDSIVCAMK	17.4119	Q9D9X8-2 Isoform 2 of Sperm acrosome membrane-associated protein 3 OS=Mus musculus GN=Spaca3 # Q9D9X8 Sperm acrosome membrane-associated protein 3 OS=Mus musculus GN=Spaca3 PE=1 SV=2 #
LVVVDFSATWC*GPCK	16.3576	P10639 Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3 #
GDCVECMAC*SDNTVR	15.8999	Q3V100 Mannose-6-phosphate isomerase OS=Mus musculus GN=Mpi PE=1 SV=1 # Q924M7 Mannose-6-phosphate isomerase OS=Mus musculus GN=Mpi PE=1 SV=1 #
GC*FHAEIVPVTTTVLNDK	15.6275	Q8VCH0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 # Q3UKM0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 #
C*LTQQAVALQR	14.1924	A0A0R4J140 Clustered mitochondria protein homolog OS=Mus musculus GN=Cluh PE=1 SV=1 # Q5SW19 Clustered mitochondria protein homolog OS=Mus musculus GN=Cluh PE=1 SV=2 #
SNPVPILIPC*HR	13.9669	P26187 Methylated-DNA--protein-cysteine methyltransferase OS=Mus musculus GN=Mgmt PE=1 SV=3 #
SCYDLSC*HAR	13.7237	Q9CZD3 Glycine--tRNA ligase OS=Mus musculus GN=Gars PE=1 SV=1 #
QQLNIHGLLPPC*IISQELQVLR	13.4741	P06801 NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=2 #
VTMGGQC*IALAPDDSLLVPAGTSYVWER	12.7238	Q78JT3 3-hydroxyanthranilate 3#4-dioxygenase OS=Mus musculus GN=Haao PE=1 SV=1 #
AEAEDGLLLYC*GESEHGRGDFMSLALIR	12.2401	Q4VBE4 Pikachurin OS=Mus musculus GN=Egflam PE=1 SV=1 # Q4VBE4-2 Isoform 2 of Pikachurin OS=Mus musculus GN=Egflam #

Peptide	L/H Ratio	Protein
SLHDALC*VVK	11.7280	P11983 T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 PE=1 SV=3 # P11983-2 Isoform 2 of T-complex protein 1 subunit alpha OS=Mus musculus GN=Tcp1 #
NELFTDSEC*QEISAVTGNPVHESLK	11.2470	Q99J39 Malonyl-CoA decarboxylase# mitochondrial OS=Mus musculus GN=Mlycd PE=1 SV=1 # Q99J39-2 Isoform Cytoplasmic+peroxisomal of Malonyl-CoA decarboxylase# mitochondrial OS=Mus musculus GN=Mlycd #
VLTLDTMNPC*VR	11.1320	Q566C3 Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=1 SV=1 # Q8QZR5 Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=1 SV=3 #
TANVFEQIC*GLQQGDHLALILPR	11.0886	Q91VA0 Acyl-coenzyme A synthetase ACSM1# mitochondrial OS=Mus musculus GN=Acsm1 PE=1 SV=1 #
FPEELTQTFMSC*NLITGMFQR	10.9365	Q4FZK2 Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=1 # Q9D8N0 Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3 #
SSPSLSILAGGQC*NESVGYYVEPCIIESK	10.6104	Q8CHT0 Delta-1-pyrroline-5-carboxylate dehydrogenase# mitochondrial OS=Mus musculus GN=Aldh4a1 PE=1 SV=3 #
STLATSSSQPVWLTAMDC*PTSGVVGLVNCLR	10.5261	A0A0U1RNJ1 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=1 # P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 #
LALYTAC*GGVNPQQCLPITLDVGTENEELLKDPLYIGLR	10.1246	P06801 NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=2 #
SQLQSVLLCGIETQAC*ILNTALDLLHR	9.7930	P85094 Isochorismatase domain-containing protein 2A OS=Mus musculus GN=Isoc2a PE=1 SV=1 #
WAC*SHLSPLRPDPFCGFHFFCLLR	9.7805	F6XZN9 Histone-lysine N-methyltransferase KMT5C (Fragment) OS=Mus musculus GN=Suv420h2 PE=1 SV=1 #
VAC*ITEQVLTLVNKR	9.4517	Q91YQ5 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=1 SV=1 #
AWVWNTHADFADEC*PKPELLAIR	9.3504	H7BX22 Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=1 # P34022 Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2 #
SYC*NDQSTGDIK	9.2659	P00493 Hypoxanthine-guanine phosphoribosyltransferase OS=Mus musculus GN=Hprt1 PE=1 SV=3 #
TPESTC*SLSSPFLR	9.2320	Q9JK23 Proteasome assembly chaperone 1 OS=Mus musculus GN=Psmg1 PE=1 SV=1 # D3Z795 Proteasome assembly chaperone 1 OS=Mus musculus GN=Psmg1 PE=1 SV=1 #
TGIQTSC*LCPVFVNTGFTK	8.9175	Q8VCR2-2 Isoform 2 of 17-beta-hydroxysteroid dehydrogenase 13 OS=Mus musculus GN=Hsd17b13 #
INEIVYFLPFC*HSELIQLVNK	8.8805	E9PY58 Caseinolytic peptidase B protein homolog OS=Mus musculus GN=Clpb PE=1 SV=1 # Q60649 Caseinolytic peptidase B protein homolog OS=Mus musculus GN=Clpb PE=1 SV=1 # Q3URM1 Caseinolytic peptidase B protein homolog OS=Mus musculus GN=Clpb PE=1 SV=1 #
GNDVLVIEC*NLR	8.6131	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
LRGEDGESEC*VINYVEK	8.5600	Q8R0Y6 Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1l1 PE=1 SV=1 #
QATLGAGLPISTPCTTVNKVC*ASGMK	8.4673	Q8QZT1 Acetyl-CoA acetyltransferase# mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1 #
LC*GSGFQSIVSGCQEIC*SK	8.1157	Q8BWT1 3-ketoacyl-CoA thiolase# mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 #
QFASWFDEAVQC*PDIGEANAMCVATCTR	8.0060	Q91XF0 Pyridoxine-5'-phosphate oxidase OS=Mus musculus GN=Pnpo PE=1 SV=1 #
LICC*DILDVLDK	7.9826	Q5SS40 14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1 # P62259 14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1 #
NNGC*LVVLPGTHK	7.8588	Q3TPC7 Phytanoyl-CoA dioxygenase# peroxisomal OS=Mus musculus GN=Phyh PE=1 SV=1 # O35386 Phytanoyl-CoA dioxygenase# peroxisomal OS=Mus musculus GN=Phyh PE=1 SV=1 #
IAVIGQSLFGQEVYC*QLR	7.8279	Q8R0Y6 Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1l1 PE=1 SV=1 #

Peptide	L/H Ratio	Protein
DC*LIPMGITSENVAER	7.8169	Q8VCH0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 # Q3UKM0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 #
LLEKYPQAVYTLC*SSCALNAWLAK	7.6976	Q9CUX1 52 kDa repressor of the inhibitor of the protein kinase OS=Mus musculus GN=Thap12 PE=2 SV=2 #
VVNEINIEDLC*LTK	7.6341	Q9CQB5 CDGSH iron-sulfur domain-containing protein 2 OS=Mus musculus GN=Cisd2 PE=1 SV=1 # D3Z3X4 CDGSH iron-sulfur domain-containing protein 2 OS=Mus musculus GN=Cisd2 PE=1 SV=1 #
VTTGAPIPC*GADAVVQVEDTELIR	7.6051	A0JNY3 Gephyrin OS=Mus musculus GN=Gphn PE=1 SV=1 # Q8BUV3 Gephyrin OS=Mus musculus GN=Gphn PE=1 SV=2 #
YVEPIEDVPC*GNIVGLVGVDQFLVK	7.5523	P58252 Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2 #
LQEVFGC*AIR	7.3962	Q9D0I9 Arginine--tRNA ligase# cytoplasmic OS=Mus musculus GN=Rars PE=1 SV=2 #
GLIAAIC*AGPTALLAHEVGFGCK	7.3181	Q99LX0 Protein deglycase DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1 #
VDTDGNGYISC*NELNDLFK	7.2379	Q61233 Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4 #
NINNDTTYC*IK	7.2246	Q99KR3 Beta-lactamase-like protein 2 OS=Mus musculus GN=Lactb2 PE=1 SV=1 #
QEPLGSDSEGVNC*LAYDEAIMAQQDR	7.1850	Q7TQI3 Ubiquitin thioesterase OTUB1 OS=Mus musculus GN=Otub1 PE=1 SV=2 #
AVLHPTGPLYC*PEEK	7.1245	Q8BG51-2 Isoform 2 of Mitochondrial Rho GTPase 1 OS=Mus musculus GN=Rhot1 # Q8BG51 Mitochondrial Rho GTPase 1 OS=Mus musculus GN=Rhot1 PE=1 SV=1 # Q8BG51-3 Isoform 3 of Mitochondrial Rho GTPase 1 OS=Mus musculus GN=Rhot1 # Q8BG51-4 Isoform 4 of Mitochondrial Rho GTPase 1 OS=Mus musculus GN=Rhot1 #
C*LLQIQASSGENK	7.0456	Q9Z2Z6 Mitochondrial carnitine/acylcarnitine carrier protein OS=Mus musculus GN=Slc25a20 PE=1 SV=1 #
IQFHNVKPEC*LDAYNSLTEAVLPK	7.0121	Q5SVF7 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)# isoform CRA_f OS=Mus musculus GN=Nipsnap1 PE=1 SV=1 # O55125 Protein NipSnap homolog 1 OS=Mus musculus GN=Nipsnap1 PE=1 SV=1 #
IMQNFSFQPC*K	6.9026	Q3UEN8 Cytochrome P450 3A11 OS=Mus musculus GN=Cyp3a11 PE=1 SV=1 # Q64459 Cytochrome P450 3A11 OS=Mus musculus GN=Cyp3a11 PE=1 SV=1 #
IIYGGSVTGATC*K	6.8871	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4 #
GIIC*GLTQFTNK	6.8585	Q64516-2 Isoform 2 of Glycerol kinase OS=Mus musculus GN=Gk # Q64516 Glycerol kinase OS=Mus musculus GN=Gk PE=1 SV=2 # Q64516-1 Isoform 1 of Glycerol kinase OS=Mus musculus GN=Gk #
KIQSLGDC*K	6.8340	Q8BGQ7 Alanine--tRNA ligase# cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1 #
KPASFMTSIC*DER	6.8019	Q3V117 ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1 #
LSTPLQTNC*TASESVVQSPSVATTASPATK	6.7600	P31230 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus GN=Aimp1 PE=1 SV=2 # A0A0G2JDW6 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 (Fragment) OS=Mus musculus GN=Aimp1 PE=1 SV=3 # Q3UZG4 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus GN=Aimp1 PE=1 SV=1 #
LDADIHTNTC*R	6.7531	Q9JHW4 Selenocysteine-specific elongation factor OS=Mus musculus GN=Eefsec PE=1 SV=2 # A0A0N4SUV6 Selenocysteine-specific elongation factor OS=Mus musculus GN=Eefsec PE=1 SV=1 #
AERPDGLILGMGGQTALNC*GVELFK	6.7491	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
C*LGELIC*TLNAANVPAGTEVVCAPPTAYIDFAR	6.7325	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4 #
YQALGAELNVLPFC*SQFIPMEVINAPR	6.5440	Q8R0Y6 Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1l1 PE=1 SV=1 #

Peptide	L/H Ratio	Protein
ASEDPLLNLVSPLDC*EVDAQEGDNMGR	6.4735	Q6NSR8 Probable aminopeptidase NPEPL1 OS=Mus musculus GN=Npepl1 PE=1 SV=1 #
LC*NPPVNAISPTVITEVR	6.4565	Q9DBM2 Peroxisomal bifunctional enzyme OS=Mus musculus GN=Ehhadh PE=1 SV=4 #
VC*IDSEHSSDTLLATLNK	6.4508	O08997 Copper transport protein ATOX1 OS=Mus musculus GN=Atox1 PE=1 SV=1 #
C*IGAIAMTEPGAGSDLQGVR	6.4251	A0A0R4J083 Long-chain-specific acyl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acadl PE=1 SV=1 # P51174 Long-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acadl PE=1 SV=2 #
VTVAGLAGKDPVQC*SR	6.4063	A2A816 Protein deglycase DJ-1 (Fragment) OS=Mus musculus GN=Park7 PE=1 SV=1 # Q99LX0 Protein deglycase DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1 #
CLGELIC*TLNAANVPAGTEVVCAPPTAYIDFAR	6.3492	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4 #
C*MPTFQFYK	6.3410	P10639 Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3 #
VILSSSSSC*LLPSK	6.2689	Q99KP3 Lambda-crystallin homolog OS=Mus musculus GN=Cryl1 PE=1 SV=3 # A7VMV2 Crystallin# lamda 1# isoform CRA_a OS=Mus musculus GN=Cryl1 PE=1 SV=1 #
HTAFIC*DKN	6.1744	Q8VDG5 Phosphopantothenate--cysteine ligase OS=Mus musculus GN=Ppcs PE=1 SV=1 #
SGANVLICGPNGC*GK	6.1475	P55096 ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=2 #
MQLIMLC*YNPDFEK	6.1280	P10649 Glutathione S-transferase Mu 1 OS=Mus musculus GN=Gstm1 PE=1 SV=2 #
SSGGFVWAC*K	6.1053	P54071 Isocitrate dehydrogenase [NADP]# mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3 #
IC*DGVQFGAGIR	6.0934	Q8BGH2 Sorting and assembly machinery component 50 homolog OS=Mus musculus GN=Samm50 PE=1 SV=1 #
EAPFTHFDPSCLFPAC*R	6.0705	P16015 Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3 #
VC*LIGC*GFSTGYGSAVK	6.0515	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
DCVGPEVENAC*ANPAAGTVILLENLR	5.9806	P09411 Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4 #
ALQHIIC*QLGGTVCDGEK	5.9525	Q3UEJ8 Peroxisomal sarcosine oxidase OS=Mus musculus GN=Pipox PE=1 SV=1 # Q9D826 Peroxisomal sarcosine oxidase OS=Mus musculus GN=Pipox PE=1 SV=1 #
AFVFDVLHEGC*LITPPELLR	5.8571	Q9DC50 Peroxisomal carnitine O-octanoyltransferase OS=Mus musculus GN=Crot PE=1 SV=1 #
IAVNIC*YGR	5.7827	Q3UEK4 Beta-ureidopropionase OS=Mus musculus GN=Upb1 PE=1 SV=1 # Q8VC97 Beta-ureidopropionase OS=Mus musculus GN=Upb1 PE=1 SV=1 #
C*EQPLWIPR	5.7122	E9QNW6 Platelet-activating factor acetylhydrolase 2# cytoplasmic OS=Mus musculus GN=Pafah2 PE=1 SV=1 # Q8VDG7 Platelet-activating factor acetylhydrolase 2# cytoplasmic OS=Mus musculus GN=Pafah2 PE=1 SV=2 #
NAGQTC*VCSNR	5.6765	Q8BWF0 Succinate-semialdehyde dehydrogenase# mitochondrial OS=Mus musculus GN=Aldh5a1 PE=1 SV=1 # B2RS41 Aldhehyde dehydrogenase family 5# subfamily A1 OS=Mus musculus GN=Aldh5a1 PE=1 SV=1 #
VPQC*PSGR	5.6457	Q9JKV1 Proteasomal ubiquitin receptor ADRM1 OS=Mus musculus GN=Adrm1 PE=1 SV=2 # A0A0A6YVU8 MCG119397 OS=Mus musculus GN=Gm9774 PE=4 SV=1 #
STLTDSLVC*K	5.6252	P58252 Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2 #
ITGTNAEVMPAQWEFQIGPC*EGIR	5.5048	P15105 Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6 #
GEC*YGLHAFVVPIR	5.4955	Q9R0H0 Peroxisomal acyl-coenzyme A oxidase 1 OS=Mus musculus GN=Acox1 PE=1 SV=5 # Q9R0H0-2 Isoform 2 of Peroxisomal acyl-coenzyme A oxidase 1 OS=Mus musculus GN=Acox1 #

Peptide	L/H Ratio	Protein
GNPAAVC*LLER	5.4300	K3W4L7 Phenazine biosynthesis-like domain-containing protein 2 OS=Mus musculus GN=Pbld2 PE=1 SV=1 # Q9DCG6 Phenazine biosynthesis-like domain-containing protein 1 OS=Mus musculus GN=Pbld1 PE=1 SV=2 # Q9CXN7 Phenazine biosynthesis-like domain-containing protein 2 OS=Mus musculus GN=Pbld2 PE=1 SV=1 #
ISSINSISALC*EATGADVEEVATAIGMDQR	5.3954	Q3TS38 UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1 # O70475 UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1 #
DIILVSYC*TLGSSR	5.3386	Q91WT7 3-alpha-hydroxysteroid dehydrogenase type 1 OS=Mus musculus GN=Akr1c14 PE=1 SV=1 #
GYC*VMQGYWGEPQK	5.3257	Q8VCW8 Acyl-CoA synthetase family member 2# mitochondrial OS=Mus musculus GN=Acsf2 PE=1 SV=1 #
YIGGCC*GFEPYHIR	5.3199	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=1 SV=1 #
SC*SGVEFSTSGSSNTDTGK	5.2890	Q60930 Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2 #
MHNQIPQITC*DGKR	5.2810	Q91VR5 ATP-dependent RNA helicase DDX1 OS=Mus musculus GN=Ddx1 PE=1 SV=1 #
IADQC*PSSLAIQENANALAR	5.2330	Q3UER1 Fructose-bisphosphate aldolase OS=Mus musculus GN=Aldob PE=1 SV=1 # Q91Y97 Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3 #
GTDIMYTGTLDC*WR	5.2317	P51881 ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3 # Q545A2 ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=1 #
TGSQGQC*TQVR	5.2213	P62858 40S ribosomal protein S28 OS=Mus musculus GN=Rps28 PE=1 SV=1 # Q059I1 40S ribosomal protein S28 OS=Mus musculus GN=Rps28 PE=1 SV=1 # J3QNN8 MCG49140 OS=Mus musculus GN=Gm10263 PE=3 SV=1 # G3UYV7 40S ribosomal protein S28 (Fragment) OS=Mus musculus GN=Rps28 PE=1 SV=1 #
VFSANSTAAC*TELAK	5.1655	Q9D0M1 Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Mus musculus GN=Prpsap1 PE=1 SV=1 # B1AT82 MCG6846# isoform CRA_c OS=Mus musculus GN=Prpsap1 PE=1 SV=1 #
ELAC*DDPEAEQVALLAVDYLNNHLLQGFK	5.1287	Q3UEK9 Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1 # P29699 Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1 #
VAASC*GAIQYIPTELDQVR	5.0790	Q99JX4 Eukaryotic translation initiation factor 3 subunit M OS=Mus musculus GN=Eif3m PE=1 SV=1 #
GTNTGVWVGVSGSEASEALSRDPETLLGYSMVGC*QR	5.0715	A0A0U1RNJ1 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=1 # P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 #
C*ELSSSVQTDINLPYLTMDASGPK	5.0308	P38647 Stress-70 protein# mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=3 #
VVMALGDYMGASCHAC*IGGTNVR	4.9933	Q5F2A7 Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=1 SV=1 # P60843 Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=1 SV=1 #
VIVVGNPANTNC*LTASK	4.9476	P14152 Malate dehydrogenase# cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3 #
ALTNHTVYC*STK	4.9201	Q91X52 L-xylulose reductase OS=Mus musculus GN=Dcxr PE=1 SV=2 #
QVADEGDALVAGGVSQTPSYLSC*K	4.9154	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=1 SV=1 #
LININVLSVC*K	4.9152	O70503 Very-long-chain 3-oxoacyl-CoA reductase OS=Mus musculus GN=Hsd17b12 PE=1 SV=1 #
GC*HLLVATPGR	4.8631	Q62095 ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2 # Q62167 ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3 # Q3TQX5 ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=1 #
GHIEDC*GHWTQIEKPTEVNQILIK	4.8531	P34914 Bifunctional epoxide hydrolase 2 OS=Mus musculus GN=Ephx2 PE=1 SV=2 #

Peptide	L/H Ratio	Protein
QGGFLPGGGSLHSAMTPHGPDADC*FEK	4.8491	O09173 Homogentisate 1#2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2 #
SRPYLFSNSLPPAVVGC*ASK	4.8397	O88986 2-amino-3-ketobutyrate coenzyme A ligase# mitochondrial OS=Mus musculus GN=Gcat PE=1 SV=2 #
LDINLLDNVVNC*LYHGEGAQQR	4.8372	Q6P5F9 Exportin-1 OS=Mus musculus GN=Xpo1 PE=1 SV=1 #
YKEWVDQNSPVLLNDPVLC*DVAK	4.7655	Q8VC28 Aldo-keto reductase family 1 member C13 OS=Mus musculus GN=Akr1c13 PE=1 SV=2 # Q9JLI0 Aldo-keto reductase a OS=Mus musculus GN=Akr1c12 PE=1 SV=1 #
LEVDAIVNAANSSLLGGGGVDGC*IHR	4.7630	Q922B1 O-acetyl-ADP-ribose deacetylase MACROD1 OS=Mus musculus GN=Macrod1 PE=1 SV=2 #
EVLLC*LFDEK	4.7437	C5NSA7 Tryptophan 2#3-dioxygenase OS=Mus musculus GN=Tdo2 PE=1 SV=1 # P48776 Tryptophan 2#3-dioxygenase OS=Mus musculus GN=Tdo2 PE=1 SV=2 # Q8VCW3 Tryptophan 2#3-dioxygenase OS=Mus musculus GN=Tdo2 PE=1 SV=1 #
IVSSKDYC*VTANSK	4.7427	G5E8N5 L-lactate dehydrogenase OS=Mus musculus GN=Ldha PE=1 SV=1 # P06151 L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3 # Q564E2 L-lactate dehydrogenase OS=Mus musculus GN=Ldha PE=1 SV=1 #
SGDLFNC*GSLTIR	4.7361	Q6P3A8 2-oxoisovalerate dehydrogenase subunit beta# mitochondrial OS=Mus musculus GN=Bckdhb PE=1 SV=2 #
ALNDHHVYLEGTLLKPNMVTAGHAC*TK	4.7103	Q3UER1 Fructose-bisphosphate aldolase OS=Mus musculus GN=Aldob PE=1 SV=1 # Q91Y97 Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3 #
DAEVVLC*GGTESMSQSPYCVR	4.7093	Q8BWT1 3-ketoacyl-CoA thiolase# mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 #
C*HTPPLYR	4.7057	P62717 60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1 #
AC*QGMSAVIHTAAAIDPLGAASR	4.7000	Q3UIU9 3 beta-hydroxysteroid dehydrogenase type 4 OS=Mus musculus GN=Gm10681 PE=2 SV=1 # Q61767 3 beta-hydroxysteroid dehydrogenase type 4 OS=Mus musculus GN=Hsd3b4 PE=2 SV=3 # Q61694 3 beta-hydroxysteroid dehydrogenase type 5 OS=Mus musculus GN=Hsd3b5 PE=1 SV=4 # E9Q007 Protein Gm4450 OS=Mus musculus GN=Gm4450 PE=1 SV=1 #
SFDDSGSGYC*R	4.6817	P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 #
HLLPLVQC*PTLIVHGEKDPLVPR	4.6789	Q8R164 Valacyclovir hydrolase OS=Mus musculus GN=Bphl PE=1 SV=1 #
C*AVVDVPFGGAK	4.6769	P26443 Glutamate dehydrogenase 1# mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1 #
GTQEPC*TVKPAQVEPLLR	4.6712	Q8CC86 Nicotinate phosphoribosyltransferase OS=Mus musculus GN=Naprt PE=1 SV=1 #
HGGEDYVFSLLTGYC*EPPTGVSLR	4.6680	Q9D0M3 Cytochrome c1# heme protein# mitochondrial OS=Mus musculus GN=Cyc1 PE=1 SV=1 # Q9D0M3-2 Isoform 2 of Cytochrome c1# heme protein# mitochondrial OS=Mus musculus GN=Cyc1 #
LNCQVIGASVDSHFC*HLAWINTPK	4.6640	P35700 Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1 # B1AXW6 Peroxiredoxin-1 (Fragment) OS=Mus musculus GN=Prdx1 PE=1 SV=1 # B1AXW5 Peroxiredoxin-1 (Fragment) OS=Mus musculus GN=Prdx1 PE=1 SV=7 #
C*VIAEGDLGIVQK	4.6300	Q9Z0S1 3'(2')#5'-bisphosphate nucleotidase 1 OS=Mus musculus GN=Bpnt1 PE=1 SV=2 #
GQVC*LPVISAENWKPATK	4.6131	P68037 Ubiquitin-conjugating enzyme E2 L3 OS=Mus musculus GN=Ube2l3 PE=1 SV=1 # Q561N4 MCG1032217 OS=Mus musculus GN=Ube2l3 PE=1 SV=1 #
TCSC*LDENYYK	4.6106	O09173 Homogentisate 1#2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2 #
C*VEELPEWNFDGSSTFQSEGSNSDMYLHPVAMFR	4.5660	P15105 Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6 # D3YVK1 Glutamine synthetase (Fragment) OS=Mus musculus GN=Glul PE=1 SV=7 #

