Protein Regulators of Lipid and Energy Metabolism

by

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ABSTRACT

Lipolysis or hydrolysis of triglyceride (TG) stored within intracellular lipid droplets (LD), is vital to maintaining metabolic homeostasis in mammals. Regulation of lipolysis and subsequent utilization of liberated fatty acids impacts cellular and organismal functions including body fat accumulation and thermogenesis. Adipose triglyceride lipase (ATGL) is the intracellular rate-limiting enzyme responsible for catalyzing hydrolysis of TG to diacylglycerol (DAG), the initial step of the lipolytic reaction. G0/G1 switch gene-2 (G0S2) and hypoxia-inducible gene-2 (HIG2) are selective inhibitors of ATGL. G0S2 facilitates accumulation of TG in the liver and adipose tissue, while HIG2 functions under hypoxic conditions. Sequence analysis and mutagenesis were used to confirm the presence of conserved domains between these proteins, and that these domains are required for efficient binding and inhibition of ATGL. Further analysis revealed a Positive sequence (Pos-Seq)-LD binding motif in G0S2 but not HIG2. The Pos-Seq mediated ATGL-independent localization to LD and was required for achieving maximal inhibition of ATGL activity by G0S2. Identification and mutational analysis of this motif revealed distinct mechanisms for HIG2 and G0S2 LD association. In addition to molecular characterization of known protein inhibitors of lipolysis, an intracellular member of the apolipoprotein L (ApoL) family, ApoL6, was also identified as a LD and mitochondria associated protein expressed in adipose tissue. Brown adipose tissue uses fatty acids as fuel for increasing its energy output as heat during acute responses to cold exposure. A Comprehensive Lab Animal Monitoring System was used to compare heat production at room temperature (RT) and 4oC in transgenic animals overexpressing ApoL6 in brown adipose tissue. Overexpression of

ApoL6 delayed utilization of long-chain fatty acids (LCFAs) as a fuel source while promoting an enhanced thermogenic response during initial cold exposure. ApoL6 mediated inhibition of LCFA utilization results from binding of ApoL6 to Mitochondrial Trifunctional Protein (MTP/TFP), which catalyzes mitochondrial Î²-oxidation. Indirect calorimetry and fasting acute cold exposure experiments suggest the augmented thermogenic profile of ApoL6 transgenic animals is a result of enhanced utilization of medium-chain fatty acids (MCFAs), glucose, and amino acids as fuel sources. Cumulatively these results indicate multiple mechanisms for regulation lipolysis and fatty acid utilization.

DEDICATION

To my late father, *Harold Douglas Campbell*,

Thank you for always telling me how much you loved me.

To my closest friend, *Duane Phillip O'Brien*,

Thank you for all your love and support.

Every day I wish you were still here.

To my sister *Alicia Renee Campbell*,

You were my strength when I had none.

I love you more than words can say.

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LIST OF ABBREVIATIONS

ADP	adenosine diphosphate
AMP	adenosine monophosphate
APO	apolipoprotein
APOL6	apolipoprotein L6
ATGL	adipose triglyceride lipase
ATP	adenosine triphosphate
BAT	brown adipose tissue
BH3	bcl2 homology 3
BSA	bovine serum albumin
CACT	carnitine-acylcarnitine translocase
CGI-58	comparative gene indentification-58
CPT1	carnitine palmitoyltransferase 1
CPT2	carnitine palmitoyltransferase 2
CrAT	carnitine o-acetyltransferase
DAG	diacylglycerol
DMEM	Dulbecco's Modified Eagle Medium
ER	endoplasmic reticulum
ETC	electron transport chain
FA	fatty acid
$FADH_2$	flavin adenine dinucleotide
FBS	fetal bovine serum
FSP27	fat specific protein 27
G0S2	G0/G1 switch gene-2
GFP	green
HADHA	hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase
HADHB	3-ketoacyl-CoA thiolase/acetyl-CoA acyltransferase/beta-ketothiolase
HD	hydrophobic domain
HDL	high-density lipoprotein
HIF1α	hypoxia-inducible factor-1α
HIG2	hypoxia-inducible gene 2
HSL	hormone sensitive lipase
IMM	inner mitochondrial membrane
IP	immunoprecipitation
LCFA	long chin fatty acid
LD	lipid droplet
LDL	low density lipoprotein
LPL	lipoprotein lipase
MAD	membrane addressing domain

MCFA	medium chain fatty acid
MGL	monoacylglycerol lipase
MTP/TFP	mitochondrial trifunctional protein
NADH	nicotinamide adenine dinucleotide
NLSD	neutral lipid storage disease
OA	oleic acid
PBS	phosphate buffered saline
PFD	pore-forming domain
PKA	protein kinase A
RER	respiratory exchange ratio
SCFA	short chain fatty acids
SD	standard deviation
SEM	standard error of the mean
TCA	tricarboxylic acid cycle
TG	triglyceride/triacylglycerol
UCP	uncoupling proteins
VLDL	very low-density lipoprotein
β-AR	β-adrenergic receptor

CHAPTER 1

INTRODUCTION

Obesity and Lipids

Obesity is defined as having a Body Mass Index above 30 and is characterized by the excess accumulation of fat in adipose tissue. The Center for Disease Control lists the overall prevalence of obesity in American adults at 42.4% in 2017-2018 [1]. Obesity is a risk factor for the development of insulin resistance and type 2 diabetes, as well as certain cancers and cardiovascular disease.

Dyslipidemia, which is frequently observed with dietary obesity, refers to altered levels of intracellular and circulating lipids. Lipids, which include phospholipids, cholesterol, fatty acids and triglycerides (TGs) perform a variety of cellular functions and their dysregulation can lead to metabolic and cardiovascular diseases. Fatty acids (FAs) stored as TGs are an important fuel source used by the mitochondria to meet cellular energetic demands. In obesity, TGs are the most abundantly accumulated lipid species in adipose tissue. As a result, obesity is associated with higher levels of intracellular and circulating TGs.

This study aims to answer two questions: 1) What motifs do regulatory proteins use to modulate TG breakdown; and 2) What proteins are involved in determining whether those breakdown products are used as a fuel source at the mitochondria?

Dietary and Circulating Fatty Acids

Levels of circulating and intracellular FAs and triglycerides are regulated by diet and enzymatic activity. Ingested lipids from dietary sources are packaged into chylomicrons, which are large TG-enriched molecules that also contain cholesterol and

Apolipoproteins.[2,3] Chylomicron TGs can be cleaved while in the bloodstream by lipoprotein lipase (LPL). Upon cleavage, FAs released can be absorbed into various tissue types to be utilized for fuel or esterified into TGs for storage. The remaining chylomicron remnant is then taken up by the liver.[4]

A feedback loop exists between circulating lipids available through ingestion and accumulation or hydrolysis of lipids intracellularly in adipose tissue and oxidative tissues such as muscle and liver. In a fasted state adipose tissue activates a program of cleaving stored intracellular TGs and releasing free FAs to be taken up by muscle and liver as a fuel source.[5] Free fatty acids being released from adipose tissue accumulate as TGs in the liver.[6,7] This accumulation is cyclical in that once feeding takes place, triglycerides are released from the liver in the form of TG-rich very low-density lipoprotein (VLDL), or they are hydrolyzed intracellularly, and the free fatty acids produced are consumed during mitochondrial β-oxidation.[8]

The rate at which lipids derived from diet, adipose tissue and liver reach the bloodstream has a significant impact on whole-body metabolism and cellular signaling in specific tissues. Insulin signaling, which stimulates the uptake of glucose into muscle, adipose tissue and liver, is sensitive to levels of intracellular FAs taken in from the bloodstream. High levels of intracellular fatty acids activate pro-inflammatory pathways leading to decreased phosphorylation of insulin receptor substrate ½ (IRS1/2) and impaired insulin signaling.[9,10] This lipotoxicity is responsible for many features associated with metabolic diseases including hyperlipidemia and type 2 diabetes.

In younger people hyperlipidemia can be especially dangerous as the amount of lipids also can affect the synthesis and availability of hormones. In older adults, this is considered a factor in development of certain cancers. Many hormones including estrogen and testosterone are synthesized from cholesterol precursors. Therefore, understanding the impact of circulating lipids and how lipids are metabolized intracellularly is important to our understanding of metabolic diseases.

Apolipoproteins

Fatty acids are carried into muscle and other oxidative tissues to be utilized as fuel or building material for membrane structures. Circulating lipids are complexed with apolipoproteins (Apo). Apolipoproteins associate with different lipid species including triglycerides and cholesterol. They are the protein components of chylomicrons, high density lipoprotein (HDL), low density lipoproteins (LDL), and very low-density lipoproteins (VLDL). Structurally lipoproteins are very similar to intracellular lipid droplets that consist of hydrophobic neutral lipids such as TGs and cholesteryl esters emulsified by a phospholipid monolayer with surface and integral membrane proteins attached (Figure 1).

Similar to proteins that associate with intracellular lipid droplets, apolipoproteins are amphipathic and contain both charged and hydrophobic domains. There are several apolipoprotein families, with A, B, C and E families being the most studied due to their respective association with VLDL, LDL and HDLs. Early studies of the more recently identified Apolipoprotein L (ApoL) family suggested that ApoL proteins are HDL-associated lipoproteins with an important role in lipid transport.[11] Consistent with this function, Duchateau et. al. found that plasma levels of ApoL1 correlated with circulating triglyceride and cholesterol levels in normal, hyperlipidemic and diabetic subjects.[12]

Intracellular lipolysis

Intracellular lipolysis is regulated by the ubiquitously expressed adipocyte triglyceride lipase or ATGL. ATGL is a patatin-like phospholipase domain-containing (PNPLA) family member and contains a patatin-like catalytic domain responsible for hydrolyzing ester bonds in TGs. Triglyceride molecules are composed of three fatty acyl chains esterified to a three-carbon glycerol. In adipocytes, complete lipolysis releases a glycerol molecule and 3 fatty acids. ATGL is responsible for the initial rate-limiting cleavage of a triglyceride molecule at the sn-2 position, producing a fatty acid and a diacylglycerol molecule. Subsequently that diacylglycerol is hydrolyzed by hormone sensitive lipase (HSL) from a diacylglycerol to monoacyglycerol. Monoacyglycerol lipase (MGL) cleaves the final fatty acid molecule from the glycerol backbone. Subsequently FAs produced by this process are utilized via three pathways: 1) release into the bloodstream to contribute to the pool of circulating fatty acids; 2) re-esterification into TG at ER to form new lipid droplets; and 3) entry into mitochondria for β-oxidation via carnitine-dependent shuttling to provide energy for the cell.

ATGL and its regulators are indirectly responsive to levels of circulating fatty acids. Once circulating fatty acids are transported into cells, they can function as cofactors activating or suppressing the transcription of genes needed to stimulate lipogenesis, the synthesis of new lipids, or regulate lipolysis.[13] Since ATGL is ubiquitously expressed, the lipolytic process is conserved within a wide variety of tissues. In oxidative tissues, such as skeletal muscle, free fatty acids released by lipolysis are likely to be consumed in mitochondrial β-oxidation for ATP production. While in adipose tissue, free fatty acids are more likely to be released into the bloodstream or re-esterified into triglyceride molecules.

The outcome of lipolysis is different in white adipose tissue versus oxidative tissues. White adipose tissue is designed for the efficient storage of triglycerides during nutrient surplus and for the quick release of FAs via lipolysis in response to increased systemic demand for energy. Consistently, white adipocytes contain a large unilocular lipid droplet and few mitochondria. Cold exposure, exercise and any stimulus that signals through the beta-adrenergic signaling pathway elicit a rapid lipolytic response in white adipocytes, which release fatty acids into the bloodstream where they are taken in by other tissues.

Striated muscle and brown adipose tissue are examples of oxidative tissues, where fatty acids are more likely to be consumed at the mitochondria through β-oxidation. In brown adipose tissue, FA oxidation is an important driver for heat production during cold exposure. In human newborns and rodents, brown adipose tissue is relied upon for non-shivering thermogenesis. Adult mice have a large interscapular depot of brown adipose tissue. Interscapular brown adipose tissue rapidly increases fatty acid oxidation and heat production in response to cold exposure. In adult humans, brown adipose tissue has been found along the spinal column and at the clavicle.[14,15] Human brown adipose tissue also increases its metabolic activity in response to cold exposure.[16,17] In fact, the capacity to greatly increase its metabolic activity makes brown adipose tissue an attractive target for developing therapies to treat obesity and insulin resistant disorders. The rationale is that increased uptake and thermogenic consumption of circulating glucose and FAs by brown adipose tissue would lead to mitigation of their deleterious effects in diabetes and dyslipidemia.[18]

Fatty Acid Oxidation

Brown adipose tissue takes up both glucose and fatty acids, and oxidation of fatty acids is required for thermogenesis.[19] Oxidation of short, medium, and long-chain FAs takes place in the mitochondria. Fatty acid oxidation is the enzymatic process that progressively shortens fatty chains to generate acetyl-CoA needed for further oxidation in the TCA cycle. In addition to acetyl-CoA production, fatty acid oxidation also produces reduced forms of nicotinamide adenine dinucleotide (NADH) and flavin adenine dinucleotide ($FADH_2$) that serve as electron carrier and donor to drive oxidative phosphorylation (Figure 2).

Short (SCFA) and medium-chain (MCFA) can enter the mitochondria directly, while long-chain fatty acids (LCFA) require a transport system. LCFA are first converted to LCFA-CoA by acyl-coenzyme A synthetase (ACS). Next LCFA-CoA are converted to carnitine conjugates by carnitine palmitoyltransferase 1 (CPT1). LCFA oxidation is dependent on the activity of CPT1. LCFA are transported across mitochondrial membrane as conjugates of carnitine generated by CPT1. Once in this form, Carnitine-acylcarnitine translocase (CACT) transports the fatty acid across the inner mitochondrial membrane into the mitochondrial matrix. CPT2 then converts the LCFA acylcarinitine back to LCFA acyl-CoA, which is the form required for fatty acid oxidation[20].

Mitochondrial trifunctional protein (MTP/TFP) is responsible for three of the four steps involved in LCFA oxidation. MTP/TFP is a hetero-octomeric complex composed of four α subunits and four β subunits. The MTP complex is present at the inner mitochondrial membrane and contains hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (HADHA) as the α subunit, and 3-ketoacyl-CoA thiolase/acetyl-CoA acyltransferase/beta-ketothiolase (HADHB) as the β subunit.

The four steps of fatty oxidation are diagramed in Figure 3. Briefly, the newly imported and converted Acyl-CoA is oxidized to produce 2,3-Enoyl-CoA. HADHA next catalyzes the conversion of 2,3-enoyl-CoA to 3-ketoacyl-CoA through at two-step process using its hydratase and dehydrogenase activities. HADHB then catalyzes the cleavage of 3-ketoacyl-CoA to acetyl-CoA and a shortened acyl-CoA molecule. The acetyl-CoA will be funneled into the TCA cycle and the acyl-CoA will undergo another round of oxidation (Figure 3).

Deficiency in MTP/TFP leads to defects in processing long chain fatty acids. Humans with MTP/TFP deficiency accumulate fatty acid oxidation intermediates that cannot be further metabolized. The condition is characterized by myopathy along with heart and liver dysfunction. LCFAs are a primary fuel source for these tissues. The effects of MTP/TFP deficiency become apparent especially during times of fasting, when FAs derived from adipose lipolysis serve as a major fuel source for muscle and heart. Consequently, inability to oxidize fatty acids leads to significant functional impairment in these tissues.

Thermoregulation in mammals

Muscle and brown adipose tissue utilize long chain fatty acids as a fuel source for maintaining body temperature during cold exposure. The fatty acid oxidation process generates acetyl-CoA and electron-carriers such as NADH and $FADH_2$ in support of oxidative phosphorylation at the inner mitochondrial membrane. The process of oxidative phosphorylation involves the transfer of electrons generated by fatty acid oxidation and the TCA cycle to a series of protein complexes of the electron transport chain (ETC) (Figure 2).

Complexes I through IV use electrons donated from NADH and $FADH_2$ to create a proton gradient across the inner mitochondrial membrane. This proton gradient is used as the driving force for ATP production by complex V. The electrons donated by NADH and $FADH_2$ are passed along the ETC in a series of redox reactions, pumping protons into the mitochondrial intermembrane space that creates a gradient across the inner mitochondrial membrane (IMM). Complex V, the ATP synthase, is a proton channel that allows for protons to move from the intermembrane space into the mitochondrial matrix. In coupled respiration, that gradient force is used to produce ATP from ADP and inorganic phosphate through complex V. The rate at which complex V operates regulates the rate at which oxidative phosphorylation occurs.

Oxidative phosphorylation and ATP production can be uncoupled from each other. This occurs when uncoupling proteins are present in the mitochondrial intermembrane. Uncoupling proteins (UCPs) act as channels for transport of protons from the intermembrane space into the mitochondrial matrix. In the presence of UCPs, complex V or ATP synthase is no longer the rate-limiting factor for oxidative phosphorylation. Instead, greater flux across the inner mitochondrial membrane results in increased heat production (Figure 4).

UCP-1 is highly expressed in brown adipose tissue. High levels of UCP-1 enable brown adipocytes to generate large amounts of heat during acute cold exposure. Long-term cold exposure also stimulates mitochondrial biogenesis and UCP-1 expression in white adipocytes, causing brown-like or beiging transformation of white adipose tissue.

Project Rationale

Lipolysis or the hydrolytic breakdown of TGs stored within intracellular lipid droplets is vital to maintaining metabolic homeostasis in all eukaryotes including mammals. Regulation of lipolysis and subsequent utilization of the lipolytic product, free fatty acids, impacts physiologic function at both cellular and organismal levels including body fat accumulation and non-shivering thermogenesis. Adipose tissue is the primary TG storage organ in humans and rodents. ATGL is the intracellular rate-limiting enzyme responsible for the initial step of the lipolytic process.

TG breakdown usually occurs at a low rate in the basal, unstimulated state. However, activities such as exercise or being exposed to a cold environment can stimulate high rates of lipolysis. Excessive fatty acids can lead to lipotoxic effects including insulin resistance and type 2 diabetes, therefore elucidation of all mechanisms influencing lipolysis is fundamental to our understanding of the molecular basis for the development of obesity and its associated metabolic diseases. Both basal and stimulated lipolysis are dependent on ATGL and many proteins involved in regulating the access of ATGL to TG-rich lipid droplet stores.

Previous work by the Liu laboratory discovered G0/G1 switch gene-2 (G0S2) and Hypoxia inducible gene-2 (HIG2) as protein inhibitors of ATGL. The first aim of this dissertation research was to delineate the function-structure relationship in these two ATGL inhibitors. Specifically, we chose to examine the key domains and amino acid residues in G0S2 and HIG2 that are of functional significance to subcellular localization and ATGL regulation. We hypothesized that there would be functional similarities and differences based on amino acid sequence analysis.

The second research project aimed to understand the role of an intracellular ApoL protein, AopL6, in adipocyte biology and thermoregulation. Recently we identified ApoL6 as a novel LD-associated protein that is highly expressed in white and brown adipose tissues. While white adipocytes store TG in a large unilocular LDs and few mitochondria, brown adipocytes contain multilocular small LDs and numerous mitochondria, and demonstrate a high rate of fatty acid oxidation and glucose uptake. To determine the functional role of ApoL6 in FA metabolism and thermogenic responses in vivo, we generated a transgenic mouse line that selectively overexpresses ApoL6 in brown adipose tissue (ApoL6-BAT). We hypothesized that ApoL6 regulates intracellular lipolysis through its association with LDs, and thereby inhibits mitochondrial oxidative function by decreasing the availability of free FAs available for oxidation.

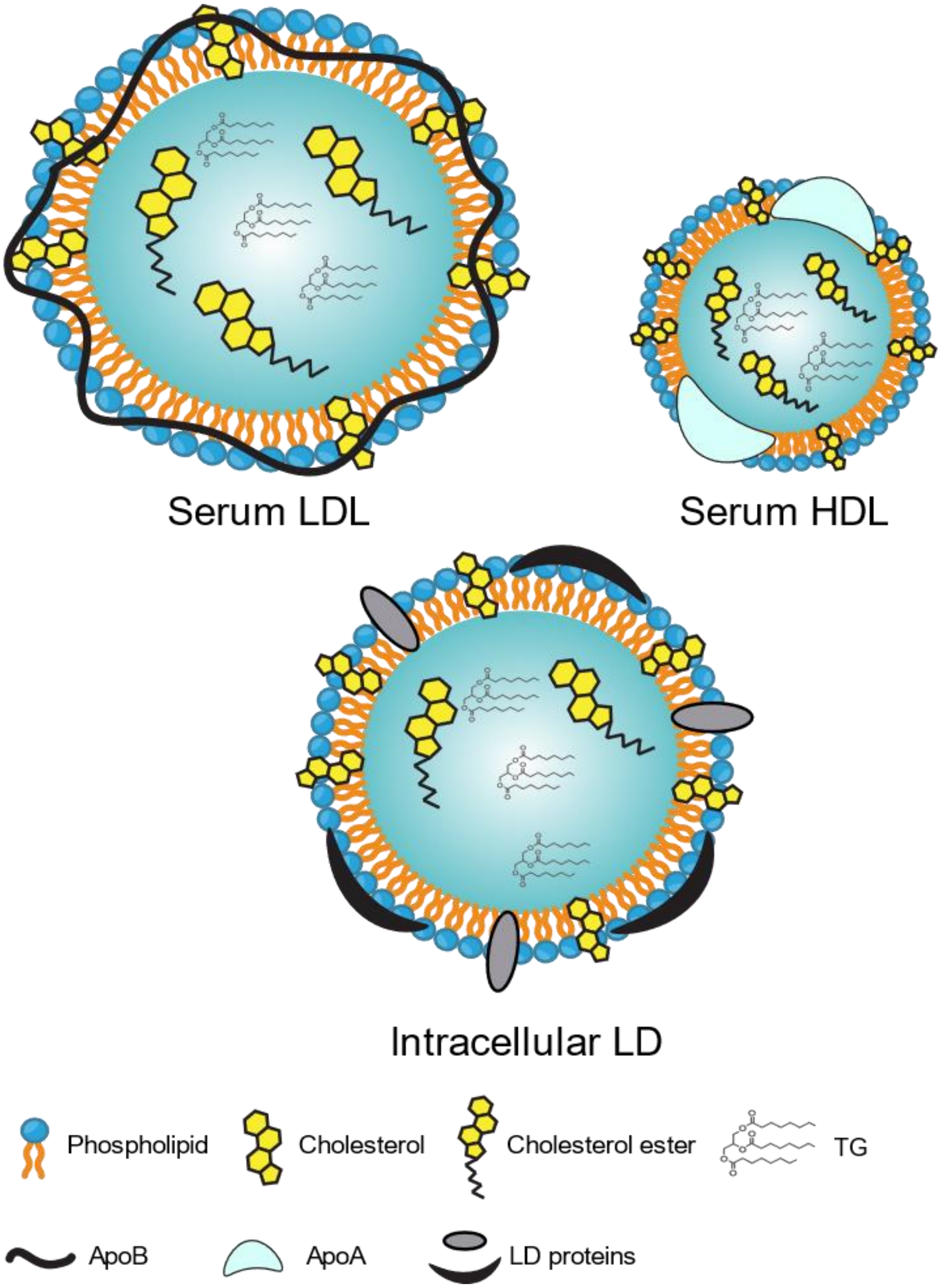


Figure 1. Serum lipoproteins and intracellular lipid droplets have structural similarities.[21]

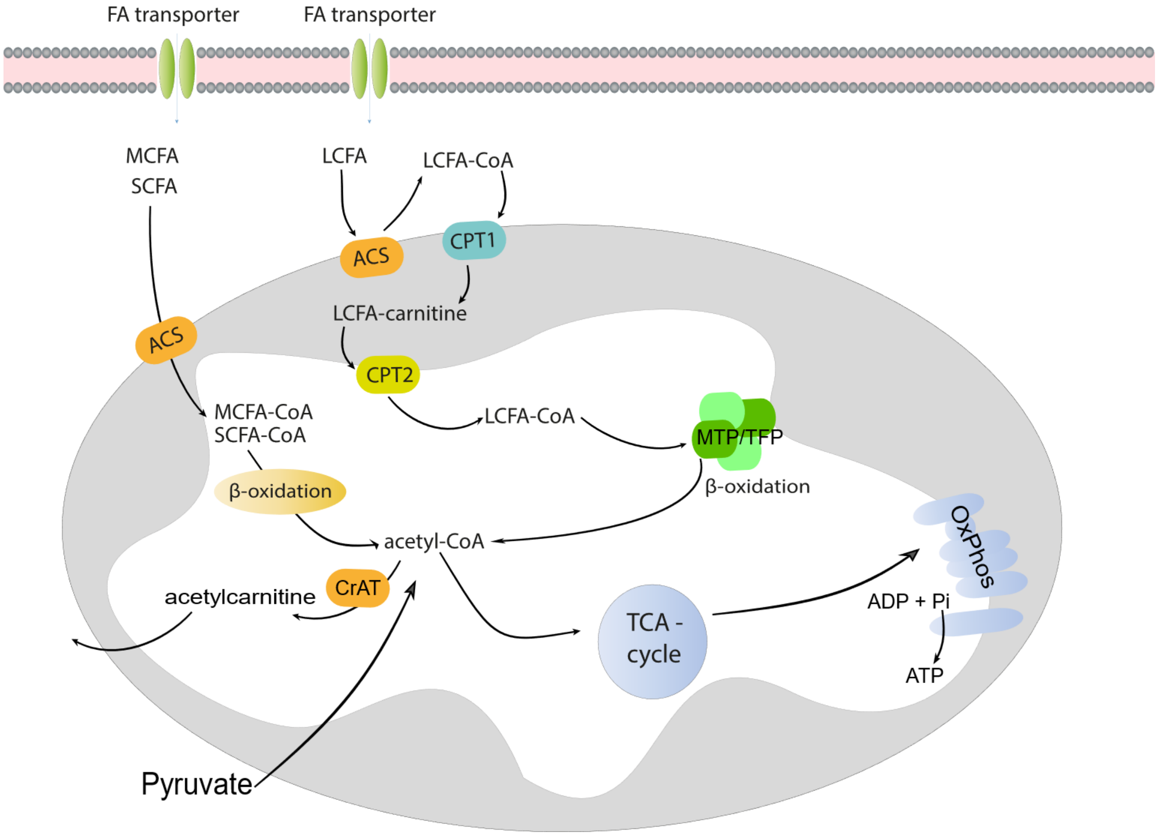


Figure 2. Diagram of mitochondrial ATP production

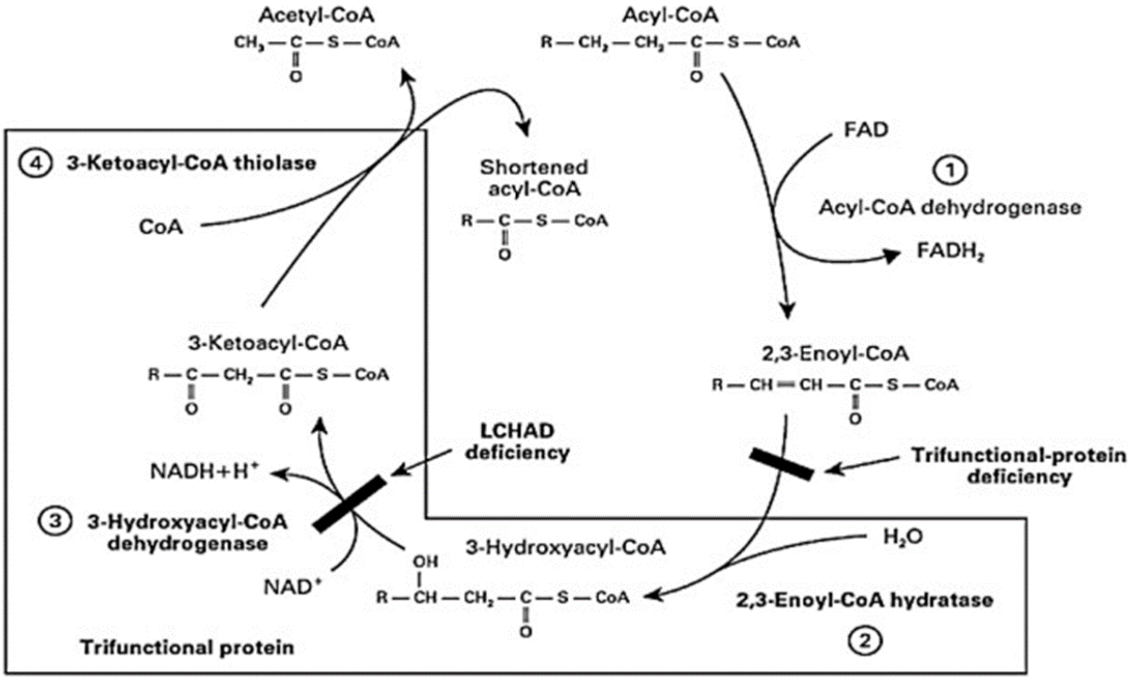


Figure 3. Diagram of LCFA β oxidation.[22] **Reproduced with permission from Idbah et. al., Copyright Massachusetts Medical Society.**

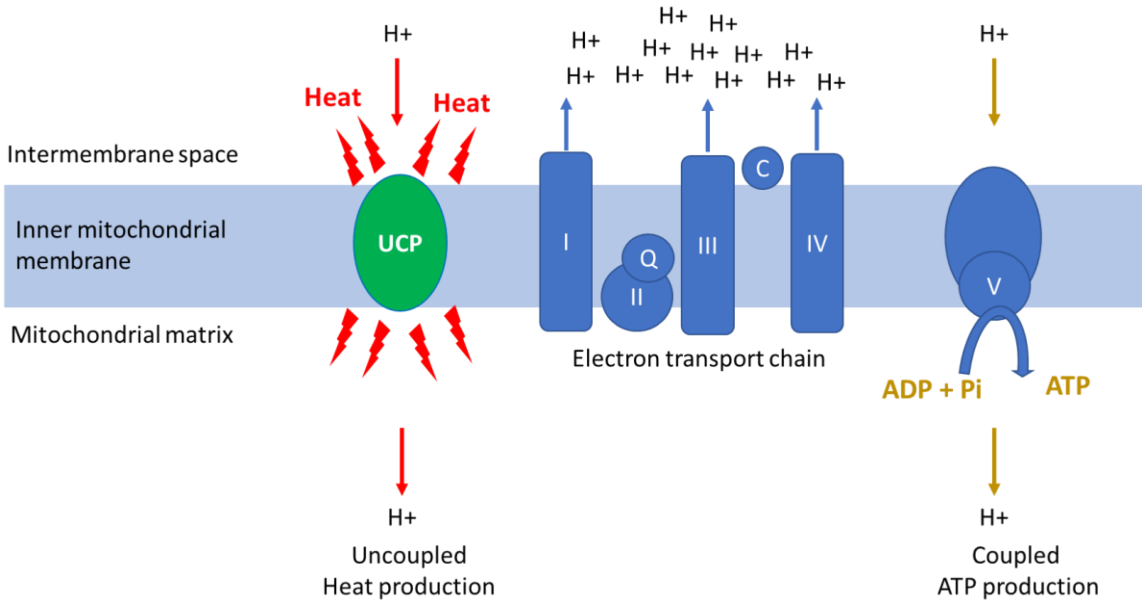


Figure 4. Mitochondrial heat production.

CHAPTER 2

CHARACTERIZATION OF FUNCTIONAL SEQUENCE MOTIFS IN PROTEIN INHIBITORS OF ADIPOSE TRIGLYCERIDE LIPASE

Introduction

Protein inhibitors of ATGL are important regulators of cellular lipid and energy metabolism. Hydrolysis of TGs stored in intracellular LDs is the primary mechanism by which adipose tissue supplies free FAs as fuel to other organs during times of nutrient scarcity or heightened metabolic demand. ATGL is the first and rate-limiting enzyme involved in TG catabolism. LDs are composed of a neutral lipid core coated by a phospholipid monolayer, and are dynamic organelles critically involved in TG storage and breakdown. ATGL acts at the LD surface and its ability to hydrolyze TG at the LD surface is tightly controlled by co-activators and repressors. Activation of ATGL lipolytic activity is controlled by comparative gene identification-58 (CGI-58), while ATGL repression is mediated by G0/G1 switch gene 2 (G0S2) and the recently identified hypoxia-inducible gene 2 (HIG2) [23–25]

The relationship between ATGL' protein structure and function has been extensively studied. Its C-terminal region contains a hydrophobic stretch of 45 amino acids that are critical for targeting it to the surface of LDs [26]. The N-terminal region of ATGL contains a patatin-like domain that is similar to the one in cytosolic phospholipase A_2 (cPLA_2), and is responsible for its TG hydrolase activity [27,28]. In addition to lipolytic activity, ATGL's patatin-like domain is the binding site for its inhibitors, G0S2 and HIG2 [24,25].

Our lab has identified G0S2 and HIG2 proteins as two structurally related, specific inhibitors of ATGL. G0S2 is a 103-amino acid protein that only exists in vertebrates and has only one isoform [29]. It is primarily expressed in liver and adipose tissue, and plays an important role as a major metabolic and energy regulator through its inhibitory action on ATGL. Previously we demonstrated that overexpression of G0S2 in adipose tissue lead to decreased adipose tissue lipolysis and impaired fatty acid utilization upon fasting [30]. When on a high fat diet, animals with adipose specific G0S2 overexpression had greater body weight and adiposity, but lower levels of circulating TG and free fatty acid compared to wild-type animals [30]. As a result of decreased systemic FA availability, transgenic animals also showed greater insulin sensitivity and glucose tolerance, indicating that G0S2 activity in adipose tissue exerts an important impact on metabolic health [30].

In addition to the role in regulating adipose tissue lipolysis, we also demonstrated that G0S2 possesses a critical function in liver. During fasting, adipose tissue lipolysis is upregulated, resulting in increased circulating fatty acids that are taken up by other tissues including the liver. Heckman et. al. showed that hepatic expression of G0S2 is increased in response to influx of adipose-derived fatty acids during fasting[31]. The hepatic G0S2 expression is dependent on the liver X receptor α (LXRα) transcription factor, and the upregulation of G0S2 is required for fasting-induced TG-LD accumulation and controlled FA oxidation in the liver[31]. Through its action in both adipose tissue and liver, G0S2 functions as an important modulator of tissue-specific partitioning of TGs and FA flux from adipose tissue to liver.

Similar to nutrient excess in adipose tissue and the fasting response in liver, hypoxia also induces the accumulation of TG-rich LDs [32,33]. Hypoxia-induced TG accumulation has been observed in a variety of cancer types[33]. HIG2 is a 63-amino acid protein whose transcription is mediated by hypoxia-inducible factor-1α (HIF1α) [34]. Zhang et. al. showed that HIG2 inhibits ATGL's lipolytic activity by binding directly to the patatin-like domain of ATGL [25]. They observed that HIG2-mediated inhibition of lipolysis is critical for tumor cell growth *in vivo*, and that loss of HIG2 sensitizes cancer cells to hypoxia-induced oxidative stress and apoptosis [25]. In a hypoxic tumor microenvironment, HIG2 inhibits ATGL-mediated intracellular lipolysis as a mechanism to promote cancer cell survival[25].

ATGL is inhibited by G0S2 and HIG2, two proteins with highly homologous hydrophobic domains (HD)[25,35,36]. A peptide that comprises the HD of G0S2 (residues 27-42) was shown to be sufficient for ATGL inhibition *in vitro* [35], while the inhibitory activity of HIG2 was abolished upon deletion of only a subset of HIG2 HD (residues 7-11)[25]. Comparison of the HD of these two proteins revealed that residues 7-11 of HIG2 and residues 27-30 of G0S2 are nearly identical sequences[25]. However, it has not yet been determined whether these analogous sequence motifs are required for G0S2 function.

On the subcellular level, HIG2 and G0S2 bind and inhibit ATGL at the LD surface. The C-terminal HD of ATGL, residues 259-337, is responsible for its localization to LDs [26]. Loss of this domain caused by genetic mutations in humans results in neutral lipid storage diseases (NLSD) characterized by excessive TG accumulation in non-adipose tissues and mild myopathy [26]. A separate study showed that G0S2 is able to anchor C-terminally truncated ATGL mutants to LDs [36]. However, the structural motifs responsible for targeting G0S2-ATGL complexes to LDs remained undefined. Here we aimed to map the specific residues and structural motifs required for G0S2- and HIG2-mediated ATGL inhibition and recruitment of such inhibitory complexes to LDs.

Methods and materials

CRISPR cell lines

Created as previously described[25]. CRISPR/Cas9-mediated gene deletion pSpCas9 (BB)−2A-Puro (pX459) V2.0 was a gift from Feng Zhang (Addgene plasmid #62988). Insert oligonucleotides that include a gRNA sequence were designed using http://crispr.mit.edu/ as follows: for HIG2 deletion, guide1-GGGTCAGTACCACACCTAAC; for ATGL deletion, guide-GACCCCGGTGACCAGCGCCG. Cells were seeded in 6-well plates and the following day transfected with pX459 plasmids containing DNA specific to HIG2 or ATGL using Lipofectamine 2000. Cells were selected under puromycin (1.5 μg/ml) for 48 hr and plated onto 96-well plates. Screening for genetic modifications was performed by immunoblotting analysis. Mutations were confirmed by direct sequencing.

Immunofluorescence and confocal microscopy

Cells were seeded on glass coverslips placed in 6-well plates and transfected with 0.25, 0.5 or 1 μg of each DNA construct using Lipofectamine 2000 according to the manufacturer's instructions. Six hours later, transfected cells were incubated with 400 μM oleic acid/0.2% BSA overnight. Following the fixation with 4% paraformaldehyde in PBS for 10 min, cells were permeabilized by 0.2% triton X-100 for 10 min, quenched with 100 mM glycine in PBS for 20 min, and then blocked with 2% BSA in PBS for 1 hr. The cells were then exposed to primary antibody for 2 hr at room temperature. Following three washes with PBS, the cells were treated for 1 hr with Alexa Fluor secondary antibodies. To visualize lipid droplets, 1 µg/ml of Bodipy 493/503 dye was added during the incubation with secondary antibodies. Samples were mounted on glass slides with SlowFade Diamond mounting medium and examined under a Zeiss LSM 800 inverted confocal microscope. Acquired images were processed and quantified manually with Zen Blue and ImageJ FIJI software. [37,38] Colocalization analysis was performed using the JACoP ImageJ plugin.[39]

In vitro transcription/translation expression

In vitro transcription/translation was carried out by using TNT SP6 High-Yield Protein Expression System (Promega) according to the manufacturer's instructions. Specifically, reactions consisting of 30 µLTNT SP6 High-Yield Wheat Germ Master Mix and 5 µg vector DNA, made up to 50 µL with molecular biology grade water were incubated for 120 min at 25°C. Then the reaction mixture was used for TG lipase activity.

Determination of TG hydrolase activity

HeLa cells were transfected with ATGL-expressing plasmids using Lipofectamine 2000 overnight and lysed on ice by sonication in a lysis buffer (0.25 M sucrose, 1 mM EDTA, 1 mM Tris-HCl pH 7.4, 1 mM DTT, 20 µg/mL leupeptin, 2 µg/mL antipain and 1 µg/mL pepstatine). The cell extract was clarified by centrifugation at 15,000 g for 10 min, and the supernatant was used as the enzyme source for the assay of TG hydrolase activity. The TG lipase activity was determined using a lipid emulsion labeled with [9,10-3H]- triolein as substrate. For G0S2 obtained from HeLa cells transfected with G0S2-expressing plasmids, 30 µl of G0S2 lysate was combined with 20 µl of ATGL lysate; For HIG2 derived from In vitro transcription/translation expression, 25 µl of In vitro transcription/translation reaction was combined with 25 µl of lysate buffer and 30 µl of ATGL lysate; Then the 80 µl HIG2/ATGL mixture was incubated with 80 µl of substrate solution for 60 min at 37°C. Reactions were terminated by adding 2.6 ml of methanol/chloroform/heptane (10:9:7) and 0.84 mL of 0.1 M potassium carbonate, 0.1 M boric acid (pH 10.5). Following centrifugation at 800 × g for 15 min, radiolabeled fatty acids in 1 ml of upper phase were measured by liquid scintillation counting.

Co-immunoprecipitation analysis

Cells were lysed in buffer containing 50 mM Tris-HCl, pH 7.4, 150 mM NaCl, 1% Triton X-100, 1 mM DTT, and protease tablet inhibitors (1 tablet per 10 ml of buffer). Anti-Flag M2-conjugated agarose gels were incubated with the lysates for 5 hr at 4°C. The beads were then washed four times with lysis buffer, and the bound proteins were eluted in SDS buffer and analyzed by immunoblotting.

Cell culture and hypoxia treatment

HeLa cells were cultured in DMEM (Invitrogen) containing 10% FBS (Invitrogen) supplemented with 100 U ml−1 penicillin/streptomycin (Invitrogen). Normoxic cells (20% O_2) were maintained at 37°C in a 5% CO_2/95% air incubator. For hypoxic exposure, cell culture plates were placed in a hypoxia incubator (Eppendorf, USA) at 0.5% O_2.

Cell adenoviral infection

HIG2 ko HeLa cells were cultured in DMEM (Invitrogen) containing 10% FBS (Invitrogen) supplemented with 100 U ml−1 penicillin/streptomycin (Invitrogen) in 12-well cell culture plates. Cells were infected with $1x10^7$ pfu/well of null, wtHIG2 or wt G0S2, $0.5x10^7$ pfu/well of TripA G0S2 adenovirus in the presence of 2.5µg/ml of polybrene for 16 h. After 16h, media was replaced with 50 µM oleic acid was added before normoxic or hypoxic treatment.

Cellular triglyceride quantification

Thermo scientific colorimetric kits were used for the determination of intracellular TG (catalog # TR22421).

Immunoblotting

Cells were lysed at 4°C in a buffer containing 50 mM Tris-HCl (pH 7.4), 150 mM NaCl, 10 mM NaF, 1% Nonidet P-40, 0.1% SDS, 0.5% sodium deoxycholate, 1.0 mM EDTA, 10% glycerol, and protease tablet inhibitors (1 tablet per 10 ml of buffer). The lysates were clarified by centrifugation at 20,000 × g, 4°C for 10 min and then mixed with equal volume of 2 × SDS sample buffer. Equivalent amounts of protein were resolved by SDSPAGE and transferred to nitrocellulose membranes. Individual proteins were blotted with primary antibodies at appropriate dilutions. Peroxide-conjugated secondary antibodies were incubated with the membrane at a dilution of 1:5000. The signals were then visualized using ECL substrate (Thermo Scientific).

Results

G0S2 can facilitate TG accumulation in the absence of HIG2.

G0S2 and HIG2 inhibit ATGL activity under different conditions; G0S2 in adipose tissue and liver, and HIG2 under hypoxia. To determine if there was any functional redundancy between these two proteins, we turned to HIG2 knockout cell lines. We overexpressed G0S2 in HIG2 knockout cells and then subjected them to hypoxic (0.5% O_2) conditions for 24hs (Figure 5). G0S2 allowed for allowed for LD accumulation above what was observed in control cells (Figure 5A).

To quantify the amount of TG accumulation with G0S2 overexpression compared to HIG2, we reintroduced wtHIG2 or wtG0S2 into HIG2 knockout cells and subjected them to hypoxic and normoxic (20% O_2) for 24hrs. At normoxia, both HIG2 and G0S2 allowed for a small but significant increase in lipid accumulation compared to control infected cells (Figure 5B). Under hypoxic conditions, G0S2 was able to facilitate TG accumulation to nearly the same level as wtHIG2 (Figure 5B). Western blot analysis showed that consistent with previous studies, HIG2 was stabilized under hypoxic conditions, but G0S2 was not (Figure 5C). These results suggest some functional or structural redundancy between G0S2 and HIG2.

Residues 27-30 of G0S2 mediate ATGL interaction and inhibition, but do not disrupt its LD localization.

G0S2' HD (residues 27-42) is sufficient to inhibit ATGL activity[35]. Deletion of G0S2' full HD causes it to lose its ATGL related functions[24]. To determine whether residues 27-30 within G0S2'HD were required for its function, we generated a series of HD deletion mutants (Figure 6A). We evaluated which subdomains are directly involved in ATGL interaction and inhibition using immunoprecipitation and lipase activity assays. Flag-tagged wtG0S2 or a deletion mutant was co-expressed with ATGL and immunoprecipitated using flag antibody conjugated beads. As expected, deletion of the entire HD Δ27-42 abolished ATGL interaction (Figure 6B). Deletion of any subdomain reduced but did not completely abolish ATGL interaction. Deletion of residues 27-30 resulted in the greatest reduction in ATGL binding (Figure 6B).

To assess the ability of the subdomain deletion mutants to inhibit ATGL activity, we performed an *in vitro* lipolysis assay. Consistent with co-immunoprecipitation results, the full HD deletion was unable to inhibit ATGL lipase activity (Figure 6C). However, despite having reduced binding to ATGL (Figure 6B), the Δ31-34, Δ35-38 and Δ39-42 mutants were as effective as wtG0S2 in inhibiting ATGL activity (Figure 6C). Of all the subdomain deletions, Δ27-30 had the greatest reduction in its ability to bind ATGL and was also the least effective at inhibiting ATGL lipase activity (Figure 6B and C).

Residues 27-30 of G0S2 are analogous to residues 7-11 of HIG2.

Sequence comparison between G0S2 and the recently identified ATGL inhibitor HIG2, revealed that residues 27-30 of G0S2 are identical to murine HIG2 residues 7-11 and nearly identical to human HIG2 ([25], Figure 7A). Our recent work identified residues 7-11 of HIG2 as being essential HIG2-mediated ATGL inhibition[25]. HIG2 residues 7-ll and G0S2 residues 27-30 mark the start of their respective HDs and have a leucine-tyrosine-X-leucine (LYXL) sequence motif. To determine whether deletion of these four residues alone could abolish G0S2' ATGL related function, we generated a deletion mutant (Δ27-30). Similar to HIG2, deletion of this motif in G0S2 abolished its ability to promote lipid droplet formation indicated by the lack of Bodipy staining (Figure 7B). These results show that residues 27-30 with the G0S2 HD are essential for G0S2' inhibitory function.

G0S2, but not HIG 2, contains a Pos-Seq motif for ER-LD sorting.

Since HIG2 and G0S2 share a conserved motif that is responsible for their ability to inhibit ATGL, we wanted to look for other similarities between their sequences. Further analysis revealed the presence of a common LD targeting motif within G0S2 but not HIG2 amino acid sequence. Positively charged residues immediately adjacent to a HD domain is common sequence arrangement in LD associated proteins [40,41]. The presence of a positive sequence (Pos-Seq) facilitates the sorting of proteins from the ER to LDs and can facilitate rapid association with the negatively charged region of the phospholipid monolayer of LDs [40,41]. G0S2 has positively charged residues upstream of its HD, while HIG2 has singular positive residues flanking its hydrophobic domains. HIG2 has a lysine at position 2 (K2) and an arginine at position 22 (R22), which are N-terminal and C-terminal to its HD (Figure 8A). G0S2 has a stretch of positive residues N-terminal to its HD at positions 20, 22, and 25 (R20, K22, K25) (Figure 8A).

We next wanted to determine whether this motif also impacted ATGL-related functions of HIG2 and G0S2. We hypothesized that G0S2 Pos-Seq mutants would have reduced association with ATGL, but HIG2-ATGL binding would remain intact. To test this, K2 and R22 of HIG2 were mutated to the hydrophobic amino acid alanine (K2AR22A). R20, K22, and K25 of G0S2 were also mutated to alanine (TripA). We then used co-immunoprecipitation and *in vitro* lipase assays to assess their impact on protein function. Mutation of the positive residues in both HIG2 and G0S2 reduced their association with ATGL (Figure 8B). Consistent with the immunoprecipitation, of these positive residue mutants had impaired ability to inhibit ATGL lipase activity in an *in vitro* (Figure 8C). Surprisingly, our results show mutation of positively charged residues in both G0S2 and HIG2 reduces ATGL binding and inhibition.

Binding to ATGL promotes LD translocation of Pos-Seq mutants of G0S2.

ATGL C-terminal mutants are catalytically active but are not targeted to LD. [24] Previous studies have shown that wtG0S2 can target ΔHD ATGL mutants to LD, but the same has not yet been determined for HIG2. Co-expression of wtHIG2 with a HD domain deletion mutant showed that it can bind to and target ΔHD ATGL to LD while allowing for TG accumulation (Figure 9A).

Pos-Seq mutants do retain some ATGL binding *in vitro* (Figure 8B) we wanted to assess whether Pos-Seq mutants can target ΔHD ATGL to LD. TripA G0S2 and K2AR22A HIG2 mutants can inhibit ΔHD ATGL lipase activity and cause it to localize to LD (Figure 9B). These results are consistent with co-immunoprecipitation results using wtATGL (Figure 8b). The patatin-like domain of ATGL is responsible for G0S2 and HIG2 binding and is intact in the ΔHD ATGL mutant. Residues 27-30 of G0S2 and 7-11 of HIG2, which mediate ATGL binding are remain intact in Pos-Seq mutants, therefore some association was expected.

G0S2 but not HIG2 contains Pos-Seq LD targeting motif.

Both HIG2 and G0S2 contain HD domains which allow for ATGL-independent association with LD (Figure 10A).[29] We sought to determine the role of these positively charged residues in ATGL-independent association of G0S2 and HIG2 with LDs. Flag-tagged wild-type or Pos-Seq mutant protein was overexpressed in ATGL-/- cells. Both wtG0S2 and wtHIG2 localized to LD (Figure 10A). The G0S2 TripA mutant failed to associate with LD but instead colocalized with the ER marker sec61 (Figure 10A). HIG2 mutants, however, did not colocalize with the ER (Figure 10B). These results indicate that the Pos-Seqs G0S2 is part of its LD targeting motif, but HIG2 has an alternate mechanism for LD association.

Discussion

Understanding mechanisms controlling fatty acid metabolism are essential for developing ways to counteract the negative effects of their dysregulation. ATGL, with its role as the rate-limiting intracellular TG hydrolase, is central to this understanding. HIG2 and G0S2 are two small protein inhibitors of ATGL. It is well established that HIG2 and G0S2 play critical roles in the regulation of lipid and energy metabolism. Inhibition of ATGL by G0S2 regulates TG storage in liver and adipose tissue, while HIG2 mediated-inhibition of ATGL promotes TG accumulation in a hypoxic tumor microenvironment [25,31,42]. Here we sought to examine the sequence similarities and identify conserved structural elements between these two proteins. We were able to confirm the requirement for the LY(V/L)LG motif for the maximal ATGL inhibition in HIG2 and show that this motif is also required for G0S2 functionality.

Binding to ATGL is not required for localization of either HIG2 or G0S2 to the LD surface. ATGL-independent localization of HIG2 and G0S2 suggests that they have separate motifs for ATGL binding and LD targeting. Hydrophobic and basic domains are commonly found within the sequence of LD-associated proteins[43]. This prompted us to further examine the sequence of both proteins for LD droplet targeting motifs.

Proteins targeted to LD surface usually contain either a HD or an amphipathic sequence, which are responsible for association with the hydrophobic fatty acid tails of the phospholipid monolayer surface of LDs[43]. In addition to hydrophobic residues, many LD-associated proteins contain a Pos-Seq, which are positively charged residues immediately adjacent to the HD or amphipathic region [40,41]. Both HIG2 and G0S2 contain HDs and in close proximity to positively charged residues. Mutation of these residues disrupted ATGL-independent localization to LD of G0S2 but not HIG2, indicating that G0S2 contains a true Pos-Seq LD targeting motif. Our results imply that G0S2, but not HIG2, is a Class I LD protein which translocates from the ER to LDs either during initial

LD formation or when mature LDs reconnect to the ER via membrane bridges[43]. This assertion is supported by the observation that mutation of this Pos-Seq to neutrally charged residues caused retention of G0S2 in the ER.