Peptide	L/H Ratio	Protein
FGCISTLSC*PTLAGSSSPAQR	4.4989	Q8CAS9 Poly [ADP-ribose] polymerase 9 OS=Mus musculus GN=Parp9 PE=1 SV=2 # Q8CAS9-2 Isoform 2 of Poly [ADP-ribose] polymerase 9 OS=Mus musculus GN=Parp9 #
TGIQTSCLC*PVFVNTGFTK	4.4721	Q8VCR2-2 Isoform 2 of 17-beta-hydroxysteroid dehydrogenase 13 OS=Mus musculus GN=Hsd17b13 #
QCFLYMVC*QTAK	4.4689	Q9DCY0 Glycine N-acyltransferase-like protein Keg1 OS=Mus musculus GN=Keg1 PE=1 SV=1 #
IQEEAGC*LIK	4.4639	P56593 Cytochrome P450 2A12 OS=Mus musculus GN=Cyp2a12 PE=1 SV=2 #
AAPISC*HVQVAHEK	4.4368	A0A0J9YUI8 Glucokinase regulatory protein OS=Mus musculus GN=Gckr PE=1 SV=1 #
DHINLPGFC*GQNPLRGPNDER	4.4117	Q9D8C9 Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp2 PE=1 SV=1 #
AGASIVGVNC*HFDPSVSLQTVK	4.4078	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=1 SV=1 #
TVVVNCNPETVSTDFDEC*DKLYFEELSLER	4.4028	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
C*ASQAGMTAYGTR	4.3849	Q9DAW9 Calponin-3 OS=Mus musculus GN=Cnn3 PE=1 SV=1 #
VC*ENIPIVLCGNK	4.3708	P62827 GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3 #
FAATRSCTIC*TLMQSR	4.3327	Q8CC96 Uncharacterized protein C6orf222 homolog OS=Mus musculus PE=2 SV=1 #
LC*DPSEQALYGK	4.2936	Q9CW42 Mitochondrial amidoxime-reducing component 1 OS=Mus musculus GN=Marc1 PE=1 SV=2 #
IAILTC*PFEPPKPK	4.2584	P80316 T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1 #
VPAFEGDDGFC*VFESNAIAYYVSNEELR	4.2555	Q4FZK2 Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=1 # Q9D8N0 Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3 #
AIC*TEAGLMALR	4.2437	P62192 26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1 # Q542I9 26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1 #
TPC*NAGTFSQPEK	4.2413	A0A140LHA2 Mitotic checkpoint protein BUB3 OS=Mus musculus GN=Bub3 PE=1 SV=1 # A0A140LIM5 Mitotic checkpoint protein BUB3 OS=Mus musculus GN=Bub3 PE=1 SV=1 # Q9WVA3 Mitotic checkpoint protein BUB3 OS=Mus musculus GN=Bub3 PE=1 SV=2 # A0A140LJ21 Mitotic checkpoint protein BUB3 (Fragment) OS=Mus musculus GN=Bub3 PE=1 SV=1 #
EAESC*DCLQGFQLTHSLGGGTGSGMGTLLISK	4.1970	P99024 Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1 # Q9D6F9 Tubulin beta-4A chain OS=Mus musculus GN=Tubb4a PE=1 SV=3 # P68372 Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1 #
VGEC*FNHAVWR	4.1905	Q9EP69 Phosphatidylinositide phosphatase SAC1 OS=Mus musculus GN=Sacm1l PE=1 SV=1 #
TSLRPQTFYDGSHC*SAR	4.1766	Q9CQ65 S-methyl-5'-thioadenosine phosphorylase OS=Mus musculus GN=Mtap PE=1 SV=1 #
AIVTTASLVPEVESVASEC*PDLK	4.1679	Q91VA0 Acyl-coenzyme A synthetase ACSM1# mitochondrial OS=Mus musculus GN=Acsm1 PE=1 SV=1 #
VNEAAC*DIAR	4.1678	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=1 SV=1 #
WTAC*YPPGPVPFPGLGNLLQVDFENIPYSFYK	4.1674	A0A0R4IZY2 Cytochrome P450 2D26 OS=Mus musculus GN=Cyp2d26 PE=1 SV=1 #
LCLNIC*VGESGDR	4.1660	E9PYL9 Protein Gm10036 OS=Mus musculus GN=Gm10036 PE=3 SV=1 # Q9CXW4 60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4 #
ASSTC*QLTFENVKVPETNILGK	4.1550	Q9DBL1 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acadsb PE=1 SV=1 #
DC*VGPEVENACANPAAGTVILLENLR	4.1444	P09411 Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4 #

Peptide	L/H Ratio	Protein
DIVLVAYC*ALGSQRPK	4.1236	G3X9Y6 Aldo-keto reductase family 1# member C19 OS=Mus musculus GN=Akr1c19 PE=1 SV=1 #
VGLGIC*YDMR	4.1032	Q9JHW2 Omega-amidase NIT2 OS=Mus musculus GN=Nit2 PE=1 SV=1 #
INILINCAAGNFLC*PASALSFNAFK	4.0884	Q3UVJ7 2-4-dienoyl-Coenzyme A reductase 2# peroxisomal OS=Mus musculus GN=Decr2 PE=1 SV=1 # Q9WV68 Peroxisomal 2#4-dienoyl-CoA reductase OS=Mus musculus GN=Decr2 PE=1 SV=1 #
VSMPICVGATAMQC*MAHVDGELATVR	4.0841	Q3UEE8 Hydroxyacid oxidase 1 OS=Mus musculus GN=Hao1 PE=1 SV=1 # Q9WU19 Hydroxyacid oxidase 1 OS=Mus musculus GN=Hao1 PE=1 SV=1 #
ALEDAQIPYSAVEQAC*VGYVYGDSTSGQR	4.0698	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 #
YLAEVAC*GDDR	4.0575	P68254 14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1 # F6VW30 14-3-3 protein theta (Fragment) OS=Mus musculus GN=Ywhaq PE=1 SV=1 # F6YY69 14-3-3 protein theta (Fragment) OS=Mus musculus GN=Ywhaq PE=1 SV=1 # P68254-2 Isoform 2 of 14-3-3 protein theta OS=Mus musculus GN=Ywhaq #
ETLSAKPGAIVLSVGGGGLLC*GVVQGLR	4.0568	Q3UEN6 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=1 # Q8VBT2 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=3 #
VDEFPLC*GHMVSDEYEQLSSEALEAAR	4.0486	B7FAU6 60S ribosomal protein L10 (Fragment) OS=Mus musculus GN=Rpl10 PE=4 SV=1 # Q6ZWV3 60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=1 SV=3 #
LPFIYGEEC*QVTSTTVK	4.0456	Q61694 3 beta-hydroxysteroid dehydrogenase type 5 OS=Mus musculus GN=Hsd3b5 PE=1 SV=4 #
QPRPQEAAEFQAEFVPIAQLAAESDFIVVSC*SLTPDTMGLCSK	4.0349	Q3T9Z2 Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1 # Q91Z53 Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1 #
EIIAVSCGPSQC*QETIR	4.0333	Q9DCW4 Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3 #
AIQSLTDTCSDDLSVVTDCMEHALTAC*HPR	4.0146	O88451 Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=1 SV=1 #
EEIVYLPC*IYR	3.9989	P17563 Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2 # Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 # D6RHN2 Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=1 # A0A0R4J135 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=1 #
LQDAFC*SR	3.9943	Q8VBT9-2 Isoform 2 of Tether containing UBX domain for GLUT4 OS=Mus musculus GN=Aspscr1 # Q8VBT9 Tether containing UBX domain for GLUT4 OS=Mus musculus GN=Aspscr1 PE=1 SV=1 #
YC*PNSVLVIIDVKPK	3.9538	A1L3B8 26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psmd7 PE=1 SV=1 # P26516 26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psmd7 PE=1 SV=2 #
VC*NYGLTFTQK	3.9491	Q3TX38 Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1 # A0A140T8V3 Protein Vdac3-ps1 OS=Mus musculus GN=Vdac3-ps1 PE=4 SV=1 # Q60931 Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1 #
IVDTPC*NEMNTDIFLEEIIQVGK	3.9437	Q6NSR8 Probable aminopeptidase NPEPL1 OS=Mus musculus GN=Npepl1 PE=1 SV=1 #
GEGILC*GTPEEVWDCIKPVASGLR	3.9299	Q9EPQ7 StAR-related lipid transfer protein 5 OS=Mus musculus GN=Stard5 PE=1 SV=2 #
VGYTPGVLTDATAELAVSLLLTTC*R	3.9034	Q3T9Z2 Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1 # Q91Z53 Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1 #
AILITGC*DSGFGFSLAK	3.9030	Q80XN0 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Mus musculus GN=Bdh1 PE=1 SV=2 #
GVLLYGPPGC*GK	3.9026	Q9D5T0 ATPase family AAA domain-containing protein 1 OS=Mus musculus GN=Atad1 PE=1 SV=1 #
C*STPEEIK	3.8902	Q4FK36 Destrin OS=Mus musculus GN=Dstn PE=1 SV=1 # Q9R0P5 Destrin OS=Mus musculus GN=Dstn PE=1 SV=3 #

Peptide	L/H Ratio	Protein
VNINGGAIALGHPLGASGC*R	3.8897	Q80X81 Acetyl-Coenzyme A acetyltransferase 3 OS=Mus musculus GN=Acat3 PE=1 SV=1 #
TAC*PGPFLQYNFDVTK	3.8869	A2AQN5 Acetyl-coenzyme A synthetase# cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=1 # Q9QXG4 Acetyl-coenzyme A synthetase# cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=2 # A2AQN4 Acetyl-coenzyme A synthetase# cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=1 #
SVSAFAPIC*NPVLC*SWGK	3.8863	Q9R0P3 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1 # H3BKH6 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1 #
ILSSPWLQVCNSFPSLIDYC*PGSHHK	3.8514	Q64458 Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29 PE=1 SV=2 #
VALVC*TGSEGSSITNSQLDAR	3.8504	Q4LDG0 Bile acyl-CoA synthetase OS=Mus musculus GN=Slc27a5 PE=1 SV=2 #
GGSVQVLEDQELTC*QPEPLVVK	3.8361	P17563 Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2 # Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 # A0A0R4J135 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=1 #
IAVYSC*PFDGMITETK	3.8294	Q3UL22 Chaperonin subunit 8 (Theta)# isoform CRA_a OS=Mus musculus GN=Cct8 PE=1 SV=1 # P42932 T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3 #
YFLQGMGYMASSC*MTR	3.8264	Q9QYG0 Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1 #
IGIASQALGIAQASLDC*AVK	3.8204	Q07417 Short-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acads PE=1 SV=2 #
NILGGTVFREPIIC*K	3.8044	P54071 Isocitrate dehydrogenase [NADP]# mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3 #
ELLTEFGYKGEETPVIVGSALC*ALEQR	3.8026	Q8BFR5 Elongation factor Tu# mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1 #
GNDQVRFELTC*YSLAPQIK	3.7948	P16460 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1 #
LLGSTIPLC*SAQWER	3.7878	P97742 Carnitine O-palmitoyltransferase 1# liver isoform OS=Mus musculus GN=Cpt1a PE=1 SV=4 # Q7TQD5 Carnitine O-palmitoyltransferase 1# liver isoform OS=Mus musculus GN=Cpt1a PE=1 SV=1 #
WDEVPDDFVEC*FILSGYR	3.7729	Q6TCG2 Progestin and adipoQ receptor family member 9 OS=Mus musculus GN=Paqr9 PE=1 SV=2 #
C*IPYAVLLEALALR	3.7664	Q9CZ04-2 Isoform 2 of COP9 signalosome complex subunit 7a OS=Mus musculus GN=Cops7a # D3Z440 COP9 signalosome complex subunit 7a (Fragment) OS=Mus musculus GN=Cops7a PE=1 SV=7 # Q9CZ04 COP9 signalosome complex subunit 7a OS=Mus musculus GN=Cops7a PE=1 SV=2 # D3YVI6 COP9 signalosome complex subunit 7a (Fragment) OS=Mus musculus GN=Cops7a PE=1 SV=1 #
DSGLWFPVDPGADASLC*GMAATGASGTNAVR	3.7464	Q7TNG8 Probable D-lactate dehydrogenase# mitochondrial OS=Mus musculus GN=Ldhd PE=1 SV=1 #
C*SYDEHAK	3.7407	Q546G4 Albumin 1 OS=Mus musculus GN=Alb PE=1 SV=1 # P07724 Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3 #
QLVLLNPYAALC*NR	3.7399	Q8VBW8 Tetratricopeptide repeat protein 36 OS=Mus musculus GN=Ttc36 PE=1 SV=1 #
SWMEGLTLQDYSEHC*K	3.7385	O35593 26S proteasome non-ATPase regulatory subunit 14 OS=Mus musculus GN=Psmd14 PE=1 SV=2 #
VQAQYPGIC*INNEVVEPSAEQIVK	3.7363	Q91VF2 Histamine N-methyltransferase OS=Mus musculus GN=Hnmt PE=1 SV=1 # A2AQK4 Histamine N-methyltransferase OS=Mus musculus GN=Hnmt PE=1 SV=1 #
TTGLVGLAVC*DTPHER	3.7291	Q9CPP6 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Mus musculus GN=Ndufa5 PE=1 SV=3 #
GVLMYGPPGC*GK	3.7166	P54775 26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2 #
VTAVIPC*FPYAR	3.7124	G3UXL2 Protein Prps1l3 OS=Mus musculus GN=Prps1l3 PE=3 SV=1 # Q9CS42 Ribose-phosphate pyrophosphokinase 2 OS=Mus musculus

Peptide	L/H Ratio	Protein
		GN=Prps2 PE=1 SV=4 # Q9D7G0 Ribose-phosphate pyrophosphokinase 1 OS=Mus musculus GN=Prps1 PE=1 SV=4 #
MGFC*SVQEDINSLCLTVVQR	3.6841	P54869 Hydroxymethylglutaryl-CoA synthase# mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2 #
C*GPGYPTPLEAMK	3.6819	Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 # A0A0R4J135 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=1 #
LNISFPATGC*QK	3.6815	P62754 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1 # Q5BLK1 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1 #
AHIMPAEFSSC*PLNSDEAVNK	3.6700	Q91V76 Ester hydrolase C11orf54 homolog OS=Mus musculus PE=1 SV=1 #
GPSIALDTAC*SSSLLALQNAYQAIR	3.6574	P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 #
AVNQPC*APDHFIQTVSHK	3.6425	Q8CC88 von Willebrand factor A domain-containing protein 8 OS=Mus musculus GN=Vwa8 PE=1 SV=2 #
SLDINC*PR	3.6406	Q05421 Cytochrome P450 2E1 OS=Mus musculus GN=Cyp2e1 PE=1 SV=1 #
MTPGC*EAEAEAEALCFFIK	3.6323	P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 #
SGTPVHC*PSPIR	3.6148	Q9JLV1 BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=2 #
YIC*TTSAIQNR	3.6040	Q3V117 ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1 #
AQNVPLPVSTLVEFVIAATDC*TAK	3.5948	Q3UEK9 Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1 # P29699 Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1 #
LECVEPNC*R	3.5912	P83882 60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=1 SV=2 # Q5M9P1 60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=1 SV=1 #
IIPGFMC*QGGDFTR	3.5755	Q5SVY2 Peptidyl-prolyl cis-trans isomerase OS=Mus musculus GN=Ppia PE=1 SV=1 # P17742 Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2 #
IAVAAQNC*YK	3.5588	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4 #
GVFCDYLEEGAQC*PSLPSYVPR	3.5494	Q62452 UDP-glucuronosyltransferase 1-9 OS=Mus musculus GN=Ugt1a9 PE=1 SV=3 #
VLYALC*R	3.5307	Q9JJW0 Peroxisomal membrane protein 4 OS=Mus musculus GN=Pxmp4 PE=1 SV=3 #
YLLQYQEPIPC*EQLVTALCDIK	3.5259	Q9R1P0 Proteasome subunit alpha type-4 OS=Mus musculus GN=Psma4 PE=1 SV=1 #
NLGVFPFPVAPYPYQLC*AVMR	3.5257	P24456 Cytochrome P450 2D10 OS=Mus musculus GN=Cyp2d10 PE=1 SV=2 #
C*GETAFIAPQCEMIPIEWVCR	3.5200	Q9DCL9 Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4 #
SYIEGYVPSQADVAVFEAVSGPPPADLC*HALR	3.5163	O70251 Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5 # G3UZ47 Elongation factor 1-beta (Fragment) OS=Mus musculus GN=Eef1b2 PE=1 SV=1 # G3UX43 Elongation factor 1-beta OS=Mus musculus GN=Eef1b2 PE=1 SV=1 #
LEAPC*QQWMELR	3.5160	Q9CRB3 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1 SV=1 # A0A0A0MQC3 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1 SV=1 #
LTTPTYGDLNHLVSATMSGVTTC*LR	3.4950	P99024 Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1 # Q9D6F9 Tubulin beta-4A chain OS=Mus musculus GN=Tubb4a PE=1 SV=3 # Q7TMM9 Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1 # B2RSN3 MCG1395 OS=Mus musculus GN=Tubb2b PE=1 SV=1 # Q9CWF2 Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1 # P68372 Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1 #
AFAFVTFADDKVAQSLC*GEDLIIK	3.4945	Q8R0B4 MCG16669# isoform CRA_a OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q8BLD4 MCG16669# isoform CRA_f OS=Mus musculus

Peptide	L/H Ratio	Protein
		GN=Tardbp PE=1 SV=1 # Q544R5 MCG16669# isoform CRA_b OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q921F2 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q6VYI4 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q6VYI5 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 # A0A087WRZ5 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 #
SIPYGC*LEEVIPYLIR	3.4855	Q8VCZ9 Probable proline dehydrogenase 2 OS=Mus musculus GN=Prodh2 PE=1 SV=1 #
LNGGLGTSMGC*K	3.4758	Q91ZJ5 UTP--glucose-1-phosphate uridylyltransferase OS=Mus musculus GN=Ugp2 PE=1 SV=3 #
LIGPNC*PGVINPGECK	3.4718	Q9WUM5 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha# mitochondrial OS=Mus musculus GN=Suclg1 PE=1 SV=4 #
C*LDAFPNLRDFLAR	3.4698	F6WHQ7 Glutathione S-transferase Mu 1 (Fragment) OS=Mus musculus GN=Gstm1 PE=1 SV=1 # P19639 Glutathione S-transferase Mu 3 OS=Mus musculus GN=Gstm3 PE=1 SV=2 # P10649 Glutathione S-transferase Mu 1 OS=Mus musculus GN=Gstm1 PE=1 SV=2 #
GSDC*GIVNVNIPTSGAEIGGAFGGEK	3.4605	Q9DBF1-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Mus musculus GN=Aldh7a1 # Q9DBF1 Alpha-aminoadipic semialdehyde dehydrogenase OS=Mus musculus GN=Aldh7a1 PE=1 SV=4 #
IVVHMAHALKPGEFGLASIC*NGGGGASALLIEK	3.4590	Q8QZT1 Acetyl-CoA acetyltransferase# mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1 #
KPWFLTNEVDEC*ENYFSR	3.4494	Q9DCN1 Peroxisomal NADH pyrophosphatase NUDT12 OS=Mus musculus GN=Nudt12 PE=1 SV=1 #
AFSC*SSFNSNTFLTR	3.4446	P46061 Ran GTPase-activating protein 1 OS=Mus musculus GN=Rangap1 PE=1 SV=2 #
C*LHTFTNNVIAER	3.4373	Q9DBW0 Cytochrome P450 4V2 OS=Mus musculus GN=Cyp4v2 PE=1 SV=1 # B2RSR0 Cytochrome P450 4V2 OS=Mus musculus GN=Cyp4v3 PE=1 SV=1 #
NYDYILSTGC*APPGK	3.4299	Q9QXF8 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=1 SV=3 #
ILVEPAC*GAALAAVYSR	3.4291	Q3UEN6 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=1 # Q8VBT2 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=3 #
FIDLLPTSLPHAVTC*DIK	3.4182	Q64458 Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29 PE=1 SV=2 #
LPQGC*AEQTMIYLAPTLTASNYLDR	3.4141	P01029 Complement C4-B OS=Mus musculus GN=C4b PE=1 SV=3 #
KTYITDPVSAPC*APPLQPK	3.4061	Q8BFW7 Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp PE=1 SV=1 # Q8BFW7-4 Isoform 4 of Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp # Q8BFW7-5 Isoform 5 of Lipoma-preferred partner homolog OS=Mus musculus GN=Lpp #
LGEWVGLC*K	3.3990	Q6ZWZ6 40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=1 #
ILQACGGNSLGSYSASQGVNC*IR	3.3954	Q8BGT5 Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=1 SV=1 #
LHLDEDYPC*SLVGNWNTWYGEQDQAVHLWR	3.3808	Q5SVF7 4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)# isoform CRA_f OS=Mus musculus GN=Nipsnap1 PE=1 SV=1 # O55125 Protein NipSnap homolog 1 OS=Mus musculus GN=Nipsnap1 PE=1 SV=1 #
SGGGGGSSGAGGGPSC*GTSSSR	3.3708	A0A140LJ01 Signal peptidase complex subunit 2 (Fragment) OS=Mus musculus GN=Spcs2 PE=1 SV=1 # A0A140LIK0 Signal peptidase complex subunit 2 OS=Mus musculus GN=Spcs2 PE=1 SV=1 # Q9CYN2 Signal peptidase complex subunit 2 OS=Mus musculus GN=Spcs2 PE=1 SV=1 # A0A140LHG8 Signal peptidase complex subunit 2 OS=Mus musculus GN=Spcs2 PE=1 SV=1 #
VGAFTVVC*K	3.3563	P05202 Aspartate aminotransferase# mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1 #
AVQMGMSSVFFNKGENC*IAAGR	3.3448	Q8R0Y6 Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Mus musculus GN=Aldh1l1 PE=1 SV=1 #

Peptide	L/H Ratio	Protein
VNC*LAPGLIK	3.3412	Q99LB2 Dehydrogenase/reductase SDR family member 4 OS=Mus musculus GN=Dhrs4 PE=1 SV=3 #
MECC*DVPAETLYDVLHDIEYR	3.3364	G3V020 PCTP-like protein (Fragment) OS=Mus musculus GN=Stard10 PE=1 SV=1 # E9PVP0 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 # G3UW37 PCTP-like protein (Fragment) OS=Mus musculus GN=Stard10 PE=1 SV=1 # Q0VG22 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 # Q9JMD3 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 #
LC*DSEAHVCFEGLDSDPTGTAYGASIPLAR	3.3267	Q8R086 Sulfite oxidase# mitochondrial OS=Mus musculus GN=Suox PE=1 SV=2 #
GHGLTC*EGQPVTSR	3.3221	A2AJL3 FGGY carbohydrate kinase domain-containing protein OS=Mus musculus GN=Fggy PE=1 SV=1 #
AGAIAPC*EVTVPAQNTGLGPEK	3.3198	Q5M8R8 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=1 # P14869 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3 #
SFSPGLPPQSC*SLTLKR	3.3180	P59266 Fat storage-inducing transmembrane protein 2 OS=Mus musculus GN=Fitm2 PE=1 SV=1 #
FLHDPSATQGFVGC*ALSSNIQR	3.3153	P17563 Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2 # Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 # A0A0R4J135 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=1 #
AAC*LESAQEPAGAWSNK	3.3100	A0A087WP83 Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1 # Q8VDJ3 Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1 # Q3U4Z7 High density lipoprotein (HDL) binding protein# isoform CRA_d OS=Mus musculus GN=Hdlbp PE=1 SV=1 #
AFQFVETHGEVC*PANWTPESPTIKPSPTASK	3.3069	P20108 Thioredoxin-dependent peroxide reductase# mitochondrial OS=Mus musculus GN=Prdx3 PE=1 SV=1 #
MQLIMLC*YNPDFTR	3.2937	F6WHQ7 Glutathione S-transferase Mu 1 (Fragment) OS=Mus musculus GN=Gstm1 PE=1 SV=1 #
MC*HPSVDGFTPR	3.2781	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
DTCLSYSPLLQNIFDEYSDYC*LTLCK	3.2660	Q3UEP4 UDP-glucuronosyltransferase OS=Mus musculus GN=Ugt2b36 PE=1 SV=1 #
ELCFEVGEGESLDLPC*GLEEAIQR	3.2626	P30416 Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus GN=Fkbp4 PE=1 SV=5 #
GTPEQPQC*GFSNAVVQILR	3.2601	Q80Y14 Glutaredoxin-related protein 5# mitochondrial OS=Mus musculus GN=Glrx5 PE=1 SV=2 #
GVAALC*IGGGMGVAMCVQR	3.2415	Q8CAY6 Acetyl-CoA acetyltransferase# cytosolic OS=Mus musculus GN=Acat2 PE=1 SV=2 #
VKDC*PPADLIIK	3.2267	Q64471 Glutathione S-transferase theta-1 OS=Mus musculus GN=Gstt1 PE=1 SV=4 #
ALTTPC*PYQLCALPR	3.2261	Q9JKY7 Cytochrome P450 CYP2D22 OS=Mus musculus GN=Cyp2d22 PE=1 SV=1 #
LILADALC*YAHTFNPK	3.2251	Q9CPY7-2 Isoform 2 of Cytosol aminopeptidase OS=Mus musculus GN=Lap3 # Q9CPY7 Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3 #
DKDFTLNDFGFMIFHSPYC*K	3.2138	Q8JZK9 Hydroxymethylglutaryl-CoA synthase# cytoplasmic OS=Mus musculus GN=Hmgcs1 PE=1 SV=1 #
NIC*FTVWDVGGQDK	3.2067	Q14BR4 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=1 SV=1 # P61750 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=1 SV=2 # P84084 ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=1 SV=2 #
GAVHQLC*QSLAGK	3.2042	D3YWR7 Dihydropteridine reductase OS=Mus musculus GN=Qdpr PE=1 SV=1 #
NIIQPPSCVLHYYNVPLC*VTEETFTK	3.2003	Q921F4 Heterogeneous nuclear ribonucleoprotein L-like OS=Mus musculus GN=Hnrnpll PE=1 SV=3 #
C*YQLPPGAR	3.1995	P10518 Delta-aminolevulinic acid dehydratase OS=Mus musculus GN=Alad PE=1 SV=1 #

Peptide	L/H Ratio	Protein
MVATGVC*R	3.1968	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
YIIWSPVC*R	3.1926	P11352 Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2 #
C*PEALFQPSFLGMESCGIHETTFNSIMK	3.1901	P60710 Actin# cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 # P63260 Actin# cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 # B2RRX1 Actin# beta OS=Mus musculus GN=Actb PE=1 SV=1 # Q4KL81 Actin# cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 #
LPC*YFENLLSYFLPQK	3.1899	G5E8S7 NmrA-like family domain containing 1# isoform CRA_a OS=Mus musculus GN=Nmral1 PE=1 SV=1 # Q8K2T1 NmrA-like family domain-containing protein 1 OS=Mus musculus GN=Nmral1 PE=1 SV=1 # Q8K2T1-3 Isoform 3 of NmrA-like family domain-containing protein 1 OS=Mus musculus GN=Nmral1 # Q8K2T1-2 Isoform 2 of NmrA-like family domain-containing protein 1 OS=Mus musculus GN=Nmral1 # D3YU12 NmrA-like family domain-containing protein 1 OS=Mus musculus GN=Nmral1 PE=1 SV=1 #
LAAFLNSMC*PR	3.1822	O08914 Fatty-acid amide hydrolase 1 OS=Mus musculus GN=Faah PE=1 SV=1 #
SPNIIMSDADMDWAVEQAHFALFFNQGQCCC*AGSR	3.1795	Q544B1 Aldehyde dehydrogenase 2# mitochondrial# isoform CRA_b OS=Mus musculus GN=Aldh2 PE=1 SV=1 # P47738 Aldehyde dehydrogenase# mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1 #
AAQDFFSTC*R	3.1793	P70697 Uroporphyrinogen decarboxylase OS=Mus musculus GN=Urod PE=1 SV=2 #
GQNNPQVCPYNLYAEQLSGSAFTC*PR	3.1549	O09173 Homogentisate 1#2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2 #
SAYALGGLGSGIC*PNKETLIDLGTK	3.1468	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
SLC*LGPTLIYSAK	3.1449	Q9CZB0 Succinate dehydrogenase cytochrome b560 subunit# mitochondrial OS=Mus musculus GN=Sdhc PE=1 SV=1 #
VTGTQFPEAPLPVPC*NPNDVSHGYVTVKPGIR	3.1421	P34914 Bifunctional epoxide hydrolase 2 OS=Mus musculus GN=Ephx2 PE=1 SV=2 #
KAAAPAPEEEMDEC*EQALAAEPK	3.1410	Q4FZK2 Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=1 # Q9D8N0 Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3 #
AVASQLDC*NFLK	3.1346	Q14AQ1 26S protease regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1 # P62334 26S protease regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1 #
SDGALVDC*GTSAQK	3.1325	Q64105 Sepiapterin reductase OS=Mus musculus GN=Spr PE=1 SV=1 #
CPALYWLSGLTC*TEQNFISK	3.1222	Q9R0P3 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1 # H3BKH6 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1 #
TAC*QEYTVTEFQPLYYVAESFNDAK	3.1090	P16331 Phenylalanine-4-hydroxylase OS=Mus musculus GN=Pah PE=1 SV=4 #
IGIVGGC*QEYTGAPYFAGISALK	3.0989	Q9CZ42 ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus GN=Carkd PE=1 SV=1 # Q9CZ42-2 Isoform 2 of ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus GN=Carkd # J3QMM7 ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus GN=Carkd PE=1 SV=1 # Q9CZ42-3 Isoform 3 of ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus GN=Carkd # J3QN06 ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus GN=Carkd PE=1 SV=1 # K3W4M4 ATP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Mus musculus GN=Carkd PE=1 SV=1 #
HGFC*GIPITDTGR	3.0987	Q3UAT9 Inosine-5'-monophosphate dehydrogenase OS=Mus musculus GN=Impdh2 PE=1 SV=1 # P24547 Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh2 PE=1 SV=2 #
METYC*NSGSTDTSSVINAVTHALTAATPYTR	3.0940	Q80XN0 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Mus musculus GN=Bdh1 PE=1 SV=2 #
LNVIC*PGFVDTPILESIEKEENMGQYIEYK	3.0938	Q8VCC1 15-hydroxyprostaglandin dehydrogenase [NAD(+)] OS=Mus musculus GN=Hpgd PE=1 SV=1 #

Peptide	L/H Ratio	Protein
VIITEIDPINALQAAMEGYEVTTMDEAC*K	3.0917	P50247 Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3 # Q3TF14 Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=1 #
GLVVLGFPC*NQFGHQENGKNEEILNSLK	3.0874	P11352 Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2 #
VFANAYLSDLGGC*IK	3.0847	P24549 Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5 #
HTGPGILSMANAGPNTNGSQFFIC*TAK	3.0834	Q5SVY2 Peptidyl-prolyl cis-trans isomerase OS=Mus musculus GN=Ppia PE=1 SV=1 # P17742 Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2 #
QAGNNQPFTLDDVQYMIFHTPFC*K	3.0758	P54869 Hydroxymethylglutaryl-CoA synthase# mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2 #
YVFITGC*DSGFGNLLAR	3.0470	Q8K5C8 Cis-retinol/androgen dehydrogenase type 3 OS=Mus musculus GN=Rdh9 PE=2 SV=1 # E9Q9P8 Protein Gm28046 OS=Mus musculus GN=Gm28046 PE=3 SV=1 # G5E8H9 MCG134493 OS=Mus musculus GN=Rdh19 PE=3 SV=1 # Q8CGV4 MCG140848 OS=Mus musculus GN=Rdh1 PE=2 SV=1 # Q9R092 17-beta-hydroxysteroid dehydrogenase type 6 OS=Mus musculus GN=Hsd17b6 PE=1 SV=1 # O88451 Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=1 SV=1 #
FDPTQFQDC*IIQGLTETGTDLEAVAK	3.0413	A0A087WQS2 Basic leucine zipper and W2 domain-containing protein 1 OS=Mus musculus GN=Bzw1 PE=1 SV=1 # Q9CQC6 Basic leucine zipper and W2 domain-containing protein 1 OS=Mus musculus GN=Bzw1 PE=1 SV=1 #
VPTPNVSVVDLTC*R	3.0370	P16858 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2 # A0A0A0MQF6 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=1 # D2KHZ9 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=GAPDH PE=1 SV=1 #
GVILTSEC*PGIFSAGLDLLEMYGR	3.0359	P42125 Enoyl-CoA delta isomerase 1# mitochondrial OS=Mus musculus GN=Eci1 PE=1 SV=2 #
GQNNPQVC*PYNLYAEQLSGSAFTCPR	3.0355	O09173 Homogentisate 1#2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2 #
IC*EFLGENLESGELELVLK	3.0303	Q8BGL3 Sulfotransferase OS=Mus musculus GN=Sult2a8 PE=1 SV=1 #
AWWQAGADLGQPDYDGHC*ALQVAEAAGNADVVALLQSFK	3.0271	A0JNU3 60 kDa lysophospholipase OS=Mus musculus GN=Aspg PE=1 SV=1 #
EC*SHITFLTIK	3.0154	G3X8T3 Carboxypeptidase OS=Mus musculus GN=Ctsa PE=1 SV=1 # Q544R6 Carboxypeptidase OS=Mus musculus GN=Ctsa PE=1 SV=1 # P16675 Lysosomal protective protein OS=Mus musculus GN=Ctsa PE=1 SV=1 #
YKPVTNQVEC*HPYFTQTK	3.0144	Q8VCX1 3-oxo-5-beta-steroid 4-dehydrogenase OS=Mus musculus GN=Akr1d1 PE=1 SV=1 #
C*TGGEVGATSALAPK	3.0095	P35979 60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2 # Q5BLK0 60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=1 # F8VQK7 Protein Gm16519 OS=Mus musculus GN=Gm16519 PE=1 SV=2 #
DIC*QSFTNLSK	3.0031	P56654 Cytochrome P450 2C37 OS=Mus musculus GN=Cyp2c37 PE=1 SV=2 # Q91X77 Cytochrome P450 2C50 OS=Mus musculus GN=Cyp2c50 PE=1 SV=2 #
YEASFPFLSLC*GR	3.0007	Q8VE95 UPF0598 protein C8orf82 homolog OS=Mus musculus PE=1 SV=1 #
AC*HPYFPLQDIVVSPPLDSLTLER	2.9877	Q91X34 Bile acid-CoA:amino acid N-acyltransferase OS=Mus musculus GN=Baat PE=1 SV=1 #
LPDSVTFEEGALIEPLSVGIYAC*R	2.9768	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 #
C*LGELICTLNAANVPAGTEVVCAPPTAYIDFAR	2.9695	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4 #

Peptide	L/H Ratio	Protein
LVSSPCC*IVTSTYGWTANMER	2.9570	P11499 Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3 # Q71LX8 Heat shock protein 84b OS=Mus musculus GN=Hsp90ab1 PE=1 SV=1 #
SPVLLDDPVLC*AMANK	2.9553	Q91WT7 3-alpha-hydroxysteroid dehydrogenase type 1 OS=Mus musculus GN=Akr1c14 PE=1 SV=1 #
ITSC*IFQLLQEAGIK	2.9502	Q9DCL9 Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4 #
VGQPGAAGPVSPMC*PGR	2.9495	Q3UEK9 Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1 # P29699 Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1 #
DIC*QSFTNLSR	2.9493	Q6XVG2 Cytochrome P450 2C54 OS=Mus musculus GN=Cyp2c54 PE=1 SV=1 #
GSHMGTVQPIPC*LLSMPTR	2.9439	Q6A0A9 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Mus musculus GN=FAM120A PE=1 SV=2 #
YLQDAGC*PVFLYEFQHTPSSFAK	2.9437	Q63880-2 Isoform 2 of Carboxylesterase 3A OS=Mus musculus GN=Ces3a # Q63880 Carboxylesterase 3A OS=Mus musculus GN=Ces3a PE=1 SV=2 #
VSLYYESLC*GACR	2.9372	Q9ESY9 Gamma-interferon-inducible lysosomal thiol reductase OS=Mus musculus GN=Ifi30 PE=1 SV=3 #
VAAVETEHGSIQTPC*VVNCAGVWASK	2.9327	Q3TWI2 Sarcosine dehydrogenase OS=Mus musculus GN=Sardh PE=1 SV=1 # Q99LB7 Sarcosine dehydrogenase# mitochondrial OS=Mus musculus GN=Sardh PE=1 SV=1 #
FLYEC*PWR	2.9319	G5E8R3 Pyruvate carboxylase OS=Mus musculus GN=Pcx PE=1 SV=1 # E9QPD7 Pyruvate carboxylase OS=Mus musculus GN=Pcx PE=1 SV=1 #
NLVFSSSATVYGNPQYLPLDEAHPTGGC*TNPYGK	2.9289	Q8R059 UDP-glucose 4-epimerase OS=Mus musculus GN=Gale PE=1 SV=1 #
VLVC*GAGPVGMVTLLVAK	2.9221	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 #
VCVATC*NR	2.9168	Q91WG8 Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Mus musculus GN=Gne PE=1 SV=1 # Q3UW64 Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Mus musculus GN=Gne PE=1 SV=1 # Q3TCI8 Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Mus musculus GN=Gne PE=1 SV=1 #
TMLQNC*LPR	2.9107	Q9QXE0 2-hydroxyacyl-CoA lyase 1 OS=Mus musculus GN=Hacl1 PE=1 SV=2 # D3YZ54 2-hydroxyacyl-CoA lyase 1 OS=Mus musculus GN=Hacl1 PE=1 SV=2 #
VVNSETPVVVDFHAQWC*GPCK	2.8993	A2A439 Thioredoxin# mitochondrial OS=Mus musculus GN=Txn2 PE=1 SV=1 # G3UX99 Thioredoxin# mitochondrial (Fragment) OS=Mus musculus GN=Txn2 PE=1 SV=1 # P97493 Thioredoxin# mitochondrial OS=Mus musculus GN=Txn2 PE=1 SV=1 # G3UZY2 Thioredoxin# mitochondrial (Fragment) OS=Mus musculus GN=Txn2 PE=1 SV=1 #
EAAALGSHGSC*SSEVEK	2.8884	Q5HZY7 ATPase# H+ transporting# lysosomal V1 subunit G1 OS=Mus musculus GN=Atp6v1g1 PE=1 SV=1 # Q9CR51 V-type proton ATPase subunit G 1 OS=Mus musculus GN=Atp6v1g1 PE=1 SV=3 #
GLC*GAIHSSVAK	2.8852	Q91VR2 ATP synthase subunit gamma# mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1 # Q3UD06 ATP synthase subunit gamma OS=Mus musculus GN=Atp5c1 PE=1 SV=1 # Q8C2Q8 ATP synthase subunit gamma OS=Mus musculus GN=Atp5c1 PE=1 SV=1 #
SDDHVVSGTLVTPLPAVLGHEGAGIVESVGEGVTC*VKPGDK	2.8835	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
MISQSC*LSNIEK	2.8828	Q8BGL3 Sulfotransferase OS=Mus musculus GN=Sult2a8 PE=1 SV=1 #
WGWNDVFC*DSKHNSICEMK	2.8798	Q9JKF4-3 Isoform 3 of C-type lectin domain family 6 member A OS=Mus musculus GN=Clec6a # Q9JKF4 C-type lectin domain family 6 member A OS=Mus musculus GN=Clec6a PE=1 SV=1 # Q3U3M9 C-type lectin domain family 6 member A OS=Mus musculus GN=Clec4n PE=1 SV=1 # Q9JKF4-2 Isoform 2 of C-type lectin domain family 6 member A OS=Mus musculus GN=Clec6a #

Peptide	L/H Ratio	Protein
DLDKANYLSQALQAGTVWINC*YDVFGAQSPFGGYK	2.8783	Q544B1 Aldehyde dehydrogenase 2# mitochondrial# isoform CRA_b OS=Mus musculus GN=Aldh2 PE=1 SV=1 # P47738 Aldehyde dehydrogenase# mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1 #
LC*YVALDFENEMATAASSSSLEK	2.8775	Q497E4 Actin# alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=2 SV=1 # P68033 Actin# alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE=1 SV=1 #
VPYHLVDTIAVSGC*LK	2.8680	O08573-2 Isoform 2 of Galectin-9 OS=Mus musculus GN=Lgals9 # G3X9T7 Galectin OS=Mus musculus GN=Lgals9 PE=1 SV=1 # B1AQR8 Galectin OS=Mus musculus GN=Lgals9 PE=1 SV=1 # O08573-3 Isoform 3 of Galectin-9 OS=Mus musculus GN=Lgals9 # O08573 Galectin-9 OS=Mus musculus GN=Lgals9 PE=1 SV=1 #
GKFPDVPGFSWVTPC*ISAK	2.8675	Q61176 Arginase-1 OS=Mus musculus GN=Arg1 PE=1 SV=1 #
IVLDKLEC*K	2.8651	P99025 GTP cyclohydrolase 1 feedback regulatory protein OS=Mus musculus GN=Gchfr PE=1 SV=3 # Q4VAF4 GTP cyclohydrolase 1 feedback regulatory protein OS=Mus musculus GN=Gchfr PE=1 SV=1 #
GNHEC*ASINR	2.8585	P63087-2 Isoform Gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Mus musculus GN=Ppp1cc # P62137 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE=1 SV=1 # P63087 Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Mus musculus GN=Ppp1cc PE=1 SV=1 # P62141 Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Mus musculus GN=Ppp1cb PE=1 SV=3 #
NFPAIGGTGPTSDTGWGC*MLR	2.8517	Q8BGE6 Cysteine protease ATG4B OS=Mus musculus GN=Atg4b PE=1 SV=2 # A0A0R4J065 Cysteine protease ATG4B OS=Mus musculus GN=Atg4b PE=1 SV=1 #
AIYHSLGLTGIPIINVNNNC*STGSTALFMAH	2.8510	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 #
QATLGAGLPISTPC*TTVNK	2.8457	Q8QZT1 Acetyl-CoA acetyltransferase# mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1 #
VPFLVLEC*PNLK	2.8442	Q78XF5 Oligosaccharyltransferase complex subunit OSTC OS=Mus musculus GN=Ostc PE=1 SV=1 #
AVLEALGSC*LNNK	2.8427	P50431 Serine hydroxymethyltransferase# cytosolic OS=Mus musculus GN=Shmt1 PE=1 SV=3 #
INISEGNC*PER	2.8353	Q61990 Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1 # Q61990-3 Isoform 3 of Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 # P60335 Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 # Q61990-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 #
C*FATQVYCK	2.8178	P25688 Uricase OS=Mus musculus GN=Uox PE=1 SV=2 # Q543J0 Uricase OS=Mus musculus GN=Uox PE=1 SV=1 #
LIDFLEC*GK	2.8102	Q8BTS0 DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Mus musculus GN=Ddx5 PE=1 SV=1 # Q61656 Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=Ddx5 PE=1 SV=2 # S4R1I6 MCG2872# isoform CRA_b OS=Mus musculus GN=Ddx5 PE=1 SV=1 #
AGAPPGLFNVVQGGAATGQFLC*HHR	2.8031	Q3U367 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 # Q9JLJ2 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 #
LVSSPC*CIVTSTYGWTANMER	2.7895	P11499 Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3 # Q71LX8 Heat shock protein 84b OS=Mus musculus GN=Hsp90ab1 PE=1 SV=1 #
ESLALIAEQGLENC*WR	2.7862	O35423-2 Isoform Peroxisomal of Serine--pyruvate aminotransferase# mitochondrial OS=Mus musculus GN=Agxt # O35423 Serine--pyruvate aminotransferase# mitochondrial OS=Mus musculus GN=Agxt PE=1 SV=3 #
ITEFC*HR	2.7802	P09103 Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=2 #
NYLPAINGIVFLVDC*ADHSR	2.7772	Q99JZ4 GTP-binding protein SAR1a OS=Mus musculus GN=Sar1a PE=1 SV=1 #

Peptide	L/H Ratio	Protein
GENVSTGEVEC*VLSSLDFLEEVNVYGVPVPGCEGK	2.7745	Q4LDG0 Bile acyl-CoA synthetase OS=Mus musculus GN=Slc27a5 PE=1 SV=2 #
VC*LIGCGFSTGYGSAVK	2.7706	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
MEC*CDVPAETLYDVLHDIEYR	2.7675	G3V020 PCTP-like protein (Fragment) OS=Mus musculus GN=Stard10 PE=1 SV=1 # E9PVP0 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 # G3UW37 PCTP-like protein (Fragment) OS=Mus musculus GN=Stard10 PE=1 SV=1 # Q0VG22 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 # Q9JMD3 PCTP-like protein OS=Mus musculus GN=Stard10 PE=1 SV=1 #
AIQDAGC*QVLK	2.7674	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=1 SV=1 #
ASVGFGGSC*FQK	2.7601	Q3TS38 UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1 # O70475 UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1 #
LPACVVDC*GTGYTK	2.7570	Q99JY9 Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3 # Q3ULF7 Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=1 #
AQGTGELTQLLNSLC*TAIK	2.7560	Q9QXD6 Fructose-1#6-bisphosphatase 1 OS=Mus musculus GN=Fbp1 PE=1 SV=3 #
SGQGAFGNMC*R	2.7503	Q564E8 60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=1 # Q9D8E6 60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3 #
LQEALDAEMLEDEAGVGGAGPGGAC*K	2.7471	Q00PI9 Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Mus musculus GN=Hnrnpul2 PE=1 SV=2 #
ITWSELSESGLPLC*DVVINLAGENILNPLR	2.7446	Q5M8N4 Epimerase family protein SDR39U1 OS=Mus musculus GN=Sdr39u1 PE=1 SV=1 # Q5M8N4-2 Isoform 2 of Epimerase family protein SDR39U1 OS=Mus musculus GN=Sdr39u1 #
NANC*SIEESFQR	2.7435	P38060 Hydroxymethylglutaryl-CoA lyase# mitochondrial OS=Mus musculus GN=Hmgcl PE=1 SV=2 #
SC*EAGYSPSYK	2.7323	P10605 Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2 #
LSIQC*YLR	2.7313	P54869 Hydroxymethylglutaryl-CoA synthase# mitochondrial OS=Mus musculus GN=Hmgcs2 PE=1 SV=2 #
DVLSGDGFDAVICLGNSFAHLPDC*K	2.7299	Q9QXF8 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=1 SV=3 #
FYDVALDTGDKVVQC*GR	2.7297	Q9DBE0 Cysteine sulfinic acid decarboxylase OS=Mus musculus GN=Csad PE=1 SV=1 #
HELQANC*YEEVKDR	2.7278	F8WGL3 Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=1 # P18760 Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3 #
C*PGLLTPSQIKPGTYK	2.7175	Q9CRB3 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1 SV=1 # A0A0A0MQC3 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1 SV=1 #
GEGMSQAATIC*R	2.7168	P35505 Fumarylacetoacetase OS=Mus musculus GN=Fah PE=1 SV=2 #
WFTPVSEVPLC*GHATLASAAVLFHK	2.7162	K3W4L7 Phenazine biosynthesis-like domain-containing protein 2 OS=Mus musculus GN=Pbld2 PE=1 SV=1 # Q9DCG6 Phenazine biosynthesis-like domain-containing protein 1 OS=Mus musculus GN=Pbld1 PE=1 SV=2 #
KLYPSESYLQNYEVAYPDC*SPVHLISEASLVDLNTR	2.7111	Q922Q1 Mitochondrial amidoxime reducing component 2 OS=Mus musculus GN=Marc2 PE=1 SV=1 #
VTPGSTCAVFGLGGVGLSVIIGC*K	2.7078	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
NLSDLIDLVPSLC*EDLLSSVDQPLK	2.6974	P47757-4 Isoform 3 of F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb # P47757-2 Isoform 2 of F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb # A2AMW0 Capping protein (Actin filament) muscle Z-line# beta# isoform CRA_a OS=Mus musculus GN=Capzb PE=1 SV=1 # P47757 F-actin-capping protein subunit beta OS=Mus musculus

Peptide	L/H Ratio	Protein
		GN=Capzb PE=1 SV=3 # F7CAZ6 F-actin-capping protein subunit beta (Fragment) OS=Mus musculus GN=Capzb PE=1 SV=1 #
SPNIIMSDADMDWAVEQAHFALFFNQGQCC*CAGSR	2.6942	Q544B1 Aldehyde dehydrogenase 2# mitochondrial# isoform CRA_b OS=Mus musculus GN=Aldh2 PE=1 SV=1 # P47738 Aldehyde dehydrogenase# mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1 #
VVGYFVSGC*DPTIMGIGPVPAINGALKK	2.6899	Q8BWT1 3-ketoacyl-CoA thiolase# mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 #
AEFGGLAPNCTVVC*LSGQK	2.6793	A0A0R4J110 Iodothyronine deiodinase OS=Mus musculus GN=Dio1 PE=1 SV=1 # Q61153 Type I iodothyronine deiodinase OS=Mus musculus GN=Dio1 PE=1 SV=3 #
LIENTDAAC*K	2.6763	Q9DCM2 Glutathione S-transferase kappa 1 OS=Mus musculus GN=Gstk1 PE=1 SV=3 #
WNTYIPLHYC*K	2.6746	Q8C7E7 Starch-binding domain-containing protein 1 OS=Mus musculus GN=Stbd1 PE=1 SV=1 #
LSYYPHC*LASFTELVR	2.6652	Q9QXF8 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=1 SV=3 #
C*PGGQSPWTGVSQFLQTSQK	2.6618	Q922E4 Ethanolamine-phosphate cytidylyltransferase OS=Mus musculus GN=Pcyt2 PE=1 SV=1 # Q3USD5 Ethanolamine-phosphate cytidylyltransferase OS=Mus musculus GN=Pcyt2 PE=1 SV=1 #
AYLMSQPLAYHTPDC*GK	2.6611	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=1 SV=1 #
IGPALSC*GNTVVVKPAEQTPLTALHLASLIK	2.6604	P24549 Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5 #
VILITPPPLC*EAAWEK	2.6506	Q9DB29 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Mus musculus GN=Iah1 PE=1 SV=1 #
TSAC*FEPSLDYMVTK	2.6463	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
LSVFRPGVLLC*DR	2.6448	Q3U816 Oxidoreductase HTATIP2 OS=Mus musculus GN=Htatip2 PE=1 SV=1 # Q9Z2G9 Oxidoreductase HTATIP2 OS=Mus musculus GN=Htatip2 PE=1 SV=3 #
TWYVQATC*ATQGTGLYEGLDWLSNELSK	2.6441	Q14BR4 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=1 SV=1 # P61750 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=1 SV=2 #
DNCQC*SDCYLHSAK	2.6438	Q924Y0 Gamma-butyrobetaine dioxygenase OS=Mus musculus GN=Bbox1 PE=1 SV=1 #
DYPLELFMSQC*YGNVNDPGK	2.6424	Q3U3J1 2-oxoisovalerate dehydrogenase subunit alpha# mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1 #
TGC*TFPEKPDFH	2.6405	P55264 Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2 #
LLPAITILGC*R	2.6386	Q922H4 Mannose-1-phosphate guanyltransferase alpha OS=Mus musculus GN=Gmppa PE=1 SV=1 #
DLNYC*FSGMSDHR	2.6376	O35737 Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3 # Q811L7 Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=2 # Q8C2Q7 Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=1 #
LAGIC*TIQLK	2.6366	E9PUL7 Protein Nat8f1 OS=Mus musculus GN=Nat8f1 PE=1 SV=1 #
FCQQHDIVIVAHSPLGTC*R	2.6356	Q8VCX1 3-oxo-5-beta-steroid 4-dehydrogenase OS=Mus musculus GN=Akr1d1 PE=1 SV=1 #
LC*DFGVSGQLIDSMANSFVGTR	2.6354	Q3TMJ8 Dual-specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=1 # P31938 Dual specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2 # Q63932 Dual specificity mitogen-activated protein kinase kinase 2 OS=Mus musculus GN=Map2k2 PE=1 SV=2 # Q91YS7 Dual-specificity mitogen-activated protein kinase kinase 2 OS=Mus musculus GN=Map2k2 PE=1 SV=1 #
C*PSTHSEELR	2.6326	O09172 Glutamate--cysteine ligase regulatory subunit OS=Mus musculus GN=Gclm PE=1 SV=1 # Q4FJZ6 Gclm protein OS=Mus musculus GN=Gclm PE=1 SV=1 #

Peptide	L/H Ratio	Protein
KLGESC*IFAPANVTSEK	2.6264	Q99N15 17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase OS=Mus musculus GN=Hsd17b10 PE=1 SV=1 #
C*TPACVSFGPK	2.6228	Q3U2G2 Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1 # Q61316 Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1 #
ITCLC*QVPQNAANR	2.6157	Q8BGQ7 Alanine--tRNA ligase# cytoplasmic OS=Mus musculus GN=Aars PE=1 SV=1 #
NQSFC*PTVNLDKLWTLVSEQTR	2.6026	P14115 60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=1 SV=5 #
TLTQC*SWLLDGFPR	2.6017	Q9WTP7 GTP:AMP phosphotransferase AK3# mitochondrial OS=Mus musculus GN=Ak3 PE=1 SV=3 #
SLSPEQNC*PR	2.5992	Q9R233 Tapasin OS=Mus musculus GN=Tapbp PE=1 SV=2 # Q3TCU5 Tapasin OS=Mus musculus GN=Tapbp PE=1 SV=1 # Q9R233-2 Isoform Short of Tapasin OS=Mus musculus GN=Tapbp #
YKPVCNQVEC*HLYLNQSQMLDYCK	2.5942	Q91WT7 3-alpha-hydroxysteroid dehydrogenase type 1 OS=Mus musculus GN=Akr1c14 PE=1 SV=1 #
VGGIC*TVIQTK	2.5939	Q8VCB3 Glycogen [starch] synthase# liver OS=Mus musculus GN=Gys2 PE=1 SV=2 #
LDTMTSALLSCHAAC*GVSVVVGVPPNAQNLSMNPMLLLLGR	2.5911	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
VTVLTHC*NTGALATAGYGTALGVIR	2.5881	Q9CQT1 Methylthioribose-1-phosphate isomerase OS=Mus musculus GN=Mri1 PE=1 SV=1 #
TVYTFVGQPEC*VVEGALHAAR	2.5809	Q91XD4 Formimidoyltransferase-cyclodeaminase OS=Mus musculus GN=Ftcd PE=1 SV=1 #
YLPDTLLLEEC*GLLR	2.5771	O88587 Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=2 # O88587-2 Isoform Soluble of Catechol O-methyltransferase OS=Mus musculus GN=Comt #
IVSNASCTTNC*LAPLAK	2.5767	V9GXA7 Protein Gm15294 OS=Mus musculus GN=Gm15294 PE=3 SV=1 #
ESLNANIVDAINQAADC*WGIR	2.5662	Q99JB2 Stomatin-like protein 2# mitochondrial OS=Mus musculus GN=Stoml2 PE=1 SV=1 # A2AG41 Stomatin-like protein 2# mitochondrial (Fragment) OS=Mus musculus GN=Stoml2 PE=1 SV=9 #
C*VLTTVDPDTGIIDRK	2.5649	Q922Q1 Mitochondrial amidoxime reducing component 2 OS=Mus musculus GN=Marc2 PE=1 SV=1 #
IGC*LKPSIPEDTAAFIR	2.5649	Q9DBG1 Sterol 26-hydroxylase# mitochondrial OS=Mus musculus GN=Cyp27a1 PE=1 SV=1 #
ITAFVPNDGC*LNFIEENDEVLVAGFGR	2.5609	P62267 40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=1 SV=3 #
FLSC*YDPINIQFTSGTTGNPK	2.5597	Q8VCW8 Acyl-CoA synthetase family member 2# mitochondrial OS=Mus musculus GN=Acsf2 PE=1 SV=1 #
NALANPLYC*PDYR	2.5591	Q9DB77 Cytochrome b-c1 complex subunit 2# mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1 #
LC*GSGFQSIVSGCQEICSK	2.5565	Q8BWT1 3-ketoacyl-CoA thiolase# mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 #
VCLLGC*GISTGYGAAVNTAK	2.5554	Q6P5I3 S-(hydroxymethyl)glutathione dehydrogenase OS=Mus musculus GN=Adh5 PE=1 SV=2 # P28474 Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3 #
IIPTLEEGLQLPSPTATSQLPLESDAVEC*LNYQHYK	2.5543	P61979 Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1 # H3BK96 Heterogeneous nuclear ribonucleoprotein K (Fragment) OS=Mus musculus GN=Hnrnpk PE=1 SV=7 # P61979-2 Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk #
IHMGNC*AENTAK	2.5540	Q8QZT1 Acetyl-CoA acetyltransferase# mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1 #
CPEALFQPSFLGMESC*GIHETTFNSIMK	2.5534	P60710 Actin# cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 # P63260 Actin# cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 # B2RRX1 Actin# beta OS=Mus musculus GN=Actb PE=1 SV=1 # Q4KL81 Actin# cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 #