Our results indicate that the ATGL-independent sorting of G0S2 to LDs happens at the ER, and that the Pos-Seq of G0S2 is an essential regulator of that sorting. ATGL-independent sorting of G0S2 to LDs from the ER also suggests a mechanism by which G0S2 can encounter ATGL already anchored to LD surfaces.

ATGL itself is a Class II LD binding protein. After being translated in the cytosol, Class II LD proteins bind directly to the LD surface via amphipathic and hydrophobic regions. The C-terminal HD of ATGL, residues 259-337, mediate its LD association but not its association with HIG2 or G0S2[26]. Binding of a HD mutant of ATGL to either wild-type HIG2 or G0S2 allows for recruitment of mutant ATGL to the LD surface. The mechanism of this recruitment had yet to be determined. Our data provide insight into the order and required domains for that recruitment.

Expression of the ER-sequestered Pos-Seq mutant of G0S2, with a cytosolic HD mutant of ATGL resulted in recruitment of both proteins to LD surfaces. This suggests that binding of ATGL to G0S2 can take place at the ER membrane, and that the resulting complex can migrate onto LDs. This constitutes an additional mechanism by which ATGL and G0S2 can be recruited to LD surfaces. Migration of an ATGL-G0S2 complex from the ER to LDs is potentially specific to the ATGL-G0S2 relationship as HIG2 does not contain a Pos-Seq and did not become sequestered in the ER following mutation of its positive residues.

Maier *et. al*. showed that HIG2 is present at points of contact between ER and LD membranes and that knockout of the HIG2 gene prevents hypoxia-induced LD formation in macrophages[44]. Our data suggests that HIG2 does not migrate onto the surface of LDs from the ER during nascent LD formation, but rather is localized to LD after they have already formed. Further analysis to understand the exact mechanism is required.

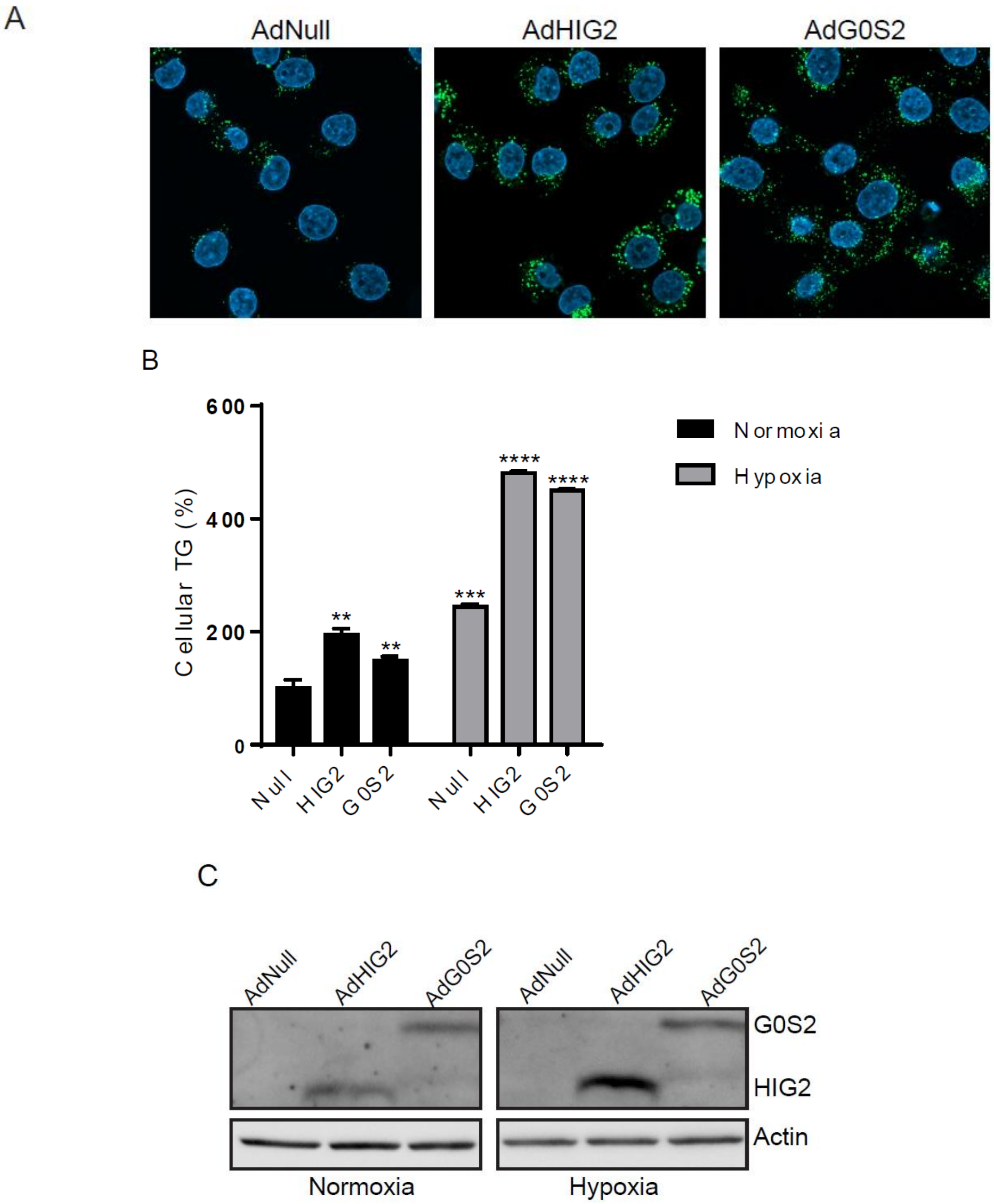


Figure 5. G0S2 can facilitate TG accumulation in the absence of HIG2. (A) HIG2-/- Hela loaded with were infected with control, HIG2 or G0S2 adenovirus overnight. 18-24hr later fresh media containing 50uM oleic acid was added. Infected cells we incubated at Normoxia (20% O2 or hypoxia 0.5% O2 for 24hrs. Cells were fixed and stained for LD (bodipy, green) and dapi (blue). (B) TG quantification of A **p<0.001, ****p<0.00001. (C) Western blot for HIG2 and G0S2 adenoviral protein.

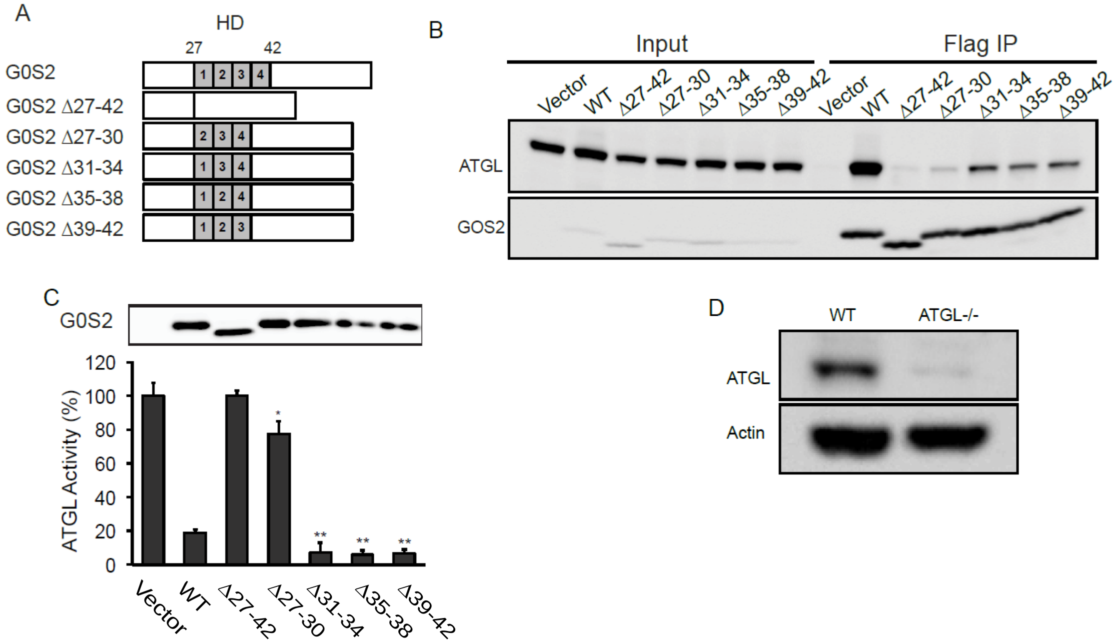


Figure 6. Residues 27-30 mediate ATGL binding and inhibition. (A) Diagrams of G0S2 HD mutants. Δ27-42 is a complete deletion of G0S2 HD, while all other mutants (Δ27-30, Δ31-34, Δ35-38, and Δ39-42) are deletions of 4 amino acids within G0S2' HD. (B) Immunoprecipitation of flag-tagged G0S2. Hela were transfected with wtATGL and a flag-tagged G0S2 constructs overnight. G0S2 was immunoprecipitated using flag-beads. (C) ATGL in vitro lipase activity assay performed in the presence of wt G0S2 or G0S2 HD mutants. $*p<0.05$, $**p<0.001$ (D) Western blot confirming ATGL-/- Hela cells generated using CRISPR-CAS9.

Hu HIG2 6 NLYLLGVVLTLLS I FVRVME 25
Hu G0S2 26 KLYVLGSVLALFGVVLGLME 44
Mus HIG2 6 NLYVLG IMLTLLS I FVRVME 25

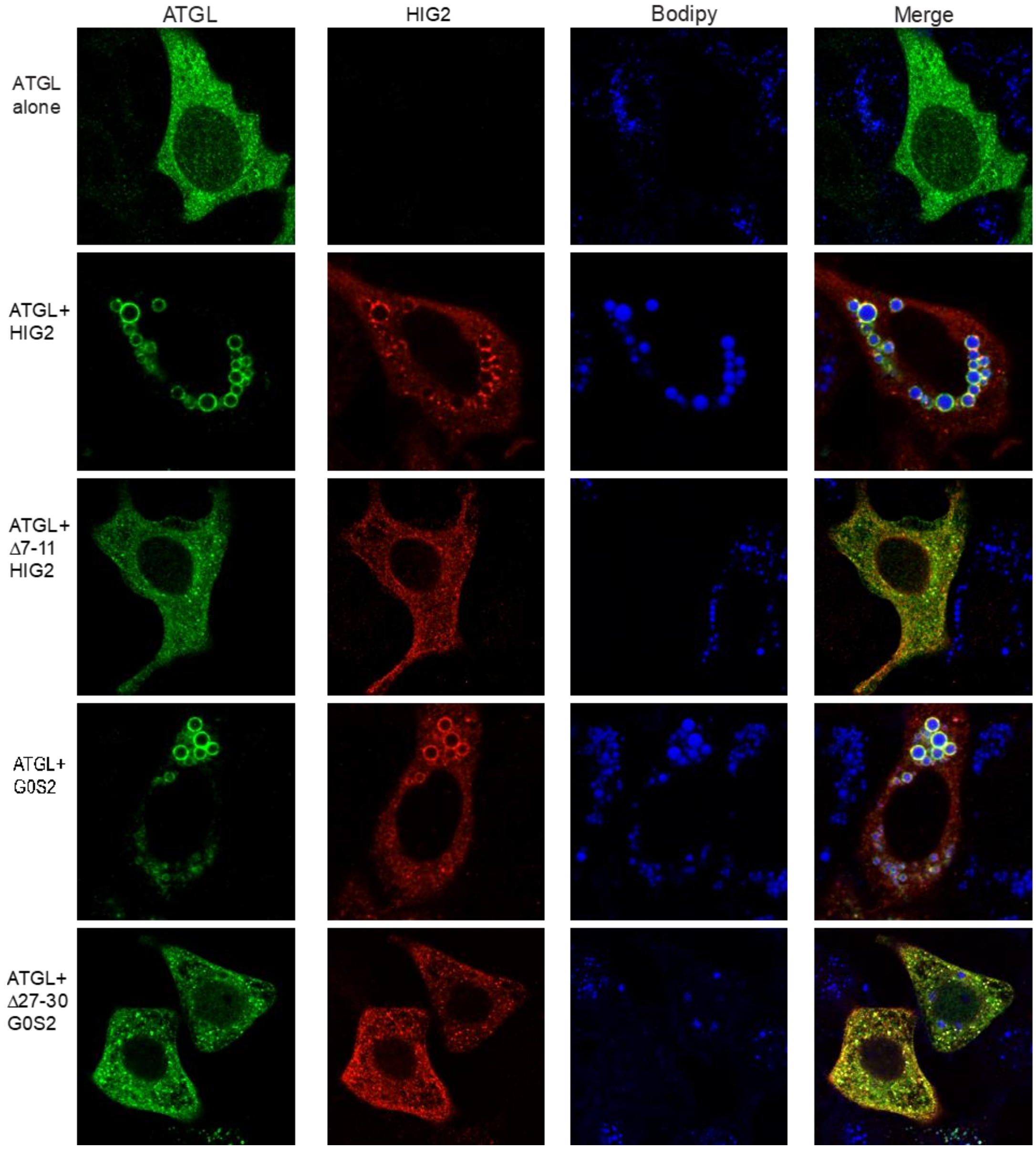


Figure 7. HIG2 and G0S2 have conserved LY(V/L)LG motifs. (A) Diagram of HIG2 and G0S2 HD domains. (B) Hela cells loaded with 200uM oleic acid were transfected with myc-tagged ATGL (green), and flag-tagged WT or deletion mutants of HIG2 and G0S2. 18-24hr later cells were fixed and stained for LD (bodipy, blue) and flag (red).

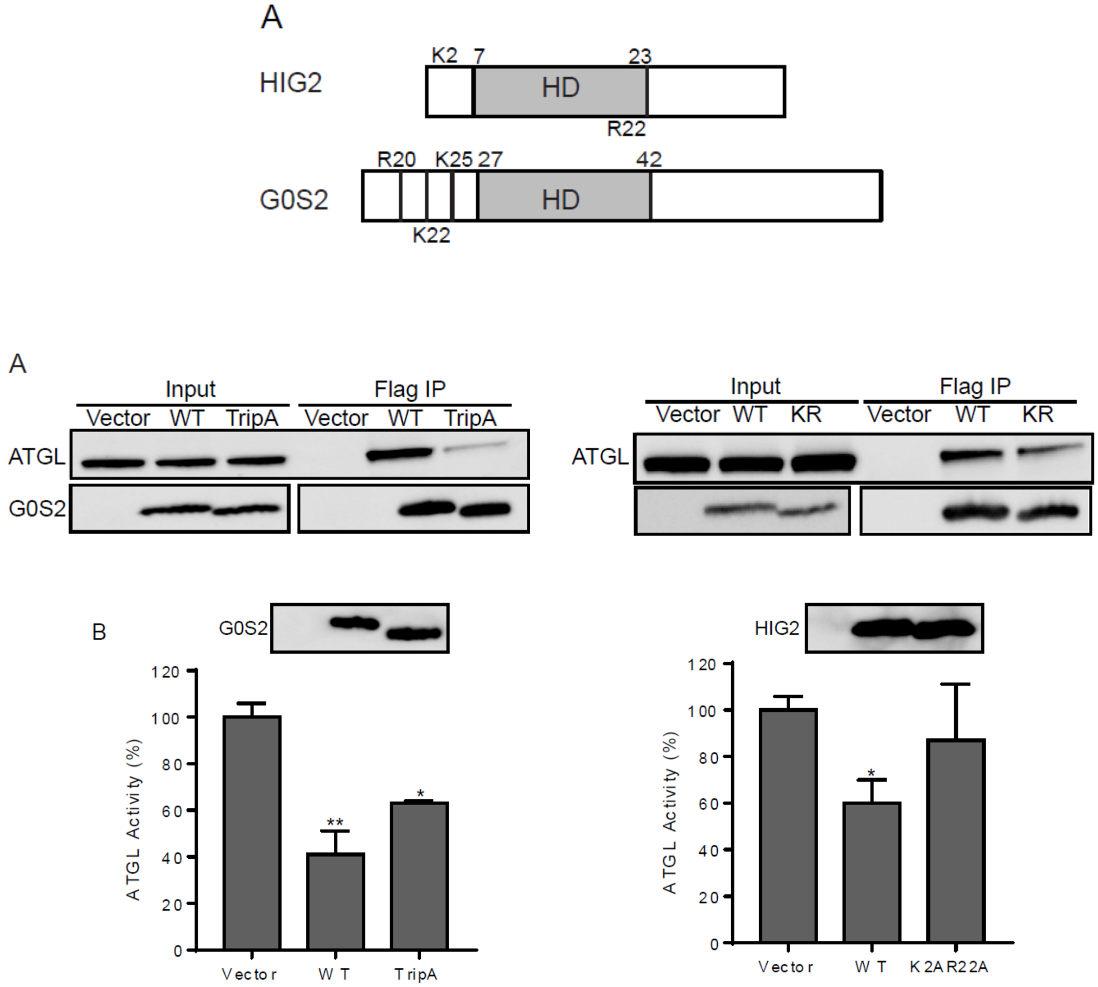


Figure 8. Mutation of positively charged reduces inhibitory function of HIG2 and G0S2. (A) Diagram of positive charged residues in HIG2 and G0S2. (B) Immunoprecipitation of flag-tagged G0S2and HIG2. Hela were transfected with wt ATGL and a flag-tagged G0S2 or HIG2 construct overnight. G0S2 or HIG2 was immunoprecipitated using flag-beads. (C) ATGL in vitro lipase activity assay performed in the presence of in vitro translated wt G0S2, G0S2 TripA mutant, wtHIG2 or K2AR22AHIG2 *p<0.05.

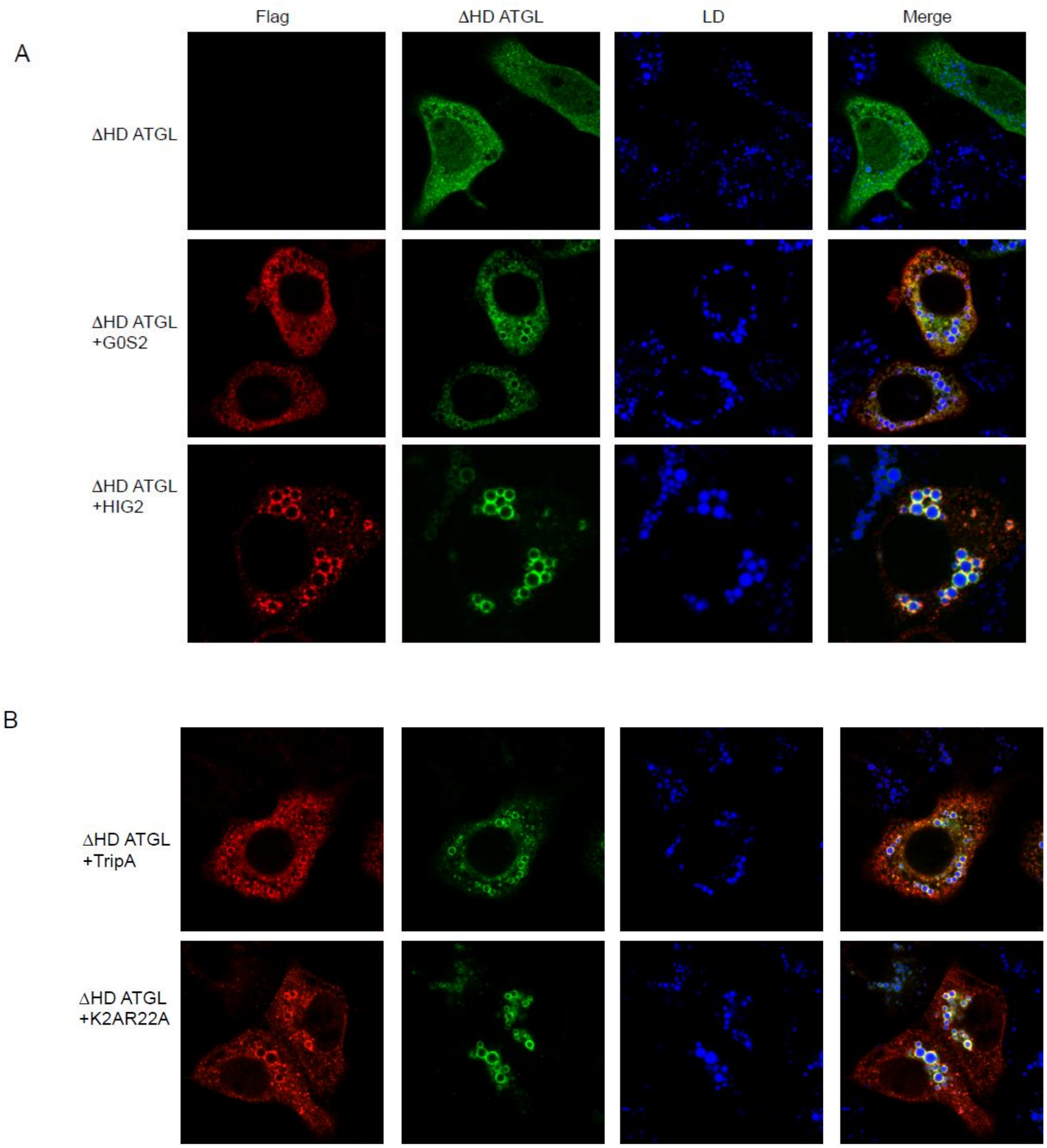


Figure 9. Binding to ATGL can bring Pos-Seq mutants to LD surface. Hela cells loaded with 200uM oleic acid were transfected with myc-tagged ΔHDATGL (green), and flag-tagged WT (A) or Pos-Seq (B) mutants of HIG2 and G0S2. 18-24hr later cells were fixed and stained for LD (bodipy, blue) and flag (red).

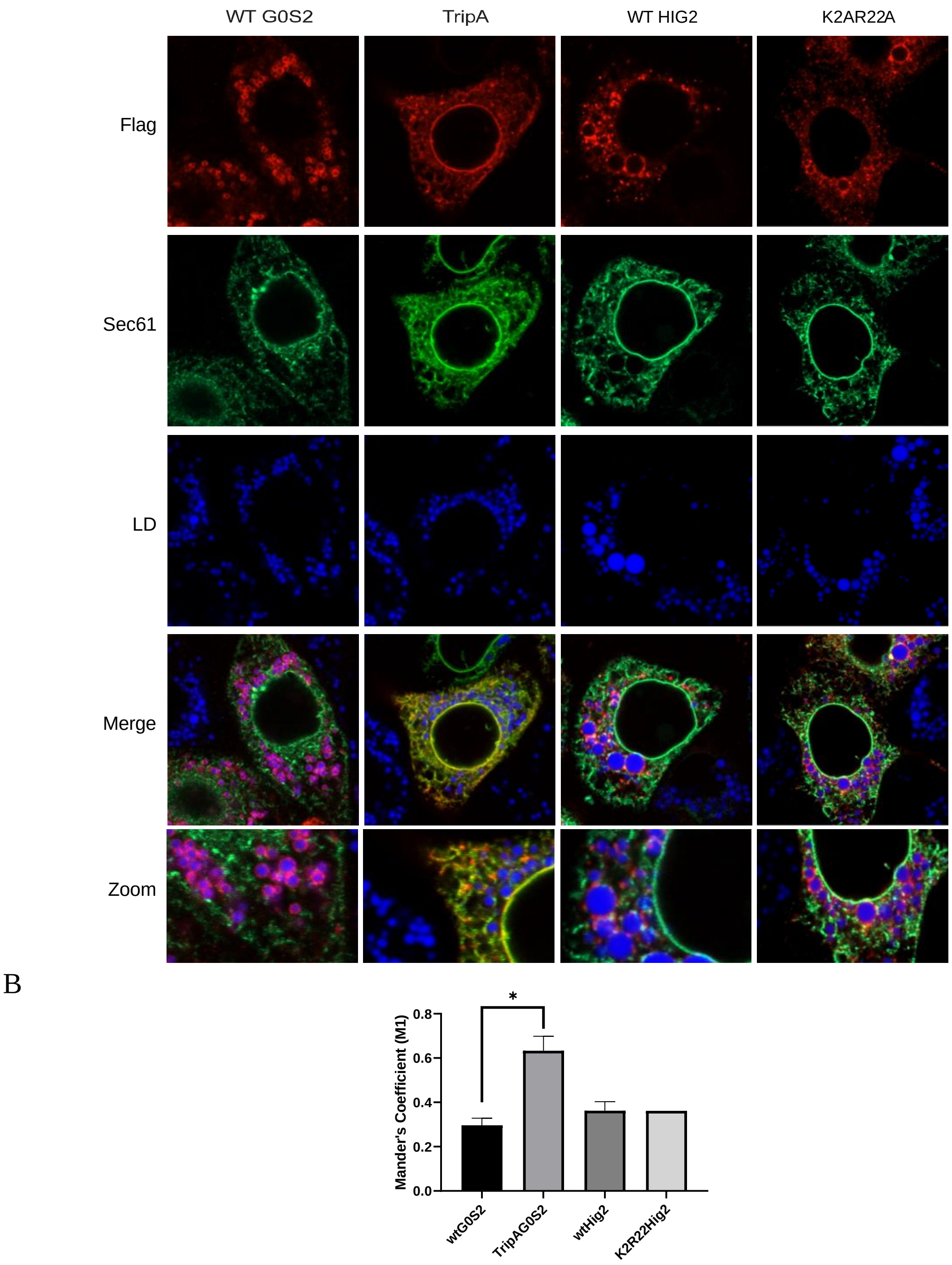


Figure 10. G0S2 but not HIG2 contains a Pos-Seq LD targeting motifs. (A) ATGL-/- Hela loaded with 200uM oleic acid were transfected with ER marker Sec61-GFP (green), flag-tagged WTor Pos-Seq mutants. 18-24hr later cells were fixed and stained for LD (bodipy, blue) and flag (red). (B) Mander's colocalization coefficient (M1) between Sec61 and flag-tagged wt or mutant HIG2 and G0S2.

CHAPTER 3

CHARACTERIZATION OF APOL6 FUNCTIONAL DOMAINS

Introduction

Apolipoprotein L family of lipoproteins is comprised of six members (L1-L6) with significant sequence homology[45]. ApoL transcripts are expressed in a variety of tissues, and analysis of their amino acid sequences revealed several predicted amphipathic helices, which are common in lipids and cellular membrane binding proteins[46]. ApoL1, the most studied member of the ApoL family, is secreted into the bloodstream. However ApoL6, is remains intracellular.[47,48]

ApoL1, is a lipid-binding protein component of high-density lipoprotein (HDL). ApoL1 is secreted into the bloodstream and by virtue of its pore forming abilities, confers resistance to the blood-borne parasite *Trypanosoma brucei brucei.* [49,50] The domains important in regulating ApoL1 phenotypes include a Pore-Forming Domain (PFD) downstream of an N-terminal signal peptide sequence, which is required for destabilizing the mitochondrial and lysosomal membranes of its parasitic target. [49] Downstream of the PFD is the membrane addressing domain (MAD), which is required for ApoL1 association with lysosomal and mitochondrial membranes[49]. Lastly, the C-terminal domain encodes an amphipathic helix, which mediates the interaction of ApoL1 with its parasitic target (SRA-interactive domain)[49]. While they are known to enhance its trypanolytic activity, C-terminal mutations of ApoL1 are implicated in the development of chronic kidney disease[51]. These mutants accumulate within podocytes, leading to mitochondria-induced cell death[52]. A recent study demonstrated that both wild type and mutant ApoL1 translocate into mitochondrial matrix, where oligomerization of mutant proteins activates the opening of mitochondrial permeability transition pore (mPTP).[53] In a separate study, wild-type ApoL1 was found to localize to LDs in podocytes.[52] Coexpression of wild-type ApoL1 with mutant ApoL1 enabled recruitment of the latter to lipid droplets, accompanied by reduced cell death. This was thought to explain the recessive pattern of the kidney disease inheritance.

The domains of the other ApoL family members are described relative to ApoL1. Unlike ApoL1, ApoL6 lacks an N-terminal signal peptide required for secretion into the bloodstream. This suggests that ApoL6 functions intracellularly. Consistent with other members of the ApoL family including ApoL1, ApoL6 contains a Bcl-2 Homology 3 (BH3) domain that mediates its apoptotic function. Liu et. al. showed that intracellular accumulation of ApoL6 resulted in activation of both caspase 8- and mitochondria-dependent caspase 9 apoptotic pathways[54,55]. The ability of ApoL6 to induce apoptosis was dependent on the presence of an intact BH3 domain[54].

Outside of its ability to induce apoptosis in cancer cell lines, a recent report by Tan et. al. suggests that ApoL6 has a role in adipocyte biology. While investigating the role of microRNA 10b-5p in adipocytes, they found that ApoL6 was a target of miRNA10b-5p, and that upregulation of ApoL6 through suppression of miRNA10b-5p resulted in enhanced differentiation of mouse 3T3-L1 preadipocytes into adipocytes[56]. They also found that upregulation of ApoL6 was common in certain obesity-related cancers including pancreatic adenocarcinoma [56]. These findings support the need for further study of the role of ApoL6 in adipocytes.

A main function of adipocytes is the storage and release of fatty acids. In response to heightened energy demand, signaling through β-adrenergic receptors stimulates adipocyte lipolysis and release of fatty acids. These fatty acids are then taken up and metabolized by other tissues to produce energy. Previous studies show that ApoL6 is a fatty acid binding protein [47,57]. ApoL6 has been shown to interact with 18-carbon fatty acids including stearic acid, which is commonly found in white adipose tissue [54,58].

Despite the ability of ApoL6 to associate with fatty acids, early functional studies have focused on its ability to induce apoptosis via its Bcl-2 Homology 3 (BH3) domain. The findings from Tan et. al., however, suggests there may be a role for ApoL6 in adipocyte biology. Our aim in this study was to determine the function of ApoL6 in mature adipocytes. Based on the absence of a signal peptide and predicted amphipathic helical domains, we hypothesized that ApoL6, like ApoL1, was an intracellular protein that is capable of localizing to both lipid droplets and mitochondria.

Indeed, we found that ApoL6 can associate with immature lipid droplets and is highly expressed in adipose tissue of wild-type mice. We also found that ApoL6 contains a mitochondrial localization sequence in its C-terminal region and that ApoL6 associates with mitochondrial fatty acid oxidation proteins. Lastly, we show that ApoL6 transcript is downregulated in response to β-adrenergic stimulation. Our results suggest ApoL6 plays a significant role in the regulation of adipocyte fatty acid and energy metabolism.

Methods and Materials

Lipolysis assay

Method as previously described [25]. Isoproterenol (ISO) was obtained from Sigma-Aldrich. Reagents for tissue culture were obtained from Invitrogen. Lipolysis was measured as the rate of glycerol and free fatty acid release by using 3T3-L1 Lipolysis Assay kit (Zenbio). Ten days after differentiation induction, adipocytes in six-well dishes were washed twice with serum- and phenol red-free DMEM containing 2% FA-free BSA and then incubated in 2.5 ml of the same medium in the presence or absence of 10 μM isoproterenol. Aliquots of the culture medium were collected after 1 h. The amounts of glycerol and FFA released were determined according to the manufacturer's instructions. Lysates were then prepared from the remaining cells, and protein concentrations in the lysates were determined and used to normalize the lipolytic signals. Statistical analysis was determined by Student's *t* test.

Co-immunoprecipitation analysis

Cells were lysed in buffer containing 50 mM Tris-HCl, pH 7.4, 150 mM NaCl, 1% Triton X-100, 1 mM DTT, and protease tablet inhibitors (1 tablet per 10 ml of buffer). Anti-Flag M2-conjugated agarose gels were incubated with the lysates for 5 hr at 4°C. The beads were then washed four times with lysis buffer, and the bound proteins were eluted in SDS buffer and analyzed by immunoblotting.

Mass Spectrometry

Flag-bead immunoprecipitated lysates were heated at 95 °C for 4 minutes in SDS sample loading buffer and were separated on by 4-20% gradient SDS polyacrylamide gels. Mass spectrometry method as previously described[59]. Gels were stained with Bio Safe Coomassie G-250 Stain (Bio-Rad, Berkeley, CA) and each lane of the gel was cut into 8 slices, destained twice and dehydrated. Gel pieces were dried by vacuum centrifugation and rehydrated with trypsin solution and incubated at 37 °C overnight. Digestion was terminated using 5% formic acid. Supernatants were transferred to a clean polypropylene tube. The extraction procedure was repeated using 0.5% FA, and the two extracts were combined. The resulting peptide mixtures were purified by solid phase extraction (C_{18}

ZipTip) and eluted with 4 µl of 50% ACN:1% FA (v/v) and 4 µl of 80% ACN:1% FA (v/v). The eluates were combined and dried by vacuum centrifugation, and 6 µl of 0.1% FA (v/v) was added followed by sonication for 2 minutes. Mass spectrometry - LC-ESI-MS/MS was performed on a Thermo Electron (San Jose, CA) Orbitrap Elite Velos Pro fitted with an EASY source (Thermo Electron, San Jose, CA).

T37i adipocyte differentiation

Method as described previously. [60,61] Cells were kept in maintenance culture in DMEM/F12 Glutamax supplement (Life technologies) containing 10% FBS (BioWhittaker), 100 IU/mL penicillin and 10 mg/mL streptomycin (Life technologies). For differentiation, cells were kept at complete confluency and after two days 2 nM triiodothyronine (Sigma-Aldrich) and 2 µM insulin (Sigma-Aldrich) was added to the medium for 9 days. During differentiation, medium was replaced every two days and cells were used for experiments between differentiation day 10–12.

3T3L1 differentiation

Method as previously described[62]. Reagents: IBMX stock solution (0.25 mM IBMX in 0.5 N KOH solution, Sterilize through a sterile 0.22-µm filter and store at −20°C) Insulin stock solution (167 µM (1 mg/mL) in 0.02 M HCl, Sterilize through a sterile 0.22-µm filter, Store at −20°C for long term, 4°C for 1 month) Dexamethasone stock solution (10 mM in 100% ethanol (store at −20°C)). Differentiation Media I (DMEM/10% FBS, 1:500 IBMX stock solution, 1:1000 insulin stock solution, 1:10,000 dexamethasone stock solution). Differentiation Media II (10% FBS/DMEM, 1:1000 insulin stock solution). Method: Prior to differentiation, 3T3-L1 preadipocytes are routinely maintained in DMEM/10% FBS in 15cm cell culture dishes. Upon reaching confluence, add fresh DMEM/10% FBS and incubate for 2 more days. To initiate differentiation, 25 mL of Differentiation Media I (Day 0) freshly made from stock solutions of different components. Three days later (Day 3), the media become more viscous. Change media to 25 mL of Differentiation Media II. Two days later (Day 5), remove Differentiation Media II and replace with 25 mL of normal DMEM/10% FBS. Two to three days later (Day 7–Day 8), cells should be fully differentiated and ready for subsequent functional experiments.

3T3-L1 and T37i adipocyte adenoviral overexpression

Method as previously described[62]. DPBS and DMEM/10% FBS are prewarmed to 37 °C in water bath before the experiment. Six-well plates are precoated with collagen solution. Make a 1:250 dilution of collagen type I solution in DPBS and add 2.5 mL/well diluted collagen solution to the plates. Plates are placed in a tissue culture incubator for 1 h and then washed with DPBS prior to the seeding of cells. Differentiated adipocytes (Day 7 or 8) in 15-cm plates are washed twice with DPBS. 5 mL of 0.25% trypsin–EDTA solution is added to each plate followed by gentle swirling to evenly coat cells. The trypsin–EDTA solution is removed by aspiration and the cells are placed in the tissue culture incubator for 3–5 min. 10–15 mL of DMEM/10% FBS is added into each plate. Cells are dispersed by gentle pipetting and then transferred to a 50-mL conical tube. The volume is adjusted to ~40 mL. After further mixing by inversion, the cells are then split (3 mL/well) into the six-well plates precoated with collagen. Gentle shaking is applied to distribute the cells evenly. One 15-cm plate of adipocytes can be divided into 2 six-well plates. After 2 days of standard incubation at 37 °C, cells are washed twice with room temperature DPBS. 2.0 mL serum-free DMEM containing 5 μg/mL of polybrene and an appropriate amount of adenovirus (2×10^8 pfu) is added into each well. Seal plates with parafilm, placed securely in microplate adaptors, and centrifuged for 1 h at 800×g at room temperature. In order to ensure the same centrifugal force of each well in the plate, following 30 min of centrifugation the plate can be inverted for another 30 min of centrifugation. After centrifugation, parafilm is removed and the plates are placed in the tissue culture incubator. After 4 h, 2.0 mL of DMEM/10% FBS is added to each well in a step to aid cell recovery. Do not remove the virus-containing media at this point. After an overnight incubation, the virus-containing media is removed and replaced with fresh DMEM/10% FBS. After 2 more days of incubation, the cells are ready for functional analyses.

3T3-L1 adipocyte siRNA knockdown

Method as previously described[62]. DPBS and DMEM/10% FBS are prewarmed to 37 °C in water bath before the experiment. Six-well plates are precoated with collagen solution. Make a 1:250 dilution of collagen type I solution in DPBS and add 2.5 mL/well diluted collagen solution to the plates. Plates are placed in a tissue culture incubator for 1 h and then washed with DPBS prior to the seeding of cells. Differentiated adipocytes (Day 7 or 8) in 15-cm plates are washed twice with DPBS. 5 mL of 0.25% trypsin–EDTA solution is added to each plate followed by gentle swirling to evenly coat cells. The trypsin–EDTA solution is removed by aspiration and the cells are placed in the tissue culture incubator for 3–5 min. 10–15 mL of DMEM/10% FBS is added into each plate. Cells are dispersed by gentle pipetting and then transferred to a 50-mL conical tube. The volume is adjusted to ~40 mL. After further mixing by inversion, the cells are then split (3 mL/well) into the six-well plates precoated with collagen. Gentle shaking is applied to distribute the cells evenly. Dilute Lipofectamine® RNAiMAX Reagent (Invitrogen) in Opti-MEM® Medium (Invitrogen), Dilute siRNA in Opti-MEM® Medium, Add diluted siRNA to diluted Lipofectamine® RNAiMAX Reagent (1:1 ratio), Incubate 5 minutes at room temperature, Add siRNA-lipid complex to wells containing 3T3-L1 adipocytes, Incubate cells for 24 h at 37°C. Then, analyze transfected cells. The following double-stranded stealth siRNA oligonucleotides (Invitrogen) were used: mouse FSP27, sense 5′-GCACAAUCGUGGAGACAGAAG-3′ and antisense 5′-UAUUCUUCUGUCUCCACGAUU-3′; Control oligonucleotides with comparable GC content were also from Invitrogen.

Fatty acid oxidation

Method as previously described[25]. Cells in 6-well plates were washed with PBS, and then incubated with 2 ml of BSA-complexed oleate (0.2 mM unlabeled plus 2 μCi/ml of [9, 10- ^{3}H] oleate and 0.2% BSA) in serum-free medium. Six hours later, the medium was collected for measuring ^3H_2O production. Excess [9,10- ^{3}H]- oleate in the medium was removed by precipitating twice with an equal volume of 10% trichloroacetic acid with 2% BSA. After centrifugation at 15,000 × g for 3 min at 4°C, the supernatants (0.5 ml) were extracted with 2.5 ml of chloroform/methanol (2:1, v/v) and 1 ml of 2 M KCl/HCl (1:1, v/v), following by centrifuged at 3,000 × g for 5 min. The aqueous phase containing ^3H_2O was collected and subjected to liquid scintillation counting and data was normalized by protein contents.

mRNA isolation and qPCR

Total RNA was isolated from mouse tissue samples using the RNeasy Plus Mini Kit (Qiagen). cDNA was synthesized from total RNA by High-Capacity cDNA Reverse

Transcription Kit (Applied Biosystems). The resulting cDNA was subjected to real-time PCR analysis with SYBGreen PCR Master Mix (Invitrogen) on an Applied Biosystems 7900 HT Real-Time PCR System. PCR primers ApoL6 forward TACTCTCTGGGAGGACTGGAA reverse TCACCAGAGTCTTGCTCTCT. β-actin forward GGCTGTATTCCCCTCCATCG reverse CCAGTTGGTAACAATGCCATGT. Data were analyzed using the comparative cycle threshold (ΔΔCt) method normalized to β-actin.

Immunofluorescence and confocal microscopy

Cells were seeded on glass coverslips placed in 6-well plates and transfected with 0.25, 0.5 or 1 µg of each DNA construct using Lipofectamine 2000 according to the manufacturer's instructions. Six hours later, transfected cells were incubated with 400 µM oleic acid/0.2% BSA overnight. Following the fixation with 4% paraformaldehyde in PBS for 10 min, cells were permeabilized by 0.2% triton X-100 for 10 min, quenched with 100 mM glycine in PBS for 20 min, and then blocked with 2% BSA in PBS for 1 hr. The cells were then exposed to primary flag monoclonal antibody (1:300) for 2 hr at room temperature. Following three washes with PBS, the cells were treated for 1 hr with Alexa Fluor secondary antibodies. To visualize lipid droplets, 1 µg/ml of Bodipy 493/503 dye was added during the incubation with secondary antibodies. Samples were mounted on glass slides with SlowFade Diamond mounting medium and examined under a Zeiss LSM 800 inverted confocal microscope. Acquired images were processed and quantified manually with Zen Blue and ImageJ FIJI software. Mouse anti-Flag M2 (Sigma, #F1804, 1:1000 dilution); Mouse anti-Actin (Sigma, #A1978, clone AC-15, 1:10,000 dilution)

Mice

Wild-type C57BLK6 mice were housed and fed a normal chow diet (test diet no. 5001, 4.5-5% total fat) and water *ad libitum* consistent with IACUC protocol A21514-14-R17 (Regulation of adipose lipolysis and relevant metabolic processes. At 16 weeks, tissues were harvested for protein and mRNA analysis.)

Statistical analysis

Values are expressed as mean ± SD for in vitro studies and ± SEM for mice. Statistical significance was evaluated by Student *t* test. Differences were considered significant at $P < 0.05$.

Results

ApoL6 contains analogous domains to ApoL1 but lacks an N-terminal signal peptide.

Figure 11A compares the protein domains of ApoL1 to ApoL6. Like ApoL1, ApoL6 includes a PFD, MAD and an SRA-interacting domain (Figure 11A). However, ApoL6 lacks a signal peptide. The absence of a signal peptide suggests that ApoL6 is not secreted from cells. Both proteins contain a BH3 domain within their PFDs and have been shown to initiate apoptosis in malignant cells[49,57,63]. Consistent with this, a role for ApoL6 in inducing apoptotic death in cancer cells has already been described in the literature [54,63,64]. However, a role for the ApoL6 in non-cancerous cells has not yet been fully described. Recent reports suggest that ApoL6 has a role in adipocyte biology [56].

ApoL6 is expressed in mouse adipose tissue.

Consistent with the Tan et. al. conclusion that ApoL6 is an important regulator of adipocyte differentiation and biology, we found that ApoL6 is abundantly expressed in white and brown adipose tissue depots (Figure 11B top). ApoL6 transcript was also detected in skeletal muscle tissue, but we have chosen to focus on examining its function in adipocytes first. Elucidating ApoL6 function in adipocytes may provide insights into its function in skeletal muscle. ApoL6 mRNA transcript results were confirmed using Western blotting (Figure 11B bottom).

ApoL6 associates is lipid droplets.

The absence of an N-terminal signal peptide indicates that ApoL6 functions intracellularly. Since the structures of intracellular lipid droplets and serum lipoproteins are very similar[21], we sought to determine whether ApoL6 could associate with lipid droplets. We generated an N-terminal flag-tagged ApoL6 construct and overexpressed it in oleic acid (OA) loaded Hela cells (Figure 12). Overexpression of the wild-type ApoL6 revealed that it associates with lipid droplets (Figure 12B).

To determine which domains in ApoL6 allow for lipid droplet binding, we generated a series of truncation and deletion mutants (Figure 12A). These mutants were constructed with N-terminal flag tags and overexpressed in OA loaded Hela cells. The confocal microscopic imaging revealed that 2 domains are required for ApoL6 interaction with lipid droplets (Figure 12B). Deletion of the membrane addressing domain, residues 137-198, disrupts lipid droplet localization (Figure 12B), mutants lacking the pore-forming domain, residues 1-135, are also unable to localize to lipid droplets (Figure 12B). Deletion of the BH3 domain does not hinder lipid droplet association (Figure 12B).

ApoL6 contains domains that influence mitochondrial morphology and function.

Previous reports used cytochrome c release and production of reactive oxygen species as an indicator of mitochondrial involvement in ApoL6 induced cell death in non-adipose cell types [54,64]. Apolipoprotein L family member, ApoL1, was shown to directly insert into the mitochondrial membrane of both lower and higher eukaryotes[49]. Based on these observations, we sought to determine whether ApoL6 can impact mitochondrial morphology or function. To do this, we generated a series of ApoL6 deletion mutants based on analogous domains in ApoL1 (Figure 12A). Two of the mutants generated displayed a mitochondrial phenotype (Figure 13). Wild-type ApoL6 localized to lipid droplets and had no obvious impact on mitochondrial function based on intact IMM potential indicated by Mitotracker staining. (Figure 13B). The deletion of its BH3 domain (ΔBH3) resulted in ApoL6 mutant that remained localized to lipid droplets, but disrupted IMM potential as indicated by the failure of Mitotracker Red to accumulate within mitochondrial matrix (Figure 13B). Deletion of the first 135 amino acids (Δ1-135) of ApoL6, which corresponds to the ApoL1 pore-forming domain (PFD), resulted in an ApoL6 variant that localized exclusively to mitochondria and induced mitochondrial fragmentation (Figure 13B). Mitotracker Red accumulated in these mitochondria despite Δ1-135 ApoL6 induced fragmentation, indicative of intact IMM potential (Figure 13B). Although the wild-type ApoL6 did not impact the IMM potential, analysis of the ΔBH3 and Δ1-135 deletion mutants suggests there may be conditions under which wild-type ApoL6 can impact mitochondrial morphology and function. These results also indicate that ApoL6 contains a mitochondrial localization sequence in its C-terminal domain (aa135-321).

ApoL6 interacts with Mitochondrial Trifunctional Protein

In order to determine whether full-length ApoL6 associated with any mitochondrial proteins, we utilized a mass spectrometry interactome approach. We overexpressed wild-type flag-tagged ApoL6 OA-loaded Hela cells, then performed an immunoprecipitation (IP) using anti-flag agarose beads. Resulting isolates were separated by SDS page and prepared for mass spectrometry. We identified 2000 proteins with at least 1 peptide associated with ApoL6, but only 107 of these proteins had at least 5 unique peptides and at least 5-fold greater interaction with ApoL6 compared to control (Figure 14A). Enrichment analysis indicated that fatty acid metabolism proteins were the most enriched in this group Figure 14B).

Two of the most abundant unique peptides associated with ApoL6 are hydroxyacyl-CoA dehydrogenase alpha (HADHA) and hydroxyacyl-CoA dehydrogenase beta (HADHB), subunits of Mitochondrial Trifunctional Protein (MTP/TFP, Table 1). HADHA and HADHB catalyze 3 of 4 steps in β-oxidation of long chain fatty acids (LCFA). β-oxidation of LCFA occurs at the mitochondrial inner membrane, which suggests that the functional activity of ApoL6 may be at the mitochondria. This idea is supported by ApoL6 association with TOM40, an OMM-embedded subunit of the translocase of the outer membrane (TOM) complex responsible for transporting proteins into the mitochondria (Table 1). Full mass spectrometry results can be found in Appendix A.

MTP/TFP is made up of 4 subunits of HADHA bound to 4 subunits of HADHB, making it a hetero-octomer. To confirm ApoL6 interaction with MTP/TFP subunits, we performed a co-IP of overexpressed flag-tagged proteins. IP results show that ApoL6 binds directly to HADHB but not HADHA (Figure 15A). Using deletion mutants, we were able to determine that the C-terminal domain of ApoL6 is required for binding to HADHB (Figure 15B). This association is unique to ApoL6, as ApoL1 does not bind to HADHB (Figure 15B).

Since ApoL6 associates the MTP/TFP complex, we next sought to determine the effects of ApoL6 overexpression on fatty acid oxidation (FAO). T37i are a murine cell line used to mimic brown adipocytes [60,65]. Brown adipocytes are responsible for non-shivering thermogenesis and have the capacity to significantly increase energy expenditure[66]. Unlike white adipocytes, brown adipocytes have a high number of mitochondria and oxidize fatty acids to produce heat. To determine whether ApoL6 could impact fatty acid oxidation we overexpressed ApoL6 in T37i adipocytes.

After differentiation, T37i adipocytes were infected with ApoL6 overexpressing-adenovirus. FAO was assessed by measuring the amount of radio-labeled water produced after 5-hour incubation with radio-labeled oleate. Apol6 overexpression resulted in a significant 22% reduction in the FAO capacity of T37i brown adipocytes (Figure 15C).

ApoL6 associates with FSP27 deficient lipid droplets.

The formation of large lipid droplets is characteristic of white adipocytes. We hypothesized that ApoL6 would associate with lipid droplets in 3T3L1 adipocytes, as it did in our Hela cell model (Figure 12B). Unlike our Hela cell model, however, overexpressed ApoL6 did not localized to the large lipid droplets present in the 3T3L1 adipocytes (Figure 16A).

Mature lipid droplets have FSP27 on their surface [67]. FSP27 facilitates the accumulation of TG into existing lipid droplets causing them to expand [67–69]. FSP27 is not expressed in Hela cells but is abundant in adipocytes. We hypothesized that FSP27 was inhibiting ApoL6 association with lipid droplets. To test this, we knocked down FSP27 expression using siRNA. Knock-down of FSP27 allowed for ApoL6 localization to the surface of lipid droplets in 3T3L1 adipocytes (Figure 16A). This result suggests that ApoL6 can associate with immature lipid droplets not coded by FSP27.

A major function of white adipose tissue is the storage and hydrolysis of lipids in response to energetic demand. Energetic demand increases during heighted physical activity and cold exposure. Both conditions initiate β-adrenergic signaling cascade mediated by cyclic AMP and PKA. [70,71]This signaling cascade activates a lipolytic program that leads to the release of free fatty acids that can be utilized as fuel by fatty acid oxidation.[70,71] We assessed the effects of both ApoL6 knockdown and overexpressed ApoL6 in 3T3-L1 adipocytes. Knockdown of ApoL6 protein resulted in reduced basal lipolysis in 3T3L1-adipocytes However, stimulated lipolysis was unaffected (Figure 16B). We next sought to determine the effect of ApoL6 overexpression on 3T3-L1 adipocytes lipolysis.

ApoL6 overexpression induced a small but significant increase in lipolysis as measured by the release of glycerol and free fatty acid into the cell culture media (Figure 16C). Stimulation with the β-AR agonist, isoproterenol, in conjunction with ApoL6 overexpression increased the amount of fatty acid released from 3T3-L1 adipocytes into the media but not the amount of glycerol released (Figure 16C). This suggests that the overall rate of stimulated lipolysis was not increased by the overexpression of ApoL6, but rather there was an increase in the rate of efflux of fatty acids from stimulated cells.

ApoL6 is regulated by β-adrenergic signaling.

Since manipulating ApoL6 protein levels had varied effects of basal and stimulated lipolysis (Figure 16B and C), we sought to determine whether ApoL6 transcription was responsive to β-adrenergic stimulation. We treated 3T3L1 adipocytes with IBMX, a phosphodiesterase inhibitor that stabilizes cyclic AMP (cAMP) or H89, a potent PKA inhibitor. IBMX treatment significantly reduced ApoL6 transcript while H89 increased ApoL6 transcript levels (Figure 17A).