Peptide	L/H Ratio	Protein
LIYDAVDIC*DTWEAMEK	2.5503	Q3UEM0 Estradiol 17 beta-dehydrogenase 5 OS=Mus musculus GN=Akr1c6 PE=1 SV=1 #
AFGSSGGGC*ISEGYAYYTDSGPVFVK	2.5379	Q9ER35 Fructosamine-3-kinase OS=Mus musculus GN=Fn3k PE=1 SV=1 #
NC*VILPHIGSATYK	2.5377	Q3T9Z2 Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1 # Q91Z53 Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1 #
LPQPPEGQC*YSN	2.5364	B7ZBY7 Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=4 SV=1 # E9PY39 Protein Gm20431 OS=Mus musculus GN=Gm20431 PE=4 SV=1 # Q9CZY3 Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus GN=Ube2v1 PE=1 SV=1 #
EMNSAFAHLPQGVLWTC*K	2.5277	Q8JZZ0 UDP-glucuronosyltransferase 3A2 OS=Mus musculus GN=Ugt3a2 PE=1 SV=2 #
GYVSCALGC*PYEGK	2.5248	P38060 Hydroxymethylglutaryl-CoA lyase# mitochondrial OS=Mus musculus GN=Hmgcl PE=1 SV=2 #
ILSLIC*NNSSEKPTAQQLQILWK	2.5236	P27612 Phospholipase A-2-activating protein OS=Mus musculus GN=Plaa PE=1 SV=4 #
VVAVDC*GIK	2.5200	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
AGSDGESIGNC*PFSQR	2.5054	Q543N5 Chloride intracellular channel protein OS=Mus musculus GN=Clic4 PE=1 SV=1 # Q9QYB1 Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=3 #
SHC*FTQAMMSQPK	2.5012	B1ARD1 Phosphatidylethanolamine N-methyltransferase (Fragment) OS=Mus musculus GN=Pemt PE=1 SV=1 # Q61907-2 Isoform 2 of Phosphatidylethanolamine N-methyltransferase OS=Mus musculus GN=Pemt # Q61907 Phosphatidylethanolamine N-methyltransferase OS=Mus musculus GN=Pemt PE=1 SV=4 #
VCLIGC*GFSTGYGSAVK	2.4979	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
ELELLFGC*HVEGDAAETPPRPR	2.4913	Q3TMJ8 Dual-specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=1 # P31938 Dual specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2 #
EDTHHLANYIPQC*SIDSLFEGTWYLVR	2.4909	Q8JZK9 Hydroxymethylglutaryl-CoA synthase# cytoplasmic OS=Mus musculus GN=Hmgcs1 PE=1 SV=1 #
NLQLSC*LSTEQNQHLQASLSR	2.4869	Q8VCZ9 Probable proline dehydrogenase 2 OS=Mus musculus GN=Prodh2 PE=1 SV=1 #
GLATFC*LDK	2.4855	Q80UU9 Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2 # Q3TXU8 Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=1 # O55022 Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4 #
HNADFC*YK	2.4837	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 #
C*QNEQLQTAVTQQASQIQQHK	2.4835	Q9Z1Z0 General vesicular transport factor p115 OS=Mus musculus GN=Uso1 PE=1 SV=2 # Q9Z1Z0-2 Isoform 2 of General vesicular transport factor p115 OS=Mus musculus GN=Uso1 #
SGETEDTFIADLVVGLC*TGQIK	2.4658	P17182 Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3 # Q5FW97 Alpha-enolase OS=Mus musculus GN=EG433182 PE=1 SV=1 #
NWYIQATC*ATSGDGLYEGLDWLSNQLR	2.4620	P84078 ADP-ribosylation factor 1 OS=Mus musculus GN=Arf1 PE=1 SV=2 #
LATGSC*SYPQSSPALEKPGR	2.4602	Q3V449 Nicotinamide-nucleotide adenylyltransferase OS=Mus musculus GN=Nmnat1 PE=1 SV=1 # Q9EPA7 Nicotinamide/nicotinic acid mononucleotide adenylyltransferase 1 OS=Mus musculus GN=Nmnat1 PE=1 SV=2 #
VC*FGIQLLNAVAR	2.4596	E9Q3B9 Monoglyceride lipase OS=Mus musculus GN=Mgll PE=1 SV=1 # O35678 Monoglyceride lipase OS=Mus musculus GN=Mgll PE=1 SV=1 # D3YYS6 Monoglyceride lipase OS=Mus musculus GN=Mgll PE=1 SV=1 #

Peptide	L/H Ratio	Protein
AC*QSIYPLHDVFVR	2.4533	P97351 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3 # Q564F3 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a1 PE=1 SV=1 #
DPPLFLISC*FSPSFHDFPELR	2.4472	Q9DCE9 Protein Igtp OS=Mus musculus GN=Igtp PE=1 SV=1 #
NC*LTNFHGMDLTR	2.4459	P97351 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3 # Q564F3 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a1 PE=1 SV=1 #
EWGFC*LNSR	2.4455	P26150 3 beta-hydroxysteroid dehydrogenase/Delta 5-- 4-isomerase type 3 OS=Mus musculus GN=Hsd3b3 PE=1 SV=3 #
GSPCDPTFILSC*APCNVICSIIFQNR	2.4438	Q64458 Cytochrome P450 2C29 OS=Mus musculus GN=Cyp2c29 PE=1 SV=2 #
GYENGNFVGPTIISNVKPSMTC*YK	2.4437	Q9EQ20 Methylmalonate-semialdehyde dehydrogenase [acylating]# mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1 #
VLLSIC*SLLCDPNPDDPLVPEIAR	2.4429	P62838 Ubiquitin-conjugating enzyme E2 D2 OS=Mus musculus GN=Ube2d2 PE=1 SV=1 # A0A0G2JGL0 Ubiquitin-conjugating enzyme E2 D3 OS=Mus musculus GN=Ube2d3 PE=1 SV=1 # P61079 Ubiquitin-conjugating enzyme E2 D3 OS=Mus musculus GN=Ube2d3 PE=1 SV=1 # Q3UT95 MCG121966 OS=Mus musculus GN=Ube2d2a PE=1 SV=1 # Q4QQL2 MCG22362# isoform CRA_a OS=Mus musculus GN=Ube2d3 PE=1 SV=1 # A0A0G2JE32 Ubiquitin-conjugating enzyme E2 D3 (Fragment) OS=Mus musculus GN=Ube2d3 PE=1 SV=1 #
GLC*AIAQAESLR	2.4408	Q5YLW3 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1 # P62908 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1 #
FIDLVPNSLPHEVTC*DIK	2.4375	Q91X77 Cytochrome P450 2C50 OS=Mus musculus GN=Cyp2c50 PE=1 SV=2 #
WSSC*NIFSTQDHAAAAIAK	2.4369	P50247 Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3 # Q3TF14 Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=1 #
VIPLFSPQC*GECR	2.4335	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
C*LLTTVDPDTGISDR	2.4305	Q9CW42 Mitochondrial amidoxime-reducing component 1 OS=Mus musculus GN=Marc1 PE=1 SV=2 #
TVVNISSLC*ALQPYK	2.4303	Q64105 Sepiapterin reductase OS=Mus musculus GN=Spr PE=1 SV=1 #
AGDTVIPLYIPQCGEC*K	2.4301	Q6P5I3 S-(hydroxymethyl)glutathione dehydrogenase OS=Mus musculus GN=Adh5 PE=1 SV=2 # P28474 Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3 #
VTDGALVVVDCVSGVC*VQTETVLR	2.4263	P58252 Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2 #
YFAGNLASGGAAGATSLC*FVYPLDFAR	2.4241	P51881 ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3 # Q545A2 ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=1 #
YCVGDEVSMADVC*LVPQVANAER	2.4233	Q9WVL0 Maleylacetoacetate isomerase OS=Mus musculus GN=Gstz1 PE=1 SV=1 #
LIIAGTSC*YSR	2.4223	P50431 Serine hydroxymethyltransferase# cytosolic OS=Mus musculus GN=Shmt1 PE=1 SV=3 #
C*KLCYPQSPDMQPFIMGIHIIDR	2.4202	P70365-4 Isoform 4 of Nuclear receptor coactivator 1 OS=Mus musculus GN=Ncoa1 # P70365 Nuclear receptor coactivator 1 OS=Mus musculus GN=Ncoa1 PE=1 SV=2 # P70365-2 Isoform 2 of Nuclear receptor coactivator 1 OS=Mus musculus GN=Ncoa1 # P70365-3 Isoform 3 of Nuclear receptor coactivator 1 OS=Mus musculus GN=Ncoa1 #
GSEVNVIGIGTSVVTC*PK	2.4173	Q8CC86 Nicotinate phosphoribosyltransferase OS=Mus musculus GN=Naprt PE=1 SV=1 #
IVFVLC*SALNPWNKEMGDHLVK	2.4121	P49429 4-hydroxyphenylpyruvate dioxygenase OS=Mus musculus GN=Hpd PE=1 SV=3 #
GQHMSEQFSQVNC*LNKVPVLK	2.4024	Q61133 Glutathione S-transferase theta-2 OS=Mus musculus GN=Gstt2 PE=1 SV=4 #

Peptide	L/H Ratio	Protein
C*PGIPSWFGL	2.4004	O35972 39S ribosomal protein L23# mitochondrial OS=Mus musculus GN=Mrpl23 PE=1 SV=1 #
LSVLAVDPSSC*TSGGSLLGDK	2.3991	Q8C7H1 Methylmalonic aciduria type A homolog# mitochondrial OS=Mus musculus GN=Mmaa PE=1 SV=1 #
HSGFGLCYC*K	2.3852	P50285 Dimethylaniline monooxygenase [N-oxide-forming] 1 OS=Mus musculus GN=Fmo1 PE=1 SV=1 #
ERVC*NLIDSGTK	2.3763	Q9EQ20 Methylmalonate-semialdehyde dehydrogenase [acylating]# mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1 #
VQQEIDEVIGQVQC*PEMADQAR	2.3736	Q9JKY7 Cytochrome P450 CYP2D22 OS=Mus musculus GN=Cyp2d22 PE=1 SV=1 #
NGGTLQTCALRPMC*IYGER	2.3732	P26150 3 beta-hydroxysteroid dehydrogenase/Delta 5-- 4-isomerase type 3 OS=Mus musculus GN=Hsd3b3 PE=1 SV=3 #
GLPVSC*TAESPTPQALAAGIR	2.3710	Q3UG55 Uroporphyrinogen III synthase# isoform CRA_a OS=Mus musculus GN=Uros PE=1 SV=1 # P51163 Uroporphyrinogen-III synthase OS=Mus musculus GN=Uros PE=1 SV=1 #
AC*GANLPENFSISQIFSQAMAAR	2.3670	P34914 Bifunctional epoxide hydrolase 2 OS=Mus musculus GN=Ephx2 PE=1 SV=2 #
YLLQYQEPIPCEQLVTALC*DIK	2.3667	Q9R1P0 Proteasome subunit alpha type-4 OS=Mus musculus GN=Psma4 PE=1 SV=1 #
FNVDKPFIFNTFQC*YLK	2.3621	A0A0R4J1T9 Proline dehydrogenase 1# mitochondrial OS=Mus musculus GN=Prodh PE=1 SV=1 # Q9WU79 Proline dehydrogenase 1# mitochondrial OS=Mus musculus GN=Prodh PE=1 SV=2 #
C*EFQDAYVLLSEKK	2.3591	P63038 60 kDa heat shock protein# mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 #
FNEVSC*QQAAIQAYEDMVK	2.3589	Q8BUE4 Apoptosis-inducing factor 2 OS=Mus musculus GN=Aifm2 PE=1 SV=1 #
EC*LPLIIFLR	2.3479	Q545X8 40S ribosomal protein S4 OS=Mus musculus GN=Rps4x PE=1 SV=1 # P62702 40S ribosomal protein S4# X isoform OS=Mus musculus GN=Rps4x PE=1 SV=2 #
LLACIASRPGQC*GR	2.3476	Q497E9 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=1 # P62242 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2 #
KNASC*GTR	2.3459	E9PW43 Protein Gm10320 OS=Mus musculus GN=Gm10320 PE=4 SV=1 # Q9CQS8 Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3 #
AIVDALPPPC*ESACSLPTDVDK	2.3459	Q9D819 Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1 # Q4FK49 Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1 #
HFVC*SSAGNAGMATAYAAR	2.3456	Q3UEN6 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=1 # Q8VBT2 L-serine dehydratase/L-threonine deaminase OS=Mus musculus GN=Sds PE=1 SV=3 #
LC*YNSNHENLKPQYLEQLPAQLK	2.3429	P48774 Glutathione S-transferase Mu 5 OS=Mus musculus GN=Gstm5 PE=1 SV=1 #
IVNDNATYC*R	2.3398	Q9D6Z1 Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2 #
LGTDESC*FNMILATR	2.3388	Q07076 Annexin A7 OS=Mus musculus GN=Anxa7 PE=1 SV=2 #
KAQC*PIVER	2.3337	Q91V55 40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=1 SV=1 #
LYGIQGFC*K	2.3294	Q99LP6 GrpE protein homolog 1# mitochondrial OS=Mus musculus GN=Grpel1 PE=1 SV=1 #
NWYVQPSC*ATSGDGLYEGLTWLTSNYK	2.3284	Q3U0D7 ADP-ribosylation factor 6 OS=Mus musculus GN=Arf6 PE=1 SV=1 # P62331 ADP-ribosylation factor 6 OS=Mus musculus GN=Arf6 PE=1 SV=2 #
C*CVMMQGR	2.3017	P23492 Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2 # Q543K9 Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=1 #
GFVPVAPIC*TDKINAVDYASVK	2.3017	E9QN99 Protein ABHD14B OS=Mus musculus GN=Abhd14b PE=1 SV=1 # Q8VCR7 Protein ABHD14B OS=Mus musculus GN=Abhd14b PE=1 SV=1 #
LEYC*EALAMLR	2.3013	Q922B2 Aspartate--tRNA ligase# cytoplasmic OS=Mus musculus GN=Dars PE=1 SV=2 #

Peptide	L/H Ratio	Protein
ALANVNIGSLIC*NVGAGGPAPAAGAAPAGGAAPSTAAAPAEEK	2.2919	P47955 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1 # Q58E35 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1 #
KC*PFTGNVSIR	2.2907	P62281 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=3 # Q3UC02 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=1 #
HPESNFC*SR	2.2841	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
QVIDC*QLADVNNLGK	2.2838	Q9CPY7-2 Isoform 2 of Cytosol aminopeptidase OS=Mus musculus GN=Lap3 # Q9CPY7 Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3 #
NMSVHLSPC*FR	2.2812	P62281 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=3 # Q3UC02 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=1 #
TIQFVDWC*PTGFK	2.2812	P68369 Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 # P68373 Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1 # Q52L87 Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1 #
TVPAAVPGIC*FLSGGMSEEDATLNLNAINR	2.2745	Q3UER1 Fructose-bisphosphate aldolase OS=Mus musculus GN=Aldob PE=1 SV=1 # Q91Y97 Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3 #
SGDAAIVDMVPGKPMC*VESFSDYPPLGR	2.2678	P10126 Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 # Q58E64 Elongation factor 1-alpha OS=Mus musculus GN=Eef1a1 PE=1 SV=1 #
MLHFQEAATTVPPMC*LLPNSHYEQVMTAFGGK	2.2663	Q9QXE0 2-hydroxyacyl-CoA lyase 1 OS=Mus musculus GN=Hacl1 PE=1 SV=2 # D3YZ54 2-hydroxyacyl-CoA lyase 1 OS=Mus musculus GN=Hacl1 PE=1 SV=2 #
SFSIASDPTSASSC*YLEEHVSK	2.2630	P00186 Cytochrome P450 1A2 OS=Mus musculus GN=Cyp1a2 PE=1 SV=1 # B6VGH4 Cytochrome P450 OS=Mus musculus GN=Cyp1a2 PE=1 SV=1 #
HSMNPFC*EIAVEEAVR	2.2608	Q9DCW4 Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3 # A0A0U1RNK9 Electron transfer flavoprotein subunit beta (Fragment) OS=Mus musculus GN=Etfb PE=1 SV=1 #
VFANPEDC*AGFGKGENAK	2.2588	E9QJW0 Microsomal glutathione S-transferase 1 OS=Mus musculus GN=Mgst1 PE=1 SV=1 #
IIC*QGFTGK	2.2576	Q9WUM5 Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha# mitochondrial OS=Mus musculus GN=Suclg1 PE=1 SV=4 #
TIAEC*LADELINAAK	2.2558	Q91V55 40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=1 SV=1 #
AAVEEGIVLGGGC*ALLR	2.2535	P63038 60 kDa heat shock protein# mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 #
C*LQTDMVDITK	2.2475	E9PUL7 Protein Nat8f1 OS=Mus musculus GN=Nat8f1 PE=1 SV=1 #
AYHEQLSVAEITNAC*FEPANQMVK	2.2472	A0A0A0MQA5 Tubulin alpha-4A chain (Fragment) OS=Mus musculus GN=Tuba4a PE=1 SV=1 # P68368 Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 # P68369 Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 # P05213 Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2 #
QASEEELFC*SFQQR	2.2416	Q9DBA8 Probable imidazolonepropionase OS=Mus musculus GN=Amdhd1 PE=1 SV=1 #
IGTNLPLKPC*PR	2.2405	D6RCX5 Mitochondrial fission regulator 1-like OS=Mus musculus GN=Mtfr1l PE=1 SV=1 # Q9CWE0-2 Isoform 2 of Mitochondrial fission regulator 1-like OS=Mus musculus GN=Mtfr1l # Q9CWE0 Mitochondrial fission regulator 1-like OS=Mus musculus GN=Mtfr1l PE=1 SV=1 # D3Z0X8 Mitochondrial fission regulator 1-like (Fragment) OS=Mus musculus GN=Mtfr1l PE=1 SV=1 # D3YW54 Mitochondrial fission regulator 1-like (Fragment) OS=Mus musculus GN=Mtfr1l PE=1 SV=1 #
ANPYEC*GFDPTSSAR	2.2380	P03899 NADH-ubiquinone oxidoreductase chain 3 OS=Mus musculus GN=Mtnd3 PE=1 SV=3 #

Peptide	L/H Ratio	Protein
IHLVPC*R	2.2356	Q5SUV8 Aromatic-L-amino-acid decarboxylase OS=Mus musculus GN=Ddc PE=1 SV=1 # O88533 Aromatic-L-amino-acid decarboxylase OS=Mus musculus GN=Ddc PE=1 SV=1 #
LGSPVPSC*SVVGTISSYYVQR	2.2347	Q3TNA1 Xylulose kinase OS=Mus musculus GN=Xylb PE=1 SV=1 #
AHC*YFLTVR	2.2322	Q9QXD1 Peroxisomal acyl-coenzyme A oxidase 2 OS=Mus musculus GN=Acox2 PE=1 SV=2 #
GSSSFEC*THYSSYLEYMK	2.2314	O88587 Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=2 # O88587-2 Isoform Soluble of Catechol O-methyltransferase OS=Mus musculus GN=Comt #
VAQATC*KL	2.2297	P38060 Hydroxymethylglutaryl-CoA lyase# mitochondrial OS=Mus musculus GN=Hmgcl PE=1 SV=2 #
VIPLFSPQCGEC*R	2.2286	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
LVIVGDGAC*GK	2.2255	Q4VAE6 Ras family member A OS=Mus musculus GN=Rhoa PE=1 SV=1 # H3BL56 Rho-related GTP-binding protein RhoC OS=Mus musculus GN=Rhoc PE=1 SV=1 # Q9QUI0 Transforming protein RhoA OS=Mus musculus GN=Rhoa PE=1 SV=1 # Q62159 Rho-related GTP-binding protein RhoC OS=Mus musculus GN=Rhoc PE=1 SV=2 # A0A0A6YXF6 Transforming protein RhoA (Fragment) OS=Mus musculus GN=Rhoa PE=1 SV=1 #
YC*VRPNSGIIDPGSIVTVSVMLQPFDYDPNEK	2.2244	Q9WV55 Vesicle-associated membrane protein-associated protein A OS=Mus musculus GN=Vapa PE=1 SV=2 #
ALVDGPC*TR	2.2230	Q9CR57 60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=1 SV=3 #
FASGGC*DNLIK	2.2223	Q9D1M0 Protein SEC13 homolog OS=Mus musculus GN=Sec13 PE=1 SV=3 #
LGESC*IFAPANVTSEKEIQAALTLAK	2.2154	Q99N15 17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase OS=Mus musculus GN=Hsd17b10 PE=1 SV=1 #
ILLNACC*PGWVR	2.2148	P48758 Carbonyl reductase [NADPH] 1 OS=Mus musculus GN=Cbr1 PE=1 SV=3 # B2RXY7 Carbonyl reductase 1 OS=Mus musculus GN=Cbr1 PE=1 SV=1 #
HVQQHAKPGDPQSVLEAIDTYC*SEK	2.2094	O88587 Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=2 # O88587-2 Isoform Soluble of Catechol O-methyltransferase OS=Mus musculus GN=Comt #
ALNALC*NGLIEELNQALETFEQDPAVGAIVLTGGDK	2.2085	Q8BH95 Enoyl-CoA hydratase# mitochondrial OS=Mus musculus GN=Echs1 PE=1 SV=1 #
TLSC*LSTSTDAASVVHSTDLVVEAIVENLK	2.2046	Q61425 Hydroxyacyl-coenzyme A dehydrogenase# mitochondrial OS=Mus musculus GN=Hadh PE=1 SV=2 #
LPCIFIC*ENNR	2.2015	P35486 Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1 # Q3UFJ3 Pyruvate dehydrogenase E1 component subunit alpha OS=Mus musculus GN=Pdha1 PE=1 SV=1 #
GISC*MNTTVSESPFK	2.1967	Q9D819 Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1 # Q4FK49 Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1 #
GYSIPEC*QK	2.1955	Q80X68 Citrate synthase OS=Mus musculus GN=Csl PE=1 SV=1 #
AVAHHTDC*TFIR	2.1906	Q8K1K2 26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5 PE=1 SV=1 # P62196 26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5 PE=1 SV=1 #
GRMEC*IR	2.1903	P13745 Glutathione S-transferase A1 OS=Mus musculus GN=Gsta1 PE=1 SV=2 # D3YZV3 Glutathione S-transferase (Fragment) OS=Mus musculus GN=Gsta2 PE=3 SV=1 # D3Z6A6 Glutathione S-transferase (Fragment) OS=Mus musculus GN=Gsta2 PE=3 SV=1 # P10648 Glutathione S-transferase A2 OS=Mus musculus GN=Gsta2 PE=1 SV=3 #

Peptide	L/H Ratio	Protein
QVCQLPGLFC*YAQHIASIDGR	2.1896	Q791V5 Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtch2 PE=1 SV=1 #
TDGFLALYNGLSASLC*R	2.1895	Q9QZD8 Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=1 SV=2 #
YTIVVSATASDAAPLQYLAPYSGC*SMGEYFR	2.1854	D3Z6F5 ATP synthase subunit alpha OS=Mus musculus GN=Atp5a1 PE=1 SV=1 # Q03265 ATP synthase subunit alpha# mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1 #
LLAC*IASR	2.1817	Q497E9 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=1 # P62242 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2 #
WGLVC*AGLADMARPAEK	2.1816	Q9D023 Mitochondrial pyruvate carrier 2 OS=Mus musculus GN=Mpc2 PE=1 SV=1 #
SKPVFDFLTILQCC*PTSDGAAAAILSSEEFVQQYGLQSK	2.1786	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 #
TCSLTAASCPYFC*SVLTK	2.1776	Q91VI7 Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1 #
NPVSQC*MR	2.1768	Q8R0B4 MCG16669# isoform CRA_a OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q8BLD4 MCG16669# isoform CRA_f OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q544R5 MCG16669# isoform CRA_b OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q921F2 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q6VYI4 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 # Q6VYI5 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 # A0A087WRZ5 TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1 #
LC*YVALDFEQEMATAASSSSLEK	2.1650	P60710 Actin# cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 # P63260 Actin# cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 # B2RRX1 Actin# beta OS=Mus musculus GN=Actb PE=1 SV=1 # Q4KL81 Actin# cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 #
TWYVQATC*ATQGTGLYDGLDWLSHELSK	2.1596	P84084 ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=1 SV=2 #
VSLC*GGGYCISK	2.1572	O88451 Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=1 SV=1 #
LVVSDHSHEGWLDFC*SLIK	2.1566	Q91VA0 Acyl-coenzyme A synthetase ACSM1# mitochondrial OS=Mus musculus GN=Acsm1 PE=1 SV=1 #
NPNAVLTC*VDDSLSQEYQK	2.1551	Q3UQ44 Ras GTPase-activating-like protein IQGAP2 OS=Mus musculus GN=Iqgap2 PE=1 SV=2 #
NMMAAC*DPR	2.1524	P99024 Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1 # Q9D6F9 Tubulin beta-4A chain OS=Mus musculus GN=Tubb4a PE=1 SV=3 # Q7TMM9 Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1 # P68372 Tubulin beta-4B chain OS=Mus musculus GN=Tubb4b PE=1 SV=1 #
ILRGENHC*GIESEIVAGIPR	2.1519	P10605 Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2 #
TIVC*QESELPDELLYGR	2.1429	Q9JJK2 LanC-like protein 2 OS=Mus musculus GN=Lancl2 PE=1 SV=1 # F6RJV6 LanC-like protein 2 (Fragment) OS=Mus musculus GN=Lancl2 PE=1 SV=1 #
YC*VGDEVSMADVCLVPQVANAER	2.1407	Q9WVL0 Maleylacetoacetate isomerase OS=Mus musculus GN=Gstz1 PE=1 SV=1 #
EEVVTIDTWMQGLLKPTC*LYGQLPK	2.1385	P19157 Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2 #
GC*FKDTTPDELLSAVLTAVLQDVK	2.1371	Q8VCH0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 # Q3UKM0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 #
GEVPC*TVTTASPLDDAVLSELK	2.1349	Q9DB20 ATP synthase subunit O# mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1 #
FASYC*LTEPGSGSDAASLLTSAK	2.1203	A0A0R4J0P1 Acyl-Coenzyme A dehydrogenase family# member 8 OS=Mus musculus GN=Acad8 PE=1 SV=1 # Q9D7B6 Isobutyryl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acad8 PE=1 SV=2 #

Peptide	L/H Ratio	Protein
LQSGIC*HLFR	2.1172	Q922B2 Aspartate--tRNA ligase# cytoplasmic OS=Mus musculus GN=Dars PE=1 SV=2 #
DGGQYALVAAC*AAGGQGHAMIVEAYPK	2.1145	Q99JY0 Trifunctional enzyme subunit beta# mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1 #
MC*EIVFEDPKTPGEK	2.1086	Q8CGC7 Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4 #
AVQNAC*QILMK	2.1019	G3X982 Aldehyde oxidase 3 OS=Mus musculus GN=Aox3 PE=1 SV=1 #
NQESCGSC*YSFASMGMLEAR	2.1012	Q3UBY5 Cathepsin C# isoform CRA_b OS=Mus musculus GN=Ctsc PE=1 SV=1 # P97821 Dipeptidyl peptidase 1 OS=Mus musculus GN=Ctsc PE=1 SV=1 #
AYGGSMC*AK	2.1004	Q9D1R9 60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=1 SV=2 #
VIEINPYLLGTMSGC*AADCQYWER	2.0976	P28063 Proteasome subunit beta type-8 OS=Mus musculus GN=Psmb8 PE=1 SV=2 # G3UZW8 Proteasome subunit beta type (Fragment) OS=Mus musculus GN=Psmb8 PE=1 SV=2 #
C*ATITPDEKR	2.0925	O88844 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=Idh1 PE=1 SV=2 #
ITNKVFANPEDC*AGFGK	2.0894	E9QJW0 Microsomal glutathione S-transferase 1 OS=Mus musculus GN=Mgst1 PE=1 SV=1 #
SSAIPSPC*GK	2.0842	B1AR28 Very long-chain-specific acyl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acadvl PE=1 SV=1 # P50544 Very long-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acadvl PE=1 SV=3 #
DIGQC*LTNFSK	2.0814	P56657 Cytochrome P450 2C40 OS=Mus musculus GN=Cyp2c40 PE=1 SV=2 # K7N6C2 Protein Cyp2c68 OS=Mus musculus GN=Cyp2c68 PE=1 SV=1 # E9Q7C8 Cytochrome P450 2C40 OS=Mus musculus GN=Cyp2c40 PE=1 SV=1 # E9PXC3 Protein Cyp2c69 OS=Mus musculus GN=Cyp2c69 PE=1 SV=1 # Q569X9 Cytochrome P450# family 2# subfamily c# polypeptide 67 OS=Mus musculus GN=Cyp2c67 PE=1 SV=1 #
IKSGEEDFESLASQFSDC*SSAK	2.0769	Q3ULQ2 Peptidylprolyl isomerase OS=Mus musculus GN=Pin1rt1 PE=1 SV=1 # Q9QUR7 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 OS=Mus musculus GN=Pin1 PE=1 SV=1 #
IFSYEC*R	2.0748	P58710 L-gulonolactone oxidase OS=Mus musculus GN=Gulo PE=1 SV=3 #
YNFFC*QGTR	2.0700	Q8BHI7 Elongation of very long chain fatty acids protein 5 OS=Mus musculus GN=Elovl5 PE=1 SV=1 #
TCNVLVALEQQSPDIAQC*VHLDR	2.0592	Q91X83 S-adenosylmethionine synthase isoform type-1 OS=Mus musculus GN=Mat1a PE=1 SV=1 #
GTFASLSELHC*DK	2.0582	Beta-globin OS=Mus musculus GN=Hbbt1 PE=1 SV=1 # P02089 Hemoglobin subunit beta-2 OS=Mus musculus GN=Hbb-b2 PE=1 SV=2 #
LLSHC*LLVTLASHHPADFTPAVHASLDK	2.0542	Q91VB8 Alpha globin 1 OS=Mus musculus GN=Hba-a1 PE=1 SV=1 #
FGIIC*MEDLIHEIYTVGKR	2.0542	Q5M9N8 60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=1 # P14148 60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=1 SV=2 # F6XI62 60S ribosomal protein L7 (Fragment) OS=Mus musculus GN=Rpl7 PE=1 SV=1 #
VIILNHPGQISAGYAPVLDCHTAHIAC*K	2.0526	P10126 Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 # Q58E64 Elongation factor 1-alpha OS=Mus musculus GN=Eef1a1 PE=1 SV=1 #
AGLTVNDIDIFEINEAFASQAVYC*VEK	2.0467	Q8VCH0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 # Q3UKM0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 #
QASVGAGIPYSVPAWSCQMIC*GSGLK	2.0463	Q80X81 Acetyl-Coenzyme A acetyltransferase 3 OS=Mus musculus GN=Acat3 PE=1 SV=1 # Q8CAY6 Acetyl-CoA acetyltransferase# cytosolic OS=Mus musculus GN=Acat2 PE=1 SV=2 #
SSFATPGVNVGLFC*STPAVALGR	2.0331	Q9D7J9 Enoyl-CoA hydratase domain-containing protein 3# mitochondrial OS=Mus musculus GN=Echdc3 PE=1 SV=1 #
VIHHTTPVTSLYC*LR	2.0320	O35423-2 Isoform Peroxisomal of Serine--pyruvate aminotransferase# mitochondrial OS=Mus musculus GN=Agxt # O35423 Serine--pyruvate aminotransferase# mitochondrial OS=Mus musculus GN=Agxt PE=1 SV=3 #

Peptide	L/H Ratio	Protein
LLLGPC*TPVQYR	2.0297	P97872 Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Mus musculus GN=Fmo5 PE=1 SV=4 #
TIC*SHVQNMIK	2.0285	Q5EBQ6 60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=1 SV=1 # A0A140T8T4 Protein Rpl9-ps6 OS=Mus musculus GN=Rpl9-ps6 PE=4 SV=1 # P51410 60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=1 SV=2 # A0A0G2JES3 60S ribosomal protein L9 (Fragment) OS=Mus musculus GN=Rpl9 PE=1 SV=1 #
NMITGTSQADC*AVLIVAAGVGEFEAGISK	2.0209	P10126 Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 # Q58E64 Elongation factor 1-alpha OS=Mus musculus GN=Eef1a1 PE=1 SV=1 #
GC*STILSPEGSAQFAAQIFGLNNHLVWAK	2.0163	Q9DCL9 Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=4 #
SVFPEVDIVVPGIC*IANTDTR	2.0070	Q8C165 Probable carboxypeptidase PM20D1 OS=Mus musculus GN=Pm20d1 PE=1 SV=1 #
YLLGTSLARPC*IAR	2.0044	P16460 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1 #
YYALCGFGGVLSC*GLTHTAVVPLDLVK	2.0035	Q8VEM8 Phosphate carrier protein# mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1 #
GTLTLC*PYHSDR	2.0027	Q3TKV1 26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psmd2 PE=1 SV=1 # Q8VDM4 26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psmd2 PE=1 SV=1 #
ILATAVCHTDAYTLSGADPEGC*FPVILGHEGAGIVESVGEGVTK	1.9997	Q6P5I3 S-(hydroxymethyl)glutathione dehydrogenase OS=Mus musculus GN=Adh5 PE=1 SV=2 # P28474 Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3 #
ATFHTPFSQLGQSPEAC*SSYTFPK	1.9977	Q9WUR2-2 Isoform 2 of Enoyl-CoA delta isomerase 2# mitochondrial OS=Mus musculus GN=Eci2 # Q3TCD4 Enoyl-CoA delta isomerase 2# mitochondrial OS=Mus musculus GN=Eci2 PE=1 SV=1 # Q9WUR2 Enoyl-CoA delta isomerase 2# mitochondrial OS=Mus musculus GN=Eci2 PE=1 SV=2 #
GKEAPFTHFDPSC*LFPACR	1.9955	P16015 Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3 #
LC*FLDKVEPQATISEIK	1.9954	G3UWE1 MCG11048# isoform CRA_c OS=Mus musculus GN=Tecr PE=1 SV=1 # Q9CY27 Very-long-chain enoyl-CoA reductase OS=Mus musculus GN=Tecr PE=1 SV=1 # Q52L67 Gpsn2 protein OS=Mus musculus GN=Tecr PE=1 SV=1 #
VC*GYDTPFPHIFEPFYIPDKWK	1.9910	Q6P3A8 2-oxoisovalerate dehydrogenase subunit beta# mitochondrial OS=Mus musculus GN=Bckdhb PE=1 SV=2 #
TPPLGSAQVPLADCVLTFLAMECAC*PDIDTYR	1.9888	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=1 SV=1 #
AETSDVANAVLDGADC*IMLSGETAK	1.9853	G3X925 Pyruvate kinase OS=Mus musculus GN=Pklr PE=1 SV=1 # E9Q509 Pyruvate kinase OS=Mus musculus GN=Pklr PE=1 SV=1 #
DQTC*TPVPVKR	1.9845	Q9EQF5 Dihydropyrimidinase OS=Mus musculus GN=Dpys PE=1 SV=2 #
QHC*AYTIAK	1.9748	B1AX77 Hydroxysteroid dehydrogenase-like protein 2 (Fragment) OS=Mus musculus GN=Hsdl2 PE=1 SV=1 # Q2TPA8 Hydroxysteroid dehydrogenase-like protein 2 OS=Mus musculus GN=Hsdl2 PE=1 SV=1 # B1AX78 Hydroxysteroid dehydrogenase-like protein 2 OS=Mus musculus GN=Hsdl2 PE=1 SV=1 #
SNPGGFGIAPHC*LDEGTVR	1.9717	Q9CXS4 Centromere protein V OS=Mus musculus GN=Cenpv PE=1 SV=2 # Q9CXS4-2 Isoform 2 of Centromere protein V OS=Mus musculus GN=Cenpv #
IPFLEFSC*PGVPPGLETLK	1.9713	E9QNL5 Sulfotransferase OS=Mus musculus GN=Sult1a1 PE=1 SV=1 #
LVVPATQC*GSLIGK	1.9667	P60335 Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 #
SGLTPNDVDVIELHDC*FSVNELITYEALGLCPEGQGGTLVDRGDNTYGGK	1.9624	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 #
VGIGPGSVC*TTR	1.9592	Q99L27 GMP reductase 2 OS=Mus musculus GN=Gmpr2 PE=1 SV=2 #

Peptide	L/H Ratio	Protein
KYESAYGTQFTPC*QLLLDHANNSSK	1.9529	Q8BMS1 Trifunctional enzyme subunit alpha# mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 #
NVLVIGTTGSQTTFLPEGELPEC*AR	1.9493	A2ADY9 Protein DDI1 homolog 2 OS=Mus musculus GN=Ddi2 PE=1 SV=1 #
HIGDGC*HLTR	1.9491	Q9DD20 Methyltransferase-like protein 7B OS=Mus musculus GN=Mettl7b PE=1 SV=2 #
NYLPAINGIVFLVDC*ADHER	1.9459	Q9CQC9 GTP-binding protein SAR1b OS=Mus musculus GN=Sar1b PE=1 SV=1 # Q0VGU0 GTP-binding protein SAR1b OS=Mus musculus GN=Sar1b PE=1 SV=1 #
VFFIESIC*NDPDIIAENIK	1.9452	P70266 6-phosphofructo-2-kinase/fructose-2#6-bisphosphatase 1 OS=Mus musculus GN=Pfkfb1 PE=1 SV=2 #
AEHSFAGVPC*GIMDQLIALLGQK	1.9420	Q9R0N0 Galactokinase OS=Mus musculus GN=Galk1 PE=1 SV=2 #
C*MALSTAILVGEAK	1.9406	Q9EQ20 Methylmalonate-semialdehyde dehydrogenase [acylating]# mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1 #
TC*NVLVALEQQSPDIAQCVHLDR	1.9373	Q91X83 S-adenosylmethionine synthase isoform type-1 OS=Mus musculus GN=Mat1a PE=1 SV=1 #
VVVVGC*R	1.9362	P47199 Quinone oxidoreductase OS=Mus musculus GN=Cryz PE=1 SV=1 #
SAC*GVCPGR	1.9329	Q9D1R9 60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=1 SV=2 #
C*MTEEIFGPVTCVVPFDSEEEVITR	1.9323	Q8BH00 Aldehyde dehydrogenase family 8 member A1 OS=Mus musculus GN=Aldh8a1 PE=1 SV=1 #
VNPLGGAIALGHPLGC*TGAR	1.9311	Q921H8 3-ketoacyl-CoA thiolase A# peroxisomal OS=Mus musculus GN=Acaa1a PE=1 SV=1 # Q8VCH0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 # Q3UKM0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 #
ISLGLPVGAVINC*ADNTGAK	1.9227	P62830 60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1 #
TEAQPFDPTFILAC*APCNVICSILFNER	1.9216	E9Q5K4 Protein Cyp2c44 OS=Mus musculus GN=Cyp2c44 PE=1 SV=1 #
SEGGFIWAC*K	1.9190	O88844 Isocitrate dehydrogenase [NADP] cytoplasmic OS=Mus musculus GN=Idh1 PE=1 SV=2 #
VQQAPIEEHWIIEC*NDGVFQR	1.9143	O35969 Guanidinoacetate N-methyltransferase OS=Mus musculus GN=Gamt PE=1 SV=1 # O35969-2 Isoform 2 of Guanidinoacetate N-methyltransferase OS=Mus musculus GN=Gamt #
IGC*FALSEPGNGSDAGAASTTAR	1.9134	Q07417 Short-chain specific acyl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acads PE=1 SV=2 #
NQESC*GSCYSFASMGMLEAR	1.9037	Q3UBY5 Cathepsin C# isoform CRA_b OS=Mus musculus GN=Ctsc PE=1 SV=1 # P97821 Dipeptidyl peptidase 1 OS=Mus musculus GN=Ctsc PE=1 SV=1 #
VWNLANC*K	1.9005	P68040 Receptor of activated protein C kinase 1 OS=Mus musculus GN=Rack1 PE=1 SV=3 #
VC*ISILHAPGDDPMGYESSAER	1.8973	Q3U431 Ubiquitin-conjugating enzyme E2 G2 OS=Mus musculus GN=Ube2g2 PE=1 SV=1 # P60605 Ubiquitin-conjugating enzyme E2 G2 OS=Mus musculus GN=Ube2g2 PE=1 SV=1 #
YNLTPTIFFCATPPDDGNLC*R	1.8950	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 #
TLFAGLEPHIPNAYC*NCMIQVLYFLEPVR	1.8911	Q8BGF7 PAB-dependent poly(A)-specific ribonuclease subunit PAN2 OS=Mus musculus GN=Pan2 PE=1 SV=1 # Q8BGF7-2 Isoform 2 of PAB-dependent poly(A)-specific ribonuclease subunit PAN2 OS=Mus musculus GN=Pan2 # Q8BGF7-3 Isoform 3 of PAB-dependent poly(A)-specific ribonuclease subunit PAN2 OS=Mus musculus GN=Pan2 # Q8BGF7-4 Isoform 4 of PAB-dependent poly(A)-specific ribonuclease subunit PAN2 OS=Mus musculus GN=Pan2 #
LCEESGAEPQEAVLQQLHQLPKGGLDLTTQSLTVETC*R	1.8900	A2AC11 Leucine-rich repeat-containing protein 45 (Fragment) OS=Mus musculus GN=Lrrc45 PE=4 SV=1 # Q8CIM1 Leucine-rich repeat-containing protein 45 OS=Mus musculus GN=Lrrc45 PE=2 SV=2 # E9PVE2 Leucine-rich repeat-containing protein 45 OS=Mus musculus GN=Lrrc45 PE=1 SV=1 #

Peptide	L/H Ratio	Protein
LTEGC*SFR	1.8866	Q6ZWU9 40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3 # A0A0G2JDW7 40S ribosomal protein S27 (Fragment) OS=Mus musculus GN=Rps27 PE=1 SV=1 # Q6ZWY3 40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=1 SV=3 #
VNQAIWLLC*TGAR	1.8854	Q91V55 40S ribosomal protein S5 OS=Mus musculus GN=Rps5 PE=1 SV=1 #
AATFFGC*IGIDK	1.8806	P55264 Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2 #
VAASDWTFLHC*LPR	1.8768	P11725 Ornithine carbamoyltransferase# mitochondrial OS=Mus musculus GN=Otc PE=1 SV=1 # Q8R1A8 Ornithine carbamoyltransferase# mitochondrial OS=Mus musculus GN=Otc PE=1 SV=1 # Q543H3 Ornithine carbamoyltransferase# mitochondrial OS=Mus musculus GN=Otc PE=1 SV=1 #
LLEETGIC*VVPGSGFGQR	1.8732	Q8BGT5 Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=1 SV=1 #
TFQDC*YSSK	1.8710	Q8BH95 Enoyl-CoA hydratase# mitochondrial OS=Mus musculus GN=Echs1 PE=1 SV=1 #
SCGSSC*AVHDLIFWR	1.8685	Q9ES97-3 Isoform 3 of Reticulon-3 OS=Mus musculus GN=Rtn3 #
GVQDIVVGEGTHFLIPWVQKPIIFDC*R	1.8675	P67778 Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1 #
C*GESPVWEEASQSLLFVDIPSK	1.8531	Q64374 Regucalcin OS=Mus musculus GN=Rgn PE=1 SV=1 #
DDYEVSC*PELDQLVEAALSVPGVYGSR	1.8528	Q9R0N0 Galactokinase OS=Mus musculus GN=Galk1 PE=1 SV=2 #
FNIWGGSLSLGHPFGATGC*R	1.8514	Q99JY0 Trifunctional enzyme subunit beta# mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1 #
VAC*IGAWHPAR	1.8507	P27659 60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=1 SV=3 #
IDATQVEVNPFGETPEGQVVC*FDAK	1.8497	Q9Z2I8-2 Isoform 2 of Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Mus musculus GN=Suclg2 # Q9Z2I8 Succinyl-CoA ligase [GDP-forming] subunit beta# mitochondrial OS=Mus musculus GN=Suclg2 PE=1 SV=3 #
SAGAC*TAAAFLR	1.8463	Q9CPY7-2 Isoform 2 of Cytosol aminopeptidase OS=Mus musculus GN=Lap3 # Q9CPY7 Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3 #
TPPLGSAQVPLADCVLTFLAMEC*ACPDIDTYR	1.8458	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=1 SV=1 #
NFYGGNGIVGAQVPLGAGIALAC*K	1.8455	P35486 Pyruvate dehydrogenase E1 component subunit alpha# somatic form# mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1 # Q3UFJ3 Pyruvate dehydrogenase E1 component subunit alpha OS=Mus musculus GN=Pdha1 PE=1 SV=1 #
KC*GLQGFDGIV	1.8433	A0A0J9YU79 Ketohexokinase OS=Mus musculus GN=Khk PE=1 SV=1 #
IC*TTLIGLEEHLNALDR	1.8424	Q8VC30 Triokinase/FMN cyclase OS=Mus musculus GN=Tkfc PE=1 SV=1 #
GTSGNVALLELGC*GTGANFQFYPQGCK	1.8413	Q9DD20 Methyltransferase-like protein 7B OS=Mus musculus GN=Mettl7b PE=1 SV=2 #
KEPGAYDWSSIVQHAC*ELEGDR	1.8354	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=1 SV=1 #
EVESVTPEHC*IFASNTSALPINQIAAVSK	1.8331	Q8BMS1 Trifunctional enzyme subunit alpha# mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 #
FGIEAFSDC*LR	1.8304	Q80XN0 D-beta-hydroxybutyrate dehydrogenase# mitochondrial OS=Mus musculus GN=Bdh1 PE=1 SV=2 #
LPC*SLDSEATQCPVPLSYVPK	1.8303	Q63886 UDP-glucuronosyltransferase 1-1 OS=Mus musculus GN=Ugt1a1 PE=1 SV=2 #
LGPNYLQIPVNC*PYR	1.8300	P24270 Catalase OS=Mus musculus GN=Cat PE=1 SV=4 #
C*MAVNFFGTVEVTK	1.8276	P51658 Estradiol 17-beta-dehydrogenase 2 OS=Mus musculus GN=Hsd17b2 PE=1 SV=2 #
IGAFGYMEC*SAK	1.8255	Q4VAE6 Ras family member A OS=Mus musculus GN=Rhoa PE=1 SV=1 # Q9QUI0 Transforming protein RhoA OS=Mus musculus GN=Rhoa PE=1

Peptide	L/H Ratio	Protein
		SV=1 # A0A0A6YXF6 Transforming protein RhoA (Fragment) OS=Mus musculus GN=Rhoa PE=1 SV=1 #
EQSDFC*PWYIGLPFIPYLDNLPNFNR	1.8179	Q8R050 Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Mus musculus GN=Gspt1 PE=1 SV=2 # Q8R050-2 Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Mus musculus GN=Gspt1 #
ADHQPLTEASYVNLPTIALC*NTDSPLR	1.8173	P14206 40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4 #
LQILNSIFPGIGC*PVPR	1.8122	Q3KNM2 E3 ubiquitin-protein ligase MARCH5 OS=Mus musculus GN=March5 PE=1 SV=1 # A0A0R4J1H0 E3 ubiquitin-protein ligase MARCH5 OS=Mus musculus GN=March5 PE=1 SV=1 # A2RTC8 E3 ubiquitin-protein ligase MARCH5 OS=Mus musculus GN=March5 PE=1 SV=1 #
YVVCFDPLDGSSNIDC*LVSIGTIFGIYR	1.8070	Q9QXD6 Fructose-1#6-bisphosphatase 1 OS=Mus musculus GN=Fbp1 PE=1 SV=3 #
DNSIIAQATSAAEAFC*AVK	1.7878	Q61635 GTP-binding protein OS=Mus musculus GN=Ifi47 PE=1 SV=1 #
VNECTEILSSPGC*QIFNAVPILIDYCPGR	1.7843	E9PXC3 Protein Cyp2c69 OS=Mus musculus GN=Cyp2c69 PE=1 SV=1 # Q569X9 Cytochrome P450# family 2# subfamily c# polypeptide 67 OS=Mus musculus GN=Cyp2c67 PE=1 SV=1 #
LFLLADEVYQDNVYSPDC*R	1.7779	Q8BGT5 Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=1 SV=1 #
TIGGGDDSFTTFFC*ETGAGK	1.7755	A0A0A0MQA5 Tubulin alpha-4A chain (Fragment) OS=Mus musculus GN=Tuba4a PE=1 SV=1 # P68368 Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 #
TNELGDGGVGLVLQGLQNPTC*K	1.7655	Q91VI7 Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=1 SV=1 #
LQTQPPSLSGQPPMYSGTLDC*FR	1.7634	Q9Z2Z6 Mitochondrial carnitine/acylcarnitine carrier protein OS=Mus musculus GN=Slc25a20 PE=1 SV=1 #
LLC*GGGAAADR	1.7549	Q544B1 Aldehyde dehydrogenase 2# mitochondrial# isoform CRA_b OS=Mus musculus GN=Aldh2 PE=1 SV=1 # P47738 Aldehyde dehydrogenase# mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1 #
GALMANFLTQGQVC*CNGTR	1.7546	Q3U367 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 # Q9JLJ2 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 #
LNLPINIIGLAPLC*ENMPSGK	1.7462	Q9CPY7-2 Isoform 2 of Cytosol aminopeptidase OS=Mus musculus GN=Lap3 # Q9CPY7 Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3 #
VDASVALLC*DIQNTIINNLFR	1.7416	Q9DBL1 Short/branched chain specific acyl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Acadsb PE=1 SV=1 #
LTLLEVGC*GTGANFK	1.7412	Q8C6B0 MCG20149# isoform CRA_a OS=Mus musculus GN=Mettl7a1 PE=1 SV=1 #
TGVGINNGDDVDFFVLLDNVAAEQVHSLLNC*PALER	1.7393	Q8BP40 Lysophosphatidic acid phosphatase type 6 OS=Mus musculus GN=Acp6 PE=1 SV=1 #
AIQSLTDTC*SDDLSVVTDCMEHALTACHPR	1.7343	O88451 Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=1 SV=1 #
AQAWC*YSK	1.7311	Q4FJQ0 MCG130610 OS=Mus musculus GN=Rab7 PE=1 SV=1 # P51150 Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2 #
QMPVHYGC*K	1.7139	Q3U3J1 2-oxoisovalerate dehydrogenase subunit alpha# mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1 #
FCTPASQC*PIIDPAWESPEGVPIEGIIFGGR	1.7008	Q9Z2V4 Phosphoenolpyruvate carboxykinase# cytosolic [GTP] OS=Mus musculus GN=Pck1 PE=1 SV=1 #
FAELVYTGFWHSPEC*EFVR	1.6988	P16460 Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1 #
YMACC*LLYR	1.6946	A0A0A0MQA5 Tubulin alpha-4A chain (Fragment) OS=Mus musculus GN=Tuba4a PE=1 SV=1 # P68368 Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 # P68369 Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 # P68373 Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1 # P05213 Tubulin alpha-1B chain