Cell culture experiments using 3T3-L1 adipocytes indicated that ApoL6 transcript is downregulated in response to β-AR stimulation (Figure 17A). To validate this response in animals, we used an acute cold exposure experimental design. Cold exposure activates β-adrenergic receptor signaling resulting in increased lipolysis and fatty acid oxidation to produce heat.[72] Fasted wild-type mice were subjected to 4-degree cold exposure or kept at room temperature conditions. After 4 hours gonadal, inguinal and brown adipose tissue were collected and ApoL6 transcript was assessed. Consistent with the 3T3-L1 cell culture model ApoL6 expression was significantly down regulated in gonadal and brown adipose tissue in response to cold exposure (Figure 17B).

Discussion

Apolipoprotein L family members are becoming an interesting and diverse group of proteins warranting extensive study. ApoL family members have been characterized as pro-apoptotic BH3 domain containing proteins. Previous reports on ApoL6 function show that it can induce mitochondrial-dependent apoptosis in a variety of cancer cell lines and smooth muscle cell [54,64]. However, this is not the full scope of their function as recent studies have begun to suggest. ApoL1 mutants have been implicated in chronic kidney diseases, and ApoL2 has been found to be an anti-apoptotic protein. To our particular interest, ApoL6 has been implicated in adipocyte biology and function [56,73–76].

ApoL proteins contain predicted amphipathic helices within their amino acid sequence[46]. Amphipathic helices are common features of lipoproteins and lipid-droplet binding proteins [41,43]. Tan et. al. showed that ApoL6 was a target of miRNA10b-5p, and that the upregulation of ApoL6 can influence the differentiation of 3T3-L1 cells into adipocytes[56]. Here we sought to further expounded upon the role of ApoL6 in adipocyte biology.

Sequence comparison showed that ApoL6 lacked a signal peptide found in ApoL1, suggesting that ApoL6 functions intracellularly (Figure 11). Our initial studies overexpressing wild-type ApoL6 showed localization to with FSP27-deficient LDs (Figures 12 and 16). This is significant as nascent LDs budding off from the endoplasmic reticulum lack FSP27. [67,77] Whether ApoL6 associates immediately after budding or is present at the ER has yet to be determined. The functional significance of ApoL6 localization should also be examined. Nascent droplets can form as a result of activated lipolysis during β-adrenergic stimulation. It is possible that sequestering ApoL6 at LDs prevents it from localizing to mitochondria and inhibiting fatty acid oxidation.

Domain mapping using internal and truncation mutants suggests that the C-terminal domain of ApoL6 contains a mitochondrial localization sequence (Figure 13). We also found that ApoL6 associates with TOM 40 (Figure 14, Table 1). TOM40 is the core channel protein of the translocase of the outer membrane (TOM) complex responsible to importing proteins into mitochondria [78,79]. This result along with the determination that the ApoL6 C-terminal domain, specifically residues 237-321, interacts with the HADHB subunit of MTP/TFP open the possibility that ApoL6 functions at the mitochondria. This would be a unique function from ApoL1 cytotoxic mitochondrial activity as ApoL1 does not associate with HADHB (Figure 15B).

Further evidence of ApoL6 involvement in fatty acid utilization was provided by observing the impact of ApoL6 overexperssion on lipolysis. β-adrenergic stimulation of adipocytes increases lipolysis freeing fatty acids to be utilized at the mitochondria. We found that overexpression of ApoL6 during beta-adrenergic stimulation led to an increase in the release of free fatty acids (Figure 14). However, there was no significant difference in glycerol compared to stimulated controls (Figure 14). This suggests there was no difference in the rate of stimulated lipolysis between control and ApoL6 overexpressing cells. Instead, it suggests that ApoL6 may influence fatty acid efflux. It is possible that ApoL6 overexpression led to a defect in the ability of 3T3-L1 adipocytes to utilize free fatty acids intracellularly. This resulted in greater release of fatty acid s from adipocytes because they could not be efficiently oxidized at the mitochondria.

In support of this idea, mass spectrometry protein interaction data showed that HADHA and HADHB, subunits of mitochondrial trifunctional protein, interact with ApoL6 (Figure 13). Disruption of this complex by ApoL6 could lead to a defect in long-chain fatty acid oxidation, and thereby promoting greater release of fatty acids for cells. Further studies are required to determine how ApoL6 is affecting fatty acid transport and intracellular utilization.

Results from *in vitro* studies on lipolysis prompted us to determine the impact of β- adrenergic stimulation on the expression of ApoL6. We found that β-adrenergic signaling downregulated endogenous ApoL6 transcript *in vitro* and *in vivo* (Figure 17). This suggests that conditions that stimulate increased fatty acid release downregulate ApoL6 expression possibly as a way to allow for enhanced β-oxidation by the mitochondria.

In our analysis of ApoL6 tissue distribution, we found that ApoL6 is expressed in both brown and white adipose tissue depots (Figure 11B). White and Brown adipose tissue serve different functions in mammals. It is the responsibility of white adipose (gonadal, inguinal, etc.) to efficiently store triglyceride in large unilocular lipid droplets. It is typically the job of brown adipose to function in thermoregulation. Both adipose tissue types upregulate their rates of lipolysis and fatty acid oxidation in response to cold exposure and β-adrenergic stimulation.[71,80] Consistent with our IBMX 3T3-L1 *in vitro* results, we also found that endogenous ApoL6 transcript is downregulated in both white and brown adipose tissue in response to cold exposure, which stimulates β-adrenergic signaling (Figure 17).

Distinguishing between direct effects on lipolysis and effects on lipolysis as secondary to mitochondrial fatty acid oxidation phenotypes is an important next step for this project. We have shown that ApoL6 can associate with FSP27 deficient lipid droplets and has the ability to impact mitochondrial morphology and function. The presence of ApoL6 on nascent FSP27-deficient lipid droplets may be facilitating the increase in lipolysis observed in unstimulated 3T3-L1 adipocytes overexpressing ApoL6 (Figure 14). White adipose tissue has large FSP27 coated lipid droplets and very few mitochondria, while brown adipose tissue has a large number of mitochondria and smaller lipid droplets coated by a FSP27-related protein, CIDEA [67,68,81]. These differences in the cellular makeup of white and brown adipose tissue require follow-up investigation of ApoL6 involvement in lipolysis of both tissue types.

Although direct lipolytic effects are a possibility, our work here strongly suggests non-cytotoxic mitochondrial functions for ApoL6. As most groups have studied ApoL6 mitochondrial function in the context of cell death, we are widening the field of possible functions for this protein. We would predict that levels of ApoL6 are tightly regulated in adipocytes as its expression can facilitate the differentiation process, but dysregulation leading to excessive accumulation of ApoL6 can cause cell death. Data derived from our work have contributed to the understanding of its regulation in adipocytes, but further study into the protein functions is required.

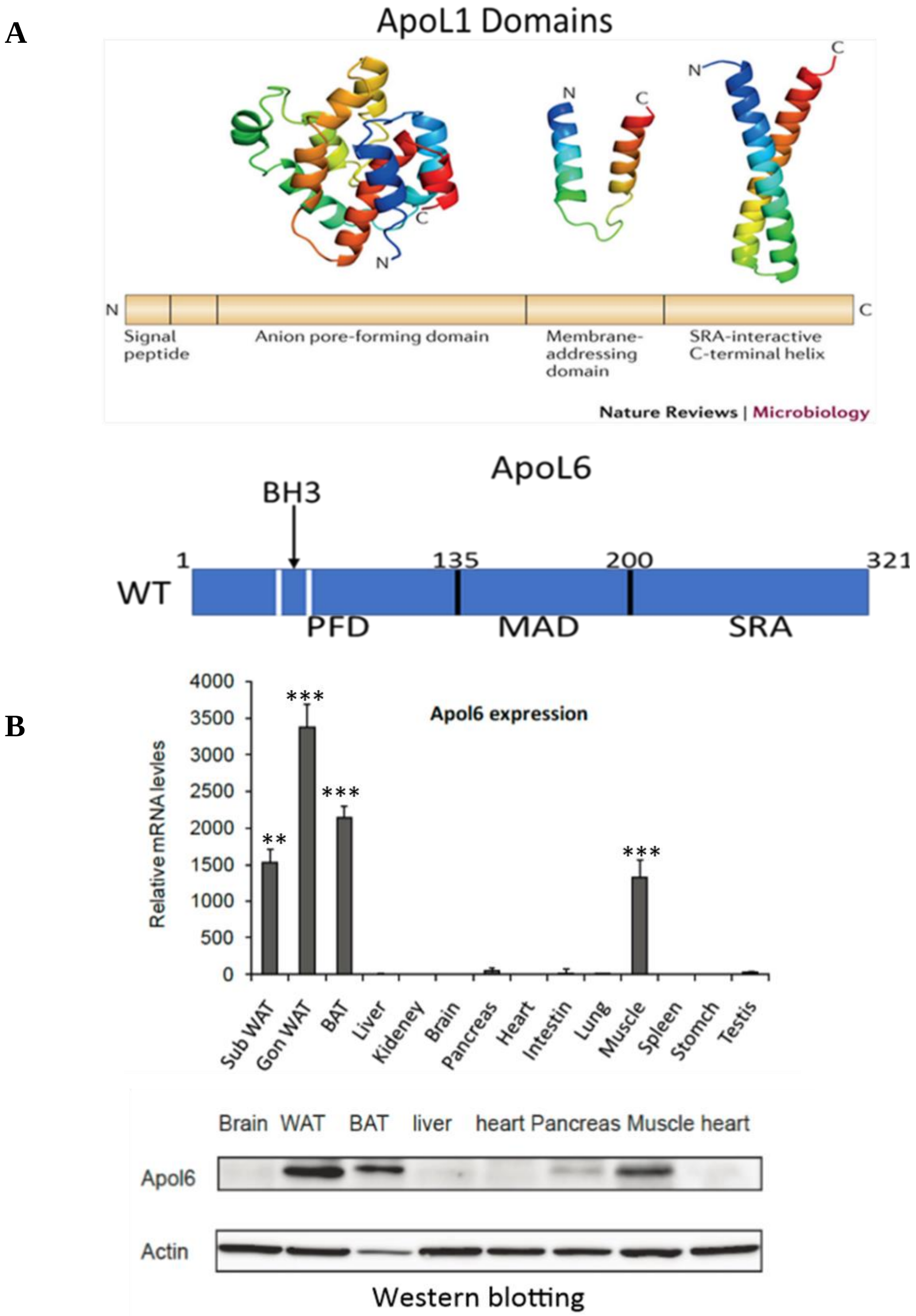


Figure 11. ApoL6 lacks a signal peptide and is expressed in adipose tissue. (**A**) Comparison of ApoL1 domains published by Pays et. al. compared to ApoL6 domains[50]. (**B**) ApoL6 mRNA(top) and protein expression(bottom) in 20-week cold wild-type mice (Zhang unpublished data).

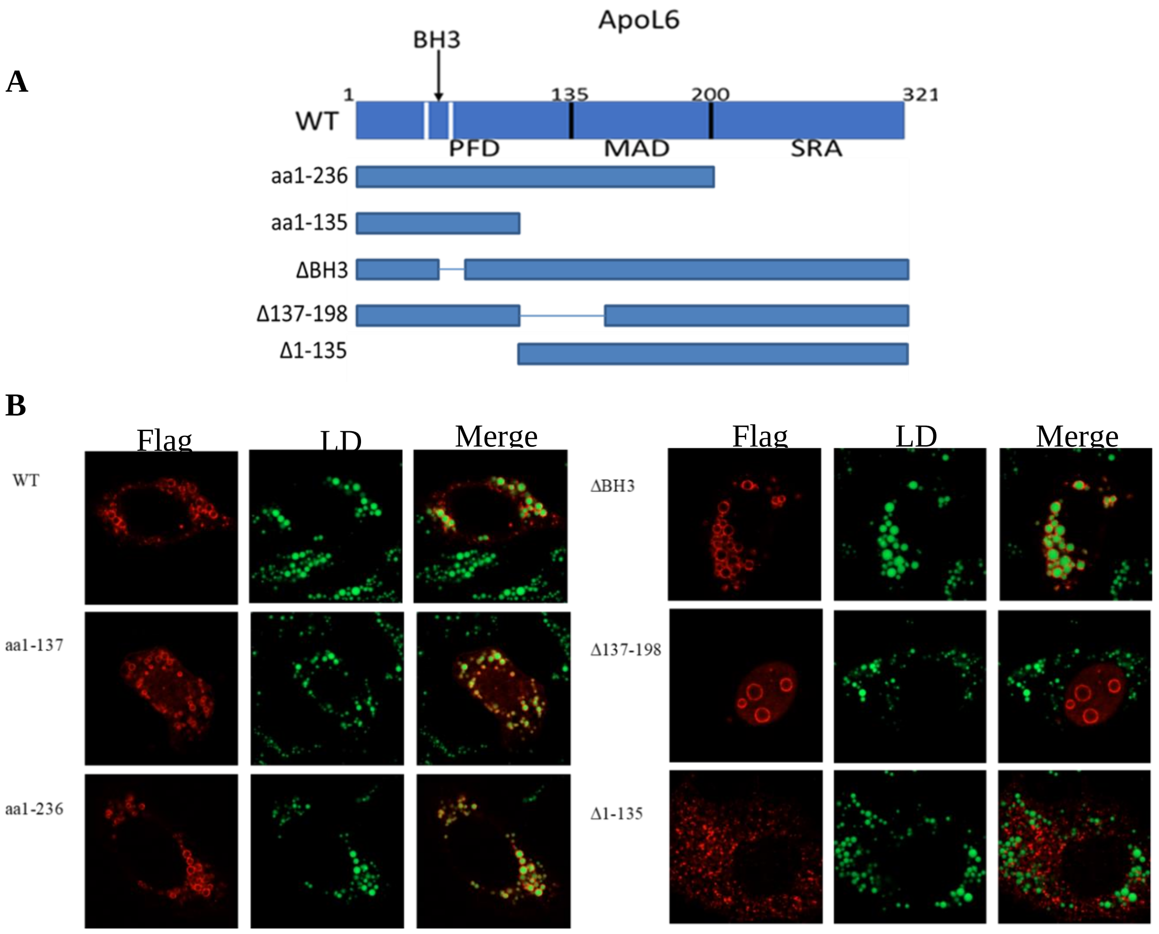


Figure 12. ApoL6 associates with lipid droplets. (**A**)Diagram of N-terminal flag-tagged wild-type and deletion mutants ApoL6. (**B**) Hela cells were cultured overnight in 400uM OA then transfected overnight with flag-tagged ApoL6 plasmids. Cells were stained for flag (red) and lipid droplets (green).

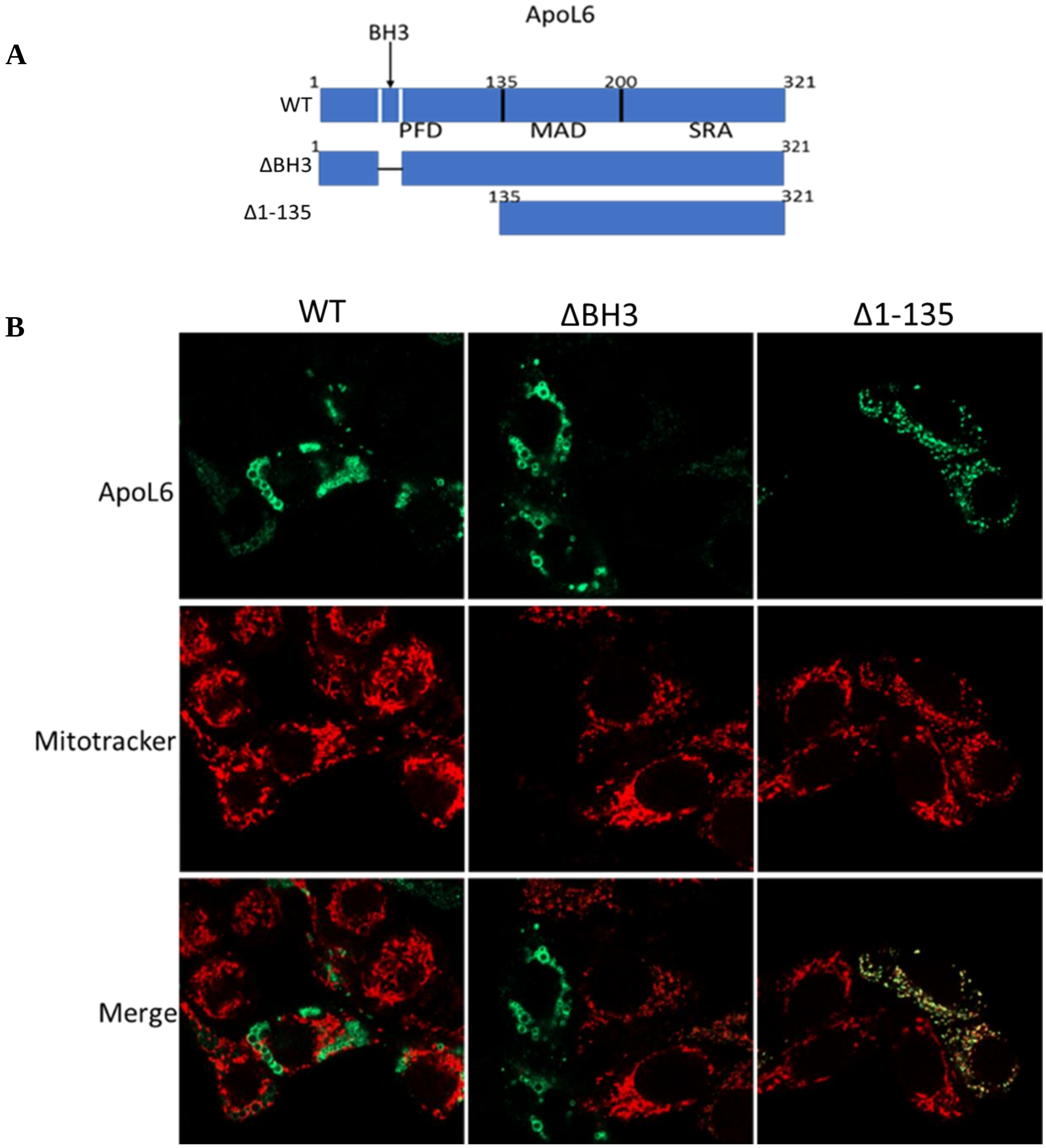


Figure 13. ApoL6 C-terminal domain interacts with mitochondria. (**A**)Diagram of N-terminal flag-tagged wild-type and deletion mutants ApoL6. (**B**) Hela cells were cultured overnight in 400uM OA then transfected overnight with flag-tagged ApoL6 plasmids. Cells were stained for flag (green) and mitochondria (Mitotracker Red).

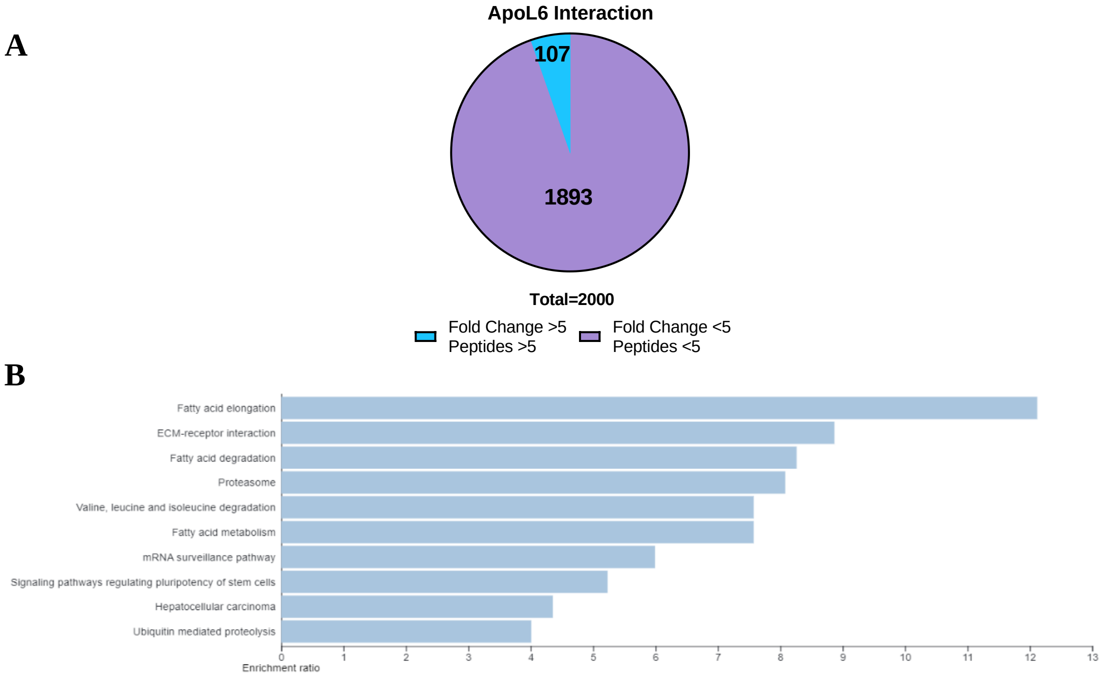


Table 1

	Gene	Fold Change ApoL6/ Control	NTSC ApoL6	NTSC Control	TUPC ApoL6	TUPC Control
Glypican-1	GPC1	78.9	81.4	1.0	33	1
Peroxisomal biogenesis factor 19	PEX19	15.5	7.8	0.5	5	0
Trifunctional enzyme subunit beta, mitochondrial	HADHB	13.3	82.4	6.2	51	5
NAD-dependent protein deacetylase sirtuin-1	SIRT1	13.1	13.6	1.0	14	1
Trifunctional enzyme subunit alpha, mitochondrial	HADHA	11.1	171.6	15.5	95	14
Mitochondrial import receptor subunit TOM40	TOMM40	5.6	5.8	1.0	6	1

Figure 14. ApoL6 binding partners. (A) Summary pie chart of number of binding partners. **(B)** Enrichment analysis of binding partner with greater than 5-fold change cover control.
Table 1. ApoL6 binding partners with largest fold change and unique peptide count.

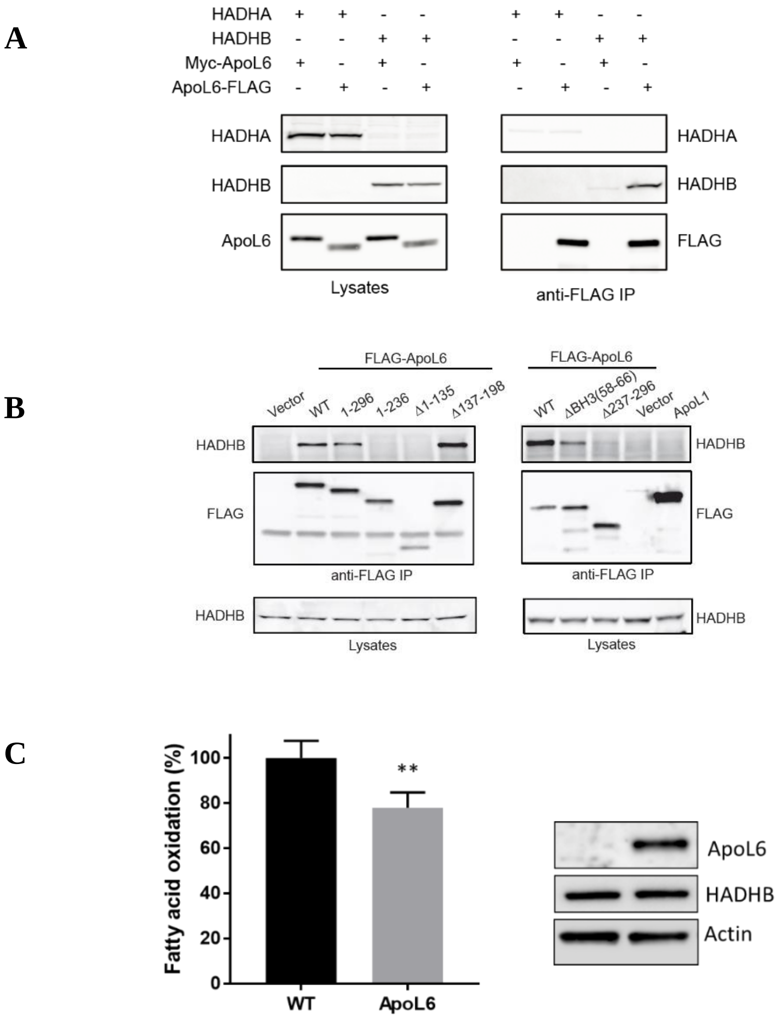


Figure 15. ApoL6 interacts with mitochondrial protein HADHB and inhibits LCFA oxidation. (A) Immunoprecipitation of overexpressed HADHB with wild-type flag-tagged ApoL6 from in Hela cells. **(B)** Immunoprecipitation of overexpressed HADHB with deletion mutants of flag-tagged ApoL6 in Hela cells. (**C**) T37i adipocytes infected with null or ApoL6 adenovirus were incubated 5 hours with radio labeled oleate. After 5 hours, media was assayed for radio-labeled water. Inset Western blot to confirm ApoL6 overexpression in T37i cells.**$p<0.001$

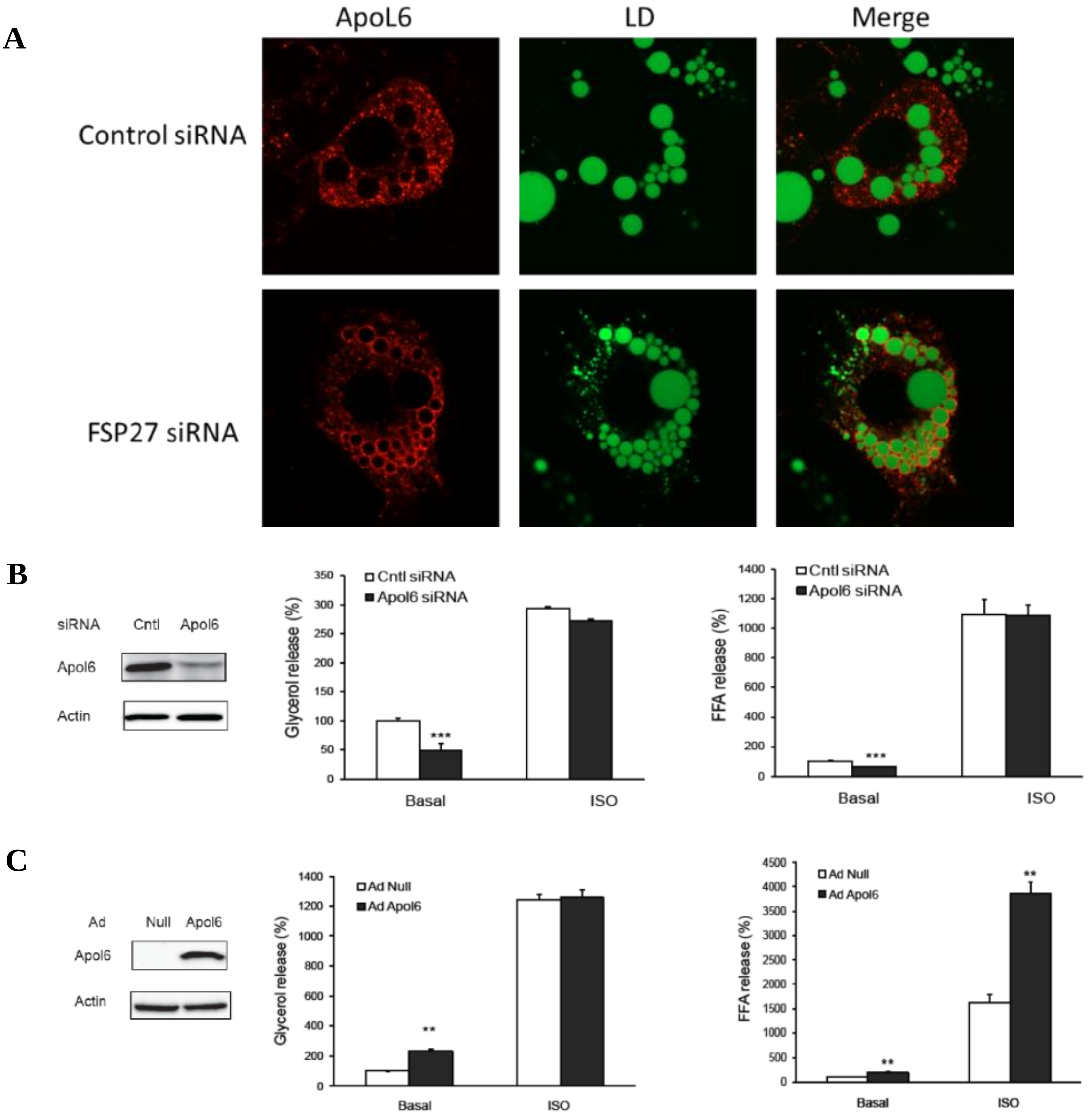


Figure 16. ApoL6 associates with FSP27-deficient lipid droplets and increases basal lipolysis. (**A**) Immunoflorescence of 3T3-L1 adipocytes overexpressing ApoL6 (red) with and without FSP27 knock down. Lipid droplets (green). **(B)** TG lipolysis assay in 3T3L1-adipocytes with ApoL6 knockdown. Inset is western blot to confirm ApoL6 knockdown. **(C)** TG lipolysis assay in 3T3L1-adipocytes with ApoL6 adenoviral overexpression. Inset is western blot to confirm ApoL6 overexpression.**p<0.001

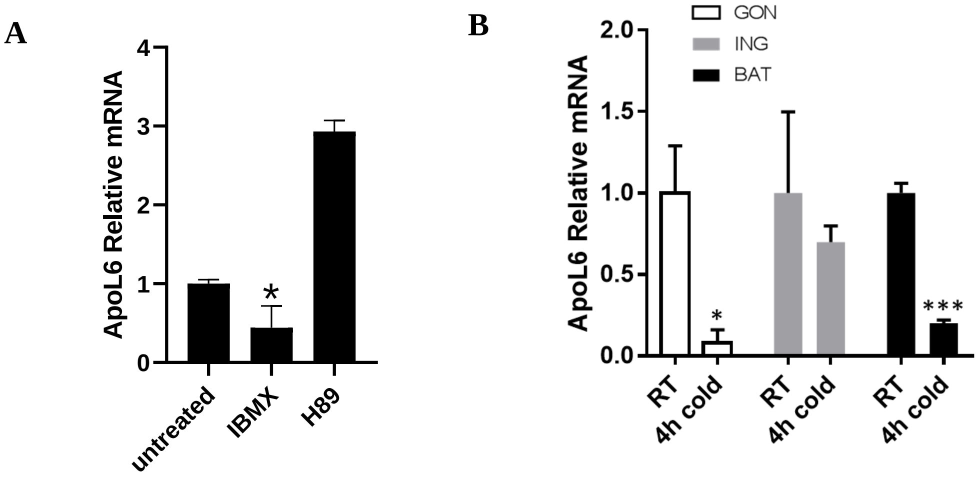


Figure17. ApoL6 transcription is decreased by β-adrenergic signaling. (A) 3T3L1 adipocytes untreated or treated for 6 hours with 1mM IBMX or 50µM H89. (**B**) 20-week cold wild-type mice were fasted for 2h then housed at 4^{o}C for 4 h. After 4 hours, adipose tissue was collected and analyzed for ApoL6 mRNA n=6 *p<0.05, ***p<0.0001.

CHAPTER 4

AUGMENTED THERMOGENIC RESPONSE IN MICE OVEREXPRESSING APOL6 IN BROWN ADIPOSE TISSUE

Introduction

Brown adipose tissue functions to dissipate energy in the form of heat in rodents and humans. Imaging studies have shown that adult humans have brown adipose tissue depots at the neck, clavicle and spinal cord[82,83]. Higher levels of brown adipose tissue are observed in younger, leaner people and in people experiencing seasonal and long-term cold exposure [82,84,85]. Brown adipose tissue drastically increases its glucose and fatty acid uptake and energy expenditure in response to cold exposure and β-adrenergic signaling [72,86,87]. Because of its metabolic properties, brown adipose tissue in humans could potentially be used to treat obesity and loss of insulin sensitivity in adults[18,88,89].

Brown adipose tissue is mitochondria dense and is stimulated by the sympathetic nervous system signaling through β3-adrenergic receptors[72]. During cold and β-adrenergic stimulation, heat production is enhanced by uncoupling ATP production from oxidative phosphorylation a process mediated by uncoupling protein UCP1.

The rate of intracellular lipolysis in both white and brown adipose tissue also increases as β-Oxidation of LCFAs generates acetyl-CoA required for the tricarboxylic (TCA) cycle and heat production. However intracellular lipolysis within brown adipocytes is not required for cold-induced thermogenesis[19]. Shin et. al. showed that circulating free fatty acids released from white adipose tissue depots are sufficient to fuel thermogenesis in brown adipose tissue during cold exposure[19]. Regardless of the source of fatty acids, mitochondrial β-oxidation of LCFAs is required for thermogenesis by brown adipose tissue [19].

We have identified ApoL6 as a novel protein involved in regulating lipolysis and fatty acid oxidation. Our *in vitro* studies using 3T3-L1 adipocytes overexpressing ApoL6 show that ApoL6 can associate with FSP27-deficient lipid droplets and increase basal lipolysis (Figure 16). We show that upon β-adrenergic stimulation, ApoL6 overexpression increases fatty acid release from differentiated adipocytes, but not the overall rate of lipolysis (Figure16B and C). Additional *in vitro* studies showed that ApoL6 overexpression inhibits oxidation of the 18-carbon LCFA oleate (Figure 15C). We also demonstrate that the C-terminal domain of ApoL6 can associate with mitochondria, and that full length ApoL6 can interact with subunits of MTP/TFP (Table 1, Figure 15A and B). These data suggest that ApoL6 inhibits fatty acid oxidation by binding directly to MTP/FTP.

Upon stimulation, brown adipose tissue increases its uptake of both glucose and fatty acids and oxidizes the compounds to produce heat. Recent work has shown that glucose is also a significant source of carbon for the TCA cycle. Hui et. al. show that glycolysis feeds into the TCA cycle through lactate production under fasted conditions in a variety of tissues, including adipose tissue[90]. Subsequent studies by Winther et. al. and Jeong et. al. show that limiting intracellular glycolysis impairs brown adipocyte glucose uptake and stimulated thermogenesis [91,92].

Notably, Wang et. al. *in vivo* using [U-^{13}C] glucose, a fully metabolizable glucose tracer, show increased glucose oxidation in brown adipose tissue during long-term cold exposure.[93] They use mass spectrometry analysis to trace [U-^{13}C] glucose derived metabolites through the TCA cycle providing direct evidence of glucose oxidation in response to cold exposure.[93] Furthermore, they demonstrate the role of mitochondrial pyruvate carrier (MPC) in this process. Importantly, they show that inhibition of MPC blocked cold and β-adrenergic agonist stimulated glucose oxidation, and that *in vivo* MPC inhibition impaired thermoregulation in cold-exposed mice.[93] These studies highlight the important role of glucose oxidation in brown adipose tissue mediated thermogenesis.

Since both fatty acid oxidation and glycolysis are important in thermogenesis, many animal and human studies rely on indirect calorimetry to assess whether carbohydrates (glucose) or fatty acids are being consumed metabolically. The use of metabolic chambers allows for such a distinction by measuring both the amount of oxygen consumed as well as the amount of C02 being expelled. This information is then used to calculate a respiratory exchange ratio or RER. The respiratory exchange ratio is the volume of expelled CO2 divided by the volume of oxygen consumed from the metabolic chamber (VCO_2/VO_2). The resulting ratio lies between 0.7 and 1, with 0.7 being indicative of fatty acid metabolism and 1 being indicative of glucose metabolism.

Here we use metabolic chambers, namely the Oxymax Comprehensive lab animal monitoring system (CLAMS), to determine the metabolic effects of ApoL6 overexpression in the brown adipose tissue of transgenic mice. We have confirmed that ApoL6 is endogenously expressed in mouse adipose tissue, and that its transcript is downregulated by cold exposure (Figure 17B). These results suggest that our transgenic ApoL6 brown adipose tissue (ApoL6-BAT) model will have a decreased ability to utilize fatty acids at room temperature and during cold exposure. Using indirect calorimetry, we obtained data that suggests ApoL6-BAT mice are defective in oxidative utilization of LCFAs. Unexpectedly, however ApoL6-BAT animals displayed an enhanced thermogenic response during cold exposure, which may be explained by reciprocal upregulation of glucose oxidation.

Materials and Methods

Mice

C57BL6 wild-type and transgenic mice were housed, fed a normal chow diet (test diet no. 5001, 4.5-5% total fat) and provided water *ad libitum* consistent with IACUC protocol A21514-14-R17 (Regulation of adipose lipolysis and relevant metabolic processes).

Generation of Transgenic Mice

To generate transgenic mice with tissue-specific overexpression of ApoL6 in adipose tissue, murine ApoL6 cDNA full sequence (National Center for Biotechnology Information reference sequence: NM_028010.1) was subcloned into a pBluescript II SK(+) vector containing a 5.4-kB adipocyte FA binding protein (aP2) promoter (Addgene) with *Sma*I and *Not*I restriction enzyme sites on the 5′ and 3′ ends, respectively. The completed aP2-ApoL6-poly(A) construct was confirmed by sequencing. Through the Mayo Clinc Transgenic and Knockout Mouse Core, the transgene fragment was released by *Sal*I digestion, purified, and microinjected into fertilized eggs of C57BL/6J mice. Tail DNA genotyping revealed a transgenic founder line with successful germ line transmission. aP2-ApoL6 transgenic mice and wild-type (WT) C57BL/6J littermates were maintained in the animal facility at Mayo Clinic

Arizona. All mice were given free access to water and were fed a standard chow diet (test diet no. 5001, 10% calories as fat).

Mouse Genotyping

Genomic DNA was extracted from 1-3mm tail snips from mouse pups. Sigma REDExtract-N-Amp tissue PCR kits were used. Briefly, 50ul of Extraction Solution reagent was mixed with 12.5ul of Tissue Preparation Solution. 62.5ul mixture was added to tail snip. Reactions were incubated for 10 minutes at room temperature, then 3min at 95^oC. 50ul of Neutralization Solution was added to stop the reaction. 4 ul of DNA was used for subsequent genotyping PCR reaction.

Body composition analysis

Body composition data for 16-week-old female and male wild type and ApoL6-BAT mice was acquired by whole body metabolic profiling using a Bruker minispec Body Composition Analyzer (Brunker Corp.) through the Mayo Clinic Mouse Metabolic Phenotyping Laboratory.

Oxymax-CLAMS

Female mice were individually placed in a Oxymax- for a multiday study. Standard 12-h light (7:00 a.m. to 7:00 p.m.) and dark (7:00 p.m. to 7:00 a.m.) cycles were maintained throughout the experiment. Mice were allowed an environmental acclimation period of 24 h at 23 degrees prior to starting the experiment at 7:00 a.m. Mice were allowed normal chow and water *ad libitum*.

Glucose and Insulin Tolerance Tests

Method as previously described. [25] For the glucose and insulin tolerance tests, fasted mice were injected intraperitoneally with glucose (2 g/kg) or insulin (0.85

units/kg). Blood glucose levels were monitored at indicated times from the tail vein using a glucometer (Freestyle; Abbott Diabetes Care).

Acute cold Exposure

20-week old transgenic ApoL6-BAT mice and aged matched litter mates were fasted for 2 hours. After fasting mice were move to 4 degrees without food but with access to hydration (Hydrogel). Temperatures were taken rectally at time 0 and at one hour increments thereafter. Termination of the experiment at 2 hours, blood and gonadal, inguinal and Brown adipose tissue was collected.

Serum Triglyceride, NEFA and glucose analysis

Plasma glucose (Wako), total TG (Thermo Fisher Scientific), free FAs (FFAs) (Wako) levels were quantified using enzyme colorimetric assays according to the manufacturer's instructions.

RNA extraction and Real-time PCR

Total RNA was isolated from mouse tissue samples using the RNeasy Plus Mini Kit (Qiagen). cDNA was synthesized from total RNA by High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems). The resulting cDNA was subjected to real-time PCR analysis with SYBGreen PCR Master Mix (Invitrogen) on an Applied Biosystems 7900 HT Real-Time PCR System. PCR primers ApoL6 forward TACTCTCTGGGAGGACTGGAA reverse TCACCAGAGTCTTGCTCTCT. β-actin forward GGCTGTATTCCCCTCCATCG reverse CCAGTTGGTAACAATGCCATGT. Data were analyzed using the comparative cycle threshold (ΔΔCt) method normalized to β-actin.

Immunoblotting

Cells were lysed at 4°C in a buffer containing 50 mM Tris-HCl (pH 7.4), 150 mM NaCl, 10 mM NaF, 1% Nonidet P-40, 0.1% SDS, 0.5% sodium deoxycholate, 1.0 mM EDTA, 10% glycerol, and protease tablet inhibitors (1 tablet per 10 ml of buffer). The lysates were clarified by centrifugation at 20,000 × g, 4°C for 10 min and then mixed with equal volume of 2 × SDS sample buffer. Equivalent amounts of protein were resolved by SDSPAGE and transferred to nitrocellulose membranes. Individual proteins were blotted with primary antibodies at appropriate dilutions. Peroxide-conjugated secondary antibodies were incubated with the membrane at a dilution of 1:5000. The signals were then visualized using ECL substrate (Thermo Scientific).

Proteinase K Protection Assay

Protocol adapted from Shah et. al and Ryan et al. [53,94] Brown adipose tissue was isolated from wild-type and ApoL6-BAT mice. Mitochondrial pellets were obtained using differential centrifugation and resuspended in STE buffer (250 mM sucrose, 5 mM Tris, 2 mM EGTA; pH 7.4). Samples were incubated on ice with STE only, 1µg/ml or 2µg/ml Proteinase K only, or 1µg/ml or 2µg/ml Proteinase K with 0.1% Triton X-100 for 1 hour. After 1 hour, 5 mM PMSF was added to stop the reaction. Samples were then incubation on ice for 10minutes, then boiled in SDS loading buffer in preparation for immunoblotting.

Metabolite Mass Spectrometry

Method from Gu et al. [95] Brown adipose tissue was removed from wild-type and ApoL6-BAT mice and stored at -80°C until use. Proteins were precipitated by mixing 50 μL of serum with 250 μL of cold methanol. After 20 min incubation at −20 °C, the mixture was centrifuged at 14 000 RCM for 20 min. The supernatant was transferred into a clean 2.0 mL Eppendorf vial and then dried under vacuum (Eppendorf Vacufuge). The obtained residue was reconstituted in 400 μL of Solvent C (40% Solvent A/60% Solvent B, see details in the LC–MS section) prior to MS analysis. In addition, 5 samples were prepared by reconstituting the metabolite residues from 50 μL of serum containing spiked U–^{13}C^{15}N-amino acids, into 200 μL (1:4 dilution), 400 μL (1:8 dilution), 600 μL (1:12 dilution), 1 200 μL (1:24 dilution), and 2 400 μL (1:48 dilution) of Solvent C.

Statistical analysis

Values are expressed as mean ± SEM. Statistical significance was evaluated by Student *t* test. Differences were considered significant at $P < 0.05$.

Results

Female transgenic mice express high levels of ApoL6 in their Brown adipose tissue.

ApoL6 transgenic mice were created as described in the methods and materials. Quantitative PCR analysis was used to determine the relative mRNA amounts of ApoL6 transcript in adipose tissue of both male and female transgenic mice. Male transgenic mice did not show a significant increase in ApoL6 transcript in any of the adipose tissue depots assayed (Figure 18A). Female transgenic mice however showed a nearly 50-fold increase in ApoL6 transcript in their brown adipose tissue only (Figure 18A). We confirmed ApoL6 protein expression in the brown adipose tissue of female transgenic animals by Western blot analysis (Figure 18B). Since only female transgenic animals overexpressed ApoL6 mRNA and protein, we proceeded with female transgenic mice (ApoL6-BAT) only for all subsequent experiments.

Overexpressed ApoL6 is localized in the mitochondria but does not impact transcription of MTP/TFP.

Our immunoprecipitation experiments indicated that ApoL6 binds to the HADHB subunit of MTP/TFP (Figure 15A). Therefore, we sought to determine if ApoL6-BAT mice had any changes in HADHA and HADHB expression. Analysis of HADHA and HADHB transcripts showed no significant difference between wild-type and ApoL6-BAT animals in gonadal, inguinal, and brown adipose tissue. (Figure 18C).

MTP/TFP is localized to the mitochondria. HADHB binding to ApoL6 suggests that ApoL6 also localizes to mitochondria. The presence of a membrane addressing domain in ApoL6 suggests that it localizes to membranous regions. For these reasons, we sought to determine whether ApoL6 is embedded in mitochondrial membranes in brown adipose tissue of transgenic animals. We performed a proteinase K digestion of mitochondria isolated from ApoL6-BAT mice. Without dissolution of the inner and outer mitochondrial membranes by triton X-100 detergent, ApoL6 was protected from proteinase K digestion (Figure 18D). Mitochondrial proteins not embedded in membranes, HADHA and TOMM20, were sensitive to proteinase K activity with and without disruption of membranes by triton X-100 (Figure 18D).

ApoL6-BAT mice have less lean mass but improved glucose tolerance.

To begin to assess metabolic differences between wild-type and ApoL6-BAT mice, we examined body weight and body composition on a 16-week normal chow diet. Transgenic animals had no significant difference in food consumption and body weight during the 16-week feeding study (Figure 19A). However, NMR body composition analysis revealed that transgenic animals have significantly more body fat (7.6% WT vs 9.3% ApoL6-BAT) and a significantly less lean body mass (76.9% WT vs 75.6% ApoL6-BAT) (Figure 19B).

The higher body fat and less lean mass observed in ApoL6-BAT animals suggests that ApoL6-BAT mice might have impaired glucose and insulin tolerance. To assess differences in glucose and insulin sensitivities, we performed intraperitoneal glucose tolerance (IGTT) and insulin tolerance tests (ITT). Despite higher adiposity and less lean mass, transgenic animals have improved glucose tolerance and normal insulin sensitivity (Figure 19C and D).

ApoL6-BAT mice have reduced amino acid metabolites.

Brown adipose tissue specific overexpression of ApoL6 produced whole body changes in lean mass and body fat percentage as well as improvements in glucose tolerance. To begin to assess metabolic changes happening locally with brown adipose tissue, we utilized mass spectrometry analysis. Water-soluble metabolites were extracted form brown adipose tissue as described in the methods and materials section. Over 300 metabolites were identified, however only 105 were present in all samples and had spectral counts greater than 1000. 22 out of the 105 metabolites were significantly different between wild-type and ApoL6-BAT animals. When these metabolites were subjected to enrichment analysis, amino acid metabolism pathways were significantly enriched (Figure 20A). 12 out of the 22 were amino acids and amino acid metabolites. Figure 20B compares spectral counts of these 12 amino acids between wild-type and transgenic animals. For all 12 metabolites, there is significantly reduced abundance in ApoL6-BAT animals.

ApoL6-BAT mice are less active and have lower RER that WT mice at RT.

In addition to body composition and metabolite analysis we also examined the respiratory rate and activity of wild-type and ApoL6-BAT animals using an Oxymax

CLAMS unit. Based on the observed reduction in FAO observed in Figure 15, and the determination that ApoL6 in embedded in mitochondrial membranes (Figure 18), we hypothesized that ApoL6-BAT animals would have greater carbohydrate utilization and therefore a higher RER than wild-type animals. To carry out this experiment, animals were acclimated to a Oxymax CLAMS unit for 24 hours at 23 degrees Centigrade. After acclimation, we began collecting data for a period of 48 hours.

Graphs of VO_2, VCO_2 and RER over 48 hours show similar cycling profiles between light and dark cycles (Figure 21A). Despite the similar profiles, ApoL6-BAT mice have lower average oxygen consumption and CO2 release over the 48-hour period. (Table 2). ApoL6-BAT animals have similar body weight and heat profiles despite being less active than wild-type animals (Figure 21A bottom, 21B and Table 2). Surprisingly, however, the average RER of ApoL6-BAT animals is lower than wild-type animals (Table 2). This suggests that ApoL6-BAT animals are using more fatty acids not less as we expected.

ApoL6-BAT mice produce more heat during cold exposure without decreasing RER.

Since ApoL6-BAT animals have lower RER at room temperature (Figure 21), we wanted to determine the metabolic impact of ApoL6 overexpression on β-adrenergic stimulated lipolysis. To do this, we analyzed the respiratory capacity and heat production of wild-type versus transgenic animals at cold temperatures using the Oxymax-CLAMS unit. Both wild-type and ApoL6-BAT animals were exposed to 4ºC for 48 hours.

Graphs of VO_2, VCO_2 and RER over 48 hours show similar cycling profiles between light and dark cycles (Figure 22A). Despite the similar profiles, there were significant differences in average oxygen consumption, CO_2 and heat production between wild-type and ApoL6-BAT mice (Figure 22Aand B).

Unlike the room temperature results, average oxygen consumption and CO_2 production in ApoL6-BAT mice was higher during the cold exposure (Table 3). ApoL6-BAT animals also generated more heat during both light and dark cycles and had higher average heat production overall compared to wild-type animals (Figure 22B and Table 3).

As expected, wild-type animals showed a significant decrease in RER during cold exposure (Table 3). This indicates greater utilization of fatty acids as a fuel source to produce heat. In ApoL6-BAT mice, although heat production and oxygen consumption were increased during cold exposure, the average RER over the 48-hour period was not significantly different from the average RER of wild-type animals. (Figure 22 and Table 3). The average RER of ApoL6-BAT animals was the same at both room temperature and cold exposure (Table 3). This indicates no change in carbohydrate versus fatty acid utilization in these animals. Activity levels, food consumption, and body weight were consistent between the two groups (Figure 22 and Table 3).

ApoL6-BAT mice consume more food and produce more heat than wild-type mice during first 24 hours of cold exposure.

Average RER over 48 hours of cold exposure was not significantly different between ApoL6-BAT and wild-type mice, however within the initial 24 hours of cold exposure RER was significantly different between the 2 groups (Figure 23A). During the first 24 hours of cold exposure, wild-type animals showed a significant decrease in their RER compared to room temperature controls (Figure 23A). Unlike wild-type animals, ApoL6-BAT mice showed no difference in their respiratory exchange ratio compared to room temperature controls (Figure 23A).

During this initial 24-hour period, heat production increased in both groups, however, ApoL6-BAT mice produced significantly more heat than wild-type animals (Figure 23B and Table 4). ApoL6-BAT animals also consumed more food during this initial 24-hour period (Table 4). These results suggest that ApoL6-BAT mice are producing a greater amount of heat but not switching their metabolic substrate from carbohydrates to fats as observed in wild-type animals. The observation that ApoL6-BAT animals consumed more food during this initial period may be the source of fuel for additional heat production.

ApoL6-BAT mice have higher body temp during fasting cold exposure.

For the duration of the 48-hour cold challenge, ApoL6-BAT mice produced more heat (Figure 22). During the first 24 hours of cold exposure, ApoL6-BAT animals consumed significantly more food (Table 4). To determine transgenic mice were able to better thermoregulate during cold exposure without increased food consumption, we measured body temperature in an acute fasted condition. Wild-type and ApoL6-BAT mice were fasted for 2 hours then exposed to 4^{o}C for 4 hours.

ApoL6-BAT mice were better able to maintain their body temperatures during the acute cold exposure. Both wild-type and transgenic animals saw a gradual decline in body temperature within 2 hours of cold exposure. By 3 hours however, transgenic animals had a significantly higher body temperature compared to wild-type animals (Figure 24). The difference in body temperature between wild-type and transgenic animals was even greater by the 4-hour timepoint (Figure 24). Animals were sacrificed at 4 hours due to the extremely low body temperatures of wild-type mice.

ApoL6-BAT mice do not show a cold induced decrease in adipose tissue.

Divergence in body temperatures between ApoL6-BAT and wild-type mice began between the 2- and 3-hour time points (Figure 24). We sought to assess metabolic changes happening between wild-type and ApoL6-BAT mice during this time. To do this, we exposed mice fasted for 2 hours to 2 hours of cold exposure. After 2 hours at 4^oC while fasting, wild-type mice had a significant decrease in overall body weight while ApoL6-BAT mice did not (Figure 25A).