Peptide	L/H Ratio	Protein
		OS=Mus musculus GN=Tuba1b PE=1 SV=2 # Q52L87 Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1 #
TC*FSMVPALQK	1.6935	P85094 Isochorismatase domain-containing protein 2A OS=Mus musculus GN=Isoc2a PE=1 SV=1 #
LLC*GLLSDR	1.6919	P34884 Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2 # Q545F0 MCG3124# isoform CRA_b OS=Mus musculus GN=Mif PE=1 SV=1 #
VTPGSTC*AVFGLGGVGLSVIIGCK	1.6913	P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=2 # Q3UKA4 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=1 SV=1 #
EYRPSLVLELGAYC*GYSAVR	1.6903	O88587 Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=2 # O88587-2 Isoform Soluble of Catechol O-methyltransferase OS=Mus musculus GN=Comt #
DSQDFSSYLSDGLHLSPMGNEFLFLNLC*PLLDK	1.6902	Q9DB29 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Mus musculus GN=Iah1 PE=1 SV=1 #
ILADSINSEVGILC*HALQK	1.6833	P16331 Phenylalanine-4-hydroxylase OS=Mus musculus GN=Pah PE=1 SV=4 #
TELLDHPGITLSTIC*PGPVHSNIYQNYLTR	1.6801	A0A140LIS8 Uncharacterized protein OS=Mus musculus PE=3 SV=1 #
QQGAGDLC*PSHLVAPADLGSSLFANIPGYK	1.6792	A0A0A0MQN4 Ubiquitin-like modifier-activating enzyme ATG7 OS=Mus musculus GN=Atg7 PE=1 SV=1 # Q9D906 Ubiquitin-like modifier-activating enzyme ATG7 OS=Mus musculus GN=Atg7 PE=1 SV=1 #
TAC*YGHFGR	1.6729	Q91X83 S-adenosylmethionine synthase isoform type-1 OS=Mus musculus GN=Mat1a PE=1 SV=1 #
IQLMIVC*CSPDFEK	1.6710	P19639 Glutathione S-transferase Mu 3 OS=Mus musculus GN=Gstm3 PE=1 SV=2 #
ASATGMIIMDSVEVPEENVLPNVSSLAGPFGC*LNTAR	1.6704	A0A0A0MQ68 Glutaryl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Gcdh PE=1 SV=1 # Q60759 Glutaryl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Gcdh PE=1 SV=2 #
EVGTSYGC*YFVPAFSGLYAPYWEPSAR	1.6656	Q64516-2 Isoform 2 of Glycerol kinase OS=Mus musculus GN=Gk # Q64516 Glycerol kinase OS=Mus musculus GN=Gk PE=1 SV=2 # Q64516-1 Isoform 1 of Glycerol kinase OS=Mus musculus GN=Gk #
GLQGSFEELC*R	1.6636	P41216 Long-chain-fatty-acid--CoA ligase 1 OS=Mus musculus GN=Acsl1 PE=1 SV=2 # D3Z041 Long-chain-fatty-acid--CoA ligase 1 OS=Mus musculus GN=Acsl1 PE=1 SV=1 #
VLELYLDLLSQPC*R	1.6634	Q64471 Glutathione S-transferase theta-1 OS=Mus musculus GN=Gstt1 PE=1 SV=4 #
LVC*ISDYEQHVR	1.6616	Q3UEE8 Hydroxyacid oxidase 1 OS=Mus musculus GN=Hao1 PE=1 SV=1 # Q9WU19 Hydroxyacid oxidase 1 OS=Mus musculus GN=Hao1 PE=1 SV=1 #
GMPFELC*FLVQR	1.6608	O08573-2 Isoform 2 of Galectin-9 OS=Mus musculus GN=Lgals9 # G3X9T7 Galectin OS=Mus musculus GN=Lgals9 PE=1 SV=1 # B1AQR8 Galectin OS=Mus musculus GN=Lgals9 PE=1 SV=1 # O08573-3 Isoform 3 of Galectin-9 OS=Mus musculus GN=Lgals9 # O08573 Galectin-9 OS=Mus musculus GN=Lgals9 PE=1 SV=1 #
YWLC*AATGPSIK	1.6587	P68040 Receptor of activated protein C kinase 1 OS=Mus musculus GN=Rack1 PE=1 SV=3 #
DVQIGDIVTVGEC*RPLSK	1.6566	P62281 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=3 # Q3UC02 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=1 SV=1 #
NEEDVGAGDQGLMFGYATDETEEC*MPLTIVLAHK	1.6522	Q91X83 S-adenosylmethionine synthase isoform type-1 OS=Mus musculus GN=Mat1a PE=1 SV=1 #
TGVAC*SVSQAQKDELILEGNDIELVSNSAALIQQATTVK	1.6520	Q5EBQ6 60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=1 SV=1 # A0A140T8T4 Protein Rpl9-ps6 OS=Mus musculus GN=Rpl9-ps6 PE=4 SV=1 # P51410 60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=1 SV=2 # A0A0G2JES3 60S ribosomal protein L9 (Fragment) OS=Mus musculus GN=Rpl9 PE=1 SV=1 #
LALNC*VGGK	1.6429	Q9DCS3 Trans-2-enoyl-CoA reductase# mitochondrial OS=Mus musculus GN=Mecr PE=1 SV=2 #

Peptide	L/H Ratio	Protein
ATYDKLC*K	1.6361	P62852 40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=1 SV=1 # Q58EA6 40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=1 SV=1 #
DVGAETLLHSC*KK	1.6186	Q9D1A2 Cytosolic non-specific dipeptidase OS=Mus musculus GN=Cndp2 PE=1 SV=1 #
MHSVGIC*GSDVHYWEHGR	1.6111	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 #
INPYMSSPC*HIEMILTEK	1.6050	Q6ZWZ7 60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=1 SV=1 # Q9CPR4 60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=1 SV=3 #
PVCNQVEC*HPYLNQGK	1.5843	Q3UEM0 Estradiol 17 beta-dehydrogenase 5 OS=Mus musculus GN=Akr1c6 PE=1 SV=1 #
QAIDDDC*NQTGQMTAGLLDWPQGTFASQVTLEGDKVK	1.5786	Q9DCW4 Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3 # A0A0U1RNK9 Electron transfer flavoprotein subunit beta (Fragment) OS=Mus musculus GN=Etfb PE=1 SV=1 #
C*AWGQQPDLAANEAQLLR	1.5768	Q9WVJ2 26S proteasome non-ATPase regulatory subunit 13 OS=Mus musculus GN=Psmd13 PE=1 SV=1 # B2RT97 26S proteasome non-ATPase regulatory subunit 13 OS=Mus musculus GN=Psmd13 PE=1 SV=1 #
AC*DLWEQILR	1.5764	A3KMP2 Tetratricopeptide repeat protein 38 OS=Mus musculus GN=Ttc38 PE=1 SV=2 #
SGQC*AAGAPVLQFTNCR	1.5754	Q8JZV7 N-acetylglucosamine-6-phosphate deacetylase OS=Mus musculus GN=Amdhd2 PE=1 SV=1 #
MVNSVEGC*ADDALAGLVASNPDLQLLQGHR	1.5591	Q8VC30 Triokinase/FMN cyclase OS=Mus musculus GN=Tkfc PE=1 SV=1 #
VDLNSNGFIC*DYELHELFK	1.5553	Q99K51 Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3 #
ILATAVC*HTDAYTLSGADPEGCFPVILGHEGAGIVESVGEGVTK	1.5476	Q6P5I3 S-(hydroxymethyl)glutathione dehydrogenase OS=Mus musculus GN=Adh5 PE=1 SV=2 # P28474 Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3 #
LGTLHGGLTATLVDSISTMALMC*TER	1.5461	Q4VA32 Acyl-coenzyme A thioesterase 13 OS=Mus musculus GN=Acot13 PE=1 SV=1 # Q9CQR4 Acyl-coenzyme A thioesterase 13 OS=Mus musculus GN=Acot13 PE=1 SV=1 #
AVNTLNEALEFANSVGYPC*LLR	1.5413	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
AFQVWC*VGNEALVGPR	1.5408	O70503 Very-long-chain 3-oxoacyl-CoA reductase OS=Mus musculus GN=Hsd17b12 PE=1 SV=1 #
RPYGVGLLIAGYDDMGPHIFQTC*PSANYFDCR	1.5219	Q3TS44 Proteasome subunit alpha type OS=Mus musculus GN=Psma1 PE=1 SV=1 # Q9R1P4 Proteasome subunit alpha type-1 OS=Mus musculus GN=Psma1 PE=1 SV=1 #
LWNTLGVC*K	1.5183	P68040 Receptor of activated protein C kinase 1 OS=Mus musculus GN=Rack1 PE=1 SV=3 #
YNLTPTIFFC*ATPPDDGNLCR	1.5099	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 #
YLAAAFPSAC*GK	1.4988	Q9Z2V4 Phosphoenolpyruvate carboxykinase# cytosolic [GTP] OS=Mus musculus GN=Pck1 PE=1 SV=1 #
ITQLSAPHC*K	1.4859	Q8BH00 Aldehyde dehydrogenase family 8 member A1 OS=Mus musculus GN=Aldh8a1 PE=1 SV=1 #
AEPPQC*TSLAWSADGQTLFAGYTDNLVR	1.4775	P68040 Receptor of activated protein C kinase 1 OS=Mus musculus GN=Rack1 PE=1 SV=3 #
GHSELDTAFMYC*DGQSENILGGLGLGLGSGDCTVK	1.4704	Q8CG76 Aflatoxin B1 aldehyde reductase member 2 OS=Mus musculus GN=Akr7a2 PE=1 SV=3 #
QC*SSGLQAVANIAGGIR	1.4673	Q8VCH0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 # Q3UKM0 3-ketoacyl-CoA thiolase B# peroxisomal OS=Mus musculus GN=Acaa1b PE=1 SV=1 #
EPGEVC*FPGGK	1.4474	Q99P30 Peroxisomal coenzyme A diphosphatase NUDT7 OS=Mus musculus GN=Nudt7 PE=1 SV=2 #
ELEVLLMC*NK	1.4470	P62911 60S ribosomal protein L32 OS=Mus musculus GN=Rpl32 PE=1 SV=2 #

Peptide	L/H Ratio	Protein
AAVPC*FSVTVEQDDILPGALR	1.4419	A7MCT6 Ethanolamine kinase 2 OS=Mus musculus GN=Etnk2 PE=1 SV=1 #
SAPALAC*GNAMIFKPSPFTPVSALLLAEIYTK	1.4409	Q3U367 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 # Q9JLJ2 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 #
HGIPDETC*NNYQAK	1.4342	Q545I6 Cathepsin Z OS=Mus musculus GN=Ctsz PE=1 SV=1 # Q9WUU7 Cathepsin Z OS=Mus musculus GN=Ctsz PE=1 SV=1 #
IQLMIVCC*SPDFEK	1.4127	P19639 Glutathione S-transferase Mu 3 OS=Mus musculus GN=Gstm3 PE=1 SV=2 #
SLC*LAQEICR	1.4109	Q3URE1 Acyl-CoA synthetase family member 3# mitochondrial OS=Mus musculus GN=Acsf3 PE=1 SV=2 #
ASVAQLTQELGTAFFQQQQLPAAMADTFLEHLC*LLDIDSEPVAAR	1.3991	G3X925 Pyruvate kinase OS=Mus musculus GN=Pklr PE=1 SV=1 # E9Q509 Pyruvate kinase OS=Mus musculus GN=Pklr PE=1 SV=1 #
C*LHPLASETFVSK	1.3942	A2AEY0 Four and a half LIM domains protein 1 (Fragment) OS=Mus musculus GN=Fhl1 PE=1 SV=1 # P97447-2 Isoform 2 of Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 # A2AEX7 Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 PE=1 SV=1 # A2AEX8 Four and a half LIM domains 1# isoform CRA_b OS=Mus musculus GN=Fhl1 PE=1 SV=1 # A2AEY1 Four and a half LIM domains protein 1 (Fragment) OS=Mus musculus GN=Fhl1 PE=1 SV=7 # P97447 Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 PE=1 SV=3 # A2AEY2 Four and a half LIM domains 1# isoform CRA_c OS=Mus musculus GN=Fhl1 PE=1 SV=1 # A2AEX6 Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 PE=1 SV=1 #
STVNTAVALTLAC*FGTQR	1.3870	Q61176 Arginase-1 OS=Mus musculus GN=Arg1 PE=1 SV=1 #
EIASLDSENIDEILNNADVALVNFYADWC*R	1.3853	Q9D1Q6 Endoplasmic reticulum resident protein 44 OS=Mus musculus GN=Erp44 PE=1 SV=1 #
TATAVAHC*K	1.3836	P14131 40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=1 SV=4 # A4FUS1 40S ribosomal protein S16 OS=Mus musculus GN=Rps16 PE=1 SV=1 #
TNHIGHTGYLNTVTVSPDGSLC*ASGGK	1.3552	P68040 Receptor of activated protein C kinase 1 OS=Mus musculus GN=Rack1 PE=1 SV=3 #
LHPAPEATVAATC*AFPSVQAAVDSTVQILQAAVPVAR	1.3501	Q7TNG8 Probable D-lactate dehydrogenase# mitochondrial OS=Mus musculus GN=Ldhd PE=1 SV=1 #
ADC*TITMADSDLLALMTGK	1.3437	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 #
VAVTGGTHGNEMC*GVYLAR	1.3346	Q91XE4 N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming) OS=Mus musculus GN=Acy3 PE=1 SV=1 #
VCETDGC*SSEAK	1.3305	Q4VAA9 Methionine aminopeptidase 1 OS=Mus musculus GN=Metap1 PE=1 SV=1 # Q8BP48 Methionine aminopeptidase 1 OS=Mus musculus GN=Metap1 PE=1 SV=1 #
LC*SNTQMLWDQTSSEIR	1.3283	Q8K5C8 Cis-retinol/androgen dehydrogenase type 3 OS=Mus musculus GN=Rdh9 PE=2 SV=1 # E9Q9P8 Protein Gm28046 OS=Mus musculus GN=Gm28046 PE=3 SV=1 # O54909 Cis-retinol androgen dehydrogenase 1 OS=Mus musculus GN=Rdh16 PE=1 SV=1 #
FMADC*PHTIGVEFGTR	1.3244	Q50HX4 RAB14 protein OS=Mus musculus GN=Rab14 PE=1 SV=1 # Q91V41 Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3 #
LLDLVQQSC*NYK	1.3146	Q9D0T1 NHP2-like protein 1 OS=Mus musculus GN=Snu13 PE=1 SV=4 #
GLYAAFDC*TATMK	1.3080	G5E8R3 Pyruvate carboxylase OS=Mus musculus GN=Pcx PE=1 SV=1 # E9QPD7 Pyruvate carboxylase OS=Mus musculus GN=Pcx PE=1 SV=1 #
HFC*PNVPIILVGNK	1.2739	Q4VAE6 Ras family member A OS=Mus musculus GN=Rhoa PE=1 SV=1 # H3BL56 Rho-related GTP-binding protein RhoC OS=Mus musculus GN=Rhoc PE=1 SV=1 # Q9QUI0 Transforming protein RhoA OS=Mus musculus GN=Rhoa PE=1 SV=1 # Q62159 Rho-related GTP-binding protein RhoC OS=Mus musculus GN=Rhoc PE=1 SV=2 # A0A0A6YXF6

Peptide	L/H Ratio	Protein
		Transforming protein RhoA (Fragment) OS=Mus musculus GN=Rhoa PE=1 SV=1 #
TNLC*ATWEALEACKDAGLVK	1.2415	Q8VCX1 3-oxo-5-beta-steroid 4-dehydrogenase OS=Mus musculus GN=Akr1d1 PE=1 SV=1 #
SVSAFAPICNPVLC*SWGK	1.2396	Q9R0P3 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1 # H3BKH6 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=1 SV=1 #
ELEAVC*QDVLSLLDNYLIK	1.2339	P61982 14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2 # A8IP69 14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=1 #
VAPEEVSEVIFGHVLTAGC*GQNPTR	1.2293	Q80X81 Acetyl-Coenzyme A acetyltransferase 3 OS=Mus musculus GN=Acat3 PE=1 SV=1 # Q8CAY6 Acetyl-CoA acetyltransferase# cytosolic OS=Mus musculus GN=Acat2 PE=1 SV=2 #
IAVHC*TVR	1.2288	E9PYL9 Protein Gm10036 OS=Mus musculus GN=Gm10036 PE=3 SV=1 # Q9CXW4 60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4 #
SLVANLAAANC*YK	1.2209	P55264 Adenosine kinase OS=Mus musculus GN=Adk PE=1 SV=2 #
AQTPIPNLYLTGQDIFTC*GLMGALQGALLCSSAILK	1.2166	Q64FW2 All-trans-retinol 13#14-reductase OS=Mus musculus GN=Retsat PE=1 SV=3 #
GYGC*AGVSSVAYGLLTR	1.2031	A0A0A0MQ68 Glutaryl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Gcdh PE=1 SV=1 # Q60759 Glutaryl-CoA dehydrogenase# mitochondrial OS=Mus musculus GN=Gcdh PE=1 SV=2 #
LGTMEELANLATFLC*SDYASWINGAVIR	1.1978	Q9CQ62 2#4-dienoyl-CoA reductase# mitochondrial OS=Mus musculus GN=Decr1 PE=1 SV=1 # Q4FJK0 2#4-dienoyl-CoA reductase# mitochondrial OS=Mus musculus GN=Decr1 PE=1 SV=1 #
ILC*GEGVDQLSLPLR	1.1559	Q8BH00 Aldehyde dehydrogenase family 8 member A1 OS=Mus musculus GN=Aldh8a1 PE=1 SV=1 #
STC*TINYSTSLPLAQGIK	1.1519	Q9DBF1-2 Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Mus musculus GN=Aldh7a1 # Q9DBF1 Alpha-aminoadipic semialdehyde dehydrogenase OS=Mus musculus GN=Aldh7a1 PE=1 SV=4 #
YWLQNPGELQRPSFSAMPVLANPAATAAC*CR	1.1452	Q91XE4 N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming) OS=Mus musculus GN=Acy3 PE=1 SV=1 #
C*KHFELGGDK	1.1444	P83882 60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=1 SV=2 # Q5M9P1 60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=1 SV=1 #
CPC*LPLLSPSLLDVPCR	1.1438	F8VPN4 Protein Agl OS=Mus musculus GN=Agl PE=1 SV=1 #
AHQLVLPPC*DVVIK	1.1414	Q6A0A9 Constitutive coactivator of PPAR-gamma-like protein 1 OS=Mus musculus GN=FAM120A PE=1 SV=2 #
WLHC*MTDDPPTTNPPTAR	1.1367	Q7TMF3 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Mus musculus GN=Ndufa12 PE=1 SV=2 # A0A0R4J275 MCG11204# isoform CRA_b OS=Mus musculus GN=Ndufa12 PE=1 SV=1 #
DYNFVNGSC*MLYEANHVR	1.1277	Q9DBB8 Trans-1#2-dihydrobenzene-1#2-diol dehydrogenase OS=Mus musculus GN=Dhdh PE=1 SV=1 #
SPLIIFSDC*NMENAVK	1.1272	Q3U367 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 # Q9JLJ2 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 #
HLDVVPAQPVAPAC*PVLVLVGQHDSPEFHR	1.0945	Q8K4H1-2 Isoform 2 of Kynurenine formamidase OS=Mus musculus GN=Afmid # Q8K4H1 Kynurenine formamidase OS=Mus musculus GN=Afmid PE=1 SV=1 # B1AQL0 Kynurenine formamidase (Fragment) OS=Mus musculus GN=Afmid PE=1 SV=1 #
THLC*DVEIPGQGPMR	1.0760	Q8VDK1 Nitrilase homolog 1 OS=Mus musculus GN=Nit1 PE=1 SV=2 # Q8VDK1-2 Isoform 2 of Nitrilase homolog 1 OS=Mus musculus GN=Nit1 #
C*EMASTGEVACFGEGIHTAFLK	1.0725	Q8C196 Carbamoyl-phosphate synthase [ammonia]# mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 #
FCCVDVLEILPYLSC*LTASDQDR	1.0546	Q8VCF0 Mitochondrial antiviral-signaling protein OS=Mus musculus GN=Mavs PE=1 SV=1 #
SSGLNLC*TGTGSK	1.0407	Q8C5H8 NAD kinase 2# mitochondrial OS=Mus musculus GN=Nadk2 PE=1 SV=2 #

Peptide	L/H Ratio	Protein
GC*LLYGPPGTGK	1.0359	Q14AQ1 26S protease regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1 # P62334 26S protease regulatory subunit 10B OS=Mus musculus GN=Psmc6 PE=1 SV=1 #
IWEFYGSTEGNVGLMNYVGHC*GAVGR	1.0306	Q4LDG0 Bile acyl-CoA synthetase OS=Mus musculus GN=Slc27a5 PE=1 SV=2 #
ILAFPC*NQFGR	1.0146	S4R1E5 Glutathione peroxidase OS=Mus musculus GN=Gpx4 PE=1 SV=1 # O70325 Phospholipid hydroperoxide glutathione peroxidase# mitochondrial OS=Mus musculus GN=Gpx4 PE=1 SV=4 # Q76LV0 Glutathione peroxidase OS=Mus musculus GN=Gpx4 PE=1 SV=2 # O70325-2 Isoform Cytoplasmic of Phospholipid hydroperoxide glutathione peroxidase# mitochondrial OS=Mus musculus GN=Gpx4 #
GWGLYC*AGK	1.0031	Q64105 Sepiapterin reductase OS=Mus musculus GN=Spr PE=1 SV=1 #
AVLLQSPPPC*ISQWR	0.9879	Q3U5Q7 UMP-CMP kinase 2# mitochondrial OS=Mus musculus GN=Cmpk2 PE=1 SV=2 #
VFIMDNC*EELIPEYLNFIR	0.9233	Q80Y52 Heat shock protein 90# alpha (Cytosolic)# class A member 1 OS=Mus musculus GN=Hsp90aa1 PE=1 SV=2 # P07901 Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4 #
AVQC*LNTSSK	0.8626	A2AN08-5 Isoform 5 of E3 ubiquitin-protein ligase UBR4 OS=Mus musculus GN=Ubr4 # A2AN08 E3 ubiquitin-protein ligase UBR4 OS=Mus musculus GN=Ubr4 PE=1 SV=1 # A2AN08-3 Isoform 3 of E3 ubiquitin-protein ligase UBR4 OS=Mus musculus GN=Ubr4 #
WFTPEAEFPLC*GHATLASAAVLFQK	0.8534	Q9CXN7 Phenazine biosynthesis-like domain-containing protein 2 OS=Mus musculus GN=Pbld2 PE=1 SV=1 #
AHNC*TR	0.8210	P58710 L-gulonolactone oxidase OS=Mus musculus GN=Gulo PE=1 SV=3 #
VLLSICSLLC*DPNPDDPLVPEIAR	0.8098	P62838 Ubiquitin-conjugating enzyme E2 D2 OS=Mus musculus GN=Ube2d2 PE=1 SV=1 # A0A0G2JGL0 Ubiquitin-conjugating enzyme E2 D3 OS=Mus musculus GN=Ube2d3 PE=1 SV=1 # P61079 Ubiquitin-conjugating enzyme E2 D3 OS=Mus musculus GN=Ube2d3 PE=1 SV=1 # Q3UT95 MCG121966 OS=Mus musculus GN=Ube2d2a PE=1 SV=1 # Q4QQL2 MCG22362# isoform CRA_a OS=Mus musculus GN=Ube2d3 PE=1 SV=1 # A0A0G2JE32 Ubiquitin-conjugating enzyme E2 D3 (Fragment) OS=Mus musculus GN=Ube2d3 PE=1 SV=1 #
PYEC*GICGRTYNHVSSLIR	0.7284	H9KUY5 Zinc finger protein 865 OS=Mus musculus GN=Zfp865 PE=1 SV=1 # Q3U3I9 Zinc finger protein 865 OS=Mus musculus GN=Znf865 PE=2 SV=1 #
SDFNLENLAIC*GSNLFTAGTETTSTTLR	0.6702	E9Q5K4 Protein Cyp2c44 OS=Mus musculus GN=Cyp2c44 PE=1 SV=1 #
AVTLQGNLDPC*ALYASEEEIGR	0.6605	P70697 Uroporphyrinogen decarboxylase OS=Mus musculus GN=Urod PE=1 SV=2 #
NC*PHVVVGTPGR	0.6438	Q8VDW0 ATP-dependent RNA helicase DDX39A OS=Mus musculus GN=Ddx39a PE=1 SV=1 #
SVPFLPLLGGC*VDDTILSR	0.6243	Q3TBW2 39S ribosomal protein L10# mitochondrial OS=Mus musculus GN=Mrpl10 PE=1 SV=2 #
ILDIAC*WVHHK	0.5865	Q3UCD9 Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1 # P18242 Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1 # F8WIR1 Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1 #
ASC*TTNC*LSPLAKVIHDNFGIVEGLMTTVHAITATQK	0.5310	S4R1W1 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm3839 PE=1 SV=1 #
C*WSSDTYNPVPGVMHGVPSSNNYQGGFGTTLMAK	0.5270	Q99L13 3-hydroxyisobutyrate dehydrogenase# mitochondrial OS=Mus musculus GN=Hibadh PE=1 SV=1 #
VTDKLTPIHDHIFCC*R	0.5260	Q60692 Proteasome subunit beta type-6 OS=Mus musculus GN=Psmb6 PE=1 SV=3 #
ISGADINSIC*QESGMLAVR	0.5153	P54775 26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=2 #
DNTIEHLLPLFLAQLKDEC*P	0.5091	Q76MZ3 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3 #

Peptide	L/H Ratio	Protein
SLEAAC*LALDVGYR	0.5021	Q8VC28 Aldo-keto reductase family 1 member C13 OS=Mus musculus GN=Akr1c13 PE=1 SV=2 # Q9JLI0 Aldo-keto reductase a OS=Mus musculus GN=Akr1c12 PE=1 SV=1 #
IGEIVAEMDVPLHC*R	0.4537	Q9DB26 Phytanoyl-CoA dioxygenase domain-containing protein 1 OS=Mus musculus GN=Phyhd1 PE=1 SV=2 # A0A0R4J137 Phytanoyl-CoA dioxygenase domain-containing protein 1 OS=Mus musculus GN=Phyhd1 PE=1 SV=1 # A2AQZ2 Phytanoyl-CoA dioxygenase domain-containing protein 1 (Fragment) OS=Mus musculus GN=Phyhd1 PE=1 SV=1 #
C*LNNLAASQLK	0.3235	O35465 Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Mus musculus GN=Fkbp8 PE=1 SV=2 # O35465-2 Isoform 2 of Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Mus musculus GN=Fkbp8 #
LFQLVMKGLLYEC*CVEFCQSK	0.1952	Q8CGF6 WD repeat-containing protein 47 OS=Mus musculus GN=Wdr47 PE=1 SV=2 #
AVC*MLSNTTAIAEAWAR	0.1917	A0A0A0MQA5 Tubulin alpha-4A chain (Fragment) OS=Mus musculus GN=Tuba4a PE=1 SV=1 # P68368 Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 #
VC*HTDAYTLSGADPEGC*FPVILGHEGAGIVESVGEGVTK	0.1823	Q6P5I3 S-(hydroxymethyl)glutathione dehydrogenase OS=Mus musculus GN=Adh5 PE=1 SV=2 # P28474 Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3 #
LC*PPVPGQALMGMVVSPPTPSEPSFK	0.1690	Q566C3 Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=1 SV=1 # Q8QZR5 Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=1 SV=3 #
C*LSSATDPQTK	0.1632	Q3UPL0-2 Isoform 2 of Protein transport protein Sec31A OS=Mus musculus GN=Sec31a # Q3UPL0 Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2 #
EASGLVLLSSC*PQTASR	0.1410	Q14AI6 RNA pseudouridylate synthase domain-containing protein 3 OS=Mus musculus GN=Rpusd3 PE=2 SV=1 # F6WLR1 RNA pseudouridylate synthase domain-containing protein 3 (Fragment) OS=Mus musculus GN=Rpusd3 PE=1 SV=1 # B7ZMQ0 MCG132976# isoform CRA_b OS=Mus musculus GN=Rpusd3 PE=1 SV=1 # Q14AI6-2 Isoform 2 of RNA pseudouridylate synthase domain-containing protein 3 OS=Mus musculus GN=Rpusd3 # F6UDW0 RNA pseudouridylate synthase domain-containing protein 3 (Fragment) OS=Mus musculus GN=Rpusd3 PE=1 SV=1 #
TPPLGSAQVPLADC*VLTFLAMECACPDIDTYR	0.1343	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=1 SV=1 #
C*IPSQAVAFTTYELMK	0.1107	Q8C0K5 Graves disease carrier protein homolog OS=Mus musculus GN=Slc25a16 PE=1 SV=1 #

Table 7. Overlapping Protein Targets with L/H ratio >1.5 from Mouse Livers Treated in vivo with Glyphosate or in vitro with Glyosylate