We presumed that the weights of the adipose tissue depots are indicators of lipolytic activity. A decrease in the weights of these fat pads suggests that lipolytic activity is higher during cold exposure. There was a statistically significant difference between wild-type and transgenic animals in both brown adipose tissue and gonadal adipose depots (Figures 25B left and middle). Wild-type animals showed a decrease in the weight of both gonadal and brown adipose fat pads after 2 hours of cold exposure. However, ApoL6-BAT animals did not (Figures 25B left and middle). This suggests that ApoL6-BAT animals are deficient in their rapidly increase lipolysis during acute cold exposure. The weight of the inguinal fat pad was not different between cold temperature and room temperature animals (Figure 23B right).

ApoL6-BAT mice have lower circulating free fatty acids and glucose levels after 2h cold exposure.

Decreases in circulating triglyceride concomitant with increases in circulating free fatty acids is an indicator of increased lipolysis. We measured the levels of circulating triglycerides and non-esterified fatty acids as indicators of lipolytic capacity. We compared levels of circulating fatty acids in wild type versus transgenic animals at room temperature and after 2 hours of cold exposure. Wild-type animals had a significant decrease in circulating triglycerides after 2 hours of cold exposure while ApoL6-BAT mice did not (Figure 25C, left). The levels of circulating free fatty acids increased significantly in wild-type animals after 2 hours of cold exposure (Figure 25C, right). ApoL6-BAT mice had a lower level of circulating free fatty acids compared to wild-type (Figure 24B). This suggests that there is a decrease in lipolytic activity which regulates free fatty acid levels in the blood.

To determine whether there were differences in carbohydrate utilization between wild-type and ApoL6-BAT mice, we also assayed serum glucose levels. There was no difference in the circulating glucose levels of wild-type animals after cold exposure, while ApoL6-BAT mice showed a significant decrease in serum glucose levels (Figure 24D). Taken together these results indicate that ApoL6 overexpressing mice are deficient in their ability to stimulate lipolysis in response to cold exposure and suggests they may be compensating by using carbohydrates as a fuel source.

Brown adipose tissue of ApoL6-BAT mice have reduced metabolic flux during acute cold exposure.

To assess changes in brown adipose tissue metabolism during cold exposure in both wild-type and ApoL6-BAT mice, we utilized mass spectrometry. Water soluble metabolites were extracted from BAT of wild-type and ApoL6-BAT animals after 2-hours at 4^{o}C. We compared to fold changes of the 105 identified metabolites between cold and room temperature animals (Figure 26A). Heat mapping of the relative fold changes revealed that ApoL6-BAT animals have an overall different profile than wild-type animals (Figure 26A). The range of fold changes is significantly different between groups. Wild-type animals have fold changes ranging from 0.3 to 7-fold increase, while ApoL6-BAT animals range from 0.4 to 2.7. (Figure 26B).

Of the 105 metabolites identified, 28 were significantly different in room temperature compared to cold exposure in wild-type animals (Figure 26C). Only 4 metabolites were different in ApoL6-BAT mice (Figure 26C). Palmitic acid was the only significantly different metabolite shared between the 2 groups.

Analysis of serum glucose levels after 2-hour cold exposure showed that ApoL6-BAT animals had less circulating glucose (Figure 25C). Recently Wang et. al., using a metabolizable glucose tracer, showed decreased glucose abundance in the brown adipose tissue of mice held under chronic cold exposure[93]. This led us to speculate that glucose was the fuel source used in the brown adipose tissue of ApoL6-BAT mice to produce excess heat. Examination of glucose abundance from brown adipose tissue revealed that is not the case. While wild-type animals showed a small decrease in glucose after 2-hour cold exposure, no significant difference was observed in glucose levels in the brown adipose tissue of neither wild-type nor transgenic animals (Figure 26D).

Table 5 shows the metabolites with the largest significant fold change between wildtype and transgenic animals. Wildtype animals saw a sevenfold increase in nucleotides in the nucleotide cytosine which may reflect increases in transcription. APOL 6 animals showed no increase in cytosine levels. Wild type animals also had a 3.6-fold increase in creating production. This reflects an increase in the use of creatine monophosphate for energy production. Transgenic animals showed no such increase.

The 4 metabolites that are significantly different in room temperature compared to cold in ApoL6-BAT are highlighted in bold in Table 5. The largest fold changes observed in ApoL6-BAT were in epinephrine (2.3-fold), acetylyglucosamine (1.6-fold) and oxidized glutathione (1.6-fold) (Table 5). Although both groups showed a significant reduction in palmitic acid between room temperature and cold (50% in wild-type and 40% ApoL6-BAT), Apol6-BAT mice are utilizing significantly less compared to wild-type animals (Table 5). ApoL6-BAT mice have an altered metabolite profile compared to wild type mice under cold conditions. A complete list of all identified metabolites can be found in appendix B.

ApoL6-BAT show increases in amino acid metabolites in during cold exposure.

Mass spectrometry analysis of wildtype and ApoL6-BAT animals revealed a difference in amino acid metabolites present in their brown adipose tissue (Figure 20). To determine whether this difference persisted through cold induced metabolic changes we compared these metabolites after cold exposure. The wild type animals showed no difference in amino acid metabolites present in room temperature compared to cold samples (Figure 27A and B). ApoL6-BAT animals however, showed an increase in the amount of amino acid metabolites present following the 2-hour cold exposure (Figure 27A and B). This increase did not reach statistical significance for any one amino acid metabolite, however across all amino acid metabolites, ApoL6-BAT mice had an average increase of 1.7-fold while wild-type animals had no overall change (Figure 27C). During cold exposure, the levels of amino acid metabolites in ApoL6-BAT increased to levels equal wild-type animals. This increase could indicate greater protein breakdown in the brown adipose tissue of ApoL6-animals.

Only two amino acid metabolites, adenosyl-L-homocysteine and citrulline, remained significantly lower in ApoL6-BAT compared to wild-type after cold exposure (Figure 27A). Neither of these metabolites are incorporated into protein but citrulline is an intermediate in arginine production. Reduced citrulline maybe indicative of reduced levels of arginine, which is used for protein synthesis. Unfortunately, arginine spectral counts did not meet our designed quality control parameters.

Adenosyl-L-homocysteine is an amino acid derivative that functions as the methyl group donor during the synthesis of carnitine and creatine. Reduced levels of adenosyl-L-homocysteine after during cold exposure may be indicative of defects in long chain fatty acid (LCFA) metabolism and ATP production via the creatine phosphate pathway. This result is consistent with the observation that ApoL6-BAT animals did not have an increase in creatinine during cold exposure (Table 5). Creatinine is a breakdown product on creatine-phosphate during ATP production.

Transgenic mice have lower acetylcarnitine levels during acute cold exposure.

Set enrichment analysis of the 31 metabolites that were statistically different between room temperature and cold exposure brown adipose tissue revealed that the most significantly enrich groups related to fatty acid and amino acid metabolism. Figure 27 analyzed the differences in amino acids and pointed to a potential defect in fatty acid metabolism suggested by reduced adenosyl-L-homocysteine levels at room temperature and during cold exposure.

Adenosyl-L-homocysteine is involved in carnitine synthesis. Carnitine is of particular importance to fatty acid metabolism because it is conjugated to LCFAs to allow for transport across mitochondrial membranes into the matrix via carnitine-acylcarnitine translocase (CACT).[96,97] Once the LCFA is released into the mitochondrial matrix, carnitine is converted to acetylcarnitine by carnitine O-acetyltransferase (CrAT) and shuttled out of the mitochondria.

Carnitine levels in both wildtype and ApoL6-BAT at room and cold temperatures were not significantly different, however differences in acetylcarnitine we detected. Specifically, there was an increase in acetylcarnitine levels in the brown adipose tissue of wild type animals after cold exposure, but this increase was not detected in transgenic animals (Figure 28B). This increase indicates increased cycling of carnitine into and out of the mitochondrial matrix in wild-type but not ApoL6-BAT animals.

ApoL6-BAT animals use more medium chain fatty acids during acute cold exposure.

Adenosyl-L-homocysteine and acylcarnitine results as well as set enrichment analysis point to changes in fatty acid oxidation in ApoL6-BAT animals. We examined fatty acid abundance present in the brown adipose tissue of wild type in transgenic animals. Mass spectrometry data for 10 fatty acids identified in brown adipose tissue of both groups is shown in Figure 29A. In wild-type animals 7 out of the 10 identified fatty acids show a decrease in abundance following cold exposure (Figure 29A). ApoL6-BAT animals however only show a reduction in palmitic acid (Figure 29A). This suggests that transgenic animals are utilizing less fatty acids then wild type animals.

To assess relative changes in these fatty acids within the group we looked at the relative abundance or fold change of each identified fatty acid. When fatty acids were grouped according to their chain lengths, MCFA ranging from 6 to 11 carbons and long chain fatty acids being 12 or more carbons, it became clear that ApoL6-BAT animals were utilizing more medium chain fatty acids (Figure 29B). Of the MCFAs identified 2 were being utilized more in ApoL6-BAT animals compared to wild-type. Specifically, 6-carbon (C6) and 8-carbon (C8) fatty acids have a greater fold reduction in ApoL6-BAT animals compared to wild-type (Figure 29B). C6 fatty acid hexanoic acid had 38% reduction in ApoL6-BAT animals following cold exposure compared to 12% in wild-type. Caprylic acid (C8) had a 26% decrease in wild-type animals compared to 52% in ApoL6-BAT mice. C10 fatty acids were similar between groups (Figure 29B).

Of the longer chain fatty acids identified, 5 out of 6 showed no difference between wild-type and transgenic animals. Palmitic acid was the one exception. ApoL6-BAT animals are utilizing less palmitic acid than wild-type animals (Figure 29C). ApoL6-BAT mice had a 35% reduction in C16 palmitic acid following cold exposure compared to 48% in wild-type mice. These results suggest that ApoL6 overexpression in brown adipose tissue is leading to increased utilization of MCFA.

Discussion

Here ApoL6 is shown to be a potentially important regulator of fatty acid utilization in brown adipose tissue. Using a transgenic overexpression model and metabolic phenotyping analysis we have demonstrated that ApoL6 in brown adipose tissue can influence whole-body energy metabolism and thermogenic responses. Transgenic animals overexpressing ApoL6 in their brown adipose tissue showed increased adiposity compared to wild-type animals on a normal chow diet and had an altered metabolic profile during cold-stimulated thermogenesis.

ApoL6-BAT mice exhibited no difference in food consumption, body weight, or insulin sensitivity as demonstrated by insulin tolerance tests. Although ApoL6-BAT animals have overall body weights consistent with wild-type animals, by 20-weeks of age ApoL6-BAT animals show significantly increased fat mass and a slight reduction in lean mass percentage. However, despite the reduction in lean mass, transgenic animals show enhanced glucose clearance compared to wild-type animals.

Analysis of ApoL6 localization using immunofluorescence indicated that the C-terminal domain localizes to the mitochondria. This result was confirmed in transgenic animals using Proteinase K protection assays of isolated mitochondria. ApoL6 was protected from Proteinase K degradation in samples lacking Triton-X, a detergent used to dissolve cellular membranes. This finding indicates that ApoL6 may integrate into mitochondrial membranes or is localized to the mitochondrial matrix. Studies of ApoL1 suggest that it translocates to the mitochondrial matrix, which suggests that ApoL6 might also be translocated to the same compartment.[53] This hypothesis is consistent with our finding that ApoL6 associates with the HADHB subunits of the MTP/FTP complex located in the mitochondrial matrix. Further biochemical fractionation and digestion assays should be performed to discern amongst these possibilities.

Because transgenic animals overexpress ApoL6 in brown adipose tissue, we used a Comprehensive Lab Animal Monitoring System to comparatively analyze heat production at room temperature (RT) and at 4^{o}C over a 48-hour period. While no difference in heat production was observed at RT, heat production was increased in ApoL6-BAT mice at housed at 4^{o}C compared to wild-type mice housed under the same conditions. The largest difference between groups occurred within the first 24 hours of cold exposure.

Over a 24-hour period at RT, respiratory exchange ratios (RERs) were similar between ApoL6-BAT and WT animals. Expectedly, cold exposure induced a reduction of RER in wild-type mice, indicative of a switch of energy substrate from carbohydrates to long-chain FAs. Interestingly, overexpression of ApoL6 in BAT prevented this switch in transgenic animals. Over the initial 24-h period at 4^{o}C, the RER of ApoL6-BAT mice remained unchanged, suggesting that ApoL6-BAT mice utilize the same ratio of carbohydrates and LCFA at 4^{o}C as at room temperature. As a result, the transgenic mice had higher average RER than wild-type mice during cold exposure. This is a striking result since increased oxidation of LCFAs is a major drive of heat production under cold stimulated conditions. Instead of exhibiting impaired in thermogenesis, as expected, ApoL6-BAT mice produced more heat than wild type animals.

One potential mechanism underlying this enhanced thermogenic response in transgenic mice is that ApoL6 overexpression in brown adipose tissue reciprocally upregulated the utilization of carbohydrates and MCFA as the sources of energy fuel. Indeed ApoL6-BAT animals consumed significantly more food than wild-type animals during the first 24 hours of cold exposure. To mitigate the confounding effects of feeding, fasted acute cold conditions were used.

Consistent with their increased thermogenic capacity during chronic cold exposure, transgenic animals also displayed higher body temperatures in the acute setting, indicating they were better equipped to thermoregulate. Specifically, transgenic animals were able to maintain a body temperature slightly below 36 ^{o}C even after 4 hours of cold exposure, while the wild-type animals could not sustain their body temperatures over the same period.

Even under fasted conditions, mice initiate a lipolytic program when acutely exposed to cold temperatures. As little as 2 hours of exposure to 4^{o}C temperatures resulted in a reduction in brown and gonadal adipose tissue mass in wild-type but not transgenic animals. This rapid decrease in adipose tissue size is most likely due to activation of a lipolytic program in brown adipose tissue to support fatty acid oxidation and thermogenesis and in white adipose tissue to release LCFA into the bloodstream. These results are in agreement with serum lipid analysis showing that there is an increase in the levels of circulating fatty acids in wild-type animals after 2 hours of fasting acute cold exposure. Transgenic animals, however, did not exhibit the same decrease in the size of these two fat depots. Instead, they showed significantly decreased levels of circulating glucose. This, in combination of increased RER observed during chronic cold exposure, suggests increased whole-body glucose oxidation as a result of ApoL6 overexpression in brown adipose tissue.

Our results suggest that there are significant differences in the metabolic profile of transgenic animals in their response to cold. Further analysis is required to elucidate the mechanisms of the augmented thermogenic profile of these animals. Specifically, using stable isotope tracers and mass spectrometry to evaluate the abundance of succinate as a marker of glucose utilization in brown adipose tissue of transgenic animals. Wang et. al. showed that in long term cold exposure, 10 days, mice use glucose as a carbon source in oxidative phosphorylation.[93] Examination of these oxidative metabolites can determine if glucose is the carbon source for the TCA intermediates.

Mass spectrometry analysis of metabolites present in the brown adipose tissue of transgenic animals supported the finding that LCFAs were not being utilized at the same rate as wild-type animals during cold exposure. Both acetylcarnitine and palmitic acid levels varied significantly between the two groups. The metabolite acetylcarnitine is one indicator of changes in levels of acetyl-CoA production and carnitine import into the mitochondrial.[98] Carnitine is a requisite conjugate to LCFAs being imported into the mitochondria.[99] Free carnitine and acetyl-CoA, are the substrates for acetylcarnitine synthesis by carnitine O-acetyltransferase (CrAT).[98,99] An increase in carnitine influx into the mitochondrial matrix along with an increase in acetyl-CoA production should result in an increase in acetylcarnitine synthesis and its efflux from the mitochondrial matrix.

An increase in acetylcarnitine could indicate increased import of carnitine into the mitochondria as a conjugate of LCFAs or signal increased acetyl-CoA production either from glucose or fatty acid oxidation.[100] No increase in acetylcarnitine levels was observed in transgenic animals suggesting that there was no increase in LCFAs imported into the mitochondria, which should occur rapidly during cold-induced lipolysis. Without LCFA oxidation, due to ApoL6 overexpression, there would be no concomitant increase in free carnitine available to CrAT. The mechanism by which ApoL6 maybe inhibiting LCFA import requires more study.

Based on the localization of ApoL6 at the mitochondria inner membrane or matrix it is unlikely that ApoL6 is directly inhibiting import the transport of carnitine conjugated LCFAs into the mitochondria. One possibility, however, is that the compensatory mechanisms developed to maintain effective metabolism in transgenic animals involves downregulating the import of LCFAs into mitochondria. This possibility is supported by the increased adiposity phenotype observed in transgenic animals. Further analysis of fatty acid metabolites and expression of fatty acid transport proteins would provide insight into the metabolic profile of ApoL6-BAT animals. A lipidomic profile to assess the abundance of long, medium, and short chain fatty acids in transgenic animals in response to cold would build on the results presented here.

ApoL6-BAT animals showed increased adiposity on a chow diet suggesting they are defective in their ability to oxidize LCFAs and therefore more efficiently store these compounds. Preliminary data from our lab suggest that LCFA-rich high fat feeding in these animals results in increased adiposity compared to wild type. This finding further supports probability of defective LCFA utilization.

Interestingly, MCFAs also seemed to be utilized to a greater extent in transgenic animals during a cold challenge compared to wild-type animals. Of the fatty acids identified in our mass spectrometry analysis, wild-type animals utilized the 16-carbon palmitic acid during cold while transgenic animals showed greater utilization of 8-carbon caprylitic acid. Challenging these animals with a diet rich in medium chain fatty acids, should serve to enhance their phenotype. MCFAs are acquired from diet and utilized in an oxidative pathway that is not dependent on carnitine transportation. ApoL6-BAT animals displayed some of the metabolic profile consistent with increased MCFA utilization, namely improved glucose tolerance despite having increased adiposity.

In addition to changes in the rate of MCFA and LCFA utilization, mass spectrometry analysis also revealed other compromised aspects of brown adipose tissue metabolism of transgenic mice. Transgenic animals displayed an overall reduced abundance of amino acid metabolites at RT. During cold exposure, there was a significant increase in amino acid metabolites in transgenic animals that was not observed in wild-type mice. This may point to greater utilization of amino acids as a source of substrates for the TCA cycle and heat production.

Our results suggest at ApoL6 acts as a modulator of LCFA utilization and that this maybe through its association with MTP/TFP which catalyzes three out of the four steps of LCFA oxidation. Further biochemical assays should be undertaken to directly determine whether and how ApoL6 binding to the HADHB subunit of MTP/TFP indeterminates impacts fatty acid oxidation and its downstream metabolic output. Another possibility is that ApoL6 is involved in tethering of the MTP/TFP complex to the inner mitochondrial membrane. To this end, further experiments should be carried out to evaluate this possibility.

Taken together, the results provide new insights into how adipocytes regulate their fuel utilization to meet the thermogenic demand. My findings also have significantly advanced the understanding of regulation and function of the previously uncharacterized ApoL6 protein in adipose tissue, while also opening up the avenue for new research questions.

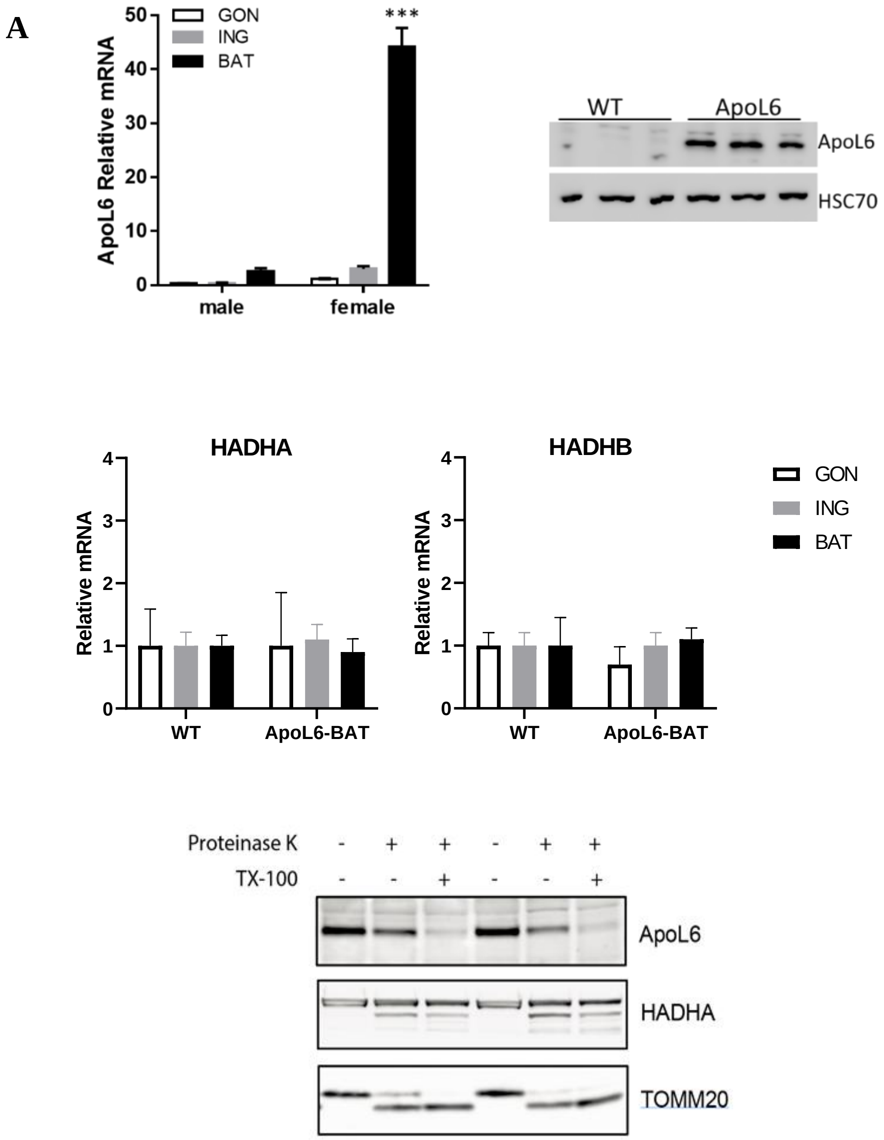


Figure 18. Female transgenic mice overexpress ApoL6 in their brown adipose tissue. **(A)** qPCR for ApoL6 using RNA from gonadal (GON), inguinal (ING) and brown (BAT) adipose tissue of male and female transgenic animals. (**B)** Western blot confirming ApoL6 protein overexpression in BAT of female transgenic animals. **(C)** HADHA and HADHB mRNA in transgenic (ApoL6-BAT) mouse adipose tissue. **(D)** Proteinase K protection assay of ApoL6 in BAT mitochondria isolated for ApoL6-BAT transgenic animals. ***p<0.0001

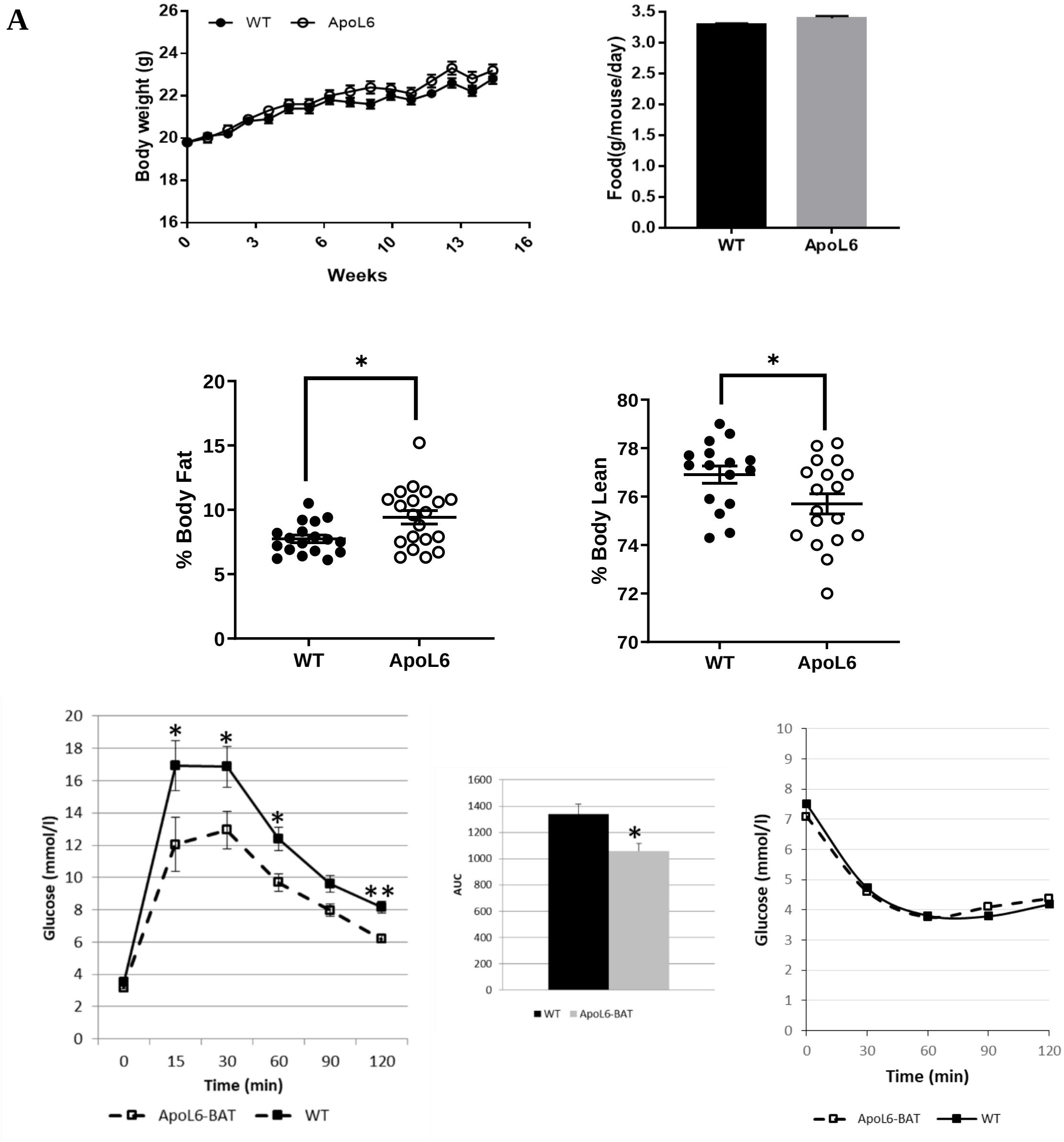


Figure 19. Female transgenic mice have enhanced glucose tolerance. WT n=16 and ApoL6-BAT n=18 animals were fed a standard chow diet and weighed weekly for 16 weeks. **(A)** Average body weight (left) and food consumption(right) per mouse per day for WT and ApoL6-BAT mice. **(B)** Body fat (left) and lean mass(right) percentage of WT and ApoL6-BAT chow fed animals determined using nuclear magnetic resonance (NMR) body composition analysis. **(C)** Intraperitoneal glucose tolerance test with corresponding area under the curve (AUC) calculation for WT (black bar) and transgenic ApoL6-BAT (grey bar) animals. **(D)** Insulin tolerance test for WT and transgenic ApoL6-BATanimals. $^*p<0.05$, $^{**}p<0.01$

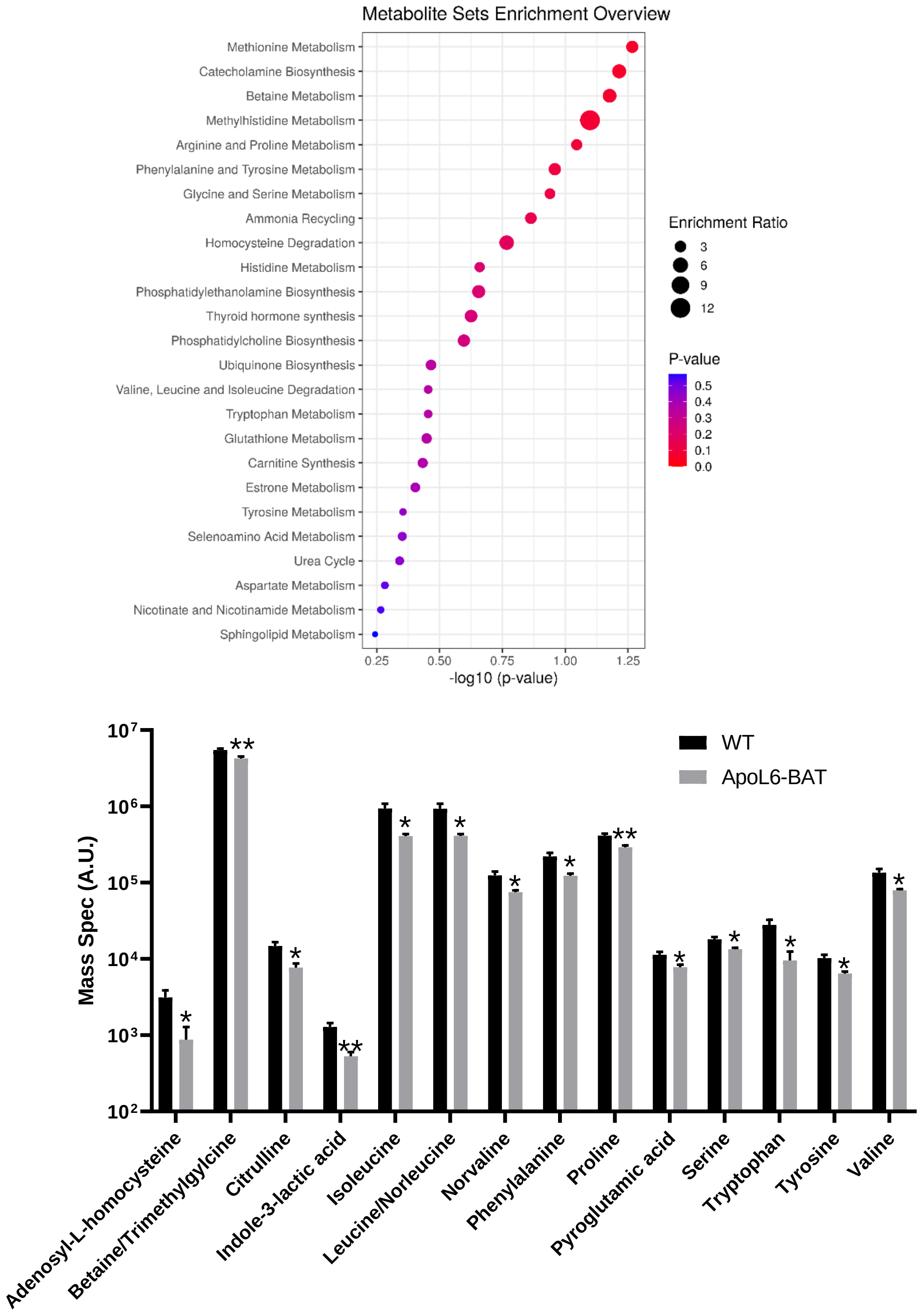
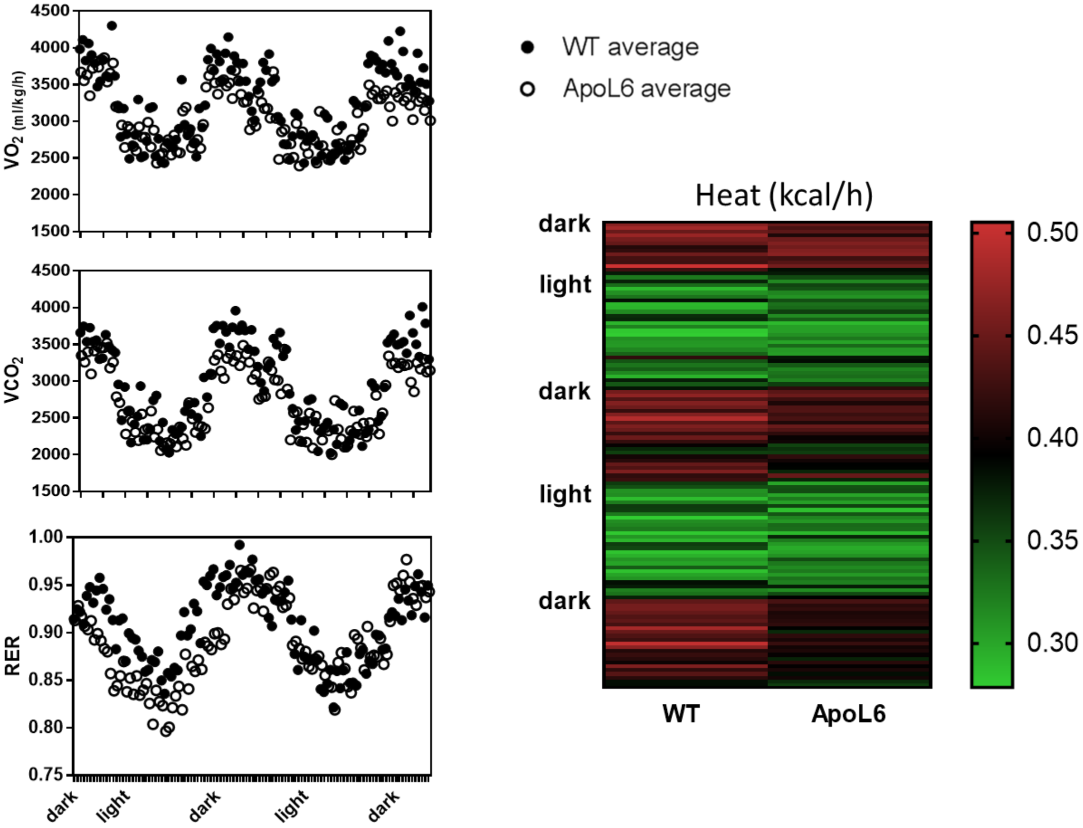


Figure 20. Decreased amino acid metabolites in brown adipose tissue of ApoL6-BAT mice. Metabolites were extracted from the BAT of wild-type (WT) and transgenic (ApoL6-BAT) animals. **(A)** Enrichment analysis of extracted metabolites. **(B)** Average mass spectrometry counts of amino acid metabolites. n=6 for both groups.



Tab

	WT	ApoL6	p value
$VO_{2(ml/kg/h)}$	3258	3063	0.003
$VCO_{2(ml/kg/h)}$	2980	2757	0.001
RER	0.91	0.89	0.003
$Heat_{(kcal/h)}$	0.38	0.37	0.1584
$Activity_{(counts)}$	2085	1419	0.0017
$Body\ weight_{(g)}$	23.7	24.7	0.299

Figure 21. ApoL6-BAT mice are less active and have lower RER that wild-type mice. 20-week-old wild-type (black circles) and ApoL6-BAT (open circles) mice were housed in CLAMS unit at 23°C for 48h, n=6 for both groups. **(A)** Oxygen consumption (VO_2), carbon dioxide production (VCO_2), and calculated respiratory exchange ratio (RER = VCO_2/VO_2) graphs over a 48h period. **(B)** Heat map of heat production over at 48h period.

Table 2. Summary of CLAMS assessment averages over 48h period at 23°C.

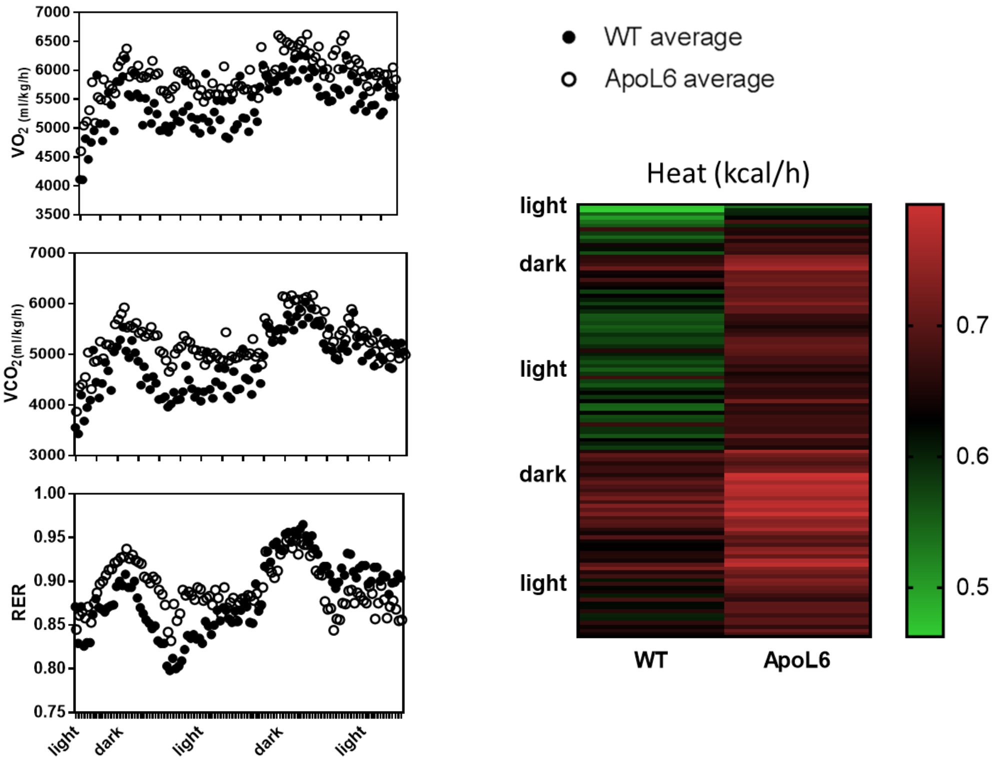


Table 3

	WT RT	ApoL6 RT	pvalue RT	WT cold	ApoL6 cold	pvalue cold
$VO_{2(ml/kg/h)}$	3258	3063	0.003	5457	5904	<0.0001
$VCO_{2(ml/kg/h)}$	2980	2757	0.001	4830	5274	<0.0001
RER	0.91	0.89	0.003	0.88	0.89	0.1235
$\text{Heat}_{(kcal/h)}$	0.38	0.37	0.1584	0.62	0.70	<0.0001
$\text{Activity}_{(counts)}$	2085	1419	0.0017	771	699	0.2427
Body $\text{weight}_{(g)}$	23.7	24.7	0.299	23.5	24.1	0.234
$\text{Food}_{(g)}$				11.9	12.7	0.3413

Figure 22. ApoL6-BAT mice produce more heat without decreasing RER. 20-week old WT (black circles) and ApoL6-BAT (open circles) mice were acclimated in CLAMS unit at 18°C for 72h then housed at 4°C for 48h. n=6 for both groups. **(A)** Oxygen consumption (VO_2), carbon dioxide production (VCO_2), and calculated respiratory exchange ratio (RER = VCO_2/VO_2) graphs over a 48h period at 4°C. **(B)** Heat map of heat production over at 48h period at 4°C.

Table 3. Summary of CLAMS assessment averages over 48h period at 4°C.

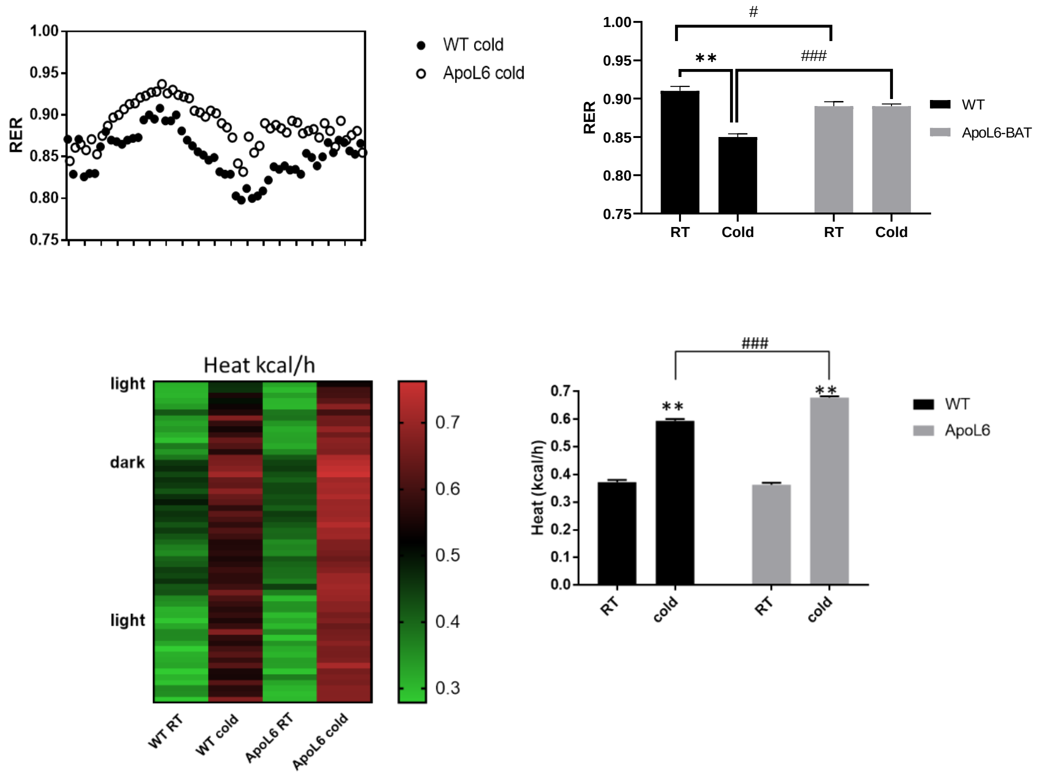
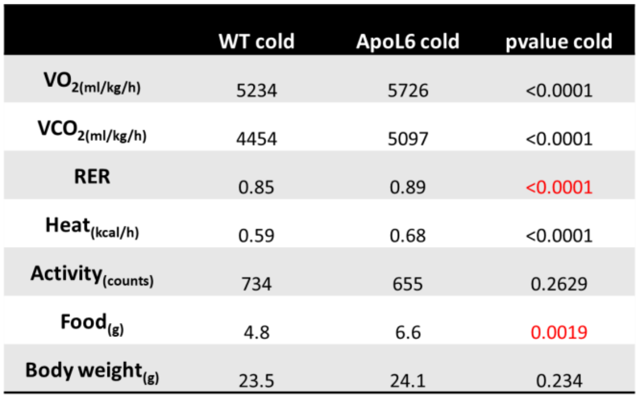


Table 4



	WT cold	ApoL6 cold	pvalue cold
$VO_{2(ml/kg/h)}$	5234	5726	<0.0001
$VCO_{2(ml/kg/h)}$	4454	5097	<0.0001
RER	0.85	0.89	<0.0001
$Heat_{(kcal/h)}$	0.59	0.68	<0.0001
$Activity_{(counts)}$	734	655	0.2629
$Food_{(g)}$	4.8	6.6	0.0019
$Body\ weight_{(g)}$	23.5	24.1	0.234

Figure 23. ApoL6-BAT mice consume more food and produce more heat than wild-type mice during first 24h of cold exposure. 20-week-old wild-type (WT black circles) and ApoL6-BAT (open circles) mice were acclimated in CLAMS unit at 23°C (RT) or 18°C for 72h then housed at 4°C (cold) for 24h. **(A)** Calculated respiratory exchange ratio (RER = VCO_2/VO_2) over initial 24h period at 4°C (right), Average RER for wild-type (black bars) and ApoL6-BAT mice (gray bars) over 24hr periods at RT and 4°C (cold). **(B)** Heat map (right) and graph (left) of average heat production over 24hr periods at RT and 4°C. # p<0.01, **p<0.001, ### p<0.0001 n=6 for both groups

Table 4. Summary of CLAMS assessment averages over initial 24h period at 4°C.

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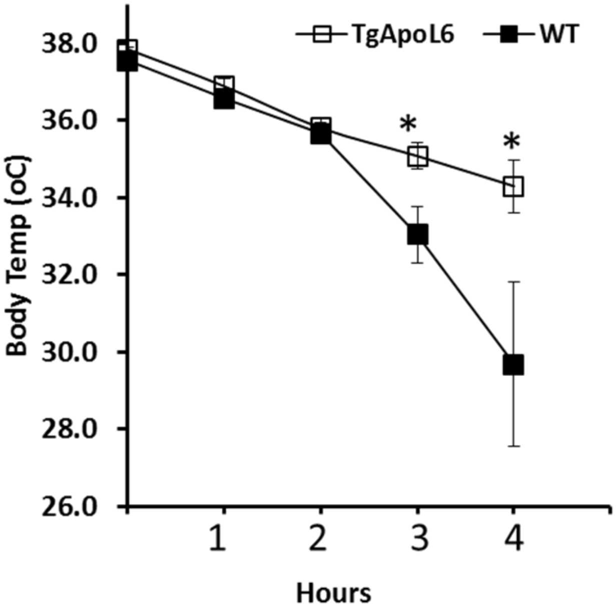


Figure 24. ApoL6-BAT mice have higher body temp during fasting cold exposure. 20-week cold wild-type (WT black squares) and ApoL6-BAT (open squares) mice were fasted for 2h then housed at 4^oC for 4 h. Body temp taken rectally every hour WT n=7 ApoL6-BAT n=8. $^*p<0.05$

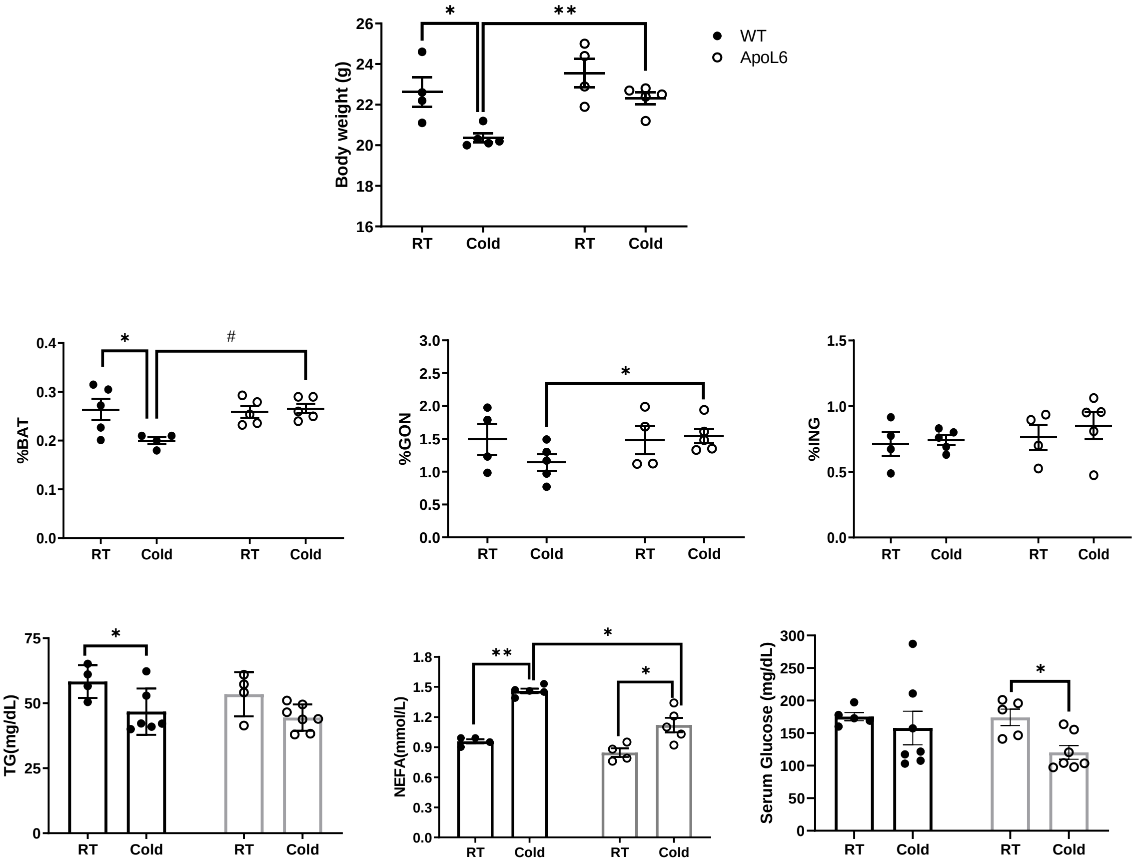
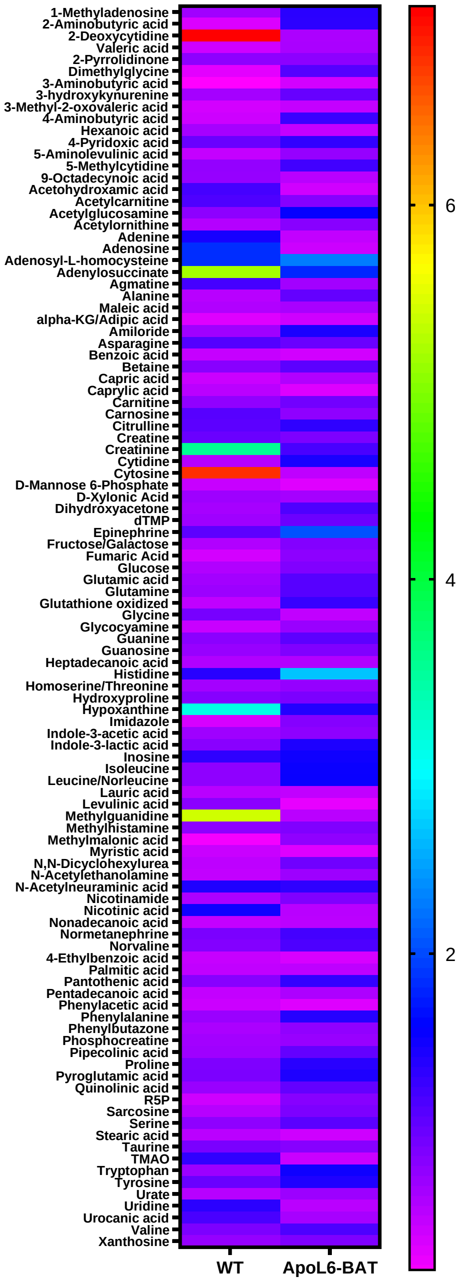
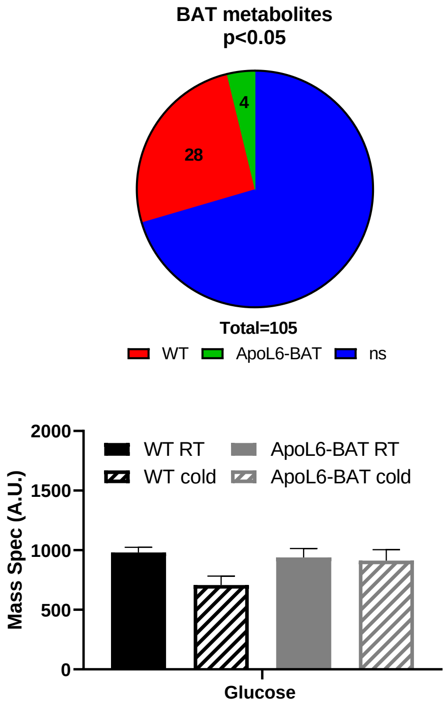


Figure 25. ApoL6-BAT mice have less fat loss and lower circulating free fatty acids after 2h cold exposure. 20-week cold WT (black circles) and ApoL6-BAT (open circles) mice were fasted for 2h then housed at RT or 4^{o}C for 2h. **(A)** Body weight of wild-type and ApoL6-BAT animals after RT and cold exposure. **(B)** At 2h, brown (BAT, left), gonadal (GON, middle), and inguinal (ING, right) fat pads were collected and weighed. Percentages are relative to total body weight. **(C)** At 2h, serum was collected and used for triglyceride (TG, left) circulating free fatty acid (NEFA, middle) and **(D)** blood glucose (right) measurements. WT n=5 ApoL6-BAT n=6. *p<0.05, # p<0.01, **p<0.001



	Range of Fold Changes	p value
WT	0.3 ±0.1 – 7.1 ±2.0	0.003
ApoL6-BAT	0.4 ±0.1 – 2.7 ±0.5	



	WT Fold Change (cold/RT)	ApoL6-BAT Fold Change (cold/RT)	p value
2-Deoxycytidine	7.1 ±2.0	0.7 ±0.3	0.020
Cytosine	6.8 ±2.1	0.6 ±0.2	0.028
Creatinine	3.6 ±1.0	0.7 ±0.1	0.024
Epinephrine	1.2 ±0.2	2.3 ±0.4	0.029
Levulinic acid	0.9 ±0.1	0.4 ±0.1	0.019
Acetylglucosamine	0.9 ±0.1	1.6 ±0.2	0.007
Oxidized Glutathione	0.6 ±0.1	1.6 ±0.2	0.003
Palmitic acid	0.5 ±0.0	0.6 ±0.0	0.025

Figure 26. ApoL6-BAT mice have less metabolic flux during acute cold exposure. 20-week cold WT (black bars) and ApoL6-BAT (gray bars) mice were fasted for 2h then housed at RT or 4^{o}C for 2h. At 2h, BAT was collected and used for mass spectrometry analysis of metabolites. **(A)** Fold change (cold/rt) of metabolites detected in BAT of wild-type (WT) and transgenic (ApoL6-BAT) animals. **(B)** Range of fold changes in BAT metabolites in wild-type compared to ApoL6-BAT mice. **(C)** Total numbers of significantly different metabolites between room temperature and cold conditions. **(D)** Glucose abundance in BAT measured my mass spec. WT n=5 ApoL6-BAT n=6. *p<0.05, **p<0.01

Table 5. Metabolites with largest fold changes during cold exposure.

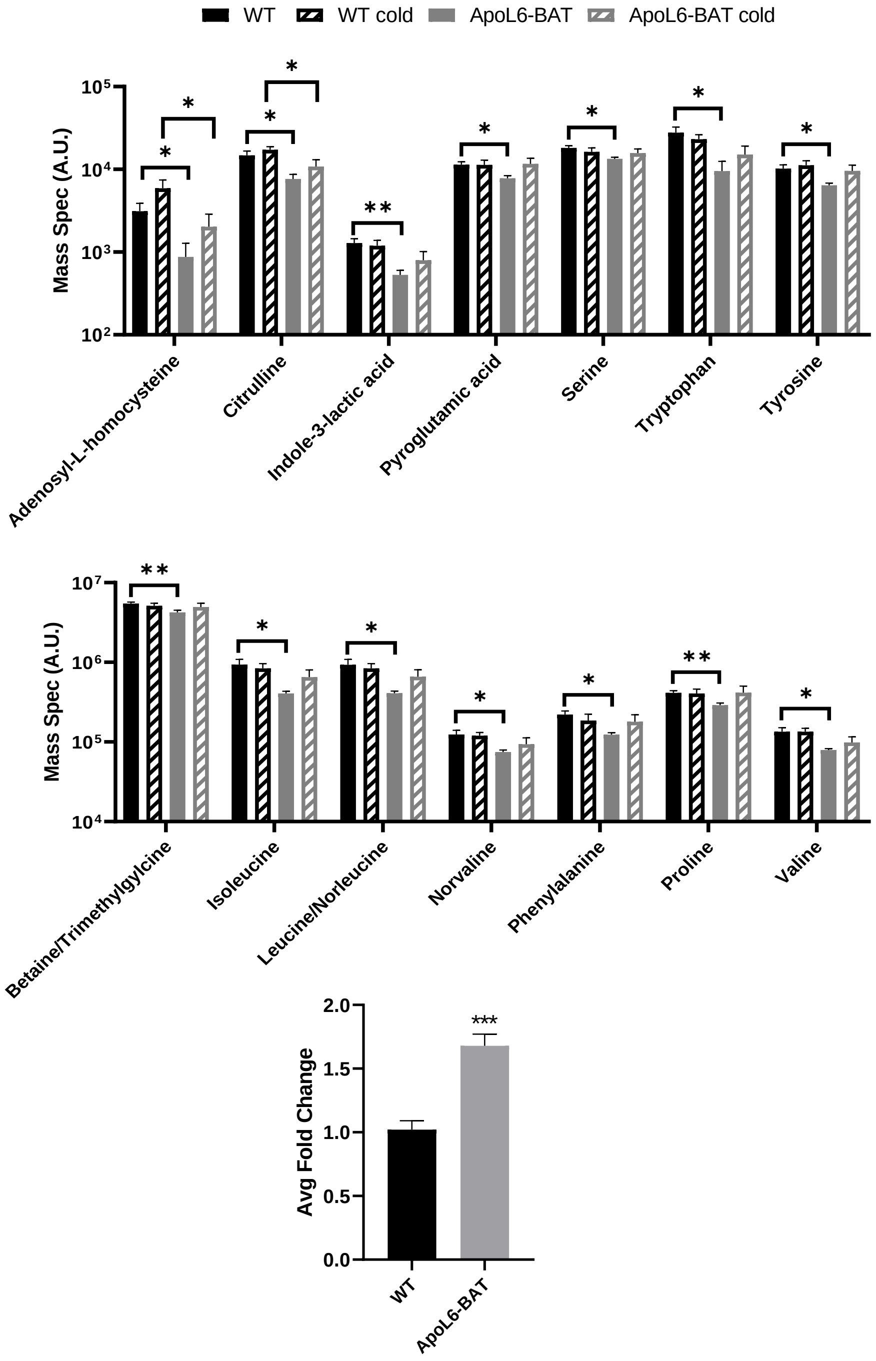


Figure 27. Increased amino acid metabolites in ApoL6-BAT during cold exposure. Metabolites were extracted from the BAT of wild-type (WT) and transgenic (ApoL6-BAT) animals. **(A)** (upper and lower) Average mass spectrometry counts of amino acid metabolites. **(B)** Average fold change of all amino acid metabolites extracted form BAT. WT n=5 ApoL6-BAT n=6. *p<0.05, **p<0.001, ***p<0.0001

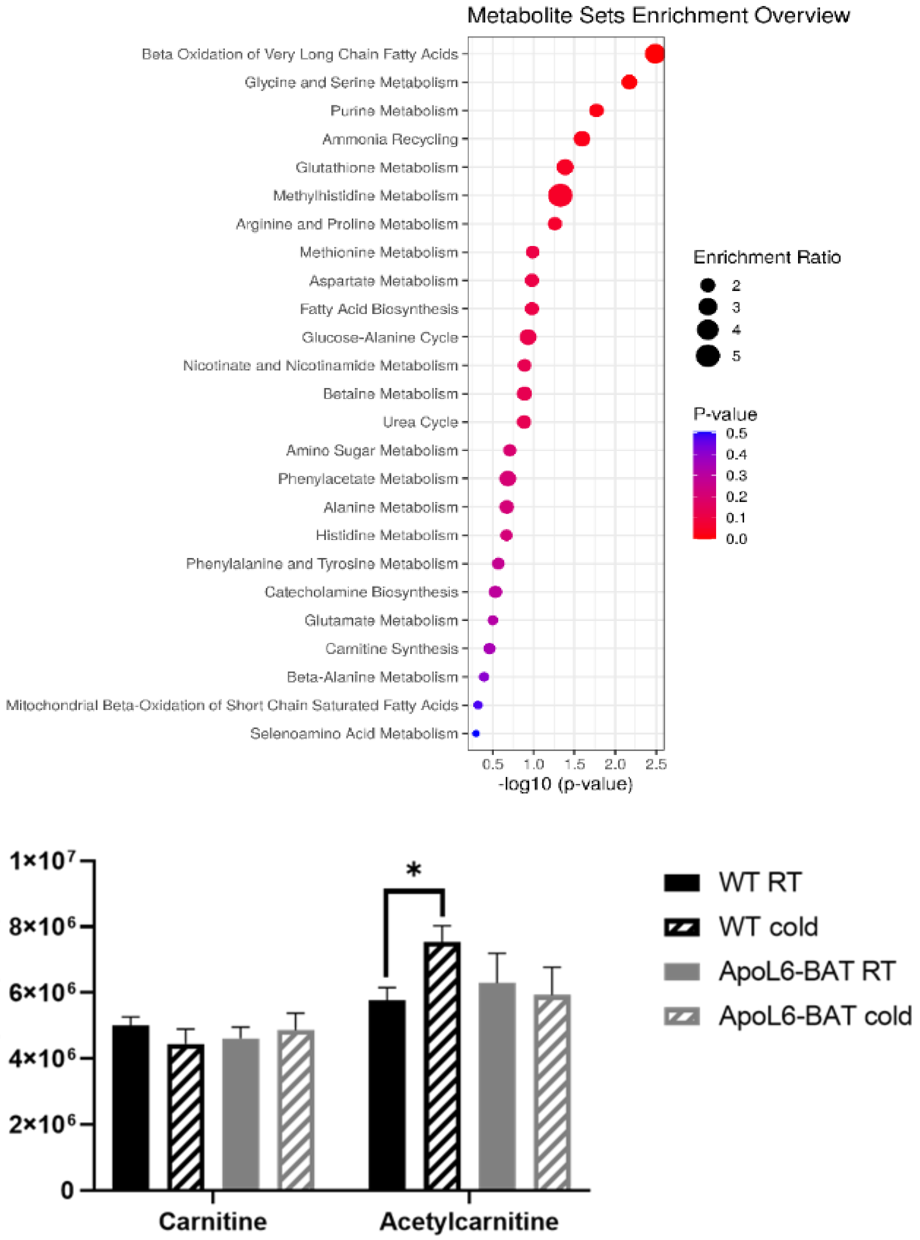


Figure 28. ApoL6-BAT have no change in acetylcarnitine during acute cold exposure. 20-week cold WT (black bars) and ApoL6-BAT (gray bars) mice were fasted for 2h then housed at RT or 4°C for 2h. At 2h, BAT was collected and used for mass spectrometry analysis of metabolites. **(A)** Enrichment analysis of extracted metabolites. **(B)** Average mass spectrometry counts of carnitine metabolites. WT n=5 ApoL6-BAT n=6. *p<0.05, **p<0.001, ***p<0.0001

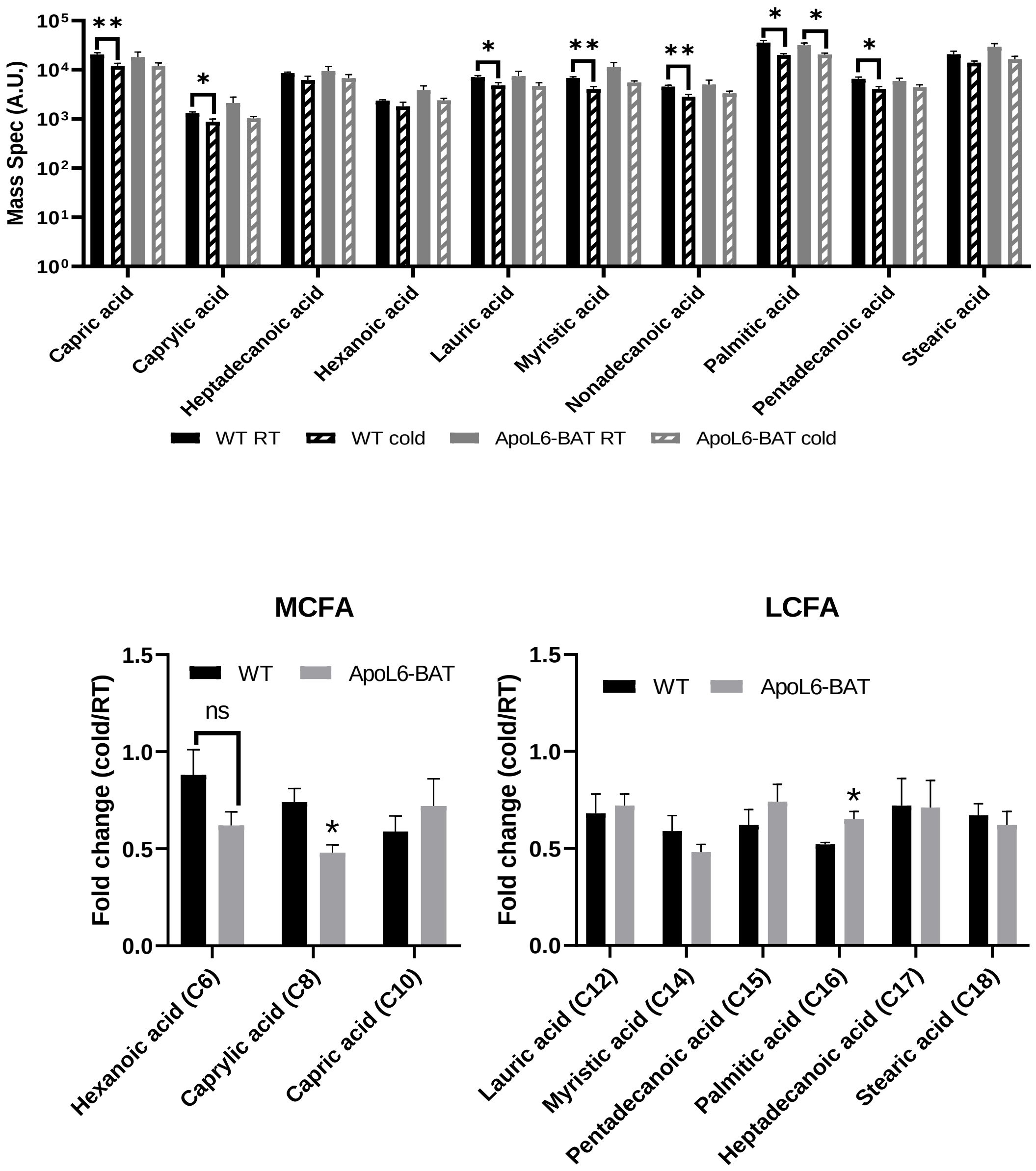


Figure 29. ApoL6-BAT animals use more shorter chain fatty acids during acute cold exposure. 20-week cold WT (black bars) and ApoL6-BAT (gray bars) mice were fasted for 2h then housed at RT or 4°C for 2h. At 2h, BAT was collected and used for mass spectrometry analysis of metabolites. **(A)** Average mass spectrometry counts of fatty acid metabolites. **(B)** Average fold change of medium and long-chain fatty acid metabolites represented in B. WT n=5 ApoL6-BAT n=6. *p<0.05, **p<0.001, ***p<0.0001

CHAPTER 5

CONCLUSIONS

Obesity, nonalcoholic hepatic steatosis (NASH) and hypoxic tumor cells all display altered lipolysis and TG storage dynamics. Central to regulation of TG metabolism in the TG lipase ATGL. Understanding the mechanisms that regulate ATGL and the utilization of the fatty acids released by its activity are essential to our understanding of metabolic and related obesity disorders. Both the ATGL inhibitors and ApoL6 projects further the understanding of both processes.

G0S2 and HIG2 are lipolytic inhibitors that associate with ATGL. G0S2 mediated inhibition of ATGL has a well established role in liver and adipose tissue TG metabolism, while HIG2 functions to inhibit ATGL in hypoxic tumor cells. Here we demonstrated the importance of the conserved LYXL motif in regulation of ATGL and discovered differences in amino acid residues important for ATGL-independent lipid droplet localization. Analysis of G0S2 and HIG2 structural similarities and differences provides insights into mechanisms of regulating ATGL and may provide a model for comparison in identifying other regulators of lipolytic enzymes.

Using mutation analysis and confocal microscopy we were able to develop the following model of G0S2-ATGL and HIG2-ATGL associations (Figure 30). G0S2 is translated at the ER and buds off with LDs as they develop. Essential to its LD localization are its HD and Pos-Seq domains. ATGL, which is translated in the cytosol, can associate with mature LDs. G0S2' interaction with ATGL is facilitated by two mechanisms. One where ATGL associates with G0S2 at the ER membrane, and two where G0S2 is translocated onto mature LD with ATGL already present via LD-ER bridges (Figure 30A). The Pos-Seq upstream of G0S2' lipid HD domain regulates G0S2'ATGL- independent sorting to LDs from the ER.

HIG2 does not contain a Pos-Seq but and has been reported to localize at points of ER lipid droplet contact with the ER.[44] Our results suggest that HIG2 is translated in the cytosol and localizes to the LD surface. The exact mechanism of the HIG2-ATGL-LD-ER connection is still unclear. One possible mechanism is HIG2 binds ATGL then anchors ATGL and the LD to the ER (Figure 30B). Another possibility is that HIG2 binds to budding lipid droplets at the ER membrane and binds to any ATGL that subsequently localizes to the LD surface (Figure 30B).

In addition to understanding lipolysis at the molecular level, identification of proteins that produce systemic changes in fatty acid utilization are essential to understanding lipid metabolism. Analysis of mouse tissues indicated endogenous ApoL6 is primarily expressed in adipose tissue and that this expression is regulated by β-adrenergic stimulation. We also show that in an *in vitro* model of brown adipocytes, ApoL6 inhibits mitochondrial fatty acid oxidation.

Mitochondria in brown adipose tissue use fatty acids as fuel for increasing their energy output as heat during acute responses to cold exposure. Increased lipolysis in white adipose tissue during cold exposure provides fatty acids to oxidative tissues to be used for mitochondria oxidation and heat production. Cold exposure was used as a metabolic challenge in transgenic mice to highlight the importance of ApoL6 in whole body metabolism. We found that transgenic animals have a greater ability to respond to acute cold exposure.

Figure 31 represents our model of altered LCFA β-oxidation and heat production in transgenic animals compared to wild-type. In wild-type animals, fatty acids are imported into the mitochondria as conjugates of carnitine via CACT and then oxidized to produce acetyl-CoA. Acetyl-CoA is used in the TCA cycle to generate NADH and $FADH_2$ needed for oxidative phosphorylation and ATP production (Figure 31A). Upon cold exposure, indicated by the red arrows, there is an increase in LCFA import into the mitochondria and oxidation by MTP/TFP. Additionally, there is also an increase in import of pyruvate into the mitochondria which can also be converted to acetyl CoA and used for in the TCA cycle.[93]

In transgenic animals that overexpress ApoL6 our results suggest impaired fatty acid oxidation in transgenic animals during initial exposure to cold temperatures. Our results suggest that there is an increase in my MCFA oxidation which is independent of MTP/TFP complexes. Our results also indicate that there may be greater import of pyruvate and amino acid metabolites into the mitochondria to be utilized for heat production.

The enhanced thermogenic response observed in transgenic animals may be a result of compensatory mechanisms established during development in these animals. These animals may have developed mechanisms that allow for efficient catabolism of glucose and amino acids for ATP production due to ApoL6 mediated inhibition of fatty acid oxidation. Our results show decreased lean mass in transgenic animals. Further analysis of ApoL6 transgenic animals could provide insight into these compensatory mechanisms.

We initially hypothesized that ApoL6 was impairing mitochondrial function through its action on fatty acid oxidation. These experiments have pointed to a much more complicated scheme that needs further analysis. While in vitro experiments showed ApoL6 localized at FSP27 deficient lipid droplets, *in vivo* analysis of ApoL6 localization suggested a mitochondrial localization in brown adipose tissue. Our data suggests that there may be some changes to ApoL6 activity and possibly localization during events that stimulate β-adrenergic signaling. Localization of ApoL6 should be examined in times of metabolic stability at room temperature with normal feeding but also at times of metabolic challenge including cold exposure. In addition to *in vivo* changes in localization there may also be changes in modifications on the ApoL6 protein. It may be useful to examine phosphorylation and other protein modifications under cold simulated conditions to further elucidate mechanisms regulating ApoL6.

Analysis of metabolites present in brown adipose tissue no increase in acetylcarnitine was observed in transgenic animals. The lack of increased acetylcarnitine may be result of no rapid increase in the availability of fatty acids because ApoL6 has impaired lipolysis, but interaction of ApoL6 with MTP/TFP may also be the reason. More studies should be conducted into the exact mechanism of ApoL6 function, including quantifying acylcarnitine metabolites. This would show if LCFAs are being imported into the mitochondria but just not being oxidized. Intracellular imaging of' lipid droplets from both room temperature in two hour fasted tissues may also provide some insight into lipid droplet dynamics in transgenic animals.

Further studies into the role of ApoL6 in other adipose tissue depots should also be undertaken. My work suggests ApoL6 may allow for more efficient storage intercellular lipids. This seems likely as its overexpression inhibited the release of fatty acids from adipose tissue under conditions of high energetic demand. ApoL6 overexpression also reduced ability of transgenic animals to oxidize the 16-carbon fatty acids palmitate during acute cold exposure. Fatty acid utilization may also be impaired at RT under normal feeding conditions as indicated by the increase adiposity of transgenic animals on a normal chow diet.

Further evaluation of what influences the metabolic shift towards fatty acids after this initial impairment should also be performed. Our metabolic chamber studies revealed that by 48 hours both wild-type and transgenic animals are both utilizing the same ration of carbohydrates to lipids. How does ApoL6 regulation change during extended periods, 10-14 days, of cold exposure? ApoL6 degradation could be enhanced or import of ApoL6 into the mitochondria may be inhibited. Elucidating the mechanism of this metabolic switch would contribute to our understanding of ApoL6 function. Additionally, more detailed mass spectrometry analysis of glucose metabolites should also be undertaken under cold conditions. It should be determined if ApoL6 overexpression is leading to increased pyruvate transport into the mitochondria via MPC activity.

A clearer understanding of ApoL6 function in adipose tissue might also be gained by making a knockout mouse model. Whole-body and adipose tissue specific knockouts should be analyzed. Both models might be needed as ApoL6 is expressed in muscle in addition to adipose tissue. Muscle has the ability to accumulate lipid droplets under certain physiological conditions including obesity. Therefore, in a whole-body model it may be difficult to separate the effects of losing ApoL6 activity in muscle versus adipose tissue.

Our ApoL6 results provide new insights into how adipocytes regulate fuel utilization. These findings also significantly advance the understanding of regulation and function of the previously uncharacterized ApoL6 protein in adipose tissue. Taken together, my work contributes to a better understanding of the cellular metabolic changes resulting from defects in lipolytic regulation.

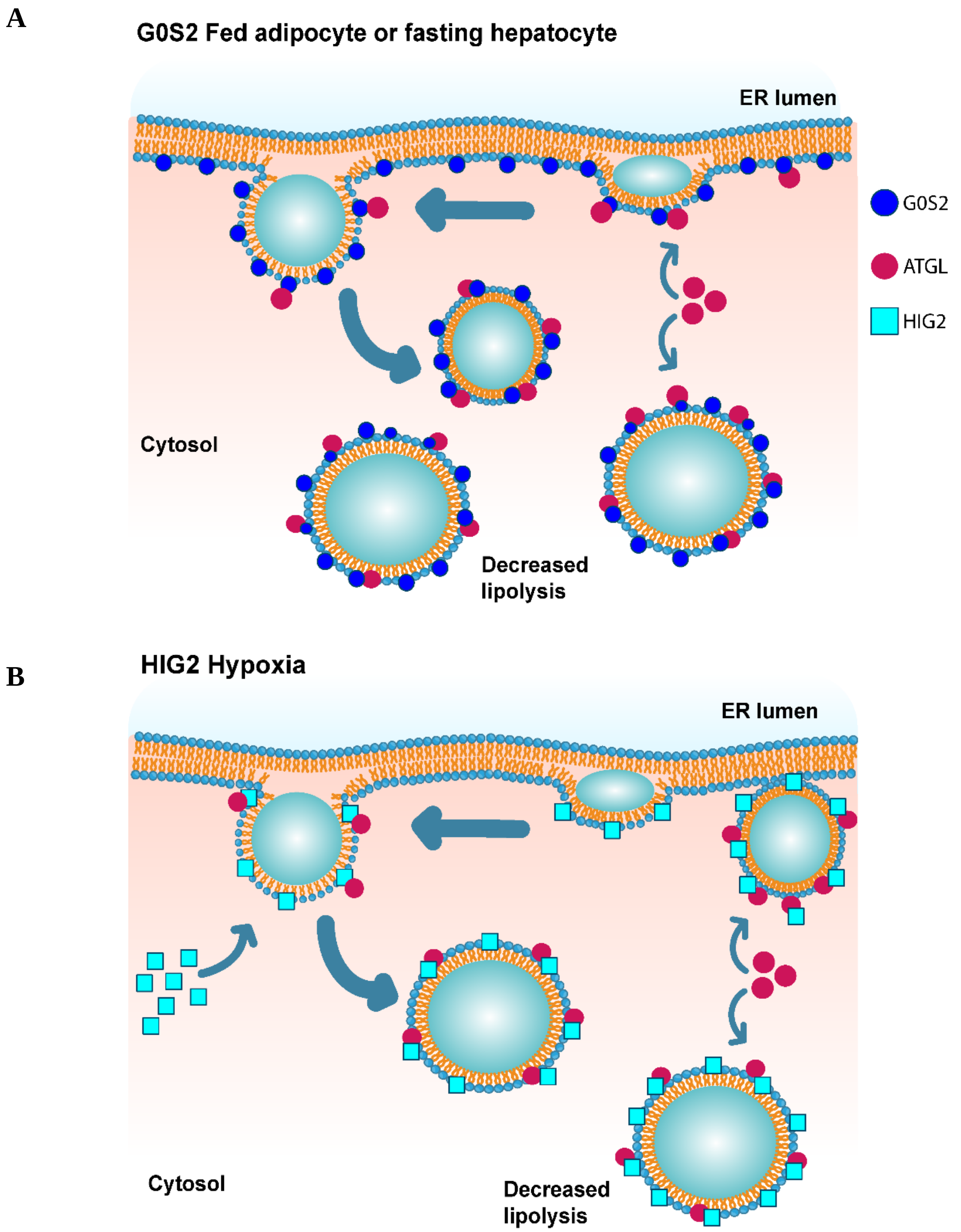


Figure 30. Model of ATGL-G0S2 and ATGL-HIG2 complex formation. (A) G0S2 interaction at ER and LD surfaces. (B) HIG2 and ATGL interactions at ER and LD surfaces.

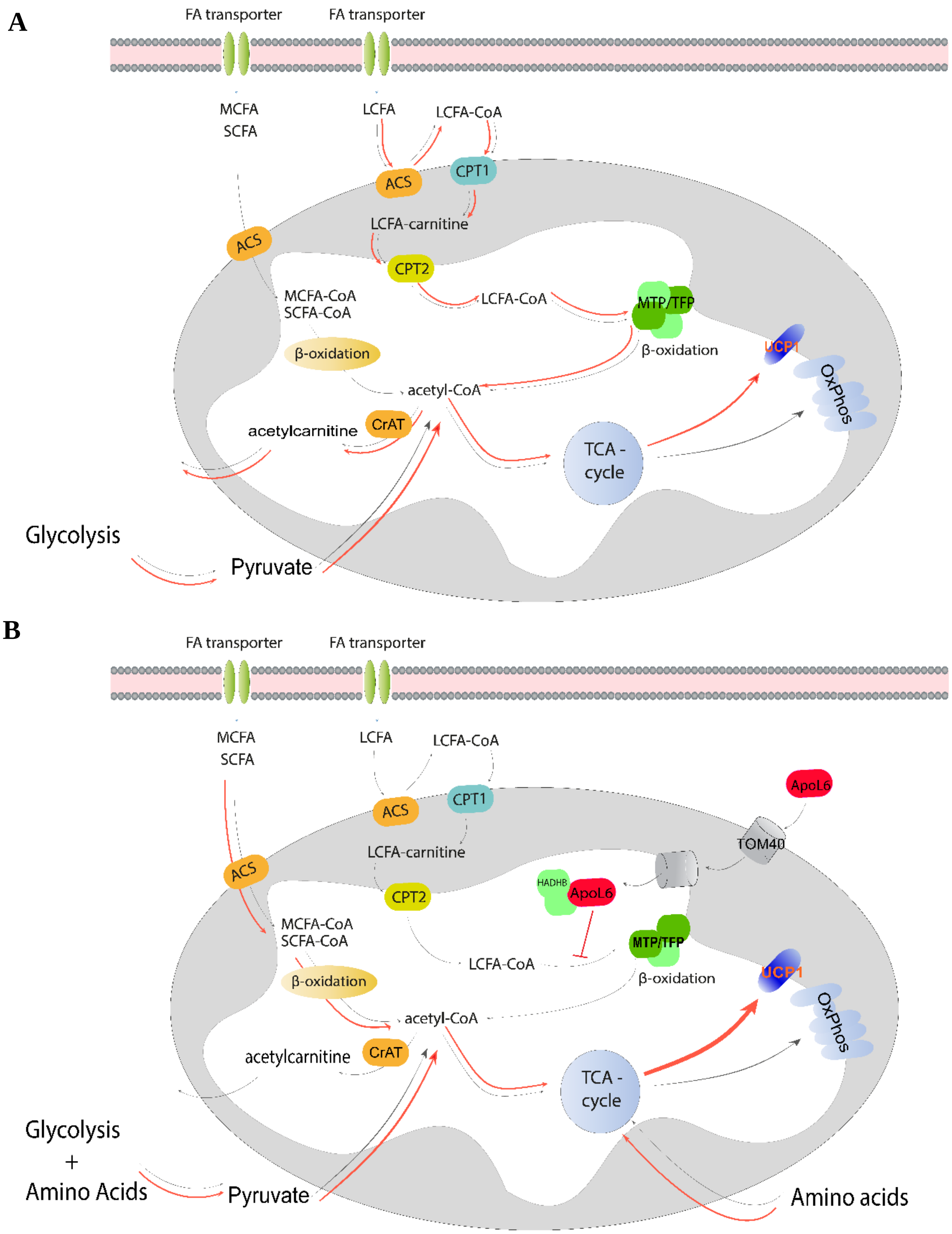


Figure 31. Model of ApoL6 mediated inhibition of LCFA oxidation. Model of fatty acid oxidation and heat production in brown adipose tissue of wild-type (A) and ApoL6-BAT (B) animals. Black arrow (RT) and cold (red arrows).

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APPENDIX A

APOL6 INTERACTING PROTEINS IDENTIFIED BY MASS SPECTROMETRY

Database used: Swissprot human Jan 2016 with a reversed sequence decoy

Protein False Discovery Rate (FDR): 0.8% : percent of the listed proteins that may be false positives. Most likely to be among the 2 or 3 peptide match proteins.

Protein Identification Criteria: > 95% probability; 2 peptide minimum; 95% peptide threshold

(TUPC) Total Unique Peptide Count: number of occurances of non-identical sequences; not counting modified forms or replicates

(NTSC) Total Spectrum Count: total number of spectrum associated with protein including modified forms and replicates after sample total spectrum count normalization

			NTSC	NTSC	TUPC	TUPC
Identified Proteins in ApoL6 compared to Flotillin with at least 8 fold increase and 5 or more peptides	**Accession Number**	**fold change ApoL6 / Flotillin**	**ApoL6**	**Flotillin**	**ApoL6**	**Flotillin**
Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2	sp|P35052|GPC1_HUMAN	78.9	81.444	1.0324	33	1
DnaJ homolog subfamily C member 16 OS=Homo sapiens GN=DNAJC16 PE=2 SV=3	sp|Q9Y2G8|DJC16_HUMAN	38.8	19.392	0.5	18	0
Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2	sp|P31431|SDC4_HUMAN	25.2	12.604	0.5	8	0
Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens GN=PBXIP1 PE=1 SV=1	sp|Q96AQ6|PBIP1_HUMAN	21.3	10.665	0.5	11	0
Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2	sp|Q8IYB3|SRRM1_HUMAN	19.7	20.361	1.0324	15	1
Regulator of nonsense transcripts 2 OS=Homo sapiens GN=UPF2 PE=1 SV=1	sp|Q9HAU5|RENT2_HUMAN	19.4	9.6958	0.5	10	0
Rho GTPase-activating protein 22 OS=Homo sapiens GN=ARHGAP22 PE=1 SV=1	sp|Q7Z5H3|RHG22_HUMAN	19.4	9.6958	0.5	9	0
Helicase with zinc finger domain 2 OS=Homo sapiens GN=HELZ2 PE=1 SV=6	sp|Q9BYK8|HELZ2_HUMAN	18.8	19.392	1.0324	20	1
Transcription elongation factor B polypeptide 3 OS=Homo sapiens GN=TCEB3 PE=1 SV=2	sp|Q14241|ELOA1_HUMAN	17.5	8.7262	0.5	9	0
Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5	sp|P39060|COIA1_HUMAN	17.5	8.7262	0.5	7	0
Protein VPRBP OS=Homo sapiens GN=VPRBP PE=1 SV=3	sp|Q9Y4B6|VPRBP_HUMAN	16.9	34.905	2.0648	33	2
Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2	sp|Q92896|GSLG1_HUMAN	15.5	7.7566	0.5	8	0
Nucleolar pre-ribosomal-associated protein 1 OS=Homo sapiens GN=URB1 PE=1 SV=4	sp|O60287|NPA1P_HUMAN	15.5	7.7566	0.5	8	0
Sphingosine-1-phosphate lyase 1 OS=Homo sapiens GN=SGPL1 PE=1 SV=3	sp|O95470|SGPL1_HUMAN	15.5	7.7566	0.5	8	0
1,4-alpha-glucan-branching enzyme OS=Homo sapiens GN=GBE1 PE=1 SV=3	sp|Q04446|GLGB_HUMAN	15.5	7.7566	0.5	8	0
Histone-lysine N-methyltransferase SETDB1 OS=Homo sapiens GN=SETDB1 PE=1 SV=1	sp|Q15047|SETB1_HUMAN	15.5	7.7566	0.5	7	0
Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens GN=PRPF4B PE=1 SV=3	sp|Q13523|PRP4B_HUMAN	15.5	7.7566	0.5	7	0
Peroxisomal biogenesis factor 19 OS=Homo sapiens GN=PEX19 PE=1 SV=1	sp|P40855|PEX19_HUMAN	15.5	7.7566	0.5	5	0
Protein ecdysoneless homolog OS=Homo sapiens GN=ECD PE=1 SV=1	sp|O95905|ECD_HUMAN	15.0	31.026	2.0648	22	2
E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1	sp|Q14669|TRIPC_HUMAN	14.6	30.057	2.0648	30	2
Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens GN=BAZ1A PE=1 SV=2	sp|Q9NRL2|BAZ1A_HUMAN	13.6	6.787	0.5	7	0
Adenomatous polyposis coli protein 2 OS=Homo sapiens GN=APC2 PE=1 SV=1	sp|O95996|APC2_HUMAN	13.6	6.787	0.5	7	0
E3 ubiquitin-protein ligase RBBP6 OS=Homo sapiens GN=RBBP6 PE=1 SV=1	sp|Q7Z6E9|RBBP6_HUMAN	13.6	6.787	0.5	7	0
Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 PE=1 SV=2	sp|P29317|EPHA2_HUMAN	13.6	6.787	0.5	7	0
Ankyrin repeat and zinc finger domain-containing protein 1 OS=Homo sapiens GN=ANKZF1 PE=1 SV=1	sp|Q9H8Y5|ANKZ1_HUMAN	13.6	6.787	0.5	7	0
Regulator of nonsense transcripts 3B OS=Homo sapiens GN=UPF3B PE=1 SV=1	sp|Q9BZI7|REN3B_HUMAN	13.6	6.787	0.5	6	0
Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3	sp|P55084|ECHB_HUMAN	13.3	82.414	6.1944	51	5
NAD-dependent protein deacetylase sirtuin-1 OS=Homo sapiens GN=SIRT1 PE=1 SV=2	sp|Q96EB6|SIR1_HUMAN	13.1	13.574	1.0324	14	1
Terminal uridylyltransferase 7 OS=Homo sapiens GN=ZCCHC6 PE=1 SV=1	sp|Q5VYS8|TUT7_HUMAN	12.2	12.604	1.0324	13	1
Digestive organ expansion factor homolog OS=Homo sapiens GN=DIEXF PE=1 SV=2	sp|Q68CQ4|DIEXF_HUMAN	12.2	12.604	1.0324	12	1
Transcriptional repressor NF-X1 OS=Homo sapiens GN=NFX1 PE=1 SV=2	sp|Q12986|NFX1_HUMAN	11.6	5.8175	0.5	6	0
Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE	sp|P98160|PGBM_HUMAN	11.6	5.8175	0.5	6	0
Centrosome-associated protein 350 OS=Homo sapiens GN=CEP350 PE=1 SV=1	sp|Q5VT06|CE350_HUMAN	11.6	5.8175	0.5	6	0
Serine/threonine-protein kinase LMTK2 OS=Homo sapiens GN=LMTK2 PE=1 SV=2	sp|Q8IWU2|LMTK2_HUMAN	11.6	5.8175	0.5	6	0
Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2	sp|Q9UGP8|SEC63_HUMAN	11.6	5.8175	0.5	6	0
Zinc finger and BTB domain-containing protein 7A OS=Homo sapiens GN=ZBTB7A PE=1 SV=1	sp|O95365|ZBT7A_HUMAN	11.6	5.8175	0.5	6	0
28S ribosomal protein S35, mitochondrial OS=Homo sapiens GN=MRPS35 PE=1 SV=1	sp|P82673|RT35_HUMAN	11.6	5.8175	0.5	6	0
Nucleolar complex protein 4 homolog OS=Homo sapiens GN=NOC4L PE=1 SV=1	sp|Q9BVI4|NOC4L_HUMAN	11.6	5.8175	0.5	6	0
Ribosomal RNA-processing protein 7 homolog A OS=Homo sapiens GN=RRP7A PE=1 SV=2	sp|Q9Y3A4|RRP7A_HUMAN	11.6	5.8175	0.5	6	0
Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	sp|P07305|H10_HUMAN	11.6	5.8175	0.5	5	0
Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2	sp|Q15050|RRS1_HUMAN	11.6	5.8175	0.5	5	0
MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2	sp|Q96T76|MMS19_HUMAN	11.4	105.68	9.2916	75	9
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	sp|P40939|ECHA_HUMAN	11.1	171.61	15.486	95	14
Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1	sp|O15355|PPM1G_HUMAN	11.0	33.935	3.0972	22	3
Adenomatous polyposis coli protein OS=Homo sapiens GN=APC PE=1 SV=2	sp|P25054|APC_HUMAN	10.8	44.6	4.1296	41	4
Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1	sp|Q86U86|PB1_HUMAN	10.3	10.665	1.0324	11	1
Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=1 SV=2	sp|Q14997|PSME4_HUMAN	10.3	10.665	1.0324	10	1
Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens GN=CIAO1 PE=1 SV=1	sp|O76071|CIAO1_HUMAN	10.0	31.026	3.0972	18	2
Centrosomal protein of 131 kDa OS=Homo sapiens GN=CEP131 PE=1 SV=3	sp|Q9UPN4|CP131_HUMAN	9.7	4.8479	0.5	5	0
Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2	sp|O43159|RRP8_HUMAN	9.7	4.8479	0.5	5	0
Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1	sp|Q8WXI9|P66B_HUMAN	9.7	4.8479	0.5	5	0
Spermatogenesis-associated serine-rich protein 2 OS=Homo sapiens GN=SPATS2 PE=1 SV=1	sp|Q86XZ4|SPAS2_HUMAN	9.7	4.8479	0.5	5	0
39S ribosomal protein L15, mitochondrial OS=Homo sapiens GN=MRPL15 PE=1 SV=1	sp|Q9P015|RM15_HUMAN	9.7	4.8479	0.5	5	0
Nucleolar protein 9 OS=Homo sapiens GN=NOP9 PE=1 SV=1	sp|Q86U38|NOP9_HUMAN	9.7	4.8479	0.5	5	0
Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4	sp|Q9UJX3|APC7_HUMAN	9.7	4.8479	0.5	5	0
Exosome complex component RRP43 OS=Homo sapiens GN=EXOSC8 PE=1 SV=1	sp|Q96B26|EXOS8_HUMAN	9.7	4.8479	0.5	5	0
Unconventional myosin-X OS=Homo sapiens GN=MYO10 PE=1 SV=3	sp|Q9HD67|MYO10_HUMAN	9.4	9.6958	1.0324	10	1
Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	sp|Q12797|ASPH_HUMAN	8.8	27.148	3.0972	24	2
Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=1 SV=3	sp|P78316|NOP14_HUMAN	8.5	8.7262	1.0324	9	1
Probable ATP-dependent RNA helicase DDX10 OS=Homo sapiens GN=DDX10 PE=1 SV=2	sp|Q13206|DDX10_HUMAN	8.5	8.7262	1.0324	9	1
Armadillo repeat-containing protein 8 OS=Homo sapiens GN=ARMC8 PE=1 SV=2	sp|Q8IUR7|ARMC8_HUMAN	8.5	8.7262	1.0324	8	1
Protein LTV1 homolog OS=Homo sapiens GN=LTV1 PE=1 SV=1	sp|Q96GA3|LTV1_HUMAN	8.5	8.7262	1.0324	8	1
Zinc finger CCCH domain-containing protein 4 OS=Homo sapiens GN=ZC3H4 PE=1 SV=3	sp|Q9UPT8|ZC3H4_HUMAN	8.5	8.7262	1.0324	6	1
Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5	sp|O00468|AGRIN_HUMAN	7.5	7.7566	1.0324	8	1
E3 ubiquitin-protein ligase TRIM56 OS=Homo sapiens GN=TRIM56 PE=1 SV=3	sp|Q9BRZ2|TRI56_HUMAN	7.5	7.7566	1.0324	8	1
Collagen alpha-1(XV) chain OS=Homo sapiens GN=COL15A1 PE=1 SV=2	sp|P39059|COFA1_HUMAN	7.5	7.7566	1.0324	8	1
Cell division cycle protein 23 homolog OS=Homo sapiens GN=CDC23 PE=1 SV=3	sp|Q9UJX2|CDC23_HUMAN	7.5	7.7566	1.0324	8	1
Probable 28S rRNA (cytosine-C(5))-methyltransferase OS=Homo sapiens GN=NSUN5 PE=1 SV=2	sp|Q96P11|NSUN5_HUMAN	7.5	7.7566	1.0324	8	1
Zinc finger SWIM domain-containing protein 8 OS=Homo sapiens GN=ZSWIM8 PE=1 SV=1	sp|A7E2V4|ZSWM8_HUMAN	7.5	15.513	2.0648	16	2
KN motif and ankyrin repeat domain-containing protein 1 OS=Homo sapiens GN=KANK1 PE=1 SV=3	sp|Q14678|KANK1_HUMAN	7.5	15.513	2.0648	13	2
RNA-binding protein 4 OS=Homo sapiens GN=RBM4 PE=1 SV=1	sp|Q9BWF3|RBM4_HUMAN	7.5	15.513	2.0648	13	2
Identified Proteins in ApoL6 compared to Flotillin with less than 8 fold increase and/or less than 5 peptides						
PHD and RING finger domain-containing protein 1 OS=Homo sapiens GN=PHRF1 PE=1 SV=3	sp|Q9P1Y6|PHRF1_HUMAN	11.6	5.8175	0.5	4	0
H/ACA ribonucleoprotein complex non-core subunit NAF1 OS=Homo sapiens GN=NAF1 PE=1 SV=2	sp|Q96HR8|NAF1_HUMAN	11.6	5.8175	0.5	3	0
ATP-dependent RNA helicase DDX55 OS=Homo sapiens GN=DDX55 PE=1 SV=3	sp|Q8NHQ9|DDX55_HUMAN	9.7	4.8479	0.5	4	0
Band 4.1-like protein 5 OS=Homo sapiens GN=EPB41L5 PE=1 SV=3	sp|Q9HCM4|E41L5_HUMAN	9.7	4.8479	0.5	4	0
Syndecan-2 OS=Homo sapiens GN=SDC2 PE=1 SV=2	sp|P34741|SDC2_HUMAN	9.7	4.8479	0.5	4	0
COP9 signalosome complex subunit 7a OS=Homo sapiens GN=COPS7A PE=1 SV=1	sp|Q9UBW8|CSN7A_HUMAN	9.7	4.8479	0.5	4	0
Transmembrane emp24 domain-containing protein 1 OS=Homo sapiens GN=TMED1 PE=1 SV=1	sp|Q13445|TMED1_HUMAN	9.7	4.8479	0.5	4	0
Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens GN=HACD3 PE=1 SV=2	sp|Q9P035|HACD3_HUMAN	9.7	4.8479	0.5	3	0
Probable helicase senataxin OS=Homo sapiens GN=SETX PE=1 SV=4	sp|Q7Z333|SETX_HUMAN	7.8	3.8783	0.5	4	0
Roundabout homolog 1 OS=Homo sapiens GN=ROBO1 PE=1 SV=1	sp|Q9Y6N7|ROBO1_HUMAN	7.8	3.8783	0.5	4	0
Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=4	sp|Q03252|LMNB2_HUMAN	7.8	3.8783	0.5	4	0
Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1	sp|Q6PJT7|ZC3HE_HUMAN	7.8	3.8783	0.5	4	0
Serine/threonine-protein kinase MARK2 OS=Homo sapiens GN=MARK2 PE=1 SV=2	sp|Q7KZI7|MARK2_HUMAN	7.8	3.8783	0.5	4	0
Oxysterol-binding protein-related protein 8 OS=Homo sapiens GN=OSBPL8 PE=1 SV=3	sp|Q9BZF1|OSBL8_HUMAN	7.8	3.8783	0.5	4	0
DnaJ homolog subfamily C member 21 OS=Homo sapiens GN=DNAJC21 PE=1 SV=2	sp|Q5F1R6|DJC21_HUMAN	7.8	3.8783	0.5	4	0
Synembryn-A OS=Homo sapiens GN=RIC8A PE=1 SV=3	sp|Q9NPQ8|RIC8A_HUMAN	7.8	3.8783	0.5	4	0
Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=1 SV=2	sp|Q99590|SCAFB_HUMAN	7.8	3.8783	0.5	4	0
Nucleolar MIF4G domain-containing protein 1 OS=Homo sapiens GN=NOM1 PE=1 SV=1	sp|Q5C9Z4|NOM1_HUMAN	7.8	3.8783	0.5	4	0
DNA excision repair protein ERCC-6 OS=Homo sapiens GN=ERCC6 PE=1 SV=1	sp|Q03468|ERCC6_HUMAN	7.8	3.8783	0.5	4	0
Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2	sp|O94832|MYO1D_HUMAN	7.8	3.8783	0.5	4	0