Peptide	Glyphosate L/H Ratio	Glyoxylate L/H Ratio	Protein
YLLQYQEPIPCEQLVTALC*DIK	8.0577	2.3667	E9PW69 Proteasome subunit alpha type OS=Mus musculus GN=Psma4 PE=3 SV=1 , Q9R1P0 Proteasome subunit alpha type-4 OS=Mus musculus GN=Psma4 PE=1 SV=1 ,
C*GPGYPTPLEAMK	6.7644	3.6819	Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 ,
DC*LIPMGITSENVAER	4.4071	7.8169	Q3UKM0 MCG21883, isoform CRA_e OS=Mus musculus GN=Acaa1b PE=2 SV=1 , Q8VCH0 3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1 ,
MISQSC*LSNIEK	4.2894	2.8828	Q8BGL3 RIKEN cDNA 2810007J24, isoform CRA_a OS=Mus musculus GN=2810007J24Rik PE=2 SV=1 ,
GGSVQVLEDQELTC*QPEPLVVK	4.1520	3.8361	P17563 Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2 , Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 ,
SFSIASDPTSASSC*YLEEHVSK	3.9389	2.2630	P00186 Cytochrome P450 1A2 OS=Mus musculus GN=Cyp1a2 PE=1 SV=1 , B6VGH4 Cytochrome P450 family 1 subfamily a polypeptide 2 OS=Mus musculus GN=Cyp1a2 PE=3 SV=1 ,
TIGGGDDSFTTFFC*ETGAGK	3.6399	1.7755	P68368 Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 ,
FLHDPSATQGFVGC*ALSSNIQR	3.5596	3.3153	P17563 Selenium-binding protein 1 OS=Mus musculus GN=Selenbp1 PE=1 SV=2 , Q63836 Selenium-binding protein 2 OS=Mus musculus GN=Selenbp2 PE=1 SV=2 ,
LPFIYGEEC*QVTSTTVK	3.4415	4.0456	Q61694 3 beta-hydroxysteroid dehydrogenase type 5 OS=Mus musculus GN=Hsd3b5 PE=1 SV=4 ,
GALMANFLTQGQVC*CNGTR	3.4413	1.7546	Q3U367 Putative uncharacterized protein OS=Mus musculus GN=Aldh9a1 PE=2 SV=1 , Q9JLJ2 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 ,
LNVIC*PGFVDTPILESIEKEENMGQYIEYK	3.3847	3.0938	Q8VCC1 15-hydroxyprostaglandin dehydrogenase [NAD+] OS=Mus musculus GN=Hpgd PE=2 SV=1 ,
C*VIAEGDLGIVQK	3.1650	4.6300	Q9Z0S1 3'(2'),5'-bisphosphate nucleotidase 1 OS=Mus musculus GN=Bpnt1 PE=1 SV=2 ,
QCFLYMVC*QTAK	3.1577	4.4689	Q9DCY0 Glycine N-acyltransferase-like protein Keg1 OS=Mus musculus GN=Keg1 PE=1 SV=1 ,
YIIWSPVC*R	3.1361	3.1926	P11352 Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2 ,
QC*SSGLQAVANIAGGIR	3.1143	1.4673	Q3UKM0 MCG21883, isoform CRA_e OS=Mus musculus GN=Acaa1b PE=2 SV=1 , Q8VCH0 3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1 ,
EAPFTHFDPSCLFPAC*R	3.0570	6.0705	P16015 Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3 ,
SGANVLICGPNGC*GK	2.9558	6.1475	P55096 ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=2 ,
LC*DFGVSGQLIDSMANSFVGTR	2.7443	2.6354	P31938 Dual specificity mitogen-activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=1 SV=2 , Q3TMJ8 Mitogen activated protein kinase kinase 1 OS=Mus musculus GN=Map2k1 PE=2 SV=1 ,
EEVVTIDTWMQGLLKPTC*LYGQLPK	2.7169	2.1385	P19157 Glutathione S-transferase P 1 OS=Mus musculus GN=Gstp1 PE=1 SV=2 ,
AC*GANLPENFSISQIFSQAMAAR	2.6822	2.3670	P34914 Epoxide hydrolase 2 OS=Mus musculus GN=Ephx2 PE=1 SV=2 ,
NGGTLQTCALRPMC*IYGER	2.4970	2.3732	P26150 3 beta-hydroxysteroid dehydrogenase/Delta 5-- 4-isomerase type 3 OS=Mus musculus GN=Hsd3b3 PE=2 SV=3 , B1ARN8 Hydroxysteroid dehydrogenase-2, delta<5 -3-beta OS=Mus musculus GN=Hsd3b3 PE=3 SV=1 ,

Peptide	Glyphosate L/H Ratio	Glyoxylate L/H Ratio	Protein
INILINCAAGNFLC*PASALSFNAFK	2.4832	4.0884	Q9WV68 Peroxisomal 2,4-dienoyl-CoA reductase OS=Mus musculus GN=Decr2 PE=1 SV=1 , Q3UVJ7 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal OS=Mus musculus GN=Decr2 PE=2 SV=1 ,
STLTDSLVC*K	2.4585	5.6252	P58252 Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2 ,
DIILVSYC*TLGSSR	2.3926	5.3386	Q91WT7 3-alpha-hydroxysteroid dehydrogenase type 1 OS=Mus musculus GN=Akr1c14 PE=2 SV=1 ,
YKPVCNQVEC*HLYLNQSQMLDYCK	2.3482	2.5942	Q91WT7 3-alpha-hydroxysteroid dehydrogenase type 1 OS=Mus musculus GN=Akr1c14 PE=2 SV=1 ,
VFSANSTAAC*TELAK	2.3103	5.1655	Q9D0M1 Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Mus musculus GN=Prpsap1 PE=1 SV=1 , B1AT82 MCG6846, isoform CRA_c OS=Mus musculus GN=Prpsap1 PE=4 SV=1 ,
AVQMGMSSVFFNKGENC*IAAGR	2.2977	3.3448	Q8R0Y6 Aldehyde dehydrogenase family 1 member L1 OS=Mus musculus GN=Aldh1l1 PE=2 SV=1 ,
GLVVLGFPC*NQFGHQENGKNEEILNSLK	2.2486	3.0874	P11352 Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2 ,
LGPNYLQIPVNC*PYR	2.2340	1.8300	P24270 Catalase OS=Mus musculus GN=Cat PE=1 SV=4 ,
C*MPTFQFYK	2.2288	6.3410	P10639 Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3 , A2AV97 Thioredoxin OS=Mus musculus GN=Txn1 PE=3 SV=1 ,
LVVPATQC*GSLIGK	2.2271	1.9667	P60335 Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 ,
C*LTQQAVALQR	2.2174	14.1924	Q5SW19-3 Isoform 3 of Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 , Q5SW19 Protein KIAA0664 OS=Mus musculus GN=Kiaa0664 PE=2 SV=2 ,
C*LQTDMVDITK	2.2111	2.2475	Q9JIZ0 Probable N-acetyltransferase CML1 OS=Mus musculus GN=Cml1 PE=1 SV=1 , E9PUL7 Uncharacterized protein OS=Mus musculus GN=Cml1 PE=4 SV=1 ,
INISEGNC*PER	2.2085	2.8353	Q61990 Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1 , P60335 Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1 , Q61990-2 Isoform 2 of Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 ,
LEAPC*QQWMELR	2.2068	3.5160	Q9CRB3 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1 SV=1 ,
VGGIC*TVIQTK	2.1579	2.5939	Q8VCB3 Glycogen [starch] synthase, liver OS=Mus musculus GN=Gys2 PE=1 SV=2 ,
VNPLGGAIALGHPLGC*TGAR	2.1491	1.9311	Q921H8 3-ketoacyl-CoA thiolase A, peroxisomal OS=Mus musculus GN=Acaa1a PE=2 SV=1 , Q3UKM0 MCG21883, isoform CRA_e OS=Mus musculus GN=Acaa1b PE=2 SV=1 , Q8VCH0 3-ketoacyl-CoA thiolase B, peroxisomal OS=Mus musculus GN=Acaa1b PE=2 SV=1 ,
YQALGAELNVLPFC*SQFIPMEVINAPR	2.1482	6.5440	Q8R0Y6 Aldehyde dehydrogenase family 1 member L1 OS=Mus musculus GN=Aldh1l1 PE=2 SV=1 ,
GLATFC*LDK	2.1294	2.4855	Q80UU9 Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2 , Q3TFP8 Uncharacterized protein OS=Mus musculus GN=Pgrmc1 PE=2 SV=1 , Q3TXU8 Progesterone receptor membrane component 1 OS=Mus musculus GN=Pgrmc1 PE=2 SV=1 , O55022 Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4 ,
SGLTPNDVDVIELHDC*FSVNELITYEALGLCPEGQGGTLVDRGDNTYGGK	2.1073	1.9624	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 ,
GSEVNVIGIGTSVVTC*PK	2.1059	2.4173	Q8CC86 Nicotinate phosphoribosyltransferase OS=Mus musculus GN=Naprt1 PE=2 SV=1 ,

Peptide	Glyphosate L/H Ratio	Glyoxylate L/H Ratio	Protein
TVYTFVGQPEC*VVEGALHAAR	2.0849	2.5809	Q91XD4 Formimidoyltransferase-cyclodeaminase OS=Mus musculus GN=Ftcd PE=1 SV=1 ,
GHSELDTAFMYC*DGQSENILGGLGLGLGSGDCTVK	2.0789	1.4704	Q8CG76 Aflatoxin B1 aldehyde reductase member 2 OS=Mus musculus GN=Akr7a2 PE=1 SV=3 ,
IQEEAGC*LIK	2.0561	4.4639	P56593 Cytochrome P450 2A12 OS=Mus musculus GN=Cyp2a12 PE=1 SV=2 ,
NINNDTTYC*IK	2.0332	7.2246	Q99KR3 Beta-lactamase-like protein 2 OS=Mus musculus GN=Lactb2 PE=1 SV=1 ,
TAC*QEYTVTEFQPLYYVAESFNDAK	2.0332	3.1090	P16331 Phenylalanine-4-hydroxylase OS=Mus musculus GN=Pah PE=1 SV=4 ,
QVADEGDALVAGGVSQTPSYLSC*K	2.0269	4.9154	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1 ,
SAGAC*TAAAFLR	2.0215	1.8463	Q9CPY7-2 Isoform 2 of Cytosol aminopeptidase OS=Mus musculus GN=Lap3 , Q9CPY7 Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3 ,
LILADALC*YAHTFNPK	2.0063	3.2251	Q9CPY7-2 Isoform 2 of Cytosol aminopeptidase OS=Mus musculus GN=Lap3 , Q9CPY7 Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3 ,
LTTPTYGDLNHLVSATMSGVTTC*LR	2.0039	3.4950	Q9D6F9 Tubulin beta-4 chain OS=Mus musculus GN=Tubb4 PE=1 SV=3 , P68372 Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1 , Q9CWF2 Tubulin beta-2B chain OS=Mus musculus GN=Tubb2b PE=1 SV=1 , B2RSN3 MCG1395 OS=Mus musculus GN=Tubb2b PE=2 SV=1 ,
LC*NPPVNAISPTVITEVR	2.0035	6.4565	Q9DBM2 Peroxisomal bifunctional enzyme OS=Mus musculus GN=Ehhadh PE=1 SV=4 ,
AIYHSLGLTGIPIINVNNNC*STGSTALFMAH	1.9974	2.8510	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 ,
GTNTGVWVGVSGSEASEALSRDPETLLGYSMVGC*QR	1.9939	5.0715	P19096 Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2 ,
DNSIIAQATSAAEAFC*AVK	1.9863	1.7878	Q61635 GTP-binding protein OS=Mus musculus GN=Ifi47 PE=2 SV=1 ,
TWYVQATC*ATQGTGLYEGLDWLSNELSK	1.9847	2.6441	P61750 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=2 SV=2 , Q14BR4 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=2 SV=1 ,
SVFPEVDIVVPGIC*IANTDTR	1.9566	2.0070	Q8C165 Probable carboxypeptidase PM20D1 OS=Mus musculus GN=Pm20d1 PE=2 SV=1 ,
TCSC*LDENYYK	1.9403	4.6106	O09173 Homogentisate 1,2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2 ,
VIEINPYLLGTMSGC*AADCQYWER	1.9259	2.0976	P28063 Proteasome subunit beta type-8 OS=Mus musculus GN=Psmb8 PE=1 SV=2 ,
ILQACGGNSLGSYSASQGVNC*IR	1.9081	3.3954	Q8BGT5 Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=2 SV=1 ,
NWYVQPSC*ATSGDGLYEGLTWLTSNYK	1.9014	2.3284	Q3U0D7 Putative uncharacterized protein OS=Mus musculus GN=Arf6 PE=2 SV=1 , P62331 ADP-ribosylation factor 6 OS=Mus musculus GN=Arf6 PE=1 SV=2 ,
ALTNHTVYC*STK	1.8954	4.9201	Q91X52 L-xylulose reductase OS=Mus musculus GN=Dcxr PE=2 SV=2 , A2AC15 Dicarbonyl L-xylulose reductase OS=Mus musculus GN=Dcxr PE=3 SV=1 ,
AAVEEGIVLGGGC*ALLR	1.8876	2.2535	P63038 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 ,

Peptide	Glyphosate L/H Ratio	Glyoxylate L/H Ratio	Protein
LSTPLQTNC*TASESVVQSPSVATTASPATK	1.8863	6.7600	P31230 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Mus musculus GN=Aimp1 PE=1 SV=2 , Q3UZG4 Putative uncharacterized protein OS=Mus musculus GN=Aimp1 PE=2 SV=1 ,
TPPLGSAQVPLADCVLTFLAMEC*ACPDIDTYR	1.8857	1.8458	P40936 Indolethylamine N-methyltransferase OS=Mus musculus GN=Inmt PE=2 SV=1 ,
ALEDAQIPYSAVEQAC*VGYVYGDSTSGQR	1.8657	4.0698	P32020 Non-specific lipid-transfer protein OS=Mus musculus GN=Scp2 PE=1 SV=3 ,
WFTPVSEVPLC*GHATLASAAVLFHK	1.8636	2.7162	Q9DCG6 Phenazine biosynthesis-like domain-containing protein 1 OS=Mus musculus GN=Pbld1 PE=2 SV=2 ,
IFSYEC*R	1.8625	2.0748	P58710 L-gulonolactone oxidase OS=Mus musculus GN=Gulo PE=1 SV=3 ,
VIVVGNPANTNC*LTASK	1.8596	4.9476	P14152 Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3 ,
LLEETGIC*VVPGSGFGQR	1.8479	1.8732	Q8BGT5 Alanine aminotransferase 2 OS=Mus musculus GN=Gpt2 PE=2 SV=1 ,
VC*FGIQLLNAVAR	1.8470	2.4596	E9Q3B9 Uncharacterized protein OS=Mus musculus GN=Mgll PE=4 SV=1 , O35678 Monoglyceride lipase OS=Mus musculus GN=Mgll PE=1 SV=1 , D3YYS6 Uncharacterized protein OS=Mus musculus GN=Mgll PE=4 SV=1 ,
ELLTEFGYKGEETPVIVGSALC*ALEQR	1.8444	3.8026	Q8BFR5-2 Isoform 2 of Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm , Q8BFR5 Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1 ,
ISLGLPVGAVINC*ADNTGAK	1.8389	1.9227	A2A6F9 Ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=3 SV=1 , P62830 60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=1 SV=1 ,
SGQGAFGNMC*R	1.8375	2.7503	Q564E8 Ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=2 SV=1 , Q9D8E6 60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3 ,
DIGQC*LTNFSK	1.8228	2.0814	E9Q7C8 Uncharacterized protein OS=Mus musculus GN=Cyp2c40 PE=3 SV=1 , Q569X9 Cytochrome P450, family 2, subfamily c, polypeptide 67 OS=Mus musculus GN=Cyp2c67 PE=2 SV=1 , P56657 Cytochrome P450 2C40 OS=Mus musculus GN=Cyp2c40 PE=2 SV=2 , E9PXC3 Uncharacterized protein OS=Mus musculus GN=Cyp2c69 PE=3 SV=1 , E9QAE5 Uncharacterized protein OS=Mus musculus GN=Cyp2c68 PE=3 SV=1 ,
VCLIGC*GFSTGYGSAVK	1.8111	2.4979	Q3UKA4 Alcohol dehydrogenase 1 (Class I), isoform CRA_c OS=Mus musculus GN=Adh1 PE=2 SV=1 , P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2 ,
VVGYFVSGC*DPTIMGIGPVPAINGALK	1.8071	2.6899	Q8BWT1 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 ,
AQGTGELTQLLNSLC*TAIK	1.8044	2.7560	Q9QXD6 Fructose-1,6-bisphosphatase 1 OS=Mus musculus GN=Fbp1 PE=2 SV=3 ,
DAEVVLC*GGTESMSQSPYCVR	1.8012	4.7093	Q8BWT1 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3 ,
VALVC*TGSEGSSITNSQLDAR	1.7992	3.8504	Q4LDG0 Bile acyl-CoA synthetase OS=Mus musculus GN=Slc27a5 PE=2 SV=2 ,
VDEFPLC*GHMVSDEYEQLSSEALEAAR	1.7802	4.0486	P86048 60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=1 , Q6ZWV3 60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3 ,
YCVGDEVSMADVC*LVPQVANAER	1.7667	2.4233	Q9WVL0 Maleylacetoacetate isomerase OS=Mus musculus GN=Gstz1 PE=1 SV=1 ,
MEC*CDVPAETLYDVLHDIEYR	1.7576	2.7675	Q66JR2 Stard10 protein (Fragment) OS=Mus musculus GN=Stard10 PE=2 SV=1 , E9PVP0 Uncharacterized protein OS=Mus musculus GN=Stard10 PE=4 SV=1 , Q0VG22 START domain containing 10 OS=Mus musculus GN=Stard10 PE=2 SV=1 , Q9JMD3 PCTP-like

Peptide	Glyphosate L/H Ratio	Glyoxylate L/H Ratio	Protein
			protein OS=Mus musculus GN=Stard10 PE=1 SV=1 , E9PVT5 Uncharacterized protein OS=Mus musculus GN=Stard10 PE=4 SV=1 ,
QASVGAGIPYSVPAWSCQMIC*GSGLK	1.7576	2.0463	Q8CAY6 Acetyl-CoA acetyltransferase, cytosolic OS=Mus musculus GN=Acat2 PE=1 SV=2 , Q80X81 Acetyl-Coenzyme A acetyltransferase 3 OS=Mus musculus GN=Acat3 PE=2 SV=1 ,
VLTLDTMNPC*VR	1.7562	11.1320	Q8QZR5 Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=2 SV=3 , Q566C3 Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=2 SV=1 ,
VFANPEDC*AGFGK	1.7548	2.2588	Q53ZD4 Microsomal glutathione S-transferase 1 OS=Mus musculus GN=Mgst1 PE=2 SV=1 , Q91VS7 Microsomal glutathione S-transferase 1 OS=Mus musculus GN=Mgst1 PE=1 SV=3 , E9QJW0 Uncharacterized protein OS=Mus musculus GN=Mgst1 PE=4 SV=1 ,
C*PGLLTPSQIKPGTYK	1.7466	2.7175	Q9CRB3 5-hydroxyisourate hydrolase OS=Mus musculus GN=Urah PE=1 SV=1 ,
GEGILC*GTPEEVWDCIKPVASGLR	1.7389	3.9299	D3YU00 StAR-related lipid transfer (START) domain containing 5, isoform CRA_a OS=Mus musculus GN=Stard5 PE=4 SV=1 , Q9EPQ7 StAR-related lipid transfer protein 5 OS=Mus musculus GN=Stard5 PE=2 SV=2 ,
VILSSSSSC*LLPSK	1.7287	6.2689	A7VMV2 Crystallin, lamda 1, isoform CRA_a OS=Mus musculus GN=Cryl1 PE=2 SV=1 , Q99KP3 Lambda-crystallin homolog OS=Mus musculus GN=Cryl1 PE=2 SV=3 ,
C*MALSTAILVGEAK	1.7227	1.9406	Q9EQ20 Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Mus musculus GN=Aldh6a1 PE=1 SV=1 , Q8K0L1 Aldh6a1 protein OS=Mus musculus GN=Aldh6a1 PE=2 SV=1 ,
VVMALGDYMGASCHAC*IGGTNVR	1.7198	4.9933	Q5F2A7 Eukaryotic translation initiation factor 4A1 OS=Mus musculus GN=Eif4a1 PE=2 SV=1 , P60843 Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=2 SV=1 ,
ILATAVC*HTDAYTLSGADPEGCFPVILGHEGAGIVESVGEGVTK	1.7139	1.5476	Q6P5I3 Alcohol dehydrogenase 5 (Class III), chi polypeptide OS=Mus musculus GN=Adh5 PE=2 SV=2 , P28474 Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3 ,
VNEAAC*DIAR	1.7127	4.1678	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1 ,
IIYGGSVTGATC*K	1.7092	6.8871	P17751 Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3 ,
ASVGFGGSC*FQK	1.7067	2.7601	D3Z3F7 Uncharacterized protein OS=Mus musculus GN=Ugdh PE=4 SV=1 , O70475 UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1 , Q3TS38 UDP-glucose dehydrogenase OS=Mus musculus GN=Ugdh PE=2 SV=1 ,
NIC*FTVWDVGGQDK	1.7052	3.2067	P84084 ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=2 SV=2 , P61750 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=2 SV=2 , Q14BR4 ADP-ribosylation factor 4 OS=Mus musculus GN=Arf4 PE=2 SV=1 ,
GLIAAIC*AGPTALLAHEVGFGCK	1.7040	7.3181	Q99LX0 Protein DJ-1 OS=Mus musculus GN=Park7 PE=1 SV=1 , A2A813 Parkinson disease (Autosomal recessive, early onset) 7 OS=Mus musculus GN=Park7 PE=4 SV=1 , A2A815 Parkinson disease (Autosomal recessive, early onset) 7 (Fragment) OS=Mus musculus GN=Park7 PE=4 SV=1 ,
SGDAAIVDMVPGKPMC*VESFSDYPPLGR	1.7036	2.2678	P10126 Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3 , Q58E64 Elongation factor 1-alpha OS=Mus musculus GN=Eef1a1 PE=2 SV=1 ,
VLVC*GAGPVGMVTLLVAK	1.6928	2.9221	Q64442 Sorbitol dehydrogenase OS=Mus musculus GN=Sord PE=1 SV=3 ,
NMSVHLSPC*FR	1.6894	2.2812	D3Z3M6 MCG49907 OS=Mus musculus GN=Gm9808 PE=3 SV=1 , P62281 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3 , Q3UC02 MCG23457 OS=Mus musculus GN=Rps11 PE=2 SV=1 , E9PXE7 Uncharacterized protein OS=Mus musculus GN=Rps11 PE=3 SV=1 ,

Peptide	Glyphosate L/H Ratio	Glyoxylate L/H Ratio	Protein
IGPALSC*GNTVVVKPAEQTPLTALHLASLIK	1.6801	2.6604	P24549 Retinal dehydrogenase 1 OS=Mus musculus GN=Aldh1a1 PE=1 SV=5 ,
AVLEALGSC*LNNK	1.6795	2.8427	P50431 Serine hydroxymethyltransferase, cytosolic OS=Mus musculus GN=Shmt1 PE=1 SV=3 ,
CPALYWLSGLTC*TEQNFISK	1.6790	3.1222	Q9R0P3 S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=2 SV=1 ,
ITAFVPNDGC*LNFIEENDEVLVAGFGR	1.6734	2.5609	Q9CZI5 Uncharacterized protein OS=Mus musculus GN=Rps23 PE=2 SV=1 , P62267 40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3 ,
FYDVALDTGDKVVQC*GR	1.6723	2.7297	Q9DBE0 Cysteine sulfinic acid decarboxylase OS=Mus musculus GN=Csad PE=2 SV=1 ,
AERPDGLILGMGGQTALNC*GVELFK	1.6685	6.7491	Q8C196 Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 ,
AIQSLTDTC*SDDLSVVTDCMEHALTACHPR	1.6606	1.7343	O88451 Retinol dehydrogenase 7 OS=Mus musculus GN=Rdh7 PE=2 SV=1 ,
GVLLYGPPGC*GK	1.6380	3.9026	Q9D5T0 ATPase family AAA domain-containing protein 1 OS=Mus musculus GN=Atad1 PE=1 SV=1 ,
C*VEELPEWNFDGSSTFQSEGSNSDMYLHPVAMFR	1.6367	4.5660	P15105 Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6 ,
LC*YVALDFEQEMATAASSSSLEK	1.6357	2.1650	P60710 Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 , P63260 Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 , B2RRX1 Actin, beta OS=Mus musculus GN=Actb PE=2 SV=1 , Q4KL81 Actin, gamma, cytoplasmic 1 OS=Mus musculus GN=Actg1 PE=2 SV=1 ,
NQSFC*PTVNLDKLWTLVSEQTR	1.6240	2.6026	P14115 60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=5 , D3Z6J9 Uncharacterized protein OS=Mus musculus GN=Gm5908 PE=3 SV=1 ,
DVLSGDGFDAVICLGNSFAHLPDC*K	1.6214	2.7299	A9C489 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=3 SV=1 , Q9QXF8 Glycine N-methyltransferase OS=Mus musculus GN=Gnmt PE=1 SV=3 ,
GQNNPQVC*PYNLYAEQLSGSAFTCPR	1.6064	3.0355	O09173 Homogentisate 1,2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2 ,
AYLMSQPLAYHTPDC*GK	1.6018	2.6611	O35490 Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1 ,
AIVDALPPPC*ESACSLPTDVDK	1.5994	2.3459	Q9D819 Inorganic pyrophosphatase OS=Mus musculus GN=Ppa1 PE=1 SV=1 , Q4FK49 Pyp protein OS=Mus musculus GN=Ppa1 PE=2 SV=1 , E9Q5Z3 Uncharacterized protein OS=Mus musculus GN=Ppa1 PE=4 SV=1 ,
C*LLTTVDPDTGISDR	1.5986	2.4305	Q9CW42 MOSC domain-containing protein 1, mitochondrial OS=Mus musculus GN=Mosc1 PE=1 SV=2 , D3YZZ3 Uncharacterized protein OS=Mus musculus GN=Mosc1 PE=4 SV=1 ,
CPEALFQPSFLGMESC*GIHETTFNSIMK	1.5958	2.5534	P60710 Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 , P63260 Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 , B2RRX1 Actin, beta OS=Mus musculus GN=Actb PE=2 SV=1 , Q4KL81 Actin, gamma, cytoplasmic 1 OS=Mus musculus GN=Actg1 PE=2 SV=1 ,
C*GESPVWEEASQSLLFVDIPSK	1.5910	1.8531	Q64374 Regucalcin OS=Mus musculus GN=Rgn PE=1 SV=1 ,
AWVWNTHADFADEC*PKPELLAIR	1.5885	9.3504	P34022 Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2 ,
LTLLEVGC*GTGANFK	1.5884	1.7412	Q8C6B0 MCG20149, isoform CRA_a OS=Mus musculus GN=Mettl7a1 PE=2 SV=1 , Q5K4Q9 AAM-B protein OS=Mus musculus GN=Mettl7a1 PE=2 SV=1 ,