E3 ubiquitin-protein ligase RAD18 OS=Homo sapiens GN=RAD18 PE=1 SV=2	sp|Q9NS91|RAD18_HUMAN	7.8	3.8783	0.5	4	0
La-related protein 7 OS=Homo sapiens GN=LARP7 PE=1 SV=1	sp|Q4G0J3|LARP7_HUMAN	7.8	3.8783	0.5	4	0
rRNA methyltransferase 3, mitochondrial OS=Homo sapiens GN=RNMTL1 PE=1 SV=2	sp|Q9HC36|MRM3_HUMAN	7.8	3.8783	0.5	4	0
Protein AATF OS=Homo sapiens GN=AATF PE=1 SV=1	sp|Q9NY61|AATF_HUMAN	7.8	3.8783	0.5	4	0
U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3	sp|Q9Y5J1|UTP18_HUMAN	7.8	3.8783	0.5	4	0
Coilin OS=Homo sapiens GN=COIL PE=1 SV=1	sp|P38432|COIL_HUMAN	7.8	3.8783	0.5	4	0
p21-activated protein kinase-interacting protein 1 OS=Homo sapiens GN=PAK1IP1 PE=1 SV=2	sp|Q9NWT1|PK1IP_HUMAN	7.8	3.8783	0.5	4	0
Zinc finger protein 316 OS=Homo sapiens GN=ZNF316 PE=1 SV=1	sp|A6NFI3|ZN316_HUMAN	7.8	3.8783	0.5	4	0
Suppressor of SWI4 1 homolog OS=Homo sapiens GN=PPAN PE=2 SV=1	sp|Q9NQ55|SSF1_HUMAN	7.8	3.8783	0.5	4	0
BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=BAG2 PE=1 SV=1	sp|O95816|BAG2_HUMAN	7.8	3.8783	0.5	4	0
Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens GN=ZC3H15 PE=1 SV=1	sp|Q8WU90|ZC3HF_HUMAN	7.8	3.8783	0.5	4	0
Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3	sp|Q9NQT5|EXOS3_HUMAN	7.8	3.8783	0.5	4	0
Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1	sp|P84103|SRSF3_HUMAN	7.8	3.8783	0.5	4	0
Uncharacterized protein C12orf43 OS=Homo sapiens GN=C12orf43 PE=1 SV=2	sp|Q96C57|CL043_HUMAN	7.8	3.8783	0.5	4	0
Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3	sp|P20020|AT2B1_HUMAN	7.8	3.8783	0.5	3	0
E3 ISG15--protein ligase HERC5 OS=Homo sapiens GN=HERC5 PE=1 SV=2	sp|Q9UII4|HERC5_HUMAN	7.8	3.8783	0.5	3	0
Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens GN=NMT1 PE=1 SV=2	sp|P30419|NMT1_HUMAN	7.8	3.8783	0.5	3	0
Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	sp|P11047|LAMC1_HUMAN	7.5	7.7566	1.0324	4	1
Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5	sp|Q9BTC0|DIDO1_HUMAN	6.6	20.361	3.0972	19	3
Protein virilizer homolog OS=Homo sapiens GN=KIAA1429 PE=1 SV=2	sp|Q69YN4|VIR_HUMAN	6.6	27.148	4.1296	19	4
Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1	sp|Q13823|NOG2_HUMAN	6.6	20.361	3.0972	18	3
Formin-like protein 2 OS=Homo sapiens GN=FMNL2 PE=1 SV=3	sp|Q96PY5|FMNL2_HUMAN	6.6	6.787	1.0324	7	1
(Reversed) Coiled-coil domain-containing protein 33 OS=Homo sapiens GN=CCDC33 PE=1 SV=3	Reversed_sp|Q8N5R6|CCD33_HUMAN	6.6	6.787	1.0324	2	1
YTH domain-containing protein 1 OS=Homo sapiens GN=YTHDC1 PE=1 SV=3	sp|Q96MU7|YTDC1_HUMAN	6.6	6.787	1.0324	7	1
SWI/SNF complex subunit SMARCC1 OS=Homo sapiens GN=SMARCC1 PE=1 SV=3	sp|Q92922|SMRC1_HUMAN	6.6	6.787	1.0324	7	1
G patch domain-containing protein 4 OS=Homo sapiens GN=GPATCH4 PE=1 SV=2	sp|Q5T3I0|GPTC4_HUMAN	6.6	13.574	2.0648	11	1
26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	sp|P55036|PSMD4_HUMAN	6.6	13.574	2.0648	8	2
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H	sp|Q9H4L7|SMRCD_HUMAN	6.6	6.787	1.0324	7	1
Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=1 SV=1	sp|Q8WTT2|NOC3L_HUMAN	6.6	6.787	1.0324	6	1
Ribosome production factor 2 homolog OS=Homo sapiens GN=RPF2 PE=1 SV=2	sp|Q9H7B2|RPF2_HUMAN	6.6	6.787	1.0324	7	1
Probable ATP-dependent RNA helicase DDX52 OS=Homo sapiens GN=DDX52 PE=1 SV=3	sp|Q9Y2R4|DDX52_HUMAN	6.6	6.787	1.0324	6	1
Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4	sp|Q9H3P7|GCP60_HUMAN	6.3	19.392	3.0972	13	3
E3 ubiquitin-protein ligase Hakai OS=Homo sapiens GN=CBLL1 PE=1 SV=1	sp|Q75N03|HAKAI_HUMAN	5.8	2.9087	0.5	3	0
CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1 PE=1 SV=1	sp|Q7Z460|CLAP1_HUMAN	5.8	2.9087	0.5	3	0
Protein SAAL1 OS=Homo sapiens GN=SAAL1 PE=1 SV=2	sp|Q96ER3|SAAL1_HUMAN	5.8	2.9087	0.5	2	0
DBF4-type zinc finger-containing protein 2 OS=Homo sapiens GN=ZDBF2 PE=1 SV=3	sp|Q9HCK1|ZDBF2_HUMAN	5.8	2.9087	0.5	3	0
MAP/microtubule affinity-regulating kinase 3 OS=Homo sapiens GN=MARK3 PE=1 SV=4	sp|P27448|MARK3_HUMAN	5.8	2.9087	0.5	3	0
Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	sp|P01008|ANT3_HUMAN	5.8	2.9087	0.5	3	0
BCL-6 corepressor-like protein 1 OS=Homo sapiens GN=BCORL1 PE=1 SV=1	sp|Q5H9F3|BCORL_HUMAN	5.8	2.9087	0.5	3	0
APC membrane recruitment protein 1 OS=Homo sapiens GN=AMER1 PE=1 SV=2	sp|Q5JTC6|AMER1_HUMAN	5.8	2.9087	0.5	3	0
Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN PE=1 SV=1	sp|O95453|PARN_HUMAN	5.8	2.9087	0.5	3	0
G patch domain-containing protein 2 OS=Homo sapiens GN=GPATCH2 PE=1 SV=1	sp|Q9NW75|GPTC2_HUMAN	5.8	2.9087	0.5	3	0
Nuclear valosin-containing protein-like OS=Homo sapiens GN=NVL PE=1 SV=1	sp|O15381|NVL_HUMAN	5.8	2.9087	0.5	3	0
NK-tumor recognition protein OS=Homo sapiens GN=NKTR PE=1 SV=2	sp|P30414|NKTR_HUMAN	5.8	2.9087	0.5	3	0
Pecanex-like protein 3 OS=Homo sapiens GN=PCNXL3 PE=1 SV=2	sp|Q9H6A9|PCX3_HUMAN	5.8	2.9087	0.5	3	0
E3 ubiquitin-protein ligase TRIM11 OS=Homo sapiens GN=TRIM11 PE=1 SV=2	sp|Q96F44|TRI11_HUMAN	5.8	2.9087	0.5	3	0
THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1	sp|Q96FV9|THOC1_HUMAN	5.8	2.9087	0.5	3	0
Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=1 SV=4	sp|Q9UM54|MYO6_HUMAN	5.8	2.9087	0.5	3	0
Pentatricopeptide repeat-containing protein 1, mitochondrial OS=Homo sapiens GN=PTCD1 PE=1 SV=2	sp|O75127|PTCD1_HUMAN	5.8	2.9087	0.5	3	0
Polyadenylate-binding protein-interacting protein 1 OS=Homo sapiens GN=PAIP1 PE=1 SV=1	sp|Q9H074|PAIP1_HUMAN	5.8	2.9087	0.5	2	0
A-kinase anchor protein 17A OS=Homo sapiens GN=AKAP17A PE=1 SV=2	sp|Q02040|AK17A_HUMAN	5.8	2.9087	0.5	3	0
Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	sp|P00450|CERU_HUMAN	5.8	2.9087	0.5	3	0
Uncharacterized protein KIAA1522 OS=Homo sapiens GN=KIAA1522 PE=1 SV=2	sp|Q9P206|K1522_HUMAN	5.8	2.9087	0.5	3	0
WD repeat-containing protein 70 OS=Homo sapiens GN=WDR70 PE=1 SV=1	sp|Q9NW82|WDR70_HUMAN	5.8	2.9087	0.5	3	0
Testis-specific Y-encoded-like protein 1 OS=Homo sapiens GN=TSPYL1 PE=1 SV=3	sp|Q9H0U9|TSYL1_HUMAN	5.8	2.9087	0.5	3	0
Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3	sp|Q6PIU2|NCEH1_HUMAN	5.8	2.9087	0.5	3	0
Serine/threonine-protein kinase RIO2 OS=Homo sapiens GN=RIOK2 PE=1 SV=2	sp|Q9BVS4|RIOK2_HUMAN	5.8	2.9087	0.5	3	0
Surfeit locus protein 6 OS=Homo sapiens GN=SURF6 PE=1 SV=3	sp|O75683|SURF6_HUMAN	5.8	2.9087	0.5	3	0
tRNA (uracil-5-)-methyltransferase homolog A OS=Homo sapiens GN=TRMT2A PE=1 SV=2	sp|Q8IZ69|TRM2A_HUMAN	5.8	2.9087	0.5	3	0
Cohesin subunit SA-2 OS=Homo sapiens GN=STAG2 PE=1 SV=3	sp|Q8N3U4|STAG2_HUMAN	5.8	2.9087	0.5	3	0
Casein kinase I isoform gamma-3 OS=Homo sapiens GN=CSNK1G3 PE=1 SV=2	sp|Q9Y6M4|KC1G3_HUMAN	5.8	2.9087	0.5	3	0
Phosphorylated adapter RNA export protein OS=Homo sapiens GN=PHAX PE=1 SV=1	sp|Q9H814|PHAX_HUMAN	5.8	2.9087	0.5	3	0
Probable ATP-dependent RNA helicase DDX31 OS=Homo sapiens GN=DDX31 PE=1 SV=2	sp|Q9H8H2|DDX31_HUMAN	5.8	2.9087	0.5	3	0
Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1	sp|Q9H2M9|RBGPR_HUMAN	5.8	2.9087	0.5	3	0
Multiple myeloma tumor-associated protein 2 OS=Homo sapiens GN=MMTAG2 PE=1 SV=1	sp|Q9BU76|MMTA2_HUMAN	5.8	2.9087	0.5	3	0
Protein numb homolog OS=Homo sapiens GN=NUMB PE=1 SV=2	sp|P49757|NUMB_HUMAN	5.8	2.9087	0.5	3	0
ER degradation-enhancing alpha-mannosidase-like protein 3 OS=Homo sapiens GN=EDEM3 PE=1 SV=2	sp|Q9BZQ6|EDEM3_HUMAN	5.8	2.9087	0.5	3	0
Large subunit GTPase 1 homolog OS=Homo sapiens GN=LSG1 PE=1 SV=2	sp|Q9H089|LSG1_HUMAN	5.8	2.9087	0.5	3	0
COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1	sp|Q9H9Q2|CSN7B_HUMAN	5.8	2.9087	0.5	3	0
Maltase-glucoamylase, intestinal OS=Homo sapiens GN=MGAM PE=1 SV=5	sp|O43451|MGA_HUMAN	5.8	2.9087	0.5	3	0
Cyclin-K OS=Homo sapiens GN=CCNK PE=1 SV=2	sp|O75909|CCNK_HUMAN	5.8	2.9087	0.5	3	0
Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1	sp|Q10471|GALT2_HUMAN	5.8	2.9087	0.5	3	0
Homer protein homolog 3 OS=Homo sapiens GN=HOMER3 PE=1 SV=2	sp|Q9NSC5|HOME3_HUMAN	5.8	2.9087	0.5	3	0
Regulator of microtubule dynamics protein 3 OS=Homo sapiens GN=RMDN3 PE=1 SV=2	sp|Q96TC7|RMD3_HUMAN	5.8	2.9087	0.5	3	0
Zinc finger CCCH-type with G patch domain-containing protein OS=Homo sapiens GN=ZGPAT PE=1 SV=3	sp|Q8N5A5|ZGPAT_HUMAN	5.8	2.9087	0.5	3	0
39S ribosomal protein L2, mitochondrial OS=Homo sapiens GN=MRPL2 PE=1 SV=2	sp|Q5T653|RM02_HUMAN	5.8	2.9087	0.5	3	0
Nicotinamide/nicotinic acid mononucleotide adenylyltransferase 1 OS=Homo sapiens GN=NMNAT1 PE=1 S	sp|Q9HAN9|NMNA1_HUMAN	5.8	2.9087	0.5	3	0
RNA-binding motif protein, X-linked 2 OS=Homo sapiens GN=RBMX2 PE=1 SV=2	sp|Q9Y388|RBMX2_HUMAN	5.8	2.9087	0.5	3	0
Geminin OS=Homo sapiens GN=GMNN PE=1 SV=1	sp|O75496|GEMI_HUMAN	5.8	2.9087	0.5	3	0
Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1	sp|Q05519|SRS11_HUMAN	5.8	2.9087	0.5	2	0
Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=	sp|Q9Y6D6|BIG1_HUMAN	5.6	5.8175	1.0324	6	1
Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1	sp|Q5T200|ZC3HD_HUMAN	5.6	17.452	3.0972	16	3
Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2	sp|Q6KC79|NIPBL_HUMAN	5.6	5.8175	1.0324	6	1
HMG box transcription factor BBX OS=Homo sapiens GN=BBX PE=1 SV=1	sp|Q8WY36|BBX_HUMAN	5.6	5.8175	1.0324	6	1
Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=1 SV=2	sp|P42695|CNDD3_HUMAN	5.6	11.635	2.0648	12	2
DDB1- and CUL4-associated factor 8 OS=Homo sapiens GN=DCAF8 PE=1 SV=1	sp|Q5TAQ9|DCAF8_HUMAN	5.6	5.8175	1.0324	6	1
Probable ATP-dependent RNA helicase DDX56 OS=Homo sapiens GN=DDX56 PE=1 SV=1	sp|Q9NY93|DDX56_HUMAN	5.6	11.635	2.0648	11	2
E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	sp|Q14258|TRI25_HUMAN	5.6	5.8175	1.0324	6	1
Pre-mRNA-splicing factor CWC22 homolog OS=Homo sapiens GN=CWC22 PE=1 SV=3	sp|Q9HCG8|CWC22_HUMAN	5.6	5.8175	1.0324	6	1
Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1	sp|O96008|TOM40_HUMAN	5.6	5.8175	1.0324	6	1
Periphilin-1 OS=Homo sapiens GN=PPHLN1 PE=1 SV=2	sp|Q8NEY8|PPHLN_HUMAN	5.6	5.8175	1.0324	5	1
Prolactin regulatory element-binding protein OS=Homo sapiens GN=PREB PE=1 SV=2	sp|Q9HCU5|PREB_HUMAN	5.6	5.8175	1.0324	5	1
COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	sp|Q92905|CSN5_HUMAN	5.6	5.8175	1.0324	6	1
Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens GN=BZW2 PE=1 SV=1	sp|Q9Y6E2|BZW2_HUMAN	5.6	5.8175	1.0324	6	1
U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens GN=RRP9 PE=1 SV=1	sp|O43818|U3IP2_HUMAN	5.6	5.8175	1.0324	6	1
E3 ubiquitin-protein ligase RING2 OS=Homo sapiens GN=RNF2 PE=1 SV=1	sp|Q99496|RING2_HUMAN	5.6	5.8175	1.0324	6	1
Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	sp|O15230|LAMA5_HUMAN	5.3	16.483	3.0972	17	3
Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens GN=BRIX1 PE=1 SV=2	sp|Q8TDN6|BRX1_HUMAN	5.3	16.483	3.0972	15	3
Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	sp|Q07065|CKAP4_HUMAN	5.2	10.665	2.0648	10	2
Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2	sp|Q9UIG0|BAZ1B_HUMAN	5.2	10.665	2.0648	11	2
FERM, RhoGEF and pleckstrin domain-containing protein 1 OS=Homo sapiens GN=FARP1 PE=1 SV=1	sp|Q9Y4F1|FARP1_HUMAN	5.2	10.665	2.0648	11	2
Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3	sp|O76021|RL1D1_HUMAN	5.2	10.665	2.0648	11	2
COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3	sp|Q9UNS2|CSN3_HUMAN	5.2	10.665	2.0648	9	2
Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	sp|Q9UQ35|SRRM2_HUMAN	5.1	121.2	23.745	88	22
Probable ATP-dependent RNA helicase DHX37 OS=Homo sapiens GN=DHX37 PE=1 SV=1	sp|Q8IY37|DHX37_HUMAN	5.0	15.513	3.0972	16	3

pre-rRNA processing protein FTSJ3 OS=Homo sapiens GN=FTSJ3 PE=1 SV=2	sp|Q8IY81|SPB1_HUMAN	4.9	30.057	6.1944	21	4
Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3	sp|Q14684|RRP1B_HUMAN	4.9	30.057	6.1944	21	6
Putative ATP-dependent RNA helicase DHX57 OS=Homo sapiens GN=DHX57 PE=1 SV=2	sp|Q6P158|DHX57_HUMAN	4.8	44.6	9.2916	41	9
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	sp|O95373|IPO7_HUMAN	4.7	115.38	24.778	76	21
Histone H1.1 OS=Homo sapiens GN=HIST1H1A PE=1 SV=3	sp|Q02539|H11_HUMAN	4.7	14.544	3.0972	6	1
Chromodomain-helicase-DNA-binding protein 8 OS=Homo sapiens GN=CHD8 PE=1 SV=5	sp|Q9HCK8|CHD8_HUMAN	4.7	4.8479	1.0324	5	1
(Reversed) Low-density lipoprotein receptor-related protein 1B OS=Homo sapiens GN=LRP1B PE=1 SV=2	Reversed_sp|Q9NZR2|LRP1B_HUMAN	4.7	4.8479	1.0324	2	1
Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3	sp|Q13428|TCOF_HUMAN	4.7	29.087	6.1944	22	6
Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 PE=1 SV=2	sp|Q14966|ZN638_HUMAN	4.7	14.544	3.0972	14	3
Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2	sp|Q14789|GOGB1_HUMAN	4.7	9.6958	2.0648	10	2
HEAT repeat-containing protein 5B OS=Homo sapiens GN=HEATR5B PE=1 SV=2	sp|Q9P2D3|HTR5B_HUMAN	4.7	14.544	3.0972	15	2
Kinesin-like protein KIF1C OS=Homo sapiens GN=KIF1C PE=1 SV=3	sp|O43896|KIF1C_HUMAN	4.7	4.8479	1.0324	5	1
DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens GN=POLRMT PE=1 SV=2	sp|O00411|RPOM_HUMAN	4.7	9.6958	2.0648	10	2
RNA-binding protein 27 OS=Homo sapiens GN=RBM27 PE=1 SV=2	sp|Q9P2N5|RBM27_HUMAN	4.7	9.6958	2.0648	10	2
Protein Red OS=Homo sapiens GN=IK PE=1 SV=3	sp|Q13123|RED_HUMAN	4.7	4.8479	1.0324	5	1
ELM2 and SANT domain-containing protein 1 OS=Homo sapiens GN=ELMSAN1 PE=1 SV=2	sp|Q6PJG2|EMSA1_HUMAN	4.7	4.8479	1.0324	4	1
Serine/threonine-protein kinase ULK1 OS=Homo sapiens GN=ULK1 PE=1 SV=2	sp|O75385|ULK1_HUMAN	4.7	4.8479	1.0324	5	1
Protein PAT1 homolog 1 OS=Homo sapiens GN=PATL1 PE=1 SV=2	sp|Q86TB9|PATL1_HUMAN	4.7	4.8479	1.0324	5	1
Fanconi anemia group D2 protein OS=Homo sapiens GN=FANCD2 PE=1 SV=2	sp|Q9BXW9|FACD2_HUMAN	4.7	4.8479	1.0324	5	1
DNA-directed RNA polymerase III subunit RPC1 OS=Homo sapiens GN=POLR3A PE=1 SV=2	sp|O14802|RPC1_HUMAN	4.7	4.8479	1.0324	5	1
Armadillo repeat-containing X-linked protein 3 OS=Homo sapiens GN=ARMCX3 PE=1 SV=1	sp|Q9UH62|ARMX3_HUMAN	4.7	4.8479	1.0324	5	1
Guanine nucleotide-binding protein-like 3-like protein OS=Homo sapiens GN=GNL3L PE=1 SV=1	sp|Q9NVN8|GNL3L_HUMAN	4.7	4.8479	1.0324	5	1
Nucleolar protein 10 OS=Homo sapiens GN=NOL10 PE=1 SV=1	sp|Q9BSC4|NOL10_HUMAN	4.7	4.8479	1.0324	5	1
COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4	sp|Q13098|CSN1_HUMAN	4.7	4.8479	1.0324	5	1
Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=1 SV=3	sp|Q13144|EI2BE_HUMAN	4.7	4.8479	1.0324	5	1
RISC-loading complex subunit TARBP2 OS=Homo sapiens GN=TARBP2 PE=1 SV=3	sp|Q15633|TRBP2_HUMAN	4.7	4.8479	1.0324	5	1
39S ribosomal protein L24, mitochondrial OS=Homo sapiens GN=MRPL24 PE=1 SV=1	sp|Q96A35|RM24_HUMAN	4.7	4.8479	1.0324	5	1
Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2	sp|Q9Y6M1|IF2B2_HUMAN	4.7	14.544	3.0972	11	2
U3 small nucleolar ribonucleoprotein protein IMP4 OS=Homo sapiens GN=IMP4 PE=1 SV=1	sp|Q96G21|IMP4_HUMAN	4.7	4.8479	1.0324	5	1
Protein furry homolog-like OS=Homo sapiens GN=FRYL PE=1 SV=2	sp|O94915|FRYL_HUMAN	4.5	149.31	33.037	114	28
RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2	sp|Q5JTH9|RRP12_HUMAN	4.5	36.844	8.2592	29	8
Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2	sp|Q86UE4|LYRIC_HUMAN	4.5	18.422	4.1296	16	4
Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	sp|P16401|H15_HUMAN	4.5	18.422	4.1296	8	3
E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	sp|Q7Z6Z7|HUWE1_HUMAN	4.4	286.99	65.041	189	56
Atrial natriuretic peptide receptor 1 OS=Homo sapiens GN=NPR1 PE=1 SV=1	sp|P16066|ANPRA_HUMAN	4.4	13.574	3.0972	13	3
U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens GN=PRPF3 PE=1 SV=2	sp|O43395|PRPF3_HUMAN	4.4	13.574	3.0972	13	3
Cell division cycle protein 27 homolog OS=Homo sapiens GN=CDC27 PE=1 SV=2	sp|P30260|CDC27_HUMAN	4.4	13.574	3.0972	14	3
Metastasis-associated protein MTA1 OS=Homo sapiens GN=MTA1 PE=1 SV=2	sp|Q13330|MTA1_HUMAN	4.2	8.7262	2.0648	9	2
Protein PRRC2B OS=Homo sapiens GN=PRRC2B PE=1 SV=2	sp|Q5JSZ5|PRC2B_HUMAN	4.2	8.7262	2.0648	8	2
CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3	sp|Q03701|CEBPZ_HUMAN	4.2	17.452	4.1296	18	4
Intron-binding protein aquarius OS=Homo sapiens GN=AQR PE=1 SV=4	sp|O60306|AQR_HUMAN	4.2	8.7262	2.0648	9	2
ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2	sp|Q8TDD1|DDX54_HUMAN	4.2	8.7262	2.0648	8	2
E3 ubiquitin-protein ligase listerin OS=Homo sapiens GN=LTN1 PE=1 SV=6	sp|O94822|LTN1_HUMAN	4.2	8.7262	2.0648	9	2
Serine/arginine-rich splicing factor 10 OS=Homo sapiens GN=SRSF10 PE=1 SV=1	sp|O75494|SRS10_HUMAN	4.2	8.7262	2.0648	8	1
Probable ATP-dependent RNA helicase DDX47 OS=Homo sapiens GN=DDX47 PE=1 SV=1	sp|Q9H0S4|DDX47_HUMAN	4.2	8.7262	2.0648	8	1
Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3	sp|Q14690|RRP5_HUMAN	4.1	12.604	3.0972	11	3
MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1	sp|Q3KQU3|MA7D1_HUMAN	4.1	12.604	3.0972	13	3
(Reversed) Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2	Reversed_sp|Q9NU22|MDN1_HUMAN	3.9	1.9392	0.5	2	0
(Reversed) A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAM	Reversed_sp|Q9P2N4|ATS9_HUMAN	3.9	1.9392	0.5	2	0
(Reversed) Transient receptor potential cation channel subfamily M member 1 OS=Homo sapiens GN=TRPM	Reversed_sp|Q7Z4N2|TRPM1_HUMAN	3.9	1.9392	0.5	2	0
Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2	sp|P49454|CENPF_HUMAN	3.9	1.9392	0.5	2	0
Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	sp|P13671|CO6_HUMAN	3.9	1.9392	0.5	2	0
(Reversed) Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	Reversed_sp|Q00610|CLH1_HUMAN	3.9	1.9392	0.5	2	0
PHD finger protein 3 OS=Homo sapiens GN=PHF3 PE=1 SV=3	sp|Q92576|PHF3_HUMAN	3.9	1.9392	0.5	2	0
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	sp|P01024|CO3_HUMAN	3.9	1.9392	0.5	2	0
Meiosis arrest female protein 1 OS=Homo sapiens GN=KIAA0430 PE=1 SV=6	sp|Q9Y4F3|MARF1_HUMAN	3.9	1.9392	0.5	2	0
Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2	sp|P13807|GYS1_HUMAN	3.9	1.9392	0.5	2	0
(Reversed) Regulating synaptic membrane exocytosis protein 1 OS=Homo sapiens GN=RIMS1 PE=1 SV=1	Reversed_sp|Q86UR5|RIMS1_HUMAN	3.9	1.9392	0.5	2	0
Rho GTPase-activating protein 35 OS=Homo sapiens GN=ARHGAP35 PE=1 SV=3	sp|Q9NRY4|RHG35_HUMAN	3.9	1.9392	0.5	2	0
Brefeldin A-inhibited guanine nucleotide-exchange protein 3 OS=Homo sapiens GN=ARFGEF3 PE=1 SV=3	sp|Q5TH69|BIG3_HUMAN	3.9	1.9392	0.5	2	0
Little elongation complex subunit 2 OS=Homo sapiens GN=ICE2 PE=1 SV=2	sp|Q659A1|ICE2_HUMAN	3.9	1.9392	0.5	2	0
Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3	sp|Q12830|BPTF_HUMAN	3.9	1.9392	0.5	2	0
Receptor-type tyrosine-protein phosphatase eta OS=Homo sapiens GN=PTPRJ PE=1 SV=3	sp|Q12913|PTPRJ_HUMAN	3.9	1.9392	0.5	2	0
Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2	sp|Q9UHB9|SRP68_HUMAN	3.9	1.9392	0.5	2	0
Rho GTPase-activating protein 42 OS=Homo sapiens GN=ARHGAP42 PE=1 SV=3	sp|A6NI28|RHG42_HUMAN	3.9	1.9392	0.5	2	0
Calmodulin-regulated spectrin-associated protein 1 OS=Homo sapiens GN=CAMSAP1 PE=1 SV=2	sp|Q5T5Y3|CAMP1_HUMAN	3.9	1.9392	0.5	2	0
N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2	sp|Q8NFW8|NEUA_HUMAN	3.9	1.9392	0.5	2	0
TBC1 domain family member 9B OS=Homo sapiens GN=TBC1D9B PE=1 SV=3	sp|Q66K14|TBC9B_HUMAN	3.9	1.9392	0.5	2	0
ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1	sp|Q8N766|EMC1_HUMAN	3.9	1.9392	0.5	2	0
RNA-binding protein 33 OS=Homo sapiens GN=RBM33 PE=1 SV=3	sp|Q96EV2|RBM33_HUMAN	3.9	1.9392	0.5	2	0
DnaJ homolog subfamily C member 1 OS=Homo sapiens GN=DNAJC1 PE=1 SV=1	sp|Q96KC8|DNJC1_HUMAN	3.9	1.9392	0.5	2	0
Kinesin-like protein KIF21A OS=Homo sapiens GN=KIF21A PE=1 SV=2	sp|Q7Z4S6|KI21A_HUMAN	3.9	1.9392	0.5	2	0
Crooked neck-like protein 1 OS=Homo sapiens GN=CRNKL1 PE=1 SV=4	sp|Q9BZJ0|CRNL1_HUMAN	3.9	1.9392	0.5	2	0
Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens GN=DAAM1 PE=1 SV=2	sp|Q9Y4D1|DAAM1_HUMAN	3.9	1.9392	0.5	2	0
Transcription elongation factor, mitochondrial OS=Homo sapiens GN=TEFM PE=1 SV=1	sp|Q96QE5|TEFM_HUMAN	3.9	1.9392	0.5	2	0
DnaJ homolog subfamily C member 2 OS=Homo sapiens GN=DNAJC2 PE=1 SV=4	sp|Q99543|DNJC2_HUMAN	3.9	1.9392	0.5	2	0
Ubiquitin carboxyl-terminal hydrolase 36 OS=Homo sapiens GN=USP36 PE=1 SV=3	sp|Q9P275|UBP36_HUMAN	3.9	1.9392	0.5	2	0
Torsin-4A OS=Homo sapiens GN=TOR4A PE=1 SV=2	sp|Q9NXH8|TOR4A_HUMAN	3.9	1.9392	0.5	2	0
Interferon-stimulated 20 kDa exonuclease-like 2 OS=Homo sapiens GN=ISG20L2 PE=1 SV=1	sp|Q9H9L3|I20L2_HUMAN	3.9	1.9392	0.5	2	0
Adenylate cyclase type 10 OS=Homo sapiens GN=ADCY10 PE=1 SV=3	sp|Q96PN6|ADCYA_HUMAN	3.9	1.9392	0.5	2	0
Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3	sp|Q9UIA9|XPO7_HUMAN	3.9	1.9392	0.5	2	0
Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	sp|Q9Y4L1|HYOU1_HUMAN	3.9	1.9392	0.5	2	0
Nuclear speckle splicing regulatory protein 1 OS=Homo sapiens GN=NSRP1 PE=1 SV=1	sp|Q9H0G5|NSRP1_HUMAN	3.9	1.9392	0.5	2	0
RNA polymerase II elongation factor ELL OS=Homo sapiens GN=ELL PE=1 SV=1	sp|P55199|ELL_HUMAN	3.9	1.9392	0.5	2	0
Pre-mRNA-splicing factor RBM22 OS=Homo sapiens GN=RBM22 PE=1 SV=1	sp|Q9NW64|RBM22_HUMAN	3.9	1.9392	0.5	2	0
Pre-mRNA-splicing factor 38B OS=Homo sapiens GN=PRPF38B PE=1 SV=1	sp|Q5VTL8|PR38B_HUMAN	3.9	1.9392	0.5	2	0
Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1	sp|P49711|CTCF_HUMAN	3.9	1.9392	0.5	2	0
Unhealthy ribosome biogenesis protein 2 homolog OS=Homo sapiens GN=URB2 PE=2 SV=2	sp|Q14146|URB2_HUMAN	3.9	1.9392	0.5	2	0
Glypican-3 OS=Homo sapiens GN=GPC3 PE=1 SV=1	sp|P51654|GPC3_HUMAN	3.9	1.9392	0.5	2	0
Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1	sp|P50579|MAP2_HUMAN	3.9	1.9392	0.5	2	0
(Reversed) Rap guanine nucleotide exchange factor 1 OS=Homo sapiens GN=RAPGEF1 PE=1 SV=3	Reversed_sp|Q13905|RPGF1_HUMAN	3.9	1.9392	0.5	2	0
Phosphorylase b kinase regulatory subunit alpha, liver isoform OS=Homo sapiens GN=PHKA2 PE=1 SV=1	sp|P46019|KPB2_HUMAN	3.9	1.9392	0.5	2	0
U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=1 SV=2	sp|Q53GS9|SNUT2_HUMAN	3.9	1.9392	0.5	2	0
Merlin OS=Homo sapiens GN=NF2 PE=1 SV=1	sp|P35240|MERL_HUMAN	3.9	1.9392	0.5	2	0
Centrosomal protein of 70 kDa OS=Homo sapiens GN=CEP70 PE=1 SV=2	sp|Q8NHQ1|CEP70_HUMAN	3.9	1.9392	0.5	2	0
Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3	sp|Q9NZT2|OGFR_HUMAN	3.9	1.9392	0.5	2	0
Round spermatid basic protein 1 OS=Homo sapiens GN=RSBN1 PE=1 SV=2	sp|Q5VWQ0|RSBN1_HUMAN	3.9	1.9392	0.5	2	0
Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2	sp|P14314|GLU2B_HUMAN	3.9	1.9392	0.5	2	0
3'-5' exoribonuclease 1 OS=Homo sapiens GN=ERI1 PE=1 SV=3	sp|Q8IV48|ERI1_HUMAN	3.9	1.9392	0.5	2	0
Protein ECT2 OS=Homo sapiens GN=ECT2 PE=1 SV=4	sp|Q9H8V3|ECT2_HUMAN	3.9	1.9392	0.5	2	0
Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	sp|P02774|VTDB_HUMAN	3.9	1.9392	0.5	2	0
RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3 PE=1 SV=2	sp|Q9H6T3|RPAP3_HUMAN	3.9	1.9392	0.5	2	0
Transcription factor 25 OS=Homo sapiens GN=TCF25 PE=1 SV=1	sp|Q9BQ70|TCF25_HUMAN	3.9	1.9392	0.5	2	0
Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS PE=1 SV=5	sp|Q13724|MOGS_HUMAN	3.9	1.9392	0.5	2	0
Pre-mRNA-processing factor 17 OS=Homo sapiens GN=CDC40 PE=1 SV=1	sp|O60508|PRP17_HUMAN	3.9	1.9392	0.5	2	0

Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1	sp|P39748|FEN1_HUMAN	3.9	1.9392	0.5	2	0
Zinc finger protein 622 OS=Homo sapiens GN=ZNF622 PE=1 SV=1	sp|Q969S3|ZN622_HUMAN	3.9	1.9392	0.5	2	0
Protein SDA1 homolog OS=Homo sapiens GN=SDAD1 PE=1 SV=3	sp|Q9NVU7|SDA1_HUMAN	3.9	1.9392	0.5	2	0
Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	sp|O43396|TXNL1_HUMAN	3.9	1.9392	0.5	2	0
Choline-phosphate cytidylyltransferase A OS=Homo sapiens GN=PCYT1A PE=1 SV=2	sp|P49585|PCY1A_HUMAN	3.9	1.9392	0.5	2	0
Vang-like protein 1 OS=Homo sapiens GN=VANGL1 PE=1 SV=1	sp|Q8TAA9|VANG1_HUMAN	3.9	1.9392	0.5	2	0
Anaphase-promoting complex subunit 5 OS=Homo sapiens GN=ANAPC5 PE=1 SV=2	sp|Q9UJX4|APC5_HUMAN	3.9	1.9392	0.5	2	0
Ribonuclease P protein subunit p40 OS=Homo sapiens GN=RPP40 PE=1 SV=3	sp|O75818|RPP40_HUMAN	3.9	1.9392	0.5	2	0
Calcium uptake protein 1, mitochondrial OS=Homo sapiens GN=MICU1 PE=1 SV=1	sp|Q9BPX6|MICU1_HUMAN	3.9	1.9392	0.5	2	0
U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens GN=UTP15 PE=1 SV=3	sp|Q8TED0|UTP15_HUMAN	3.9	1.9392	0.5	2	0
Myotubularin-related protein 1 OS=Homo sapiens GN=MTMR1 PE=1 SV=4	sp|Q13613|MTMR1_HUMAN	3.9	1.9392	0.5	2	0
Phenylalanine--tRNA ligase, mitochondrial OS=Homo sapiens GN=FARS2 PE=1 SV=1	sp|O95363|SYFM_HUMAN	3.9	1.9392	0.5	2	0
GRAM domain-containing protein 1B OS=Homo sapiens GN=GRAMD1B PE=1 SV=1	sp|Q3KR37|GRM1B_HUMAN	3.9	1.9392	0.5	2	0
THUMP domain-containing protein 3 OS=Homo sapiens GN=THUMPD3 PE=1 SV=1	sp|Q9BV44|THUM3_HUMAN	3.9	1.9392	0.5	2	0
Cirhin OS=Homo sapiens GN=CIRH1A PE=1 SV=1	sp|Q969X6|CIR1A_HUMAN	3.9	1.9392	0.5	2	0
RNA-binding protein 42 OS=Homo sapiens GN=RBM42 PE=1 SV=1	sp|Q9BTD8|RBM42_HUMAN	3.9	1.9392	0.5	2	0
Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	sp|P06744|G6PI_HUMAN	3.9	1.9392	0.5	2	0
Transcriptional repressor protein YY1 OS=Homo sapiens GN=YY1 PE=1 SV=2	sp|P25490|TYY1_HUMAN	3.9	1.9392	0.5	2	0
Zinc finger CCCH domain-containing protein 8 OS=Homo sapiens GN=ZC3H8 PE=1 SV=2	sp|Q8N5P1|ZC3H8_HUMAN	3.9	1.9392	0.5	2	0
RNA-binding protein with serine-rich domain 1 OS=Homo sapiens GN=RNPS1 PE=1 SV=1	sp|Q15287|RNPS1_HUMAN	3.9	1.9392	0.5	2	0
Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	sp|P69905|HBA_HUMAN	3.9	1.9392	0.5	2	0
Nucleolar protein 12 OS=Homo sapiens GN=NOL12 PE=1 SV=1	sp|Q9UGY1|NOL12_HUMAN	3.9	1.9392	0.5	2	0
Sorting nexin-27 OS=Homo sapiens GN=SNX27 PE=1 SV=2	sp|Q96L92|SNX27_HUMAN	3.9	1.9392	0.5	2	0
Transcription factor E2F6 OS=Homo sapiens GN=E2F6 PE=1 SV=1	sp|O75461|E2F6_HUMAN	3.9	1.9392	0.5	2	0
Methyltransferase-like protein 8 OS=Homo sapiens GN=METTL8 PE=2 SV=2	sp|Q9H825|METL8_HUMAN	3.9	1.9392	0.5	2	0
NEDD4 family-interacting protein 1 OS=Homo sapiens GN=NDFIP1 PE=1 SV=1	sp|Q9BT67|NFIP1_HUMAN	3.9	1.9392	0.5	2	0
Thyroid transcription factor 1-associated protein 26 OS=Homo sapiens GN=CCDC59 PE=1 SV=2	sp|Q9P031|TAP26_HUMAN	3.9	1.9392	0.5	2	0
Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	sp|P28072|PSB6_HUMAN	3.9	1.9392	0.5	2	0
Translation machinery-associated protein 16 OS=Homo sapiens GN=TMA16 PE=1 SV=2	sp|Q96EY4|TMA16_HUMAN	3.9	1.9392	0.5	2	0
Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2	sp|Q12959|DLG1_HUMAN	3.9	1.9392	0.5	2	0
Exosome complex component RRP46 OS=Homo sapiens GN=EXOSC5 PE=1 SV=1	sp|Q9NQT4|EXOS5_HUMAN	3.9	1.9392	0.5	2	0
Ig heavy chain V-III region 23 OS=Homo sapiens GN=IGHV3-23 PE=1 SV=2	sp|P01764|HV303_HUMAN	3.9	1.9392	0.5		
Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3	sp|Q12873|CHD3_HUMAN	3.8	19.392	5.162	16	5
Ryanodine receptor 1 OS=Homo sapiens GN=RYR1 PE=1 SV=3	sp|P21817|RYR1_HUMAN	3.8	3.8783	1.0324	2	1
Myosin-6 OS=Homo sapiens GN=MYH6 PE=1 SV=5	sp|P13533|MYH6_HUMAN	3.8	3.8783	1.0324	2	1
AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2	sp|Q10567|AP1B1_HUMAN	3.8	11.635	3.0972	12	3
Phosphatidylinositol 4-phosphate 5-kinase type-1 alpha OS=Homo sapiens GN=PIP5K1A PE=1 SV=1	sp|Q99755|PI51A_HUMAN	3.8	3.8783	1.0324	4	1
Pinin OS=Homo sapiens GN=PNN PE=1 SV=4	sp|Q9H307|PININ_HUMAN	3.8	11.635	3.0972	9	3
Formin-like protein 3 OS=Homo sapiens GN=FMNL3 PE=1 SV=3	sp|Q8IVF7|FMNL3_HUMAN	3.8	3.8783	1.0324	4	1
Chromodomain-helicase-DNA-binding protein 6 OS=Homo sapiens GN=CHD6 PE=1 SV=4	sp|Q8TD26|CHD6_HUMAN	3.8	3.8783	1.0324	4	1
Neuroblastoma-amplified sequence OS=Homo sapiens GN=NBAS PE=1 SV=2	sp|A2RRP1|NBAS_HUMAN	3.8	3.8783	1.0324	4	1
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	sp|P02751|FINC_HUMAN	3.8	3.8783	1.0324	4	1
Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	sp|P00558|PGK1_HUMAN	3.8	7.7566	2.0648	8	2
39S ribosomal protein L38, mitochondrial OS=Homo sapiens GN=MRPL38 PE=1 SV=2	sp|Q96DV4|RM38_HUMAN	3.8	3.8783	1.0324	4	1
Double-stranded RNA-binding protein Staufen homolog 2 OS=Homo sapiens GN=STAU2 PE=1 SV=1	sp|Q9NUL3|STAU2_HUMAN	3.8	7.7566	2.0648	8	2
General transcription factor IIF subunit 1 OS=Homo sapiens GN=GTF2F1 PE=1 SV=2	sp|P35269|T2FA_HUMAN	3.8	3.8783	1.0324	4	1
Peripheral plasma membrane protein CASK OS=Homo sapiens GN=CASK PE=1 SV=3	sp|O14936|CSKP_HUMAN	3.8	3.8783	1.0324	4	1
Protein phosphatase 1 regulatory subunit 15B OS=Homo sapiens GN=PPP1R15B PE=1 SV=1	sp|Q5SWA1|PR15B_HUMAN	3.8	11.635	3.0972	11	3
Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	sp|P09874|PARP1_HUMAN	3.8	3.8783	1.0324	4	1
THO complex subunit 5 homolog OS=Homo sapiens GN=THOC5 PE=1 SV=2	sp|Q13769|THOC5_HUMAN	3.8	3.8783	1.0324	4	1
AT-rich interactive domain-containing protein 2 OS=Homo sapiens GN=ARID2 PE=1 SV=2	sp|Q68CP9|ARID2_HUMAN	3.8	3.8783	1.0324	3	1
RNA-binding protein 47 OS=Homo sapiens GN=RBM47 PE=1 SV=2	sp|A0AV96|RBM47_HUMAN	3.8	3.8783	1.0324	4	1
Zinc finger C2HC domain-containing protein 1A OS=Homo sapiens GN=ZC2HC1A PE=1 SV=2	sp|Q96GY0|ZC21A_HUMAN	3.8	3.8783	1.0324	2	1
WD40 repeat-containing protein SMU1 OS=Homo sapiens GN=SMU1 PE=1 SV=2	sp|Q2TAY7|SMU1_HUMAN	3.8	7.7566	2.0648	6	2
Ran-binding protein 9 OS=Homo sapiens GN=RANBP9 PE=1 SV=1	sp|Q96S59|RANB9_HUMAN	3.8	3.8783	1.0324	4	1
Zinc finger CCHC-type and RNA-binding motif-containing protein 1 OS=Homo sapiens GN=ZCRB1 PE=1 SV	sp|Q8TBF4|ZCRB1_HUMAN	3.8	3.8783	1.0324	3	1
Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=1 SV=3	sp|P21127|CD11B_HUMAN	3.8	3.8783	1.0324	4	1
Cyclin-dependent kinase 11A OS=Homo sapiens GN=CDK11A PE=1 SV=4	sp|Q9UQ88|CD11A_HUMAN	3.8	3.8783	1.0324	4	1
Chromobox protein homolog 8 OS=Homo sapiens GN=CBX8 PE=1 SV=3	sp|Q9HC52|CBX8_HUMAN	3.8	3.8783	1.0324	4	1
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	sp|P06396|GELS_HUMAN	3.8	3.8783	1.0324	4	1
Protein kinase C iota type OS=Homo sapiens GN=PRKCI PE=1 SV=2	sp|P41743|KPCI_HUMAN	3.8	3.8783	1.0324	4	1
Centromere protein V OS=Homo sapiens GN=CENPV PE=1 SV=1	sp|Q7Z7K6|CENPV_HUMAN	3.8	3.8783	1.0324	4	1
Anaphase-promoting complex subunit 2 OS=Homo sapiens GN=ANAPC2 PE=1 SV=1	sp|Q9UJX6|ANC2_HUMAN	3.8	3.8783	1.0324	4	1
Serum response factor-binding protein 1 OS=Homo sapiens GN=SRFBP1 PE=1 SV=1	sp|Q8NEF9|SRFB1_HUMAN	3.8	3.8783	1.0324	4	1
RNA-binding protein PNO1 OS=Homo sapiens GN=PNO1 PE=1 SV=1	sp|Q9NRX1|PNO1_HUMAN	3.8	3.8783	1.0324	4	1
Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3	sp|P18827|SDC1_HUMAN	3.8	7.7566	2.0648	6	2
Something about silencing protein 10 OS=Homo sapiens GN=UTP3 PE=1 SV=1	sp|Q9NQZ2|SAS10_HUMAN	3.8	3.8783	1.0324	4	1
DDB1- and CUL4-associated factor 13 OS=Homo sapiens GN=DCAF13 PE=1 SV=2	sp|Q9NV06|DCA13_HUMAN	3.8	3.8783	1.0324	4	1
Monoacylglycerol lipase ABHD12 OS=Homo sapiens GN=ABHD12 PE=1 SV=2	sp|Q8N2K0|ABD12_HUMAN	3.8	3.8783	1.0324	4	1
Very long-chain acyl-CoA synthetase OS=Homo sapiens GN=SLC27A2 PE=1 SV=2	sp|O14975|S27A2_HUMAN	3.8	3.8783	1.0324	4	1
RAC-beta serine/threonine-protein kinase OS=Homo sapiens GN=AKT2 PE=1 SV=2	sp|P31751|AKT2_HUMAN	3.8	3.8783	1.0324	4	1
V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2	sp|Q15904|VAS1_HUMAN	3.8	3.8783	1.0324	4	1
Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRNPLL PE=1 SV=1	sp|Q8WVV9|HNRLL_HUMAN	3.8	7.7566	2.0648	6	1
Coiled-coil domain-containing protein 86 OS=Homo sapiens GN=CCDC86 PE=1 SV=1	sp|Q9H6F5|CCD86_HUMAN	3.8	3.8783	1.0324	3	1
Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	sp|Q9NTK5|OLA1_HUMAN	3.8	3.8783	1.0324	4	1
Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2	sp|O95793|STAU1_HUMAN	3.8	3.8783	1.0324	4	1
Importin subunit alpha-4 OS=Homo sapiens GN=KPNA3 PE=1 SV=2	sp|O00505|IMA4_HUMAN	3.8	3.8783	1.0324	4	1
Cell division cycle protein 16 homolog OS=Homo sapiens GN=CDC16 PE=1 SV=2	sp|Q13042|CDC16_HUMAN	3.8	3.8783	1.0324	4	1
Vesicle transport through interaction with t-SNAREs homolog 1B OS=Homo sapiens GN=VTI1B PE=1 SV=3	sp|Q9UEU0|VTI1B_HUMAN	3.8	3.8783	1.0324	3	1
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	sp|P07339|CATD_HUMAN	3.8	3.8783	1.0324	2	1
Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2	sp|Q14980|NUMA1_HUMAN	3.7	41.692	11.356	42	11
E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3	sp|Q9ULT8|HECD1_HUMAN	3.7	33.935	9.2916	35	9
Protein SON OS=Homo sapiens GN=SON PE=1 SV=4	sp|P18583|SON_HUMAN	3.6	26.179	7.2268	24	7
ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2	sp|Q9NVP1|DDX18_HUMAN	3.6	22.3	6.1944	20	6
Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	sp|P42704|LPPRC_HUMAN	3.5	141.56	40.263	102	37
Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens GN=USP34 PE=1 SV=2	sp|Q70CQ2|UBP34_HUMAN	3.5	14.544	4.1296	15	4
Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2	sp|Q96ST3|SIN3A_HUMAN	3.5	14.544	4.1296	15	4
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	sp|Q14974|IMB1_HUMAN	3.4	84.353	24.778	43	17
28S ribosomal protein S5, mitochondrial OS=Homo sapiens GN=MRPS5 PE=1 SV=2	sp|P82675|RT05_HUMAN	3.4	10.665	3.0972	10	3
Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4	sp|Q9Y3T9|NOC2L_HUMAN	3.4	10.665	3.0972	10	3
Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1	sp|Q92522|H1X_HUMAN	3.4	10.665	3.0972	5	3
Titin OS=Homo sapiens GN=TTN PE=1 SV=4	sp|Q8WZ42|TITIN_HUMAN	3.3	6.787	2.0648	6	2
SRSF protein kinase 2 OS=Homo sapiens GN=SRPK2 PE=1 SV=3	sp|P78362|SRPK2_HUMAN	3.3	13.574	4.1296	13	4
Transformation/transcription domain-associated protein OS=Homo sapiens GN=TRRAP PE=1 SV=3	sp|Q9Y4A5|TRRAP_HUMAN	3.3	6.787	2.0648	7	2
Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3	sp|Q8WXH0|SYNE2_HUMAN	3.3	6.787	2.0648	7	2
Emerin OS=Homo sapiens GN=EMD PE=1 SV=1	sp|P50402|EMD_HUMAN	3.3	40.722	12.389	15	8
Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4	sp|P35251|RFC1_HUMAN	3.3	33.935	10.324	32	10
Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	sp|Q96P70|IPO9_HUMAN	3.3	37.813	11.356	28	8
MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=NIFK PE=1 SV=1	sp|Q9BYG3|MK67I_HUMAN	3.3	13.574	4.1296	14	4
PAX3- and PAX7-binding protein 1 OS=Homo sapiens GN=PAXBP1 PE=1 SV=2	sp|Q9Y5B6|PAXB1_HUMAN	3.3	6.787	2.0648	7	2
PHD finger protein 6 OS=Homo sapiens GN=PHF6 PE=1 SV=1	sp|Q8IWS0|PHF6_HUMAN	3.3	6.787	2.0648	6	2
DNA-binding protein SMUBP-2 OS=Homo sapiens GN=IGHMBP2 PE=1 SV=3	sp|P38935|SMBP2_HUMAN	3.3	6.787	2.0648	7	2
Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKR	sp|O75569|PRKRA_HUMAN	3.3	6.787	2.0648	7	2
Probable dimethyladenosine transferase OS=Homo sapiens GN=DIMT1 PE=1 SV=1	sp|Q9UNQ2|DIM1_HUMAN	3.3	6.787	2.0648	7	2
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4	sp|Q9UPN3|MACF1_HUMAN	3.2	16.483	5.162	16	4

Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3	sp|Q9BZE4|NOG1_HUMAN	3.2	32.966	10.324	28	7
Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3	sp|O75691|UTP20_HUMAN	3.2	35.874	11.356	35	11
Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1	sp|Q9Y4P3|TBL2_HUMAN	3.2	26.179	8.2592	24	7
Transformer-2 protein homolog alpha OS=Homo sapiens GN=TRA2A PE=1 SV=1	sp|Q13595|TRA2A_HUMAN	3.2	16.483	5.162	9	5
Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3	sp|P48634|PRC2A_HUMAN	3.1	29.087	9.2916	26	9
Unconventional myosin-IXb OS=Homo sapiens GN=MYO9B PE=1 SV=3	sp|Q13459|MYO9B_HUMAN	3.1	22.3	7.2268	22	7
Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2	sp|Q8TEX9|IPO4_HUMAN	3.1	31.996	10.324	27	10
Probable ATP-dependent RNA helicase DDX41 OS=Homo sapiens GN=DDX41 PE=1 SV=2	sp|Q9UJV9|DDX41_HUMAN	3.1	9.6958	3.0972	9	3
Ribonuclease 3 OS=Homo sapiens GN=DROSHA PE=1 SV=2	sp|Q9NRR4|RNC_HUMAN	3.1	9.6958	3.0972	10	3
Serine/arginine-rich splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=1 SV=1	sp|Q13243|SRSF5_HUMAN	3.1	12.604	4.1296	8	3
Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	sp|Q9P2E9|RRBP1_HUMAN	3.0	99.866	33.037	57	26
Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	sp|Q14692|BMS1_HUMAN	3.0	61.083	20.648	43	15
E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2	sp|O95714|HERC2_HUMAN	3.0	21.331	7.2268	22	7
Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2	sp|Q01780|EXOSX_HUMAN	3.0	21.331	7.2268	20	7
Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=S	sp|A6NHR9|SMHD1_HUMAN	2.9	35.874	12.389	33	12
Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 PE=1 SV=3	sp|O75179|ANR17_HUMAN	2.9	32.966	11.356	24	11
Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=1 SV=2	sp|O14776|TCRG1_HUMAN	2.8	2.9087	1.0324	3	1
Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2	sp|Q9BQG0|MBB1A_HUMAN	2.8	78.536	27.875	64	24
Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2	sp|P46013|KI67_HUMAN	2.8	37.813	13.421	36	13
Chromodomain-helicase-DNA-binding protein 7 OS=Homo sapiens GN=CHD7 PE=1 SV=3	sp|Q9P2D1|CHD7_HUMAN	2.8	2.9087	1.0324	3	1
Chromodomain-helicase-DNA-binding protein 9 OS=Homo sapiens GN=CHD9 PE=1 SV=2	sp|Q3L8U1|CHD9_HUMAN	2.8	2.9087	1.0324	3	1
26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	sp|O00232|PSD12_HUMAN	2.8	34.905	12.389	26	9
Protein TASOR OS=Homo sapiens GN=FAM208A PE=1 SV=3	sp|Q9UK61|TASOR_HUMAN	2.8	2.9087	1.0324	3	1
Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3	sp|Q8TE73|DYH5_HUMAN	2.8	2.9087	1.0324	2	1
Transcriptional regulator ATRX OS=Homo sapiens GN=ATRX PE=1 SV=5	sp|P46100|ATRX_HUMAN	2.8	2.9087	1.0324	3	1
Splicing factor, suppressor of white-apricot homolog OS=Homo sapiens GN=SFSWAP PE=1 SV=3	sp|Q12872|SFSWA_HUMAN	2.8	8.7262	3.0972	9	3
Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2	sp|Q12888|TP53B_HUMAN	2.8	5.8175	2.0648	5	2
Cell growth-regulating nucleolar protein OS=Homo sapiens GN=LYAR PE=1 SV=2	sp|Q9NX58|LYAR_HUMAN	2.8	11.635	4.1296	12	4
RNA 3'-terminal phosphate cyclase-like protein OS=Homo sapiens GN=RCL1 PE=1 SV=3	sp|Q9Y2P8|RCL1_HUMAN	2.8	17.452	6.1944	18	6
Probable RNA-binding protein 19 OS=Homo sapiens GN=RBM19 PE=1 SV=3	sp|Q9Y4C8|RBM19_HUMAN	2.8	8.7262	3.0972	9	3
Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2	sp|Q99848|EBP2_HUMAN	2.8	11.635	4.1296	9	3
Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF PE=1 SV=2	sp|P10586|PTPRF_HUMAN	2.8	2.9087	1.0324	2	1
28S ribosomal protein S9, mitochondrial OS=Homo sapiens GN=MRPS9 PE=1 SV=2	sp|P82933|RT09_HUMAN	2.8	11.635	4.1296	9	4
Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4	sp|O00567|NOP56_HUMAN	2.8	11.635	4.1296	10	3
COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1	sp|P61201|CSN2_HUMAN	2.8	11.635	4.1296	11	4
Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3	sp|O76094|SRP72_HUMAN	2.8	2.9087	1.0324	3	1
Transcriptional repressor p66-alpha OS=Homo sapiens GN=GATAD2A PE=1 SV=1	sp|Q86YP4|P66A_HUMAN	2.8	5.8175	2.0648	6	2
39S ribosomal protein L1, mitochondrial OS=Homo sapiens GN=MRPL1 PE=1 SV=2	sp|Q9BYD6|RM01_HUMAN	2.8	5.8175	2.0648	6	2
Translation initiation factor eIF-2B subunit beta OS=Homo sapiens GN=EIF2B2 PE=1 SV=3	sp|P49770|EI2BB_HUMAN	2.8	8.7262	3.0972	6	2
Zinc finger protein 281 OS=Homo sapiens GN=ZNF281 PE=1 SV=1	sp|Q9Y2X9|ZN281_HUMAN	2.8	2.9087	1.0324	3	1
Pre-mRNA cleavage complex 2 protein Pcf11 OS=Homo sapiens GN=PCF11 PE=1 SV=3	sp|O94913|PCF11_HUMAN	2.8	2.9087	1.0324	3	1
Wolframin OS=Homo sapiens GN=WFS1 PE=1 SV=2	sp|O76024|WFS1_HUMAN	2.8	2.9087	1.0324	3	1
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-3 OS=Homo sapiens GN=PLCD3 PE=1 SV	sp|Q8N3E9|PLCD3_HUMAN	2.8	8.7262	3.0972	9	3
ATP-dependent RNA helicase DDX19B OS=Homo sapiens GN=DDX19B PE=1 SV=1	sp|Q9UMR2|DD19B_HUMAN	2.8	2.9087	1.0324	3	1
Periodic tryptophan protein 1 homolog OS=Homo sapiens GN=PWP1 PE=1 SV=1	sp|Q13610|PWP1_HUMAN	2.8	5.8175	2.0648	6	2
Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2	sp|Q9UI10|EI2BD_HUMAN	2.8	5.8175	2.0648	6	2
Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens GN=EIF2AK2 PE=1 SV	sp|P19525|E2AK2_HUMAN	2.8	5.8175	2.0648	6	2
Protein FAM135A OS=Homo sapiens GN=FAM135A PE=1 SV=2	sp|Q9P2D6|F135A_HUMAN	2.8	2.9087	1.0324	3	1
Liprin-beta-1 OS=Homo sapiens GN=PPFIBP1 PE=1 SV=2	sp|Q86W92|LIPB1_HUMAN	2.8	2.9087	1.0324	3	1
Secretory carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 PE=1 SV=3	sp|O14828|SCAM3_HUMAN	2.8	5.8175	2.0648	5	1
Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1	sp|O14974|MYPT1_HUMAN	2.8	2.9087	1.0324	3	1
SURP and G-patch domain-containing protein 2 OS=Homo sapiens GN=SUGP2 PE=1 SV=2	sp|Q8IX01|SUGP2_HUMAN	2.8	2.9087	1.0324	3	1
Protein RMD5 homolog A OS=Homo sapiens GN=RMND5A PE=1 SV=1	sp|Q9H871|RMD5A_HUMAN	2.8	5.8175	2.0648	6	2
Syntabulin OS=Homo sapiens GN=SYBU PE=1 SV=2	sp|Q9NX95|SYBU_HUMAN	2.8	5.8175	2.0648	5	2
Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4	sp|P06737|PYGL_HUMAN	2.8	2.9087	1.0324	3	1
DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CD3EAP PE=1 SV=1	sp|O15446|RPA34_HUMAN	2.8	2.9087	1.0324	2	1
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=	sp|O76031|CLPX_HUMAN	2.8	2.9087	1.0324	3	1
Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2	sp|Q96I24|FUBP3_HUMAN	2.8	2.9087	1.0324	3	1
28S ribosomal protein S18b, mitochondrial OS=Homo sapiens GN=MRPS18B PE=1 SV=1	sp|Q9Y676|RT18B_HUMAN	2.8	5.8175	2.0648	5	2
Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2	sp|P36952|SPB5_HUMAN	2.8	2.9087	1.0324	3	1
Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 S	sp|Q96EY7|PTCD3_HUMAN	2.8	2.9087	1.0324	3	1
STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1	sp|Q9H2G2|SLK_HUMAN	2.8	2.9087	1.0324	3	1
Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1	sp|P51648|AL3A2_HUMAN	2.8	2.9087	1.0324	3	1
Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens GN=DDX28 PE=1 SV=2	sp|Q9NUL7|DDX28_HUMAN	2.8	2.9087	1.0324	3	1
(Reversed) Deleted in lung and esophageal cancer protein 1 OS=Homo sapiens GN=DLEC1 PE=2 SV=2	Reversed_sp|Q9Y238|DLEC1_HUMAN	2.8	2.9087	1.0324	2	1
Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2	sp|Q7L014|DDX46_HUMAN	2.8	2.9087	1.0324	3	1
Small acidic protein OS=Homo sapiens GN=SMAP PE=1 SV=1	sp|O00193|SMAP_HUMAN	2.8	5.8175	2.0648	3	2
Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2	sp|Q9Y3Y2|CHTOP_HUMAN	2.8	2.9087	1.0324	3	1
Nucleolar and spindle-associated protein 1 OS=Homo sapiens GN=NUSAP1 PE=1 SV=1	sp|Q9BXS6|NUSAP_HUMAN	2.8	2.9087	1.0324	3	1
UPF0488 protein C8orf33 OS=Homo sapiens GN=C8orf33 PE=1 SV=1	sp|Q9H7E9|CH033_HUMAN	2.8	5.8175	2.0648	5	2
Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5	sp|Q01518|CAP1_HUMAN	2.8	2.9087	1.0324	2	1
7SK snRNA methylphosphate capping enzyme OS=Homo sapiens GN=MEPCE PE=1 SV=1	sp|Q7L2J0|MEPCE_HUMAN	2.8	2.9087	1.0324	3	1
Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1 PE=1 SV=1	sp|Q9H0U3|MAGT1_HUMAN	2.8	2.9087	1.0324	2	1
Serine/threonine-protein kinase PLK1 OS=Homo sapiens GN=PLK1 PE=1 SV=1	sp|P53350|PLK1_HUMAN	2.8	2.9087	1.0324	3	1
PIN2/TERF1-interacting telomerase inhibitor 1 OS=Homo sapiens GN=PINX1 PE=1 SV=2	sp|Q96BK5|PINX1_HUMAN	2.8	2.9087	1.0324	2	1
ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 PE=1 SV=2	sp|Q8N6T3|ARFG1_HUMAN	2.8	2.9087	1.0324	3	1
Exocyst complex component 2 OS=Homo sapiens GN=EXOC2 PE=1 SV=1	sp|Q96KP1|EXOC2_HUMAN	2.8	2.9087	1.0324	3	1
WD repeat-containing protein 92 OS=Homo sapiens GN=WDR92 PE=1 SV=1	sp|Q96MX6|WDR92_HUMAN	2.8	2.9087	1.0324	3	1
E3 ubiquitin-protein ligase Praja-2 OS=Homo sapiens GN=PJA2 PE=1 SV=4	sp|O43164|PJA2_HUMAN	2.8	2.9087	1.0324	3	1
RRP15-like protein OS=Homo sapiens GN=RRP15 PE=1 SV=2	sp|Q9Y3B9|RRP15_HUMAN	2.8	2.9087	1.0324	3	1
Importin subunit alpha-3 OS=Homo sapiens GN=KPNA4 PE=1 SV=1	sp|O00629|IMA3_HUMAN	2.8	2.9087	1.0324	3	1
Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2	sp|Q13616|CUL1_HUMAN	2.8	2.9087	1.0324	3	1
Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=1 SV=3	sp|Q14671|PUM1_HUMAN	2.8	2.9087	1.0324	3	1
Death domain-associated protein 6 OS=Homo sapiens GN=DAXX PE=1 SV=2	sp|Q9UER7|DAXX_HUMAN	2.8	2.9087	1.0324	3	1
Activating signal cointegrator 1 OS=Homo sapiens GN=TRIP4 PE=1 SV=4	sp|Q15650|TRIP4_HUMAN	2.8	2.9087	1.0324	3	1
Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=1 SV=2	sp|Q9H6S0|YTDC2_HUMAN	2.7	36.844	13.421	33	11
A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4	sp|Q02952|AKA12_HUMAN	2.7	16.483	6.1944	16	6
ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=1 SV=1	sp|Q9GZR7|DDX24_HUMAN	2.7	22.3	8.2592	20	8
Eukaryotic translation initiation factor 2-alpha kinase 3 OS=Homo sapiens GN=EIF2AK3 PE=1 SV=3	sp|Q9NZJ5|E2AK3_HUMAN	2.7	22.3	8.2592	19	8
COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1	sp|Q9BT78|CSN4_HUMAN	2.7	22.3	8.2592	17	8
DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2	sp|P11387|TOP1_HUMAN	2.6	34.905	13.421	29	11
Zinc finger C3H1 domain-containing protein OS=Homo sapiens GN=ZFC3H1 PE=1 SV=3	sp|O60293|ZC3H1_HUMAN	2.6	13.574	5.162	10	1
Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	sp|Q92973|TNPO1_HUMAN	2.6	10.665	4.1296	10	4
Tuftelin-interacting protein 11 OS=Homo sapiens GN=TFIP11 PE=1 SV=1	sp|Q9UBB9|TFP11_HUMAN	2.6	10.665	4.1296	10	4
FERM, RhoGEF and pleckstrin domain-containing protein 2 OS=Homo sapiens GN=FARP2 PE=1 SV=3	sp|O94887|FARP2_HUMAN	2.6	13.574	5.162	11	5
28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3 PE=1 SV=1	sp|P51398|RT29_HUMAN	2.6	10.665	4.1296	9	4
Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1	sp|Q8NCA5|FA98A_HUMAN	2.6	10.665	4.1296	10	4
Chromodomain-helicase-DNA-binding protein 5 OS=Homo sapiens GN=CHD5 PE=1 SV=1	sp|Q8TDI0|CHD5_HUMAN	2.5	18.422	7.2268	14	7
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE	sp|Q92538|GBF1_HUMAN	2.5	15.513	6.1944	13	6
RB1-inducible coiled-coil protein 1 OS=Homo sapiens GN=RB1CC1 PE=1 SV=3	sp|Q8TDY2|RBCC1_HUMAN	2.5	26.179	10.324	26	8
Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2	sp|P07942|LAMB1_HUMAN	2.5	7.7566	3.0972	8	3
Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4	sp|O60841|IF2P_HUMAN	2.5	18.422	7.2268	17	6
Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1	sp|Q2NL82|TSR1_HUMAN	2.5	15.513	6.1944	15	6
CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1 PE=1 SV=2	sp|P30622|CLIP1_HUMAN	2.5	15.513	6.1944	16	6
Chromodomain-helicase-DNA-binding protein 2 OS=Homo sapiens GN=CHD2 PE=1 SV=2	sp|O14647|CHD2_HUMAN	2.5	7.7566	3.0972	8	3

Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1	sp|Q7Z417|NUFP2_HUMAN	2.5	7.7566	3.0972	8	3
General transcription factor 3C polypeptide 5 OS=Homo sapiens GN=GTF3C5 PE=1 SV=2	sp|Q9Y5Q8|TF3C5_HUMAN	2.5	7.7566	3.0972	8	3
SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=1 SV=2	sp|Q9NWH9|SLTM_HUMAN	2.5	7.7566	3.0972	8	3
Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1	sp|Q13501|SQSTM_HUMAN	2.4	57.205	23.745	31	14
Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1	sp|Q86UP2|KTN1_HUMAN	2.4	25.209	10.324	25	10
Serine/arginine-rich splicing factor 4 OS=Homo sapiens GN=SRSF4 PE=1 SV=2	sp|Q08170|SRSF4_HUMAN	2.4	17.452	7.2268	7	4
AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1	sp|P63010|AP2B1_HUMAN	2.4	25.209	10.324	24	10
(E3-independent) E2 ubiquitin-conjugating enzyme OS=Homo sapiens GN=UBE2O PE=1 SV=3	sp|Q9C0C9|UBE2O_HUMAN	2.4	12.604	5.162	13	5
U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens GN=PRPF4 PE=1 SV=2	sp|O43172|PRP4_HUMAN	2.4	12.604	5.162	11	5
Cyclin-dependent kinase 16 OS=Homo sapiens GN=CDK16 PE=1 SV=1	sp|Q00536|CDK16_HUMAN	2.3	4.8479	2.0648	2	1
Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	sp|P01860|IGHG3_HUMAN	2.3	67.87	29.939	8	6
Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	sp|Q9H9G7|AGO3_HUMAN	2.3	4.8479	2.0648	5	2
Supervillin OS=Homo sapiens GN=SVIL PE=1 SV=2	sp|O95425|SVIL_HUMAN	2.3	4.8479	2.0648	5	2
U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1	sp|O43290|SNUT1_HUMAN	2.3	14.544	6.1944	14	6
Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4	sp|P29144|TPP2_HUMAN	2.3	26.179	11.356	24	11
Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens GN=CHD1 PE=1 SV=2	sp|O14646|CHD1_HUMAN	2.3	9.6958	4.1296	10	4
Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1 PE=1 SV=1	sp|Q6UN15|FIP1_HUMAN	2.3	4.8479	2.0648	4	2
Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	sp|P01031|CO5_HUMAN	2.3	4.8479	2.0648	5	2
General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1	sp|Q9Y5Q9|TF3C3_HUMAN	2.3	11.635	5.162	11	5
ATP-dependent RNA helicase DHX8 OS=Homo sapiens GN=DHX8 PE=1 SV=1	sp|Q14562|DHX8_HUMAN	2.3	9.6958	4.1296	9	3
Wings apart-like protein homolog OS=Homo sapiens GN=WAPL PE=1 SV=1	sp|Q7Z5K2|WAPL_HUMAN	2.3	4.8479	2.0648	5	2
Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2	sp|O00425|IF2B3_HUMAN	2.3	23.27	10.324	18	8
Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 PE=1 SV=2	sp|Q6NZY4|ZCHC8_HUMAN	2.3	4.8479	2.0648	5	2
Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=1 SV=3	sp|Q15003|CND2_HUMAN	2.3	4.8479	2.0648	5	2
Arginine and glutamate-rich protein 1 OS=Homo sapiens GN=ARGLU1 PE=1 SV=1	sp|Q9NWB6|ARGL1_HUMAN	2.3	9.6958	4.1296	5	4
Protein KRI1 homolog OS=Homo sapiens GN=KRI1 PE=1 SV=3	sp|Q8N9T8|KRI1_HUMAN	2.3	4.8479	2.0648	5	2
F-box only protein 21 OS=Homo sapiens GN=FBXO21 PE=2 SV=2	sp|O94952|FBX21_HUMAN	2.3	4.8479	2.0648	5	2
Cyclin-dependent kinase 13 OS=Homo sapiens GN=CDK13 PE=1 SV=2	sp|Q14004|CDK13_HUMAN	2.2	6.787	3.0972	4	2
MAX gene-associated protein OS=Homo sapiens GN=MGA PE=1 SV=3	sp|Q8IWI9|MGAP_HUMAN	2.2	65.931	29.939	59	29
RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2	sp|Q14498|RBM39_HUMAN	2.2	33.935	15.486	19	10
SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2	sp|Q96SB4|SRPK1_HUMAN	2.2	25.209	11.356	19	11
Neuropathy target esterase OS=Homo sapiens GN=PNPLA6 PE=1 SV=2	sp|Q8IY17|PLPL6_HUMAN	2.2	20.361	9.2916	19	9
Rho GTPase-activating protein 23 OS=Homo sapiens GN=ARHGAP23 PE=1 SV=2	sp|Q9P227|RHG23_HUMAN	2.2	18.422	8.2592	17	7
Protein SPT2 homolog OS=Homo sapiens GN=SPTY2D1 PE=1 SV=3	sp|Q68D10|SPT2_HUMAN	2.2	6.787	3.0972	5	3
Transforming acidic coiled-coil-containing protein 3 OS=Homo sapiens GN=TACC3 PE=1 SV=1	sp|Q9Y6A5|TACC3_HUMAN	2.2	6.787	3.0972	7	3
RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3	sp|Q9NW13|RBM28_HUMAN	2.2	13.574	6.1944	13	6
ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1	sp|Q9BQ39|DDX50_HUMAN	2.2	13.574	6.1944	13	5
Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2 PE=1 SV=2	sp|Q15428|SF3A2_HUMAN	2.2	6.787	3.0972	6	3
DnaJ homolog subfamily B member 2 OS=Homo sapiens GN=DNAJB2 PE=1 SV=3	sp|P25686|DNJB2_HUMAN	2.2	6.787	3.0972	5	3
Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4	sp|Q13561|DCTN2_HUMAN	2.2	6.787	3.0972	7	3
Girdin OS=Homo sapiens GN=CCDC88A PE=1 SV=2	sp|Q3V6T2|GRDN_HUMAN	2.1	104.71	49.555	74	42
Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=1 SV=4	sp|Q9Y520|PRC2C_HUMAN	2.1	68.84	33.037	59	28
General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4	sp|Q12789|TF3C1_HUMAN	2.1	49.448	23.745	45	23
Dystonin OS=Homo sapiens GN=DST PE=1 SV=4	sp|Q03001|DYST_HUMAN	2.1	10.665	5.162	11	5
Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2	sp|O15397|IPO8_HUMAN	2.1	51.387	24.778	42	21
E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens GN=MYCBP2 PE=1 SV=3	sp|O75592|MYCB2_HUMAN	2.1	8.7262	4.1296	9	4
Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3	sp|P51114|FXR1_HUMAN	2.1	41.692	19.616	33	17
Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	sp|Q9UPY3|DICER_HUMAN	2.1	8.7262	4.1296	7	4
AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=1 SV=3	sp|O00203|AP3B1_HUMAN	2.1	8.7262	4.1296	9	4
Aftiphilin OS=Homo sapiens GN=AFTPH PE=1 SV=2	sp|Q6ULP2|AFTIN_HUMAN	2.1	10.665	5.162	10	5
Muskelin OS=Homo sapiens GN=MKLN1 PE=1 SV=2	sp|Q9UL63|MKLN1_HUMAN	2.1	8.7262	4.1296	8	4
ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1	sp|Q5T9A4|ATD3B_HUMAN	2.0	103.74	51.62	55	32
Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2	sp|Q9NYF8|BCLF1_HUMAN	2.0	82.414	40.263	53	30
Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3	sp|P12270|TPR_HUMAN	2.0	39.753	19.616	37	19
Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2	sp|P51116|FXR2_HUMAN	2.0	24.239	12.389	19	9
Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=1 SV=2	sp|Q86VM9|ZCH18_HUMAN	2.0	12.604	6.1944	11	6
Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	sp|P55209|NP1L1_HUMAN	2.0	25.209	12.389	17	8
NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF PE=1 SV=2	sp|O15226|NKRF_HUMAN	2.0	16.483	8.2592	16	8
Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2	sp|Q9BVP2|GNL3_HUMAN	2.0	18.422	9.2916	16	6
Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2	sp|O95232|LC7L3_HUMAN	2.0	14.544	7.2268	8	5
Putative oxidoreductase GLYR1 OS=Homo sapiens GN=GLYR1 PE=1 SV=3	sp|Q49A26|GLYR1_HUMAN	2.0	12.604	6.1944	11	6
Putative RNA-binding protein 15 OS=Homo sapiens GN=RBM15 PE=1 SV=2	sp|Q96T37|RBM15_HUMAN	2.0	12.604	6.1944	13	6
60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	sp|Q9Y3U8|RL36_HUMAN	2.0	12.604	6.1944	5	3
WD repeat-containing protein 26 OS=Homo sapiens GN=WDR26 PE=1 SV=3	sp|Q9H7D7|WDR26_HUMAN	2.0	12.604	6.1944	12	5
Fragile X mental retardation protein 1 OS=Homo sapiens GN=FMR1 PE=1 SV=1	sp|Q06787|FMR1_HUMAN	2.0	12.604	6.1944	10	5
Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	sp|Q13813|SPTN1_HUMAN	1.9	237.55	128.02	177	105
60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	sp|P36578|RL4_HUMAN	1.9	159.01	84.656	50	33
60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	sp|Q02878|RL6_HUMAN	1.9	136.71	70.203	29	24
E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	sp|Q5T4S7|UBR4_HUMAN	1.9	71.749	37.166	64	35
Cyclin-dependent kinase 12 OS=Homo sapiens GN=CDK12 PE=1 SV=2	sp|Q9NYV4|CDK12_HUMAN	1.9	7.7566	4.1296	5	3
Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	sp|P16403|H12_HUMAN	1.9	38.783	20.648	12	6
Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	sp|P10412|H14_HUMAN	1.9	35.874	18.583	10	6
A-kinase anchor protein 13 OS=Homo sapiens GN=AKAP13 PE=1 SV=2	sp|Q12802|AKP13_HUMAN	1.9	29.087	15.486	28	14
Protein FAM111B OS=Homo sapiens GN=FAM111B PE=1 SV=1	sp|Q6SJ93|F111B_HUMAN	1.9	1.9392	1.0324	2	1
Metastasis-associated protein MTA3 OS=Homo sapiens GN=MTA3 PE=1 SV=2	sp|Q9BTC8|MTA3_HUMAN	1.9	3.8783	2.0648	4	2
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	sp|Q9Y490|TLN1_HUMAN	1.9	25.209	13.421	25	13
Melanoma-associated antigen B2 OS=Homo sapiens GN=MAGEB2 PE=1 SV=3	sp|O15479|MAGB2_HUMAN	1.9	28.118	14.454	23	12
Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3	sp|O43795|MYO1B_HUMAN	1.9	33.935	17.551	33	16
60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2	sp|P62910|RL32_HUMAN	1.9	29.087	15.486	10	8
Myosin-13 OS=Homo sapiens GN=MYH13 PE=2 SV=2	sp|Q9UKX3|MYH13_HUMAN	1.9	3.8783	2.0648	2	2
KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KH	sp|Q07666|KHDR1_HUMAN	1.9	15.513	8.2592	10	7
Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2	sp|P51532|SMCA4_HUMAN	1.9	15.513	8.2592	16	8
Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=1 SV=1	sp|P17480|UBF1_HUMAN	1.9	19.392	10.324	17	10
Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2	sp|O60488|ACSL4_HUMAN	1.9	3.8783	2.0648	3	2
Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2	sp|Q9BUJ2|HNRL1_HUMAN	1.9	19.392	10.324	17	8
Cadherin EGF LAG seven-pass G-type receptor 1 OS=Homo sapiens GN=CELSR1 PE=1 SV=1	sp|Q9NYQ6|CELR1_HUMAN	1.9	1.9392	1.0324	2	1
Kinesin-like protein KIF1B OS=Homo sapiens GN=KIF1B PE=1 SV=5	sp|O60333|KIF1B_HUMAN	1.9	3.8783	2.0648	4	2
Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	sp|P02748|CO9_HUMAN	1.9	5.8175	3.0972	3	2
Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1	sp|Q12874|SF3A3_HUMAN	1.9	15.513	8.2592	13	8
HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1	sp|O43719|HTSF1_HUMAN	1.9	9.6958	5.162	10	5
E3 ubiquitin-protein ligase SHPRH OS=Homo sapiens GN=SHPRH PE=1 SV=2	sp|Q149N8|SHPRH_HUMAN	1.9	1.9392	1.0324	2	1
Nuclear receptor-interacting protein 1 OS=Homo sapiens GN=NRIP1 PE=1 SV=2	sp|P48552|NRIP1_HUMAN	1.9	1.9392	1.0324	2	1
Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=1 SV=1	sp|Q96A65|EXOC4_HUMAN	1.9	5.8175	3.0972	6	3
(Reversed) Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	Reversed_sp|P07814|SYEP_HUMAN	1.9	1.9392	1.0324	2	1
Collagen alpha-2(IV) chain OS=Homo sapiens GN=COL4A2 PE=1 SV=4	sp|P08572|CO4A2_HUMAN	1.9	1.9392	1.0324	2	1
Poly [ADP-ribose] polymerase 12 OS=Homo sapiens GN=PARP12 PE=1 SV=1	sp|Q9H0J9|PAR12_HUMAN	1.9	5.8175	3.0972	6	3
mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2	sp|Q9UKD2|MRT4_HUMAN	1.9	15.513	8.2592	13	7
Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	sp|P26368|U2AF2_HUMAN	1.9	11.635	6.1944	12	5
Round spermatid basic protein 1-like protein OS=Homo sapiens GN=RSBN1L PE=1 SV=2	sp|Q6PCB5|RSBNL_HUMAN	1.9	7.7566	4.1296	8	4
SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1	sp|Q8TAQ2|SMRC2_HUMAN	1.9	7.7566	4.1296	8	3
Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens GN=SPATA5L1 PE=1 SV=2	sp|Q9BVQ7|SPA5L_HUMAN	1.9	11.635	6.1944	12	6
Muscleblind-like protein 3 OS=Homo sapiens GN=MBNL3 PE=1 SV=2	sp|Q9NUK0|MBNL3_HUMAN	1.9	3.8783	2.0648	4	2
RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1	sp|Q9UKM9|RALY_HUMAN	1.9	15.513	8.2592	12	8
E3 ubiquitin-protein ligase TRIM33 OS=Homo sapiens GN=TRIM33 PE=1 SV=3	sp|Q9UPN9|TRI33_HUMAN	1.9	1.9392	1.0324	2	1
MAP kinase-activating death domain protein OS=Homo sapiens GN=MADD PE=1 SV=2	sp|Q8WXG6|MADD_HUMAN	1.9	1.9392	1.0324	2	1

Serine/threonine-protein kinase WNK2 OS=Homo sapiens GN=WNK2 PE=1 SV=4	sp|Q9Y3S1|WNK2_HUMAN	1.9	1.9392	1.0324	2	1
Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3	sp|Q9UPU5|UBP24_HUMAN	1.9	1.9392	1.0324	2	1
H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3	sp|O60832|DKC1_HUMAN	1.9	11.635	6.1944	10	5
Target of EGR1 protein 1 OS=Homo sapiens GN=TOE1 PE=1 SV=1	sp|Q96GM8|TOE1_HUMAN	1.9	3.8783	2.0648	4	2
Protein pelota homolog OS=Homo sapiens GN=PELO PE=1 SV=2	sp|Q9BRX2|PELO_HUMAN	1.9	11.635	6.1944	10	6
Unconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	sp|Q9NQX4|MYO5C_HUMAN	1.9	1.9392	1.0324	2	1
MAP7 domain-containing protein 3 OS=Homo sapiens GN=MAP7D3 PE=1 SV=2	sp|Q8IWC1|MA7D3_HUMAN	1.9	9.6958	5.162	10	5
Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	sp|P48444|COPD_HUMAN	1.9	9.6958	5.162	9	5
Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	sp|Q96AG4|LRC59_HUMAN	1.9	9.6958	5.162	8	5
Negative elongation factor E OS=Homo sapiens GN=NELFE PE=1 SV=3	sp|P18615|NELFE_HUMAN	1.9	3.8783	2.0648	4	2
Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	sp|P31948|STIP1_HUMAN	1.9	1.9392	1.0324	2	1
(Reversed) Next to BRCA1 gene 1 protein OS=Homo sapiens GN=NBR1 PE=1 SV=3	Reversed_sp|Q14596|NBR1_HUMAN	1.9	1.9392	1.0324	2	1
Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=1 SV=1	sp|Q14257|RCN2_HUMAN	1.9	9.6958	5.162	7	5
Genetic suppressor element 1 OS=Homo sapiens GN=GSE1 PE=1 SV=3	sp|Q14687|GSE1_HUMAN	1.9	1.9392	1.0324	2	1
Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=1 SV=3	sp|O75152|ZC11A_HUMAN	1.9	3.8783	2.0648	4	2
Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1	sp|P46060|RAGP1_HUMAN	1.9	9.6958	5.162	9	5
Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens GN=DNTTIP2 PE=1 SV=2	sp|Q5QJE6|TDIF2_HUMAN	1.9	3.8783	2.0648	4	2
Histone-lysine N-methyltransferase EHMT2 OS=Homo sapiens GN=EHMT2 PE=1 SV=3	sp|Q96KQ7|EHMT2_HUMAN	1.9	3.8783	2.0648	3	2
Katanin p60 ATPase-containing subunit A-like 2 OS=Homo sapiens GN=KATNAL2 PE=2 SV=3	sp|Q8IYT4|KATL2_HUMAN	1.9	1.9392	1.0324	2	1
Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2	sp|O75400|PR40A_HUMAN	1.9	7.7566	4.1296	8	3
COP9 signalosome complex subunit 6 OS=Homo sapiens GN=COPS6 PE=1 SV=1	sp|Q7L5N1|CSN6_HUMAN	1.9	9.6958	5.162	10	5
ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1 PE=1 SV=2	sp|Q96TA2|YMEL1_HUMAN	1.9	7.7566	4.1296	7	4
Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1	sp|O00541|PESC_HUMAN	1.9	3.8783	2.0648	4	2
Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3	sp|O95801|TTC4_HUMAN	1.9	3.8783	2.0648	4	2
Ubiquitin carboxyl-terminal hydrolase 28 OS=Homo sapiens GN=USP28 PE=1 SV=1	sp|Q96RU2|UBP28_HUMAN	1.9	1.9392	1.0324	2	1
Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2	sp|O95819|M4K4_HUMAN	1.9	1.9392	1.0324	2	1
Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=1 SV=3	sp|O00139|KIF2A_HUMAN	1.9	3.8783	2.0648	4	2
39S ribosomal protein L19, mitochondrial OS=Homo sapiens GN=MRPL19 PE=1 SV=2	sp|P49406|RM19_HUMAN	1.9	5.8175	3.0972	6	3
Helicase-like transcription factor OS=Homo sapiens GN=HLTF PE=1 SV=2	sp|Q14527|HLTF_HUMAN	1.9	1.9392	1.0324	2	1
(Reversed) Catenin delta-2 OS=Homo sapiens GN=CTNND2 PE=1 SV=3	Reversed_sp|Q9UQB3|CTND2_HUMAN	1.9	1.9392	1.0324	2	1
RNA-binding protein 26 OS=Homo sapiens GN=RBM26 PE=1 SV=3	sp|Q5T8P6|RBM26_HUMAN	1.9	1.9392	1.0324	2	1
Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=1 SV=1	sp|O00764|PDXK_HUMAN	1.9	3.8783	2.0648	4	2
Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	sp|Q9BTV4|TMM43_HUMAN	1.9	3.8783	2.0648	4	2
Testis-expressed sequence 10 protein OS=Homo sapiens GN=TEX10 PE=1 SV=2	sp|Q9NXF1|TEX10_HUMAN	1.9	3.8783	2.0648	4	2
SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2	sp|Q9NUQ6|SPS2L_HUMAN	1.9	1.9392	1.0324	2	1
Clathrin interactor 1 OS=Homo sapiens GN=CLINT1 PE=1 SV=1	sp|Q14677|EPN4_HUMAN	1.9	1.9392	1.0324	2	1
WASH complex subunit FAM21C OS=Homo sapiens GN=FAM21C PE=1 SV=3	sp|Q9Y4E1|FA21C_HUMAN	1.9	1.9392	1.0324	2	1
Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100 PE=1 SV=3	sp|P23497|SP100_HUMAN	1.9	1.9392	1.0324	2	1
Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1	sp|Q8N1G4|LRC47_HUMAN	1.9	3.8783	2.0648	4	2
28S ribosomal protein S2, mitochondrial OS=Homo sapiens GN=MRPS2 PE=1 SV=1	sp|Q9Y399|RT02_HUMAN	1.9	5.8175	3.0972	5	3
Histone-lysine N-methyltransferase EHMT1 OS=Homo sapiens GN=EHMT1 PE=1 SV=4	sp|Q9H9B1|EHMT1_HUMAN	1.9	1.9392	1.0324	2	1
Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4	sp|Q9NV70|EXOC1_HUMAN	1.9	1.9392	1.0324	2	1
Polyhomeotic-like protein 3 OS=Homo sapiens GN=PHC3 PE=1 SV=1	sp|Q8NDX5|PHC3_HUMAN	1.9	1.9392	1.0324	2	1
Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4	sp|Q15637|SF01_HUMAN	1.9	3.8783	2.0648	3	2
Zinc finger CCCH domain-containing protein 7A OS=Homo sapiens GN=ZC3H7A PE=1 SV=1	sp|Q8IWR0|Z3H7A_HUMAN	1.9	3.8783	2.0648	4	2
Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1	sp|O00560|SDCB1_HUMAN	1.9	5.8175	3.0972	5	2
Synaptosomal-associated protein 29 OS=Homo sapiens GN=SNAP29 PE=1 SV=1	sp|O95721|SNP29_HUMAN	1.9	3.8783	2.0648	3	2
Exosome complex component MTR3 OS=Homo sapiens GN=EXOSC6 PE=1 SV=1	sp|Q5RKV6|EXOS6_HUMAN	1.9	3.8783	2.0648	4	2
Histone deacetylase complex subunit SAP130 OS=Homo sapiens GN=SAP130 PE=1 SV=1	sp|Q9H0E3|SP130_HUMAN	1.9	1.9392	1.0324	2	1
Exosome complex component RRP45 OS=Homo sapiens GN=EXOSC9 PE=1 SV=3	sp|Q06265|EXOS9_HUMAN	1.9	1.9392	1.0324	2	1
OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1	sp|Q9NX40|OCAD1_HUMAN	1.9	1.9392	1.0324	2	1
Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1	sp|Q9UJU6|DBNL_HUMAN	1.9	1.9392	1.0324	2	1
Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Homo sapiens GN=ERGIC3 PE=1 SV	sp|Q9Y282|ERGI3_HUMAN	1.9	1.9392	1.0324	2	1
Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	sp|P07384|CAN1_HUMAN	1.9	1.9392	1.0324	2	1
Dynein assembly factor 5, axonemal OS=Homo sapiens GN=DNAAF5 PE=1 SV=4	sp|Q86Y56|DAAF5_HUMAN	1.9	1.9392	1.0324	2	1
Anaphase-promoting complex subunit 4 OS=Homo sapiens GN=ANAPC4 PE=1 SV=2	sp|Q9UJX5|APC4_HUMAN	1.9	1.9392	1.0324	2	1
Methyl-CpG-binding domain protein 3 OS=Homo sapiens GN=MBD3 PE=1 SV=1	sp|O95983|MBD3_HUMAN	1.9	1.9392	1.0324	2	1
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo	sp|Q12824|SNF5_HUMAN	1.9	1.9392	1.0324	2	1
General transcription factor IIH subunit 2 OS=Homo sapiens GN=GTF2H2 PE=1 SV=1	sp|Q13888|TF2H2_HUMAN (+1)	1.9	1.9392	1.0324	2	1
Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	sp|P18669|PGAM1_HUMAN	1.9	3.8783	2.0648	4	2
DNA-3-methyladenine glycosylase OS=Homo sapiens GN=MPG PE=1 SV=3	sp|P29372|3MG_HUMAN	1.9	3.8783	2.0648	4	2
Glioma tumor suppressor candidate region gene 2 protein OS=Homo sapiens GN=GLTSCR2 PE=1 SV=2	sp|Q9NZM5|GSCR2_HUMAN	1.9	3.8783	2.0648	4	2
cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 S\	sp|P13861|KAP2_HUMAN	1.9	1.9392	1.0324	2	1
BRCA2 and CDKN1A-interacting protein OS=Homo sapiens GN=BCCIP PE=1 SV=1	sp|Q9P287|BCCIP_HUMAN	1.9	1.9392	1.0324	2	1
Zinc finger CCCH-type antiviral protein 1-like OS=Homo sapiens GN=ZC3HAV1L PE=1 SV=2	sp|Q96H79|ZCCHL_HUMAN	1.9	1.9392	1.0324	2	1
DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=1 SV=2	sp|Q9NVH1|DJC11_HUMAN	1.9	1.9392	1.0324	2	1
Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1 PE=1 SV=1	sp|O60828|PQBP1_HUMAN	1.9	1.9392	1.0324	2	1
Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3	sp|P15121|ALDR_HUMAN	1.9	1.9392	1.0324	2	1
Non-canonical poly(A) RNA polymerase PAPD5 OS=Homo sapiens GN=PAPD5 PE=1 SV=2	sp|Q8NDF8|PAPD5_HUMAN	1.9	1.9392	1.0324	2	1
Phosducin-like protein OS=Homo sapiens GN=PDCL PE=1 SV=3	sp|Q13371|PHLP_HUMAN	1.9	1.9392	1.0324	2	1
Histone deacetylase 8 OS=Homo sapiens GN=HDAC8 PE=1 SV=2	sp|Q9BY41|HDAC8_HUMAN	1.9	1.9392	1.0324	2	1
Annexin A8 OS=Homo sapiens GN=ANXA8 PE=1 SV=3	sp|P13928|ANXA8_HUMAN (+1)	1.9	1.9392	1.0324	2	1
Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1	sp|Q8IY67|RAVR1_HUMAN	1.9	1.9392	1.0324	2	1
ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2	sp|Q9NVI7|ATD3A_HUMAN	1.8	110.53	59.879	62	41
Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2	sp|Q14839|CHD4_HUMAN	1.8	45.57	25.81	39	23
Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2	sp|Q5UIP0|RIF1_HUMAN	1.8	56.235	32.004	49	31
U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=1 SV=2	sp|O15042|SR140_HUMAN	1.8	47.509	26.842	36	22
Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2	sp|Q13247|SRSF6_HUMAN	1.8	31.996	17.551	14	10
Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=1 SV=3	sp|O95248|MTMR5_HUMAN	1.8	16.483	9.2916	17	8
U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2	sp|P08621|RU17_HUMAN	1.8	24.239	13.421	14	11
Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1	sp|Q09161|NCBP1_HUMAN	1.8	16.483	9.2916	15	9
Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3	sp|Q8NB90|SPAT5_HUMAN	1.8	20.361	11.356	18	10
DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2	sp|P52701|MSH6_HUMAN	1.8	14.544	8.2592	15	8
Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	sp|Q9Y2W1|TR150_HUMAN	1.7	91.14	53.685	51	35
La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	sp|Q6PKG0|LARP1_HUMAN	1.7	79.505	46.458	58	34
60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	sp|P05388|RLA0_HUMAN	1.7	86.292	51.62	49	31
DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	sp|P11388|TOP2A_HUMAN	1.7	73.688	42.328	62	37
Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	sp|Q9NZB2|F120A_HUMAN	1.7	46.54	27.875	38	24
Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3	sp|Q7Z2W4|ZCCHV_HUMAN	1.7	43.631	25.81	31	20
Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2	sp|Q8IVF2|AHNK2_HUMAN	1.7	15.513	9.2916	13	7
Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	sp|Q8IX12|CCAR1_HUMAN	1.7	38.783	22.713	34	20
Probable global transcription activator SNF2L1 OS=Homo sapiens GN=SMARCA1 PE=1 SV=2	sp|P28370|SMCA1_HUMAN	1.7	10.665	6.1944	9	6
Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	sp|Q9UKV8|AGO2_HUMAN	1.7	10.665	6.1944	11	6
26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	sp|P62191|PRS4_HUMAN	1.7	45.57	26.842	30	20
ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36 PE=1 SV=2	sp|Q9H2U1|DHX36_HUMAN	1.7	35.874	21.68	32	19
Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2	sp|Q99459|CDC5L_HUMAN	1.7	29.087	17.551	28	15
26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	sp|P51665|PSMD7_HUMAN	1.7	42.661	24.778	30	19
AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	sp|O95782|AP2A1_HUMAN	1.7	19.392	11.356	19	11
Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1	sp|Q13547|HDAC1_HUMAN	1.7	10.665	6.1944	9	4
Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1	sp|Q5SW79|CE170_HUMAN	1.7	15.513	9.2916	16	9
R3H domain-containing protein 1 OS=Homo sapiens GN=R3HDM1 PE=1 SV=3	sp|Q15032|R3HD1_HUMAN	1.7	15.513	9.2916	15	8
Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1	sp|Q16629|SRSF7_HUMAN	1.7	22.3	13.421	15	8
General transcription factor 3C polypeptide 2 OS=Homo sapiens GN=GTF3C2 PE=1 SV=2	sp|Q8WUA4|TF3C2_HUMAN	1.7	8.7262	5.162	9	5
Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1	sp|P62995|TRA2B_HUMAN	1.7	22.3	13.421	12	10
Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	sp|P27797|CALR_HUMAN	1.7	10.665	6.1944	9	5

28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=1 SV=3	sp|Q92552|RT27_HUMAN	1.7	10.665	6.1944	10	6
Ran-binding protein 10 OS=Homo sapiens GN=RANBP10 PE=1 SV=1	sp|Q6VN20|RBP10_HUMAN	1.7	10.665	6.1944	8	6
CDKN2A-interacting protein OS=Homo sapiens GN=CDKN2AIP PE=1 SV=3	sp|Q9NXV6|CARF_HUMAN	1.7	8.7262	5.162	9	5
Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	sp|Q9NR30|DDX21_HUMAN	1.6	83.383	51.62	56	35
Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1	sp|Q7L2E3|DHX30_HUMAN	1.6	60.114	37.166	54	34
26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	sp|P17980|PRS6A_HUMAN	1.6	61.083	37.166	37	23
Tyrosine-protein kinase Yes OS=Homo sapiens GN=YES1 PE=1 SV=3	sp|P07947|YES_HUMAN	1.6	4.8479	3.0972	2	2
26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	sp|P43686|PRS6B_HUMAN	1.6	60.114	38.199	40	30
Ensconsin OS=Homo sapiens GN=MAP7 PE=1 SV=1	sp|Q14244|MAP7_HUMAN	1.6	38.783	24.778	30	20
Ankyrin repeat and KH domain-containing protein 1 OS=Homo sapiens GN=ANKHD1 PE=1 SV=1	sp|Q8IWZ3|ANKH1_HUMAN	1.6	21.331	13.421	15	13
26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	sp|O00231|PSD11_HUMAN	1.6	48.479	29.939	37	22
Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4	sp|P20742|PZP_HUMAN	1.6	14.544	9.2916	5	6
Protein argonaute-1 OS=Homo sapiens GN=AGO1 PE=1 SV=3	sp|Q9UL18|AGO1_HUMAN	1.6	4.8479	3.0972	5	3
RNA-binding protein 6 OS=Homo sapiens GN=RBM6 PE=1 SV=5	sp|P78332|RBM6_HUMAN	1.6	26.179	16.518	26	16
DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3	sp|Q02880|TOP2B_HUMAN	1.6	43.631	27.875	39	22
Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1	sp|O94776|MTA2_HUMAN	1.6	20.361	12.389	18	11
Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3	sp|Q8N3C0|ASCC3_HUMAN	1.6	18.422	11.356	18	11
Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	sp|P17844|DDX5_HUMAN	1.6	47.509	28.907	36	21
Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	sp|Q00341|VIGLN_HUMAN	1.6	26.179	16.518	26	16
Biorientation of chromosomes in cell division protein 1-like 1 OS=Homo sapiens GN=BOD1L1 PE=1 SV=2	sp|Q8NFC6|BD1L1_HUMAN	1.6	4.8479	3.0972	4	2
Putative helicase MOV-10 OS=Homo sapiens GN=MOV10 PE=1 SV=2	sp|Q9HCE1|MOV10_HUMAN	1.6	28.118	17.551	29	17
Probable ATP-dependent RNA helicase DDX20 OS=Homo sapiens GN=DDX20 PE=1 SV=2	sp|Q9UHI6|DDX20_HUMAN	1.6	24.239	15.486	23	11
Anaphase-promoting complex subunit 1 OS=Homo sapiens GN=ANAPC1 PE=1 SV=1	sp|Q9H1A4|APC1_HUMAN	1.6	13.574	8.2592	11	7
E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 PE=1 SV=2	sp|Q9UNE7|CHIP_HUMAN	1.6	27.148	16.518	23	12
Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=1 SV=2	sp|Q92769|HDAC2_HUMAN	1.6	14.544	9.2916	10	7
Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2	sp|Q92841|DDX17_HUMAN	1.6	36.844	23.745	27	17
tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	sp|Q9Y3I0|RTCB_HUMAN	1.6	24.239	15.486	21	13
Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	sp|O43390|HNRPR_HUMAN	1.6	26.179	16.518	21	13
Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2	sp|Q9Y383|LC7L2_HUMAN	1.6	14.544	9.2916	7	6
Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	sp|P02786|TFR1_HUMAN	1.6	13.574	8.2592	12	8
Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1	sp|Q15020|SART3_HUMAN	1.6	13.574	8.2592	14	8
Transportin-2 OS=Homo sapiens GN=TNPO2 PE=1 SV=3	sp|O14787|TNPO2_HUMAN	1.6	4.8479	3.0972	5	3
Neurofibromin OS=Homo sapiens GN=NF1 PE=1 SV=2	sp|P21359|NF1_HUMAN	1.6	4.8479	3.0972	5	3
cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2	sp|P17612|KAPCA_HUMAN	1.6	13.574	8.2592	11	7
Caprin-2 OS=Homo sapiens GN=CAPRIN2 PE=1 SV=1	sp|Q6IMN6|CAPR2_HUMAN	1.6	4.8479	3.0972	5	3
Kinesin-like protein KIF14 OS=Homo sapiens GN=KIF14 PE=1 SV=1	sp|Q15058|KIF14_HUMAN	1.6	6.787	4.1296	7	4
Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2	sp|P40938|RFC3_HUMAN	1.6	13.574	8.2592	12	7
Telomere length regulation protein TEL2 homolog OS=Homo sapiens GN=TELO2 PE=1 SV=2	sp|Q9Y4R8|TELO2_HUMAN	1.6	6.787	4.1296	7	4
Muscleblind-like protein 1 OS=Homo sapiens GN=MBNL1 PE=1 SV=2	sp|Q9NR56|MBNL1_HUMAN	1.6	4.8479	3.0972	5	3
Nuclear export mediator factor NEMF OS=Homo sapiens GN=NEMF PE=1 SV=4	sp|O60524|NEMF_HUMAN	1.6	6.787	4.1296	7	4
Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1	sp|Q96SI9|STRBP_HUMAN	1.6	13.574	8.2592	6	5
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=	sp|P15170|ERF3A_HUMAN	1.6	4.8479	3.0972	5	3
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV	sp|P62879|GBB2_HUMAN	1.6	4.8479	3.0972	5	3
Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 PE=1 SV=1	sp|P78346|RPP30_HUMAN	1.6	6.787	4.1296	7	4
Putative methyltransferase C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3	sp|Q5T280|CI114_HUMAN	1.6	6.787	4.1296	7	3
Ribosome biogenesis protein WDR12 OS=Homo sapiens GN=WDR12 PE=1 SV=2	sp|Q9GZL7|WDR12_HUMAN	1.6	4.8479	3.0972	5	3
Importin subunit alpha-7 OS=Homo sapiens GN=KPNA6 PE=1 SV=1	sp|O60684|IMA7_HUMAN	1.6	4.8479	3.0972	4	2
Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV	sp|Q9H0C8|ILKAP_HUMAN	1.6	4.8479	3.0972	5	3
Polycomb group RING finger protein 6 OS=Homo sapiens GN=PCGF6 PE=1 SV=2	sp|Q9BYE7|PCGF6_HUMAN	1.6	6.787	4.1296	7	3
Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1	sp|Q9Y2X3|NOP58_HUMAN	1.6	4.8479	3.0972	5	3
Tetratricopeptide repeat protein 27 OS=Homo sapiens GN=TTC27 PE=1 SV=1	sp|Q6P3X3|TTC27_HUMAN	1.6	4.8479	3.0972	5	3
Neuroguidin OS=Homo sapiens GN=NGDN PE=1 SV=1	sp|Q8NEJ9|NGDN_HUMAN	1.6	4.8479	3.0972	5	2
Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=2 SV=2	sp|Q15269|PWP2_HUMAN	1.6	4.8479	3.0972	5	2
Engulfment and cell motility protein 2 OS=Homo sapiens GN=ELMO2 PE=1 SV=2	sp|Q96JJ3|ELMO2_HUMAN	1.6	4.8479	3.0972	5	3
Ran-binding protein 6 OS=Homo sapiens GN=RANBP6 PE=1 SV=2	sp|O60518|RNBP6_HUMAN	1.6	4.8479	3.0972	4	3
DnaJ homolog subfamily C member 8 OS=Homo sapiens GN=DNAJC8 PE=1 SV=2	sp|O75937|DNJC8_HUMAN	1.6	4.8479	3.0972	2	3
E3 ubiquitin-protein ligase KCMF1 OS=Homo sapiens GN=KCMF1 PE=1 SV=2	sp|Q9P0J7|KCMF1_HUMAN	1.6	4.8479	3.0972	4	2
RNA-binding protein NOB1 OS=Homo sapiens GN=NOB1 PE=1 SV=1	sp|Q9ULX3|NOB1_HUMAN	1.6	4.8479	3.0972	5	3
Survival of motor neuron-related-splicing factor 30 OS=Homo sapiens GN=SMNDC1 PE=1 SV=1	sp|O75940|SPF30_HUMAN	1.6	4.8479	3.0972	5	3
39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2	sp|Q9BZE1|RM37_HUMAN	1.6	4.8479	3.0972	5	3
Casein kinase II subunit alpha' OS=Homo sapiens GN=CSNK2A2 PE=1 SV=1	sp|P19784|CSK22_HUMAN	1.6	4.8479	3.0972	4	3
Calcium uniporter protein, mitochondrial OS=Homo sapiens GN=MCU PE=1 SV=1	sp|Q8NE86|MCU_HUMAN	1.6	4.8479	3.0972	5	3
Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	sp|Q01082|SPTB2_HUMAN	1.5	189.07	130.08	140	101
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	sp|P19338|NUCL_HUMAN	1.5	146.41	96.013	68	51
Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	sp|O75533|SF3B1_HUMAN	1.5	127.98	85.689	90	59
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	sp|Q13200|PSMD2_HUMAN	1.5	117.32	79.494	77	51
Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	sp|O43143|DHX15_HUMAN	1.5	111.5	73.3	52	40
Cyclin-dependent kinase 9 OS=Homo sapiens GN=CDK9 PE=1 SV=3	sp|P50750|CDK9_HUMAN	1.5	10.665	7.2268	8	6
60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	sp|P62424|RL7A_HUMAN	1.5	95.018	62.976	28	19
E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=1 SV=2	sp|O95071|UBR5_HUMAN	1.5	65.931	44.393	66	39
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	sp|P46940|IQGA1_HUMAN	1.5	70.779	46.458	58	39
Protein Daple OS=Homo sapiens GN=CCDC88C PE=1 SV=3	sp|Q9P219|DAPLE_HUMAN	1.5	52.357	35.101	51	30
Poly(rC)-binding protein 3 OS=Homo sapiens GN=PCBP3 PE=2 SV=2	sp|P57721|PCBP3_HUMAN	1.5	12.604	8.2592	6	5
Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	sp|Q12906|ILF3_HUMAN	1.5	61.083	40.263	34	24
Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	sp|Q9Y678|COPG1_HUMAN	1.5	24.239	16.518	21	14
26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	sp|Q15008|PSMD6_HUMAN	1.5	42.661	27.875	32	23
26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	sp|O00487|PSDE_HUMAN	1.5	34.905	22.713	19	15
Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	sp|P08754|GNAI3_HUMAN	1.5	10.665	7.2268	9	6
Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	sp|Q12905|ILF2_HUMAN	1.5	31.026	20.648	21	15
Cytosolic purine 5'-nucleotidase OS=Homo sapiens GN=NT5C2 PE=1 SV=1	sp|P49902|5NTC_HUMAN	1.5	31.026	20.648	26	14
Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=1 SV=2	sp|Q5H9R7|PP6R3_HUMAN	1.5	27.148	18.583	24	17
WD repeat-containing protein 3 OS=Homo sapiens GN=WDR3 PE=1 SV=1	sp|Q9UNX4|WDR3_HUMAN	1.5	7.7566	5.162	8	5
60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	sp|P40429|RL13A_HUMAN	1.5	21.331	14.454	10	9
Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	sp|P51991|ROA3_HUMAN	1.5	30.057	19.616	18	13
YTH domain-containing family protein 2 OS=Homo sapiens GN=YTHDF2 PE=1 SV=2	sp|Q9Y5A9|YTHD2_HUMAN	1.5	7.7566	5.162	7	4
ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2	sp|Q9UG63|ABCF2_HUMAN	1.5	22.3	14.454	20	14
Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1	sp|Q1KMD3|HNRL2_HUMAN	1.5	12.604	8.2592	13	8
Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	sp|P04075|ALDOA_HUMAN	1.5	15.513	10.324	14	9
Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2	sp|P05455|LA_HUMAN	1.5	10.665	7.2268	11	7
Nuclear receptor corepressor 2 OS=Homo sapiens GN=NCOR2 PE=1 SV=2	sp|Q9Y618|NCOR2_HUMAN	1.5	7.7566	5.162	8	5
cAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens GN=PRKACB PE=1 SV=2	sp|P22694|KAPCB_HUMAN	1.5	12.604	8.2592	10	7
Splicing factor 45 OS=Homo sapiens GN=RBM17 PE=1 SV=1	sp|Q96I25|SPF45_HUMAN	1.5	17.452	11.356	13	10
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	sp|P08865|RSSA_HUMAN	1.5	16.483	11.356	13	11
60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	sp|P42766|RL35_HUMAN	1.5	17.452	11.356	5	4
SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	sp|Q9UH99|SUN2_HUMAN	1.5	13.574	9.2916	11	7
Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens GN=PELP1 PE=1 SV=2	sp|Q8IZL8|PELP1_HUMAN	1.5	7.7566	5.162	8	5
Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3	sp|P35250|RFC2_HUMAN	1.5	10.665	7.2268	11	7
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=	sp|P04844|RPN2_HUMAN	1.5	10.665	7.2268	10	6
U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=1 SV=2	sp|O00566|MPP10_HUMAN	1.5	7.7566	5.162	7	4
Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1	sp|P35222|CTNB1_HUMAN	1.5	7.7566	5.162	7	4
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	sp|P35579|MYH9_HUMAN	1.4	282.15	200.28	175	126
Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	sp|Q13310|PABP4_HUMAN	1.4	73.688	52.652	48	36
Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	sp|Q6P2Q9|PRP8_HUMAN	1.4	88.231	65.041	75	52
ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	sp|Q08211|DHX9_HUMAN	1.4	108.59	75.365	79	57
60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	sp|P39023|RL3_HUMAN	1.4	103.74	72.268	41	31

Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	sp|P62979|RS27A_HUMAN	1.4	95.988	69.171	7	6
Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2	sp|P24941|CDK2_HUMAN	1.4	5.8175	4.1296	3	3
60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	sp|P61313|RL15_HUMAN	1.4	63.022	44.393	17	12
ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	sp|O00571|DDX3X_HUMAN	1.4	50.418	36.134	41	29
Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2	sp|Q93009|UBP7_HUMAN	1.4	33.935	23.745	33	22
Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	sp|P58107|EPIPL_HUMAN	1.4	40.722	29.939	37	26
Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	sp|Q13464|ROCK1_HUMAN	1.4	45.57	33.037	41	29
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	sp|P12956|XRCC6_HUMAN	1.4	47.509	35.101	35	25
Rho GTPase-activating protein 21 OS=Homo sapiens GN=ARHGAP21 PE=1 SV=1	sp|Q5T5U3|RHG21_HUMAN	1.4	25.209	17.551	23	16
Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	sp|P26599|PTBP1_HUMAN	1.4	43.631	30.972	33	21
Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2	sp|P42167|LAP2B_HUMAN	1.4	45.57	32.004	22	16
26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	sp|P62333|PRS10_HUMAN	1.4	44.6	30.972	22	17
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	sp|P01023|A2MG_HUMAN	1.4	22.3	16.518	11	10
DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5	sp|O75165|DJC13_HUMAN	1.4	25.209	17.551	24	17
Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2	sp|Q08378|GOGA3_HUMAN	1.4	33.935	24.778	34	23
5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1	sp|Q9H0D6|XRN2_HUMAN	1.4	25.209	18.583	25	17
Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2	sp|P63096|GNAI1_HUMAN	1.4	12.604	9.2916	10	8
Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2	sp|Q9UKV3|ACINU_HUMAN	1.4	23.27	16.518	18	14
Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	sp|Q07955|SRSF1_HUMAN	1.4	34.905	25.81	18	16
Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A PE=1 SV=3	sp|Q8ND56|LS14A_HUMAN	1.4	26.179	18.583	18	15
Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	sp|Q9P258|RCC2_HUMAN	1.4	24.239	17.551	19	14
Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=2	sp|Q9NZI8|IF2B1_HUMAN	1.4	31.026	21.68	24	18
Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2	sp|Q99575|POP1_HUMAN	1.4	20.361	14.454	18	10
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	sp|P01857|IGHG1_HUMAN	1.4	107.62	78.462	8	8
Little elongation complex subunit 1 OS=Homo sapiens GN=ICE1 PE=1 SV=5	sp|Q9Y2F5|ICE1_HUMAN	1.4	2.9087	2.0648	3	2
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=	sp|P04843|RPN1_HUMAN	1.4	21.331	15.486	18	15
Macrophage erythroblast attacher OS=Homo sapiens GN=MAEA PE=1 SV=1	sp|Q7L5Y9|MAEA_HUMAN	1.4	15.513	11.356	14	11
Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	sp|Q9Y446|PKP3_HUMAN	1.4	12.604	9.2916	13	9
Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3	sp|Q9UKK3|PARP4_HUMAN	1.4	12.604	9.2916	13	9
Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	sp|O43592|XPOT_HUMAN	1.4	12.604	9.2916	12	9
ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2	sp|Q8NE71|ABCF1_HUMAN	1.4	12.604	9.2916	13	9
Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens GN=G3BP2 PE=1 SV=2	sp|Q9UN86|G3BP2_HUMAN	1.4	20.361	14.454	15	10
Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1	sp|O96019|ACL6A_HUMAN	1.4	8.7262	6.1944	7	6
Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	sp|P52292|IMA1_HUMAN	1.4	17.452	12.389	16	11
2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2	sp|P09543|CN37_HUMAN	1.4	17.452	12.389	18	11
Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1	sp|Q13151|ROA0_HUMAN	1.4	18.422	13.421	14	10
Unconventional myosin-Vb OS=Homo sapiens GN=MYO5B PE=1 SV=3	sp|Q9ULV0|MYO5B_HUMAN	1.4	2.9087	2.0648	3	2
Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	sp|P01876|IGHA1_HUMAN	1.4	12.604	9.2916	4	3
Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1	sp|P78344|IF4G2_HUMAN	1.4	2.9087	2.0648	3	2
Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4	sp|Q15154|PCM1_HUMAN	1.4	2.9087	2.0648	3	2
Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3	sp|Q96QR8|PURB_HUMAN	1.4	8.7262	6.1944	9	5
Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	sp|P05556|ITB1_HUMAN	1.4	2.9087	2.0648	3	2
General transcription factor 3C polypeptide 4 OS=Homo sapiens GN=GTF3C4 PE=1 SV=2	sp|Q9UKN8|TF3C4_HUMAN	1.4	5.8175	4.1296	6	3
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	sp|P02765|FETUA_HUMAN	1.4	8.7262	6.1944	3	3
28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=1 SV=1	sp|P82650|RT22_HUMAN	1.4	11.635	8.2592	12	8
Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1	sp|A0FGR8|ESYT2_HUMAN	1.4	5.8175	4.1296	6	4
Zinc finger BED domain-containing protein 5 OS=Homo sapiens GN=ZBED5 PE=2 SV=2	sp|Q49AG3|ZBED5_HUMAN	1.4	2.9087	2.0648	3	2
Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1	sp|Q9Y295|DRG1_HUMAN	1.4	11.635	8.2592	10	7
Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=1 SV=2	sp|Q9Y4I1|MYO5A_HUMAN	1.4	2.9087	2.0648	3	2
U7 snRNA-associated Sm-like protein LSm11 OS=Homo sapiens GN=LSM11 PE=1 SV=2	sp|P83369|LSM11_HUMAN	1.4	5.8175	4.1296	6	4
Lethal(3)malignant brain tumor-like protein 2 OS=Homo sapiens GN=L3MBTL2 PE=1 SV=1	sp|Q969R5|LMBL2_HUMAN	1.4	2.9087	2.0648	3	2
39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 PE=1 SV=3	sp|Q9NYK5|RM39_HUMAN	1.4	5.8175	4.1296	5	4
Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=1	sp|Q6P996|PDXD1_HUMAN	1.4	5.8175	4.1296	6	4
E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1	sp|Q96T88|UHRF1_HUMAN	1.4	2.9087	2.0648	3	2
AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=1 SV=1	sp|O14617|AP3D1_HUMAN	1.4	2.9087	2.0648	3	2
Protein FRG1 OS=Homo sapiens GN=FRG1 PE=1 SV=1	sp|Q14331|FRG1_HUMAN	1.4	2.9087	2.0648	3	2
General transcription factor IIF subunit 2 OS=Homo sapiens GN=GTF2F2 PE=1 SV=2	sp|P13984|T2FB_HUMAN	1.4	8.7262	6.1944	8	5
Anion exchange protein 2 OS=Homo sapiens GN=SLC4A2 PE=1 SV=4	sp|P04920|B3A2_HUMAN	1.4	2.9087	2.0648	2	2
BUB3-interacting and GLEBS motif-containing protein ZNF207 OS=Homo sapiens GN=ZNF207 PE=1 SV=1	sp|O43670|ZN207_HUMAN	1.4	2.9087	2.0648	3	2
Polynucleotide 5'-hydroxyl-kinase NOL9 OS=Homo sapiens GN=NOL9 PE=1 SV=1	sp|Q5SY16|NOL9_HUMAN	1.4	2.9087	2.0648	3	2
Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1	sp|Q8WX92|NELFB_HUMAN	1.4	2.9087	2.0648	3	2
WD repeat-containing protein 55 OS=Homo sapiens GN=WDR55 PE=1 SV=2	sp|Q9H6Y2|WDR55_HUMAN	1.4	2.9087	2.0648	3	2
Solute carrier family 12 member 3 OS=Homo sapiens GN=SLC12A3 PE=1 SV=3	sp|P55017|S12A3_HUMAN	1.4	2.9087	2.0648	3	2
WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1	sp|Q6UXN9|WDR82_HUMAN	1.4	5.8175	4.1296	5	3
WD repeat-containing protein 18 OS=Homo sapiens GN=WDR18 PE=1 SV=2	sp|Q9BV38|WDR18_HUMAN	1.4	5.8175	4.1296	6	4
TRAF-type zinc finger domain-containing protein 1 OS=Homo sapiens GN=TRAFD1 PE=1 SV=1	sp|O14545|TRAD1_HUMAN	1.4	2.9087	2.0648	3	2
Protein CASC3 OS=Homo sapiens GN=CASC3 PE=1 SV=2	sp|O15234|CASC3_HUMAN	1.4	2.9087	2.0648	3	2
NEDD4-like E3 ubiquitin-protein ligase WWP2 OS=Homo sapiens GN=WWP2 PE=1 SV=2	sp|O00308|WWP2_HUMAN	1.4	5.8175	4.1296	5	4
F-box only protein 22 OS=Homo sapiens GN=FBXO22 PE=1 SV=1	sp|Q8NEZ5|FBX22_HUMAN	1.4	2.9087	2.0648	3	2
S-adenosylmethionine decarboxylase proenzyme OS=Homo sapiens GN=AMD1 PE=1 SV=2	sp|P17707|DCAM_HUMAN	1.4	2.9087	2.0648	3	2
Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3	sp|P52294|IMA5_HUMAN	1.4	5.8175	4.1296	5	3
RNA-binding motif, single-stranded-interacting protein 1 OS=Homo sapiens GN=RBMS1 PE=1 SV=3	sp|P29558|RBMS1_HUMAN	1.4	2.9087	2.0648	3	2
39S ribosomal protein L44, mitochondrial OS=Homo sapiens GN=MRPL44 PE=1 SV=1	sp|Q9H9J2|RM44_HUMAN	1.4	2.9087	2.0648	3	2
Protein MEMO1 OS=Homo sapiens GN=MEMO1 PE=1 SV=1	sp|Q9Y316|MEMO1_HUMAN	1.4	2.9087	2.0648	3	2
High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	sp|P09429|HMGB1_HUMAN	1.4	2.9087	2.0648	3	2
Protein CMSS1 OS=Homo sapiens GN=CMSS1 PE=1 SV=2	sp|Q9BQ75|CMS1_HUMAN	1.4	2.9087	2.0648	3	2
G patch domain-containing protein 11 OS=Homo sapiens GN=GPATCH11 PE=1 SV=3	sp|Q8N954|GPT11_HUMAN	1.4	2.9087	2.0648	3	2
Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	sp|Q9UQ80|PA2G4_HUMAN	1.4	2.9087	2.0648	3	2
PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5	sp|Q96HC4|PDLI5_HUMAN	1.4	2.9087	2.0648	3	2
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	sp|Q09666|AHNK_HUMAN	1.3	308.32	234.35	225	174
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	sp|Q00839|HNRPU_HUMAN	1.3	93.079	70.203	55	45
Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	sp|Q13435|SF3B2_HUMAN	1.3	74.657	58.847	51	42
26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	sp|Q99460|PSMD1_HUMAN	1.3	89.201	67.106	57	46
E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2	sp|P49792|RBP2_HUMAN	1.3	45.57	36.134	46	34
Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4	sp|P16989|YBOX3_HUMAN	1.3	36.844	27.875	16	13
Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1	sp|Q14152|EIF3A_HUMAN	1.3	61.083	46.458	54	40
Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	sp|Q14764|MVP_HUMAN	1.3	73.688	54.717	56	40
Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	sp|Q92900|RENT1_HUMAN	1.3	63.022	48.523	51	40
60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	sp|P18124|RL7_HUMAN	1.3	57.205	44.393	30	25
26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	sp|P35998|PRS7_HUMAN	1.3	51.387	39.231	30	26
Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	sp|P55795|HNRH2_HUMAN	1.3	29.087	22.713	16	10
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	sp|P62753|RS6_HUMAN	1.3	48.479	37.166	21	14
Microtubule cross-linking factor 1 OS=Homo sapiens GN=MTCL1 PE=1 SV=5	sp|Q9Y4B5|MTCL1_HUMAN	1.3	26.179	20.648	23	20
Gem-associated protein 4 OS=Homo sapiens GN=GEMIN4 PE=1 SV=2	sp|P57678|GEMI4_HUMAN	1.3	27.148	21.68	25	19
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=	sp|Q5JWF2|GNAS1_HUMAN	1.3	6.787	5.162	7	5
Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	sp|Q15459|SF3A1_HUMAN	1.3	26.179	20.648	26	19
Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=	sp|Q9Y6D5|BIG2_HUMAN	1.3	6.787	5.162	7	5
Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2	sp|Q9UNF1|MAGD2_HUMAN	1.3	17.452	13.421	16	13
Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	sp|P05198|IF2A_HUMAN	1.3	23.27	17.551	15	13
Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	sp|P25786|PSA1_HUMAN	1.3	26.179	20.648	20	14
Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4	sp|Q15424|SAFB1_HUMAN	1.3	10.665	8.2592	11	8
MICOS complex subunit MIC60 OS=Homo sapiens GN=IMMT PE=1 SV=1	sp|Q16891|MIC60_HUMAN	1.3	22.3	17.551	19	17
Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	sp|Q96HS1|PGAM5_HUMAN	1.3	26.179	19.616	24	18
Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1	sp|Q9HAV4|XPO5_HUMAN	1.3	15.513	12.389	14	11
YTH domain-containing family protein 1 OS=Homo sapiens GN=YTHDF1 PE=1 SV=1	sp|Q9BYJ9|YTHD1_HUMAN	1.3	3.8783	3.0972	3	2

Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2	sp|Q96KR1|ZFR_HUMAN	1.3	15.513	12.389	14	11
UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1	sp|O60701|UGDH_HUMAN	1.3	17.452	13.421	15	11
Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1 PE=1 SV=2	sp|O75534|CSDE1_HUMAN	1.3	18.422	14.454	17	12
Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	sp|P07996|TSP1_HUMAN	1.3	13.574	10.324	14	10
Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ACAP2 PI	sp|Q15057|ACAP2_HUMAN	1.3	11.635	9.2916	12	9
Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1	sp|Q5SRE5|NU188_HUMAN	1.3	11.635	9.2916	12	9
THO complex subunit 2 OS=Homo sapiens GN=THOC2 PE=1 SV=2	sp|Q8NI27|THOC2_HUMAN	1.3	9.6958	7.2268	7	6
Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	sp|Q15427|SF3B4_HUMAN	1.3	13.574	10.324	12	9
60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	sp|P46776|RL27A_HUMAN	1.3	17.452	13.421	6	7
Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	sp|P07237|PDIA1_HUMAN	1.3	15.513	12.389	14	11
A-kinase anchor protein 11 OS=Homo sapiens GN=AKAP11 PE=1 SV=1	sp|Q9UKA4|AKA11_HUMAN	1.3	6.787	5.162	7	5
Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	sp|P38919|IF4A3_HUMAN	1.3	20.361	15.486	18	11
5'-3' exoribonuclease 1 OS=Homo sapiens GN=XRN1 PE=1 SV=1	sp|Q8IZH2|XRN1_HUMAN	1.3	6.787	5.162	7	5
Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=1 SV=1	sp|P40937|RFC5_HUMAN	1.3	11.635	9.2916	9	9
Obscurin-like protein 1 OS=Homo sapiens GN=OBSL1 PE=1 SV=4	sp|O75147|OBSL1_HUMAN	1.3	6.787	5.162	7	5
Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1	sp|Q99436|PSB7_HUMAN	1.3	13.574	10.324	10	7
Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=1 SV=2	sp|Q9BY77|PDIP3_HUMAN	1.3	9.6958	7.2268	10	7
Citron Rho-interacting kinase OS=Homo sapiens GN=CIT PE=1 SV=2	sp|O14578|CTRO_HUMAN	1.3	3.8783	3.0972	4	3
Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	sp|O60716|CTND1_HUMAN	1.3	7.7566	6.1944	8	6
Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3	sp|Q01081|U2AF1_HUMAN	1.3	6.787	5.162	7	4
Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	sp|Q08554|DSC1_HUMAN	1.3	10.665	8.2592	6	3
Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3	sp|Q12931|TRAP1_HUMAN	1.3	7.7566	6.1944	7	5
RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	sp|Q96PK6|RBM14_HUMAN	1.3	10.665	8.2592	11	8
Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	sp|P15311|EZRI_HUMAN	1.3	3.8783	3.0972	4	3
Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2	sp|Q16186|ADRM1_HUMAN	1.3	9.6958	7.2268	6	5
U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2	sp|P09661|RU2A_HUMAN	1.3	9.6958	7.2268	10	7
Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2	sp|P27694|RFA1_HUMAN	1.3	9.6958	7.2268	10	7
Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2	sp|Q00577|PURA_HUMAN	1.3	7.7566	6.1944	7	5
Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	sp|Q92945|FUBP2_HUMAN	1.3	3.8783	3.0972	4	2
Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	sp|O75367|H2AY_HUMAN	1.3	9.6958	7.2268	10	5
Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	sp|P27105|STOM_HUMAN	1.3	6.787	5.162	6	5
Integrator complex subunit 3 OS=Homo sapiens GN=INTS3 PE=1 SV=1	sp|Q68E01|INT3_HUMAN	1.3	3.8783	3.0972	4	3
Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4	sp|Q01130|SRSF2_HUMAN	1.3	3.8783	3.0972	3	3
Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1	sp|O15144|ARPC2_HUMAN	1.3	6.787	5.162	5	4
Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1	sp|P68400|CSK21_HUMAN	1.3	3.8783	3.0972	3	3
Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=2	sp|Q16630|CPSF6_HUMAN	1.3	3.8783	3.0972	3	2
Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	sp|P05089|ARGI1_HUMAN	1.3	3.8783	3.0972	3	3
Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	sp|P51858|HDGF_HUMAN	1.3	3.8783	3.0972	4	3
Glutaminyl-peptide cyclotransferase OS=Homo sapiens GN=QPCT PE=1 SV=1	sp|Q16769|QPCT_HUMAN	1.3	6.787	5.162	5	5
Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1	sp|Q52LJ0|FA98B_HUMAN	1.3	3.8783	3.0972	4	3
Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1	sp|P43487|RANG_HUMAN	1.3	3.8783	3.0972	4	3
U5 small nuclear ribonucleoprotein 40 kDa protein OS=Homo sapiens GN=SNRNP40 PE=1 SV=1	sp|Q96DI7|SNR40_HUMAN	1.3	3.8783	3.0972	4	3
Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	sp|Q9Y277|VDAC3_HUMAN	1.3	3.8783	3.0972	4	3
Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2	sp|Q14739|LBR_HUMAN	1.3	3.8783	3.0972	4	3
Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	sp|P35580|MYH10_HUMAN	1.2	73.688	64.009	63	50
Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	sp|Q15149|PLEC_HUMAN	1.2	265.66	227.13	222	188
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	sp|Q14204|DYHC1_HUMAN	1.2	258.88	210.61	210	172
Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	sp|Q9BQA1|MEP50_HUMAN	1.2	265.66	215.77	131	100
OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4 PE=1 SV=4	sp|Q01804|OTUD4_HUMAN	1.2	216.22	187.9	133	111
Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	sp|P11940|PABP1_HUMAN	1.2	84.353	70.203	54	42
Polyadenylate-binding protein 3 OS=Homo sapiens GN=PABPC3 PE=1 SV=2	sp|Q9H361|PABP3_HUMAN	1.2	31.996	26.842	20	15
General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	sp|P78347|GTF2I_HUMAN	1.2	97.927	82.592	77	57
U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	sp|O75643|U520_HUMAN	1.2	86.292	70.203	74	58
Methylcytosine dioxygenase TET2 OS=Homo sapiens GN=TET2 PE=1 SV=3	sp|Q6N021|TET2_HUMAN	1.2	57.205	47.49	50	40
Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	sp|Q14008|CKAP5_HUMAN	1.2	66.901	56.782	59	51
60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	sp|P62917|RL8_HUMAN	1.2	53.327	43.361	24	20
Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2	sp|P43243|MATR3_HUMAN	1.2	46.54	40.263	31	30
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	sp|P13010|XRCC5_HUMAN	1.2	52.357	44.393	39	32
Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1	sp|Q15366|PCBP2_HUMAN	1.2	26.179	22.713	16	17
U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2	sp|Q8WWY3|PRP31_HUMAN	1.2	55.266	45.425	31	30
Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2	sp|P14866|HNRPL_HUMAN	1.2	47.509	41.296	31	27
Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=1 SV=3	sp|Q8IWX8|CHERP_HUMAN	1.2	40.722	33.037	30	24
HLA class I histocompatibility antigen, A-68 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=4	sp|P01891|1A68_HUMAN	1.2	9.6958	8.2592	9	8
26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	sp|O43242|PSMD3_HUMAN	1.2	44.6	36.134	35	24
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	sp|P55060|XPO2_HUMAN	1.2	36.844	32.004	35	28
Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3	sp|P27816|MAP4_HUMAN	1.2	32.966	26.842	20	20
Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2	sp|Q9NTJ3|SMC4_HUMAN	1.2	31.026	26.842	32	24
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Hc	sp|O60264|SMCA5_HUMAN	1.2	25.209	20.648	23	20
Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	sp|O60506|HNRPQ_HUMAN	1.2	42.661	35.101	22	23
Nestin OS=Homo sapiens GN=NES PE=1 SV=2	sp|P48681|NEST_HUMAN	1.2	21.331	17.551	22	17
Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	sp|Q8TEQ6|GEMI5_HUMAN	1.2	31.996	26.842	30	21
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1	sp|P62136|PP1A_HUMAN	1.2	20.361	17.551	15	11
Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1	sp|P62140|PP1B_HUMAN	1.2	20.361	16.518	14	11
Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2	sp|Q8TF72|SHRM3_HUMAN	1.2	4.8479	4.1296	2	2
Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	sp|Q14151|SAFB2_HUMAN	1.2	12.604	10.324	13	10
ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	sp|Q92499|DDX1_HUMAN	1.2	26.179	22.713	24	19
Protein Wiz OS=Homo sapiens GN=WIZ PE=1 SV=2	sp|O95785|WIZ_HUMAN	1.2	17.452	14.454	17	12
Synergin gamma OS=Homo sapiens GN=SYNRG PE=1 SV=2	sp|Q9UMZ2|SYNRG_HUMAN	1.2	18.422	15.486	18	14
Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2	sp|P00533|EGFR_HUMAN	1.2	18.422	15.486	19	14
GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1	sp|P49915|GUAA_HUMAN	1.2	18.422	15.486	16	13
LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	sp|Q9UHB6|LIMA1_HUMAN	1.2	14.544	12.389	11	9
Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	sp|Q13283|G3BP1_HUMAN	1.2	22.3	18.583	16	13
Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	sp|P13797|PLST_HUMAN	1.2	8.7262	7.2268	8	7
ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	sp|P06576|ATPB_HUMAN	1.2	18.422	15.486	15	11
Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens GN=DDX23 PE=1 SV=3	sp|Q9BUQ8|DDX23_HUMAN	1.2	13.574	11.356	11	10
Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2	sp|Q14137|BOP1_HUMAN	1.2	9.6958	8.2592	9	6
Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens GN=DDX27 PE=1 SV=2	sp|Q96GQ7|DDX27_HUMAN	1.2	13.574	11.356	13	11
Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3	sp|O14979|HNRDL_HUMAN	1.2	12.604	10.324	9	8
Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2	sp|P20042|IF2B_HUMAN	1.2	9.6958	8.2592	10	8
Replication factor C subunit 4 OS=Homo sapiens GN=RFC4 PE=1 SV=2	sp|P35249|RFC4_HUMAN	1.2	12.604	10.324	12	10
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDO	sp|P39656|OST48_HUMAN	1.2	12.604	10.324	13	10
WD repeat-containing protein 43 OS=Homo sapiens GN=WDR43 PE=1 SV=3	sp|Q15061|WDR43_HUMAN	1.2	4.8479	4.1296	4	4
Putative bifunctional UDP-N-acetylglucosamine transferase and deubiquitinase ALG13 OS=Homo sapiens GI	sp|Q9NP73|ALG13_HUMAN	1.2	4.8479	4.1296	5	4
Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2	sp|Q01650|LAT1_HUMAN	1.2	9.6958	8.2592	4	4
Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1	sp|O00622|CYR61_HUMAN	1.2	8.7262	7.2268	7	6
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 S\	sp|P11177|ODPB_HUMAN	1.2	9.6958	8.2592	9	6
Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	sp|Q99733|NP1L4_HUMAN	1.2	12.604	10.324	9	6
Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3	sp|Q9HAV0|GBB4_HUMAN	1.2	4.8479	4.1296	5	4
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitocl	sp|P36957|ODO2_HUMAN	1.2	4.8479	4.1296	4	4
Transcription factor AP-2-delta OS=Homo sapiens GN=TFAP2D PE=2 SV=1	sp|Q7Z6R9|AP2D_HUMAN	1.2	4.8479	4.1296	2	1
Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	sp|Q16658|FSCN1_HUMAN	1.2	4.8479	4.1296	5	4
Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2	sp|Q15758|AAAT_HUMAN	1.2	4.8479	4.1296	4	3
Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2	sp|P06730|IF4E_HUMAN	1.2	4.8479	4.1296	5	3
Protein quaking OS=Homo sapiens GN=QKI PE=1 SV=1	sp|Q96PU8|QKI_HUMAN	1.2	4.8479	4.1296	5	4
Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	sp|O14744|ANM5_HUMAN	1.1	510	474.9	199	186

Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	sp|P21333|FLNA_HUMAN	1.1	420.8	391.28	233	215
Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2	sp|Q7Z406|MYH14_HUMAN	1.1	20.361	18.583	13	13
Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	sp|P35749|MYH11_HUMAN	1.1	29.087	26.842	22	19
Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	sp|P52732|KIF11_HUMAN	1.1	318.02	295.27	161	142
Spectrin beta chain, erythrocytic OS=Homo sapiens GN=SPTB PE=1 SV=5	sp|P11277|SPTB1_HUMAN	1.1	8.7262	8.2592	8	6
Clathrin heavy chain 2 OS=Homo sapiens GN=CLTCL1 PE=1 SV=2	sp|P53675|CLH2_HUMAN	1.1	26.179	23.745	20	16
Cyclin-dependent kinase 6 OS=Homo sapiens GN=CDK6 PE=1 SV=1	sp|Q00534|CDK6_HUMAN	1.1	5.8175	5.162	3	3
RNA binding motif protein, X-linked-like-1 OS=Homo sapiens GN=RBMXL1 PE=1 SV=1	sp|Q96E39|RMXL1_HUMAN	1.1	21.331	19.616	18	16
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	sp|P15880|RS2_HUMAN	1.1	74.657	66.073	30	27
RANBP2-like and GRIP domain-containing protein 5/6 OS=Homo sapiens GN=RGPD5 PE=1 SV=3	sp|Q99666|RGPD5_HUMAN	1.1	13.574	12.389	14	12
Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	sp|P52272|HNRPM_HUMAN	1.1	65.931	59.879	42	39
Calmodulin-regulated spectrin-associated protein 3 OS=Homo sapiens GN=CAMSAP3 PE=1 SV=2	sp|Q9P1Y5|CAMP3_HUMAN	1.1	69.809	62.976	59	46
Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	sp|P01861|IGHG4_HUMAN	1.1	71.749	62.976	8	6
Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5	sp|P09651|ROA1_HUMAN	1.1	88.231	80.527	40	33
Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens GN=HNRNPA1L2 PE=2 SV=2	sp|Q32P51|RA1L2_HUMAN	1.1	61.083	56.782	30	24
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	sp|P61978|HNRPK_HUMAN	1.1	75.627	67.106	39	38
Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	sp|P06748|NPM_HUMAN	1.1	61.083	56.782	21	29
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	sp|P16615|AT2A2_HUMAN	1.1	38.783	34.069	32	26
Influenza virus NS1A-binding protein OS=Homo sapiens GN=IVNS1ABP PE=1 SV=3	sp|Q9Y6Y0|NS1BP_HUMAN	1.1	63.022	59.879	38	37
DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	sp|Q16531|DDB1_HUMAN	1.1	57.205	53.685	51	42
Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4	sp|Q04637|IF4G1_HUMAN	1.1	49.448	45.425	40	34
Transcription initiation factor TFIID subunit 4 OS=Homo sapiens GN=TAF4 PE=1 SV=2	sp|O00268|TAF4_HUMAN	1.1	43.631	39.231	37	31
26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	sp|P62195|PRS8_HUMAN	1.1	57.205	52.652	34	36
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	sp|P62241|RS8_HUMAN	1.1	59.144	55.749	17	16
Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3	sp|Q9Y2H1|ST38L_HUMAN	1.1	80.475	73.3	47	38
Mitogen-activated protein kinase kinase kinase 7 OS=Homo sapiens GN=MAP3K7 PE=1 SV=1	sp|O43318|M3K7_HUMAN	1.1	45.57	41.296	25	24
Glutaminyl-peptide cyclotransferase-like protein OS=Homo sapiens GN=QPCTL PE=1 SV=2	sp|Q9NXS2|QPCTL_HUMAN	1.1	48.479	45.425	35	31
60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	sp|P46777|RL5_HUMAN	1.1	40.722	36.134	22	18
Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	sp|P53621|COPA_HUMAN	1.1	38.783	35.101	35	29
tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2	sp|Q08J23|NSUN2_HUMAN	1.1	41.692	37.166	38	30
Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	sp|P14618|KPYM_HUMAN	1.1	42.661	39.231	32	29
Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4	sp|P26640|SYVC_HUMAN	1.1	33.935	29.939	32	25
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	sp|Q07020|RL18_HUMAN	1.1	35.874	32.004	8	9
Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	sp|O95347|SMC2_HUMAN	1.1	35.874	34.069	35	30
Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	sp|Q86VP6|CAND1_HUMAN	1.1	28.118	25.81	29	24
60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	sp|P46778|RL21_HUMAN	1.1	30.057	27.875	13	11
26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2	sp|Q9UNM6|PSD13_HUMAN	1.1	36.844	33.037	26	23
Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	sp|Q99873|ANM1_HUMAN	1.1	32.966	28.907	21	21
Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	sp|P04899|GNAI2_HUMAN	1.1	8.7262	8.2592	8	7
Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	sp|Q15233|NONO_HUMAN	1.1	29.087	26.842	24	19
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE	sp|P36873|PP1G_HUMAN	1.1	20.361	18.583	15	12
TGF-beta-activated kinase 1 and MAP3K7-binding protein 3 OS=Homo sapiens GN=TAB3 PE=1 SV=2	sp|Q8N5C8|TAB3_HUMAN	1.1	23.27	21.68	17	17
60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	sp|P50914|RL14_HUMAN	1.1	27.148	23.745	9	6
Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4	sp|P07910|HNRPC_HUMAN	1.1	25.209	22.713	15	14
Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1	sp|Q99613|EIF3C_HUMAN	1.1	26.179	24.778	24	19
Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	sp|P52597|HNRPF_HUMAN	1.1	38.783	34.069	22	20
Liprin-alpha-1 OS=Homo sapiens GN=PPFIA1 PE=1 SV=1	sp|Q13136|LIPA1_HUMAN	1.1	12.604	11.356	12	11
Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	sp|Q8WWM7|ATX2L_HUMAN	1.1	23.27	20.648	23	19
Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	sp|P50395|GDIB_HUMAN	1.1	25.209	22.713	21	18
Protein piccolo OS=Homo sapiens GN=PCLO PE=1 SV=4	sp|Q9Y6V0|PCLO_HUMAN	1.1	5.8175	5.162	2	1
Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens GN=NOP2 PE=1 SV=2	sp|P46087|NOP2_HUMAN	1.1	19.392	17.551	19	16
Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3	sp|Q15021|CND1_HUMAN	1.1	13.574	12.389	14	12
TGF-beta-activated kinase 1 and MAP3K7-binding protein 2 OS=Homo sapiens GN=TAB2 PE=1 SV=1	sp|Q9NYJ8|TAB2_HUMAN	1.1	21.331	19.616	20	17
Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	sp|Q9Y3F4|STRAP_HUMAN	1.1	23.27	20.648	17	16
DNA-directed RNA polymerase I subunit RPA1 OS=Homo sapiens GN=POLR1A PE=1 SV=2	sp|O95602|RPA1_HUMAN	1.1	7.7566	7.2268	8	7
Phosphatidylinositol 4-kinase alpha OS=Homo sapiens GN=PI4KA PE=1 SV=3	sp|P42356|PI4KA_HUMAN	1.1	6.787	6.1944	7	6
Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1	sp|Q9NYL9|TMOD3_HUMAN	1.1	17.452	15.486	15	14
Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1	sp|O94906|PRP6_HUMAN	1.1	13.574	12.389	14	12
Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2	sp|Q14683|SMC1A_HUMAN	1.1	15.513	14.454	16	14
Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3	sp|P42285|SK2L2_HUMAN	1.1	13.574	12.389	14	12
Serine/threonine-protein kinase WNK1 OS=Homo sapiens GN=WNK1 PE=1 SV=2	sp|Q9H4A3|WNK1_HUMAN	1.1	5.8175	5.162	6	5
Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1	sp|Q9Y262|EIF3L_HUMAN	1.1	17.452	16.518	18	15
RNA cytidine acetyltransferase OS=Homo sapiens GN=NAT10 PE=1 SV=2	sp|Q9H0A0|NAT10_HUMAN	1.1	17.452	15.486	17	14
Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	sp|P61158|ARP3_HUMAN	1.1	11.635	10.324	12	10
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP	sp|Q07021|C1QBP_HUMAN	1.1	16.483	14.454	10	9
DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens GN=DNAJA3 PE=1 SV=2	sp|Q96EY1|DNJA3_HUMAN	1.1	14.544	13.421	13	12
LanC-like protein 1 OS=Homo sapiens GN=LANCL1 PE=1 SV=1	sp|O43813|LANC1_HUMAN	1.1	8.7262	8.2592	9	8
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2	sp|Q02809|PLOD1_HUMAN	1.1	10.665	9.2916	11	9
Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3	sp|Q13409|DC1I2_HUMAN	1.1	12.604	11.356	12	9
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1	sp|Q06210|GFPT1_HUMAN	1.1	5.8175	5.162	6	5
KRR1 small subunit processome component homolog OS=Homo sapiens GN=KRR1 PE=1 SV=4	sp|Q13601|KRR1_HUMAN	1.1	5.8175	5.162	4	3
Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2	sp|P49321|NASP_HUMAN	1.1	6.787	6.1944	7	5
Protein odr-4 homolog OS=Homo sapiens GN=ODR4 PE=1 SV=1	sp|Q5SWX8|ODR4_HUMAN	1.1	8.7262	8.2592	9	8
Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	sp|Q9UHD8|SEPT9_HUMAN	1.1	11.635	10.324	11	10
Kallistatin OS=Homo sapiens GN=SERPINA4 PE=1 SV=3	sp|P29622|KAIN_HUMAN	1.1	6.787	6.1944	2	2
THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3	sp|Q86V81|THOC4_HUMAN	1.1	8.7262	8.2592	8	7
Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2	sp|P31942|HNRH3_HUMAN	1.1	7.7566	7.2268	5	3
Survival motor neuron protein OS=Homo sapiens GN=SMN1 PE=1 SV=1	sp|Q16637|SMN_HUMAN	1.1	6.787	6.1944	6	5
60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	sp|P49207|RL34_HUMAN	1.1	8.7262	8.2592	3	4
Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	sp|P31930|QCR1_HUMAN	1.1	5.8175	5.162	6	5
Translation initiation factor eIF-2B subunit alpha OS=Homo sapiens GN=EIF2B1 PE=1 SV=1	sp|Q14232|EI2BA_HUMAN	1.1	5.8175	5.162	6	5
DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1	sp|Q8WXX5|DNJC9_HUMAN	1.1	5.8175	5.162	6	5
Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	sp|P01625|KV402_HUMAN (+3)	1.1	7.7566	7.2268	3	4
Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1	sp|P09497|CLCB_HUMAN	1.1	5.8175	5.162	5	5
60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	sp|P61353|RL27_HUMAN	1.1	5.8175	5.162	3	3
Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1	sp|Q9BYX7|ACTBM_HUMAN	1.0	25.209	25.81	12	16
DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	sp|P78527|PRKDC_HUMAN	1.0	170.65	168.28	145	139
Protein phosphatase 1B OS=Homo sapiens GN=PPM1B PE=1 SV=1	sp|O75688|PPM1B_HUMAN	1.0	210.4	217.84	69	65
Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	sp|Q14315|FLNC_HUMAN	1.0	135.74	137.31	111	108
Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1	sp|Q15208|STK38_HUMAN	1.0	149.31	142.47	69	66
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1	sp|Q16875|F263_HUMAN	1.0	52.357	51.62	32	28
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	sp|P02768|ALBU_HUMAN	1.0	99.866	97.045	32	31
Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	sp|Q92616|GCN1L_HUMAN	1.0	81.444	82.592	74	70
Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	sp|Q15393|SF3B3_HUMAN	1.0	84.353	85.689	67	58
Serine/threonine-protein kinase RIO1 OS=Homo sapiens GN=RIOK1 PE=1 SV=2	sp|Q9BRS2|RIOK1_HUMAN	1.0	84.353	82.592	42	34
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	sp|P62701|RS4X_HUMAN	1.0	78.536	78.462	36	30
RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3	sp|P38159|RBMX_HUMAN	1.0	25.209	24.778	19	19
Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	sp|P67809|YBOX1_HUMAN	1.0	32.966	34.069	16	16
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	sp|P48643|TCPE_HUMAN	1.0	74.657	73.3	45	46
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	sp|P61247|RS3A_HUMAN	1.0	65.931	68.138	37	28
Spindlin-3 OS=Homo sapiens GN=SPIN3 PE=1 SV=1	sp|Q5JUX0|SPIN3_HUMAN	1.0	14.544	14.454	9	8
Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	sp|O00159|MYO1C_HUMAN	1.0	48.479	50.587	43	44
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	sp|P26641|EF1G_HUMAN	1.0	46.54	47.49	34	34
Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4	sp|P31943|HNRH1_HUMAN	1.0	51.387	50.587	26	23
Uncharacterized protein C11orf84 OS=Homo sapiens GN=C11orf84 PE=1 SV=3	sp|Q9BUA3|CK084_HUMAN	1.0	39.753	41.296	22	22

Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	sp|P42166|LAP2A_HUMAN	1.0	23.27	22.713	9	9
60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	sp|P26373|RL13_HUMAN	1.0	37.813	36.134	14	14
LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3	sp|Q8WWI1|LMO7_HUMAN	1.0	30.057	29.939	30	27
Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	sp|P27824|CALX_HUMAN	1.0	31.996	32.004	27	24
Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	sp|O00410|IPO5_HUMAN	1.0	22.3	22.713	20	21
Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1	sp|Q9BXP5|SRRT_HUMAN	1.0	19.392	18.583	19	16
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	sp|P60842|IF4A1_HUMAN	1.0	27.148	26.842	21	19
60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	sp|Q02543|RL18A_HUMAN	1.0	27.148	27.875	12	12
Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4	sp|Q96N67|DOCK7_HUMAN	1.0	19.392	19.616	19	19
Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	sp|P23381|SYWC_HUMAN	1.0	22.3	21.68	21	17
Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=2	sp|Q99729|ROAA_HUMAN	1.0	20.361	19.616	16	14
Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	sp|P60228|EIF3E_HUMAN	1.0	22.3	22.713	18	18
60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	sp|P46779|RL28_HUMAN	1.0	21.331	20.648	10	11
Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3	sp|Q92621|NU205_HUMAN	1.0	11.635	11.356	12	11
Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3	sp|O95573|ACSL3_HUMAN	1.0	9.6958	9.2916	9	8
DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1	sp|Q92878|RAD50_HUMAN	1.0	12.604	12.389	13	11
V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	sp|P38606|VATA_HUMAN	1.0	10.665	10.324	10	9
Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=1 SV=4	sp|Q92974|ARHG2_HUMAN	1.0	9.6958	9.2916	10	9
Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	sp|P13489|RINI_HUMAN	1.0	11.635	11.356	10	11
Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	sp|Q9UHX1|PUF60_HUMAN	1.0	10.665	10.324	11	10
(Reversed) ZW10 interactor OS=Homo sapiens GN=ZWINT PE=1 SV=2	Reversed_sp|O95229|ZWINT_HUMAN	1.0	13.574	13.421	2	1
ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	sp|P36542|ATPG_HUMAN	1.0	12.604	12.389	10	9
Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	sp|P81605|DCD_HUMAN	1.0	10.665	10.324	5	6
60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	sp|P47914|RL29_HUMAN	1.0	9.6958	9.2916	4	2
			NTSC	**NTSC**	**TUPC**	**TUPC**
Identified Proteins in Flotillin compared to ApoL6 with at least 8 fold increase and 5 or more peptides	**Accession Number**	**fold change Flotillin / ApoL6**	**ApoL6**	**Flotillin**	**ApoL6**	**Flotillin**
BTB/POZ domain-containing protein KCTD21 OS=Homo sapiens GN=KCTD21 PE=1 SV=1	sp|Q4G0X4|KCD21_HUMAN	148.7	0.5	74.333	0	31
Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	sp|P30041|PRDX6_HUMAN	51.6	0.5	25.81	0	19
Ankyrin repeat domain-containing protein 40 OS=Homo sapiens GN=ANKRD40 PE=1 SV=2	sp|Q6AI12|ANR40_HUMAN	41.3	0.5	20.648	0	16
Vacuolar protein sorting-associated protein 13B OS=Homo sapiens GN=VPS13B PE=1 SV=2	sp|Q7Z7G8|VP13B_HUMAN	35.1	0.5	17.551	0	17
Nuclear pore complex protein Nup88 OS=Homo sapiens GN=NUP88 PE=1 SV=2	sp|Q99567|NUP88_HUMAN	31.0	0.5	15.486	0	14
Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	sp|P14735|IDE_HUMAN	31.0	0.5	15.486	0	15
ADP/ATP translocase 4 OS=Homo sapiens GN=SLC25A31 PE=2 SV=1	sp|Q9H0C2|ADT4_HUMAN	28.9	0.5	14.454	0	6
Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1	sp|Q9BYT8|NEUL_HUMAN	28.9	0.5	14.454	0	12
Activating molecule in BECN1-regulated autophagy protein 1 OS=Homo sapiens GN=AMBRA1 PE=1 SV=2	sp|Q9C0C7|AMRA1_HUMAN	28.9	0.5	14.454	0	12
FAD synthase OS=Homo sapiens GN=FLAD1 PE=1 SV=1	sp|Q8NFF5|FAD1_HUMAN	26.8	0.5	13.421	0	10
PAS domain-containing serine/threonine-protein kinase OS=Homo sapiens GN=PASK PE=1 SV=3	sp|Q96RG2|PASK_HUMAN	26.8	0.5	13.421	0	12
Methionine synthase OS=Homo sapiens GN=MTR PE=1 SV=2	sp|Q99707|METH_HUMAN	22.7	0.5	11.356	0	11
Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2	sp|P52789|HXK2_HUMAN	20.6	0.5	10.324	0	10
Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Homo sapiens GN=PIK3	sp|O00443|P3C2A_HUMAN	20.6	0.5	10.324	0	10
Erythroid differentiation-related factor 1 OS=Homo sapiens GN=EDRF1 PE=1 SV=1	sp|Q3B7T1|EDRF1_HUMAN	20.6	0.5	10.324	0	10
Tensin-3 OS=Homo sapiens GN=TNS3 PE=1 SV=2	sp|Q68CZ2|TENS3_HUMAN	20.6	0.5	10.324	0	10
Echinoderm microtubule-associated protein-like 3 OS=Homo sapiens GN=EML3 PE=1 SV=1	sp|Q32P44|EMAL3_HUMAN	20.6	0.5	10.324	0	10
Adenylyltransferase and sulfurtransferase MOCS3 OS=Homo sapiens GN=MOCS3 PE=1 SV=1	sp|O95396|MOCS3_HUMAN	20.6	0.5	10.324	0	8
Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1	sp|Q9BXW7|CECR5_HUMAN	20.6	0.5	10.324	0	9
WD repeat-containing protein 62 OS=Homo sapiens GN=WDR62 PE=1 SV=4	sp|O43379|WDR62_HUMAN	18.6	0.5	9.2916	0	7
UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	sp|Q9Y224|CN166_HUMAN	18.6	0.5	9.2916	0	8
Iporin OS=Homo sapiens GN=RUSC2 PE=1 SV=3	sp|Q8N2Y8|RUSC2_HUMAN	16.5	0.5	8.2592	0	8
BAG family molecular chaperone regulator 1 OS=Homo sapiens GN=BAG1 PE=1 SV=4	sp|Q99933|BAG1_HUMAN	16.5	0.5	8.2592	0	6
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	sp|P78371|TCPB_HUMAN	14.9	3.8783	57.814	4	40
Rap guanine nucleotide exchange factor 6 OS=Homo sapiens GN=RAPGEF6 PE=1 SV=2	sp|Q8TEU7|RPGF6_HUMAN	14.5	0.5	7.2268	0	7
RNA polymerase II-associated protein 1 OS=Homo sapiens GN=RPAP1 PE=1 SV=3	sp|Q9BWH6|RPAP1_HUMAN	14.5	0.5	7.2268	0	7
Plakophilin-4 OS=Homo sapiens GN=PKP4 PE=1 SV=2	sp|Q99569|PKP4_HUMAN	14.5	0.5	7.2268	0	7
Centrosomal protein of 76 kDa OS=Homo sapiens GN=CEP76 PE=1 SV=1	sp|Q8TAP6|CEP76_HUMAN	14.5	0.5	7.2268	0	6
Serine/threonine-protein kinase MRCK beta OS=Homo sapiens GN=CDC42BPB PE=1 SV=2	sp|Q9Y5S2|MRCKB_HUMAN	14.5	0.5	7.2268	0	7
Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=3	sp|P55735|SEC13_HUMAN	14.5	0.5	7.2268	0	5
Solute carrier family 12 member 2 OS=Homo sapiens GN=SLC12A2 PE=1 SV=1	sp|P55011|S12A2_HUMAN	14.5	0.5	7.2268	0	6
Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	sp|P20930|FILA_HUMAN	12.8	0.96958	12.389	1	11
Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	sp|O75955|FLOT1_HUMAN	12.5	77.566	969.42	27	153
TBC1 domain family member 4 OS=Homo sapiens GN=TBC1D4 PE=1 SV=2	sp|O60343|TBCD4_HUMAN	12.4	0.5	6.1944	0	6
Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	sp|P14868|SYDC_HUMAN	12.4	0.5	6.1944	0	6
Immunoglobulin-binding protein 1 OS=Homo sapiens GN=IGBP1 PE=1 SV=1	sp|P78318|IGBP1_HUMAN	12.4	0.5	6.1944	0	5
BAG family molecular chaperone regulator 4 OS=Homo sapiens GN=BAG4 PE=1 SV=1	sp|O95429|BAG4_HUMAN	12.4	0.5	6.1944	0	6
Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	sp|Q08380|LG3BP_HUMAN	12.4	0.5	6.1944	0	5
RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	sp|Q9Y265|RUVB1_HUMAN	12.4	0.5	6.1944	0	5
Myotubularin OS=Homo sapiens GN=MTM1 PE=1 SV=2	sp|Q13496|MTM1_HUMAN	12.4	0.5	6.1944	0	5
HAUS augmin-like complex subunit 6 OS=Homo sapiens GN=HAUS6 PE=1 SV=2	sp|Q7Z4H7|HAUS6_HUMAN	12.4	0.5	6.1944	0	6
Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1	sp|Q8N122|RPTOR_HUMAN	12.4	0.5	6.1944	0	6
5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=1 SV=1	sp|P54619|AAKG1_HUMAN	12.4	0.5	6.1944	0	6
Mitotic checkpoint serine/threonine-protein kinase BUB1 beta OS=Homo sapiens GN=BUB1B PE=1 SV=3	sp|O60566|BUB1B_HUMAN	11.7	0.96958	11.356	1	11
Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2	sp|P36776|LONM_HUMAN	11.2	1.9392	21.68	2	20
Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=1 SV=4	sp|P52948|NUP98_HUMAN	10.6	0.96958	10.324	1	10
Serine/threonine-protein phosphatase 4 catalytic subunit OS=Homo sapiens GN=PPP4C PE=1 SV=1	sp|P60510|PP4C_HUMAN	10.3	0.5	5.162	0	5
Kelch-like protein 28 OS=Homo sapiens GN=KLHL28 PE=2 SV=2	sp|Q9NXS3|KLH28_HUMAN	10.3	0.5	5.162	0	5
NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=	sp|O75489|NDUS3_HUMAN	10.3	0.5	5.162	0	5
Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2	sp|O95487|SC24B_HUMAN	10.3	0.5	5.162	0	5
Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2	sp|P04745|AMY1_HUMAN	10.3	0.5	5.162	0	5
Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3	sp|Q15654|TRIP6_HUMAN	9.6	0.96958	9.2916	1	9
C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4	sp|O60271|JIP4_HUMAN	9.6	0.96958	9.2916	1	9
Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4	sp|P13798|ACPH_HUMAN	9.6	0.96958	9.2916	1	8
Hermansky-Pudlak syndrome 5 protein OS=Homo sapiens GN=HPS5 PE=1 SV=2	sp|Q9UPZ3|HPS5_HUMAN	9.6	0.96958	9.2916	1	9
Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3	sp|Q8WVV4|POF1B_HUMAN	9.6	0.96958	9.2916	1	8
Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=3	sp|Q53H96|P5CR3_HUMAN	9.6	0.96958	9.2916	1	8
Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3	sp|P53992|SC24C_HUMAN	8.5	0.96958	8.2592	1	8
Protein O-GlcNAcase OS=Homo sapiens GN=MGEA5 PE=1 SV=2	sp|O60502|OGA_HUMAN	8.5	0.96958	8.2592	1	8
Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 PE=1 SV=2	sp|Q14134|TRI29_HUMAN	8.5	0.96958	8.2592	1	8
Golgi to ER traffic protein 4 homolog OS=Homo sapiens GN=GET4 PE=1 SV=1	sp|Q7L5D6|GET4_HUMAN	7.5	1.9392	14.454	2	11
Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=1 SV=3	sp|Q15477|SKIV2_HUMAN	7.5	0.96958	7.2268	1	7
Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2	sp|Q9Y3Z3|SAMH1_HUMAN	7.5	0.96958	7.2268	1	7
Tax1-binding protein 1 OS=Homo sapiens GN=TAX1BP1 PE=1 SV=2	sp|Q86VP1|TAXB1_HUMAN	7.5	0.96958	7.2268	1	7
DNA polymerase delta subunit 2 OS=Homo sapiens GN=POLD2 PE=1 SV=1	sp|P49005|DPOD2_HUMAN	7.5	0.96958	7.2268	1	7
Laminin subunit alpha-1 OS=Homo sapiens GN=LAMA1 PE=1 SV=2	sp|P25391|LAMA1_HUMAN	7.5	2.9087	21.68	3	19
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA	sp|P67775|PP2AA_HUMAN	7.5	2.9087	21.68	2	18
Identified Proteins in Flotillin compared to ApoL6 with less than 8 fold increase and/or less than 5 peptides						
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	sp|P62829|RL23_HUMAN	12.4	0.5	6.1944	0	4
Macrophage-stimulating protein