Peptide	Glyphosate L/H Ratio	Glyoxylate L/H Ratio	Protein
ASATGMIIMDSVEVPEENVLPNVSSLAGPFGC*LNTAR	1.5845	1.6704	Q60759 Glutaryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Gcdh PE=2 SV=2 ,
LTEGC*SFR	1.5650	1.8866	Q6ZWU9 40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3 , Q6ZWY3 40S ribosomal protein S27-like OS=Mus musculus GN=Rps27l PE=2 SV=3 , E9QAB4 Uncharacterized protein OS=Mus musculus GN=Gm17241 PE=3 SV=1 ,
C*MTEEIFGPVTCVVPFDSEEEVITR	1.5610	1.9323	Q8BH00 Aldehyde dehydrogenase family 8 member A1 OS=Mus musculus GN=Aldh8a1 PE=1 SV=1 ,
VPTPNVSVVDLTC*R	1.5584	3.0370	E9Q9E5 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10481 PE=3 SV=1 , E9QP42 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdhs PE=3 SV=1 , Q64467 Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Mus musculus GN=Gapdhs PE=1 SV=1 , E9PZH9 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10566 PE=3 SV=1 ,
VQQEIDEVIGQVQC*PEMADQAR	1.5427	2.3736	Q9JKY7 Cytochrome P450 CYP2D22 OS=Mus musculus GN=Cyp2d22 PE=2 SV=1 ,
ALANVNIGSLIC*NVGAGGPAPAAGAAPAGGAAPSTAAAPAEEK	1.5381	2.2919	Q58E35 MCG10168 OS=Mus musculus GN=Rplp1 PE=4 SV=1 , P47955 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1 ,
EVESVTPEHC*IFASNTSALPINQIAAVSK	1.5354	1.8331	Q8BMS1 Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1 ,
TGIQTSC*LCPVFVNTGFTK	1.5338	8.9175	A8Y5N6 Hydroxysteroid (17-beta) dehydrogenase 13 OS=Mus musculus GN=Hsd17b13 PE=3 SV=1 , A8Y5N5 Hydroxysteroid (17-beta) dehydrogenase 13 OS=Mus musculus GN=Hsd17b13 PE=3 SV=1 ,
VILITPPPLC*EAAWEK	1.5314	2.6506	Q9DB29 Isoamyl acetate-hydrolyzing esterase 1 homolog OS=Mus musculus GN=Iah1 PE=2 SV=1 ,
LNISFPATGC*QK	1.5241	3.6815	P62754 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1 , Q5BLK1 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=2 SV=1 ,
GVILTSEC*PGIFSAGLDLLEMYGR	1.5233	3.0359	Q8QZV3 Dci protein OS=Mus musculus GN=Eci1 PE=2 SV=1 ,
IPFLEFSC*PGVPPGLETLK	1.5218	1.9713	D3Z3G5 Uncharacterized protein OS=Mus musculus GN=Sult1a1 PE=4 SV=1 , Q91W19 Sulfotransferase family 1A, phenol-preferring, member 1 OS=Mus musculus GN=Sult1a1 PE=2 SV=1 , E9QNL5 Uncharacterized protein OS=Mus musculus GN=Sult1a1 PE=4 SV=1 , P52840 Sulfotransferase 1A1 OS=Mus musculus GN=Sult1a1 PE=2 SV=1 ,
GTPEQPQC*GFSNAVVQILR	1.5088	3.2601	Q80Y14 Glutaredoxin-related protein 5, mitochondrial OS=Mus musculus GN=Glrx5 PE=2 SV=2 ,
LLACIASRPGQC*GR	1.5051	2.3476	Q497E9 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=2 SV=1 , P62242 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2 , Q5SZV3 40S ribosomal protein S8 OS=Mus musculus GN=Gm11353 PE=3 SV=1 ,
VDLNSNGFIC*DYELHELFK	1.5042	1.5553	B1AX58 Plastin 3 (T-isoform) OS=Mus musculus GN=Pls3 PE=4 SV=1 , Q99K51 Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3 ,

Appendix 5. IsoTOP-ABPP profiling of DCTyne lysine-reactivity in mouse livers from mice treated with vehicle or glyphosate

Table 8 shows IsoTOP-ABPP analysis of lysine reactivity from in vivo exposure with glyphosate or vehicle. Proteomes were labeled with DCTyne, followed by appendage of a biotin-azide handle bearing a TEV recognition sequence and isotopically light (vehicle-treated) or heavy (glyphosate-treated) valine, combining of control and treated proteomes in a 1:1 ratio, avidin enrichment, tryptic digestion, release of modified peptides by TEV protease, and analysis by LC-MS/MS. Shown are modified peptides and their corresponding protein IDs that were quantified by measuring the light to heavy ratios of peptides. These tables are related to Figure 2-5.

Peptide	L/H Ratio	Protein	Protein ID
K*PWPEAQNFANSVACGSASPAELVQCLLQK	31.7276	Q8VCU1 Liver carboxylesterase 31-like OS=Mus musculus GN=Gm4738 PE=2 SV=1 ,	Gm4738
VVTIAPGLFATPLLTTLPEK*VR	3.7322	Q99N15 17beta-hydroxysteroid dehydrogenase type 10/short chain L-3-hydroxyacyl-CoA dehydrogenase OS=Mus musculus GN=Hsd17b10 PE=2 SV=1 , A2AFQ2 Hydroxysteroid (17-beta) dehydrogenase 10 OS=Mus musculus GN=Hsd17b10 PE=3 SV=1 ,	Hsd17b10
SFPFVSK*TLGVDFIDVATK	3.2656	Q8C196 Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 ,	Cps1
DFTPAAQAAFQK*VVAGVAAALAHK	3.2368	Beta-globin OS=Mus musculus GN=Hbb-b1 PE=3 SV=1 ,	Hbb-b1
K*FPLDPLITHVLPFEK	2.7982	Q3UKA4 Alcohol dehydrogenase 1 (Class I), isoform CRA_c OS=Mus musculus GN=Adh1 PE=2 SV=1 , P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2 ,	Adh1
ITSPLMEPSSIEK*IVEIDAHIGCAMSGLIADAK	2.5371	Q9Z2U1 Proteasome subunit alpha type-5 OS=Mus musculus GN=Psma5 PE=1 SV=1 , D3YX79 Proteasome subunit alpha type OS=Mus musculus GN=Gm8394 PE=3 SV=1 , Q3UPK6 Proteasome subunit alpha type OS=Mus musculus GN=Psma5 PE=2 SV=1 ,	Psma5
SSALASK*ATGYPLAFIAAK	2.4006	Q8C196 Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2 ,	Cps1
IHLSELMLEK*CPFPAGSDLAQK	1.8482	O54928 Suppressor of cytokine signaling 5 OS=Mus musculus GN=Socs5 PE=1 SV=2 ,	Socs5
SAPALACGNAMIFK*PSPFTPVSALLLAEIYTK	1.6520	Q3U367 Putative uncharacterized protein OS=Mus musculus GN=Aldh9a1 PE=2 SV=1 , Q9JLJ2 4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1 ,	Aldh9a1
LGPALATGNVVVMK*VAEQTPLTALYVANLIK	1.6108	Q544B1 Aldehyde dehydrogenase 2, mitochondrial, isoform CRA_b OS=Mus musculus GN=Aldh2 PE=2 SV=1 , P47738 Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1 ,	Aldh2
LDQGGAPLAGTNK*ETTIQGLDGLSER	1.6071	Q3UER1 Fructose-bisphosphate aldolase OS=Mus musculus GN=Aldob PE=2 SV=1 , Q91Y97 Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3 ,	Aldob
AAVSGLWGK*VNADEVGGEALGR	1.5949	Beta-globin OS=Mus musculus GN=Hbb-b1 PE=3 SV=1 ,	Hbb-b1
VITAFNDGLNHLDSLK*GTFASLSELHCDK	1.5779	Beta-globin OS=Mus musculus GN=Hbb-b1 PE=3 SV=1 ,	Hbb-b1
AALDGTPGMIGYGMAK*GAVHQLCQSLAGK	1.5696	D3YWR7 Uncharacterized protein OS=Mus musculus GN=Qdpr PE=4 SV=1 ,	Qdpr
AALDGTPGMIGYGMAK*GAVHQLCQSLAGK	1.5028	D3YWR7 Uncharacterized protein OS=Mus musculus GN=Qdpr PE=4 SV=1 ,	Qdpr
YDNSLK*IVSNASCTTNCLAPLAK	0.8331	E9Q9E5 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10481 PE=3 SV=1 , P16858 Glyceraldehyde-3-	Gapdh

Peptide	L/H Ratio	Protein	Protein ID
		phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2 , E9PYX4 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm5507 PE=3 SV=1 , D2KHZ9 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=2 SV=1 , E9PX42 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm2606 PE=3 SV=1 , E9PZP4 Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gm10313 PE=3 SV=1 ,	
IDGASPLDK*VCLIGCGFSTGYGSAVK	0.7660	Q3UKA4 Alcohol dehydrogenase 1 (Class I), isoform CRA_c OS=Mus musculus GN=Adh1 PE=2 SV=1 , P00329 Alcohol dehydrogenase 1 OS=Mus musculus GN=Adh1 PE=2 SV=2 ,	Adh1
IAK*METYCNSGSTDTSSVINAVTHALTAATPYTR	0.2203	Q80XN0 D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Mus musculus GN=Bdh1 PE=1 SV=2 ,	Bdh1
IIK*THLPLSLLPQSLLDQK	0.0461	D3Z3G5 Uncharacterized protein OS=Mus musculus GN=Sult1a1 PE=4 SV=1 , Q91W19 Sulfotransferase family 1A, phenol-preferring, member 1 OS=Mus musculus GN=Sult1a1 PE=2 SV=1 , D3Z2P8 Uncharacterized protein OS=Mus musculus GN=Sult1a1 PE=4 SV=1 , E9QNL5 Uncharacterized protein OS=Mus musculus GN=Sult1a1 PE=4 SV=1 , P52840 Sulfotransferase 1A1 OS=Mus musculus GN=Sult1a1 PE=2 SV=1 ,	Sult1a1
AVTPNQVQDLYDMMDK*EHAQR	0.0105	Q3TBH9 Putative uncharacterized protein OS=Mus musculus GN=Mical1 PE=2 SV=1 , E9PUI4 Uncharacterized protein OS=Mus musculus GN=Mical1 PE=4 SV=1 , Q8VDP3 NEDD9-interacting protein with calponin homology and LIM domains OS=Mus musculus GN=Mical1 PE=1 SV=1 , D3Z4C6 Uncharacterized protein OS=Mus musculus GN=Mical1 PE=4 SV=1 , E9PXR1 Uncharacterized protein OS=Mus musculus GN=Mical1 PE=4 SV=1 ,	Mical1
GEGYADLEYAMMVSMGAVHK*	0.0012	Q3URQ7-2 Isoform 2 of Methenyltetrahydrofolate synthase domain-containing protein OS=Mus musculus GN=Mthfsd , Q3URQ7 Methenyltetrahydrofolate synthase domain-containing protein OS=Mus musculus GN=Mthfsd PE=2 SV=1 , D3Z0Q4 Uncharacterized protein OS=Mus musculus GN=Mthfsd PE=4 SV=1 , D3Z4L1 Methenyltetrahydrofolate synthetase domain containing, isoform CRA_d OS=Mus musculus GN=Mthfsd PE=4 SV=1 , D3Z1R2 Uncharacterized protein OS=Mus musculus GN=Mthfsd PE=4 SV=1 ,	Mthfsd

Appendix 6. Lipidomic profiling of mouse livers from mice treated with vehicle or glyphosate

Table 9 shows lipidomics profiling data from mice treated with vehicle or glyphosate. Mice were treated with vehicle or glyphosate (200 mg/kg ip, once per day treatment over 7 days). Relative metabolite levels from individual mice are presented where the data for each lipid is normalized to "1" for vehicle-treated controls. Abbreviations for lipids are as followed: FFA, free fatty acid; PA, phosphatidic acid; PS, phosphatidyl serine; PE, phosphatidylethanolamine; PC, phosphatidylcholine; PG, phosphatidylglycerol; PI, phosphatidyl inositol; SM, sphingomyelin; AC, acyl carnitine; NAE, N-acylethanolamine; MAG, monoacylglycerol; DAG, diacylglycerol; TAG, triacylglycerol; PGE2/PGD2, prostaglandin E2/D2; PGJ2, prostaglandin J2; 5,6-EET, 5,6-epoxyeicosatrienoic acid; 5-HETE, 5-hydroxyeicosatetraenoic acid; PGF2alpha, prostaglandin F2-alpha; NAT, N-acyltaurine; TXB2, thromboxane B2; S1P, sphingosine-1-phosphate; "L" in front of a lipid acronym refers to "lyso" (e.g. LPA refers to lysophosphatidic acid); "e" or "p" after a lipid acronym refers to ether or plasmalogen, respectively. This table is related to Figure 2-3.

Table 9. Lipidomic profiling data form mice treated in vivo with glyphosate

Lipid	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
C16:0e/C20:4 PCe	1	0.10	2.21	0.14	0.00006
C16:0p/C20:4 PEp	1	0.12	1.90	0.06	0.00007
C18:0/C20:4 PC	1	0.12	1.90	0.08	0.00009
C18:0/C20:4 PS	1	0.13	2.34	0.16	0.00010
C16:0 Ceramide	1	0.11	1.94	0.11	0.00017
C16:0/C20:4/C16:0 TAG	1	0.10	1.73	0.08	0.00017
C18:0e/C18:1 PGe	1	0.12	1.83	0.09	0.00023
C16:0e/C18:1 PCe	1	0.12	1.88	0.10	0.00025
C18:0e/C20:4 PCe	1	0.10	2.02	0.16	0.00031
C18:0 ceramide	1	0.12	2.20	0.19	0.00032
total cholesteryl esters	1	0.15	3.48	0.44	0.00036
C16:0 SM	1	0.10	1.86	0.13	0.00037
C18:0e MAGe	1	0.29	3.95	0.48	0.00038
C16:0/C18:1 PG	1	0.15	2.07	0.14	0.00041
C16:0e/C18:1 PEe	1	0.11	1.72	0.09	0.00044
C16:0/C20:4 PC	1	0.11	1.63	0.06	0.00058
C18:0e/C20:4 PEe	1	0.11	1.63	0.07	0.00061
C16:0e glycerone phosphate	1	0.09	1.70	0.10	0.00069
C18:0e/C20:4 PSe	1	0.17	2.75	0.35	0.00099
C16:0e LPAe	1	0.10	1.56	0.04	0.00100
C18:1/C18:0 lactosylceramide	1	0.10	1.69	0.12	0.00106
pregninolone sulfate	1	0.13	1.61	0.06	0.00108
C18:0p/C20:4 PEp	1	0.09	1.53	0.10	0.00179

Lipid	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
C18:0/C20:4 DAG	1	0.10	1.71	0.15	0.00180
C18:0p/C20:4 PCp	1	0.11	1.66	0.12	0.00218
C16:0/C20:4 PS	1	0.21	2.40	0.29	0.00233
C16:0/C20:4 DAG	1	0.15	1.70	0.11	0.00267
C18:0 LPA	1	0.02	1.31	0.09	0.00315
sphinganine	1	0.13	1.65	0.12	0.00322
C18:1/C16:0 ceramide-1-P	1	0.08	1.69	0.18	0.00338
sphingosine	1	0.09	1.39	0.05	0.00347
C18:0/C18:1 PS	1	0.12	1.86	0.21	0.00369
cholesterol	1	0.10	1.39	0.04	0.00432
C16:0/C18:1 PC	1	0.11	1.46	0.07	0.00434
C16:0/C18:1 PS	1	0.13	1.72	0.17	0.00455
C16:0/C18:1/C16:0 TAG	1	0.11	1.49	0.09	0.00458
C16:0e/C18:1 PAe	1	0.07	1.36	0.08	0.00503
C18:0p LPAp	1	0.05	1.40	0.12	0.00595
C16:0/C20:4 PE	1	0.12	1.49	0.10	0.00598
C18:0/C20:4 PE	1	0.12	1.44	0.06	0.00602
C18:0/C16:0 ceramide-1-P	1	0.08	1.52	0.14	0.00627
C16:0 MAG	1	0.16	1.63	0.12	0.00629
C18:1 ceramide	1	0.13	1.59	0.13	0.00660
C18:0/C18:1 PC	1	0.10	1.40	0.07	0.00724
C18:0e LPAe	1	0.08	1.28	0.05	0.01020
C16:0e/C20:4 PSe	1	0.13	1.42	0.06	0.01032
C18:0/C18:1 PE	1	0.15	1.43	0.03	0.01120
C18:0e/C18:1 PCe	1	0.10	1.28	0.04	0.01248
C16:0e/C20:4 PCe	1	0.10	1.31	0.05	0.01341
C18:0/C18:1 PG	1	0.13	1.47	0.12	0.01350
C18:0/C18:0/C18:0 TAG	1	0.14	1.60	0.17	0.01407
C18:0e/C2:0 MAGe	1	0.14	1.41	0.06	0.01417
C18:0/C20:4/C18:0 TAG	1	0.11	1.45	0.13	0.01511
C18:0/C20:4 PA	1	0.07	1.43	0.16	0.01555
C18:0e LPIe	1	0.22	1.87	0.25	0.01752
C20:0 LPC	1	0.10	0.66	0.09	0.01813
C20:4 ceramide	1	0.09	1.28	0.07	0.01963
C16:0/C18:1 PE	1	0.11	1.36	0.10	0.02066
C18:0 SM	1	0.13	1.33	0.06	0.02071
C16:0/C18:1 DAG	1	0.17	1.49	0.13	0.02385
C18:0p/C2:0 MAGp	1	0.20	1.53	0.11	0.02390
C16:0/C16:0/C16:0 TAG	1	0.15	1.44	0.11	0.02398

Lipid	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
gamma tocopherol	1	0.20	1.86	0.30	0.02401
cholesteryl oleate	1	0.21	5.14	1.99	0.02556
C18:0/C18:1/C18:0 TAG	1	0.12	1.42	0.15	0.03059
C16:0e LPSe	1	0.23	2.68	0.74	0.03138
alpha tocopherol	1	0.10	1.30	0.10	0.03156
C16:0e/C18:1 PSe	1	0.29	2.00	0.36	0.03233
C20:4 LPG	1	0.14	0.66	0.09	0.03683
C16:0e/C20:4 PIe	1	0.16	1.42	0.10	0.03825
C18:0p LPSp	1	0.19	0.62	0.04	0.03989
C18:0e/C20:4 PGe	1	0.18	1.40	0.09	0.04161
C16:0e/C20:4 PEe	1	0.13	1.33	0.11	0.04450
C16:0e/C2:0 MAGe	1	0.16	1.55	0.24	0.04753
C18:0 MAG	1	0.17	1.57	0.25	0.04860
C2:0 ceramide	1	0.26	2.15	0.57	0.05250
C16:0e LPGe	1	0.31	2.74	0.91	0.05377
C18:0 LPE	1	0.09	0.81	0.05	0.05460
C18:0e LPSe	1	0.11	20.07	10.64	0.05541
estradiol sulfate	1	0.37	2.77	0.91	0.05553
C18:0p LPCp	1	0.11	1.32	0.14	0.05663
C22:6 MAG	1	0.13	1.38	0.18	0.06248
C18:0 LPC	1	0.09	1.22	0.09	0.06300
C18:0e/C20:4 PIe	1	0.17	1.34	0.07	0.06505
C16:0 LPS	1	0.09	1.20	0.08	0.07326
C18:0 NAT	1	0.16	1.31	0.08	0.07570
C20:4 LPS	1	0.07	1.34	0.21	0.07765
C12:0 acyl CoA	1	0.17	0.55	0.26	0.08574
C18:0e LPCe	1	0.12	1.26	0.13	0.08912
C18:0 LPG	1	0.50	0.26	0.08	0.09231
C22:0 NAT	1	0.07	1.20	0.13	0.09828
C16:0p/C20:4 PSp	1	0.23	1.49	0.27	0.09841
testosterone sulfate	1	0.17	1.30	0.13	0.09884
C18:0p MAGp	1	0.26	3.19	1.58	0.10382
phytanic acid	1	0.24	1.83	0.62	0.10542
C18:1 LPG	1	0.18	1.47	0.30	0.10791
C16:0e/C20:4 PGe	1	0.26	1.51	0.27	0.10949
C18:0/C18:1 DAG	1	0.16	1.25	0.11	0.10987
C18:1 LPE	1	0.10	0.81	0.10	0.11603
C18:1 LPA	1	0.38	1.59	0.18	0.12016
C18:0 AC	1	0.16	1.29	0.17	0.12232

Lipid	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
DHEA	1	0.34	0.49	0.23	0.12373
C16:0 LPI	1	0.13	0.75	0.18	0.13520
C18:0 NAE	1	0.25	1.37	0.19	0.13748
C18:0p LPIp	1	0.21	1.33	0.17	0.14013
C16:0 LPE	1	0.10	0.85	0.09	0.14151
C16:0 LPC	1	0.10	1.13	0.07	0.14240
DHEA-sulfate	1	0.47	1.76	0.47	0.14283
C20:4 LPC	1	0.11	1.15	0.07	0.14832
C20:4 SM	1	0.11	1.13	0.04	0.14890
C18:0e/C18:1 PSe	1	0.10	1.36	0.32	0.15054
C16:0 NAE	1	0.23	1.30	0.15	0.15135
C16:0e/C18:1 PGe	1	0.14	0.83	0.06	0.15165
C22:6 FFA	1	0.13	1.34	0.30	0.15238
C18:1 SM	1	0.10	1.12	0.05	0.15245
C16:0e LPCe	1	0.13	1.20	0.14	0.16967
C20:4 NAT	1	0.17	0.78	0.12	0.17506
C6:0 AC	1	0.23	1.95	0.97	0.18258
C18:0e/C20:4 PAe	1	0.15	1.19	0.12	0.18391
C20:4 FFA	1	0.09	0.89	0.07	0.19221
C4:0 AC	1	0.22	1.96	1.07	0.20367
C12:0 AC	1	0.20	1.28	0.26	0.20981
C18:0e LPEe	1	0.07	1.09	0.09	0.21554
C18:0e/C18:1 PEe	1	0.13	1.18	0.17	0.21828
C22:6 NAT	1	0.18	0.79	0.17	0.21957
C20:4 LPI	1	0.13	0.81	0.22	0.22134
C16:0 FFA	1	0.06	1.09	0.09	0.22233
cholic acid	1	0.17	0.84	0.08	0.23184
C16:0/C20:4 PA	1	0.08	1.13	0.16	0.23535
C18:1/C18:1/C18:1/C18:1 cardiolipin	1	0.10	1.23	0.34	0.24475
C18:0p LPGp	1	0.09	0.93	0.03	0.25173
C18:0e LPCe	1	0.14	1.13	0.12	0.25410
C20:4 LPA	1	0.15	1.15	0.18	0.26689
C18:0e/C18:1 PIe	1	0.22	1.18	0.14	0.27141
C16:0/C18:1 PI	1	0.15	1.13	0.14	0.27229
testosterone	1	0.39	1.27	0.20	0.27424
C16:0e LPEe	1	0.16	1.22	0.32	0.27909
C18:1 MAG	1	0.11	1.11	0.14	0.28200
C16:0e MAGe	1	0.12	0.91	0.08	0.28345
C18:0e LPGe	1	0.19	1.13	0.12	0.29178

Lipid	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
C2:0 AC	1	0.28	0.84	0.11	0.30127
C18:1 NAE	1	0.23	0.86	0.11	0.30366
C16:0 AC	1	0.16	1.12	0.16	0.31382
C20:0 acyl CoA	1	0.65	0.62	0.08	0.31394
C18:0 FFA	1	0.12	1.12	0.23	0.31967
C18:0/C20:4 PG	1	0.26	0.85	0.18	0.32190
C16:0 S1P	1	0.19	0.90	0.07	0.32581
C16:0/C20:4 PI	1	0.16	1.10	0.15	0.33571
C18:0 LPS	1	0.10	1.09	0.17	0.33580
C18:2 MAG	1	0.09	1.06	0.10	0.33836
C16:0e/C20:4 PAe	1	0.09	0.94	0.09	0.34345
C18:1 LPS	1	0.07	1.07	0.16	0.35860
C18:0/C18:1 PI	1	0.16	1.07	0.07	0.36590
pregninolone	1	0.16	1.07	0.12	0.37040
C18:1 NAT	1	0.27	1.11	0.13	0.37087
C16:0/C16:0 PI	1	0.20	1.09	0.18	0.37865
C18:0e/C18:1 PAe	1	0.21	1.08	0.14	0.38153
C20:4 MAG	1	0.09	1.06	0.19	0.38276
C16:0/C20:4 PG	1	0.20	1.07	0.12	0.38715
C18:0p/C20:4 PSp	1	0.16	0.94	0.15	0.39312
C16:0e/C18:1 PIe	1	0.11	0.97	0.06	0.41194
C18:0/C18:1 PA	1	0.18	1.05	0.15	0.42776
C18:1 LPI	1	0.30	1.07	0.29	0.43457
C18:2 NAT	1	0.23	0.95	0.19	0.44228
C18:1 LPC	1	0.10	0.98	0.06	0.44439
pristanic acid	1	0.36	1.06	0.21	0.45146
15-deoxyPGJ2	1	0.36	1.06	0.21	0.45146
5-HETE	1	0.36	1.06	0.21	0.45146
5,6-EET	1	0.36	1.06	0.21	0.45146
PGJ2	1	0.36	1.06	0.21	0.45146
PGE2/PGD2	1	0.36	1.06	0.21	0.45146
PGF2alpha	1	0.36	1.06	0.21	0.45146
TXB2	1	0.36	1.06	0.21	0.45146
C16:0e LPIe	1	0.36	1.06	0.21	0.45146
glucosyl-ceramide	1	0.36	1.06	0.21	0.45146
C18:1/C18:1/C18:1/C18:1 cardiolipin	1	0.36	1.06	0.21	0.45146
coenzyme A	1	0.36	1.06	0.21	0.45146
acetyl CoA	1	0.36	1.06	0.21	0.45146
C4:0 acyl CoA	1	0.36	1.06	0.21	0.45146

Lipid	Control average	Control SEM	Glyphosate average	Glyphosate SEM	P-value
acetoacetyl CoA	1	0.36	1.06	0.21	0.45146
malonyl CoA	1	0.36	1.06	0.21	0.45146
C6:0 acyl CoA	1	0.36	1.06	0.21	0.45146
C8:0 acyl CoA	1	0.36	1.06	0.21	0.45146
C10:0 acyl CoA	1	0.36	1.06	0.21	0.45146
C14:0 acyl CoA	1	0.36	1.06	0.21	0.45146
C16:0 acyl CoA	1	0.36	1.06	0.21	0.45146
C16:0/C18:1 PA	1	0.14	1.03	0.19	0.45699
C16:1 NAT	1	0.35	1.06	0.42	0.45978
C18:1 FFA	1	0.14	1.02	0.06	0.46186
C16:0 NAT	1	0.28	0.96	0.29	0.46575
C18:0p LPCp	1	0.08	0.99	0.03	0.47190
C18:0/C20:4 PI	1	0.12	1.01	0.10	0.47729
estradiol	1	0.10	0.99	0.08	0.47919
C18:0 LPI	1	0.23	1.02	0.24	0.48169
C20:4 LPE	1	0.11	1.01	0.12	0.48549
C18:0p LPEp	1	0.11	1.00	0.10	0.49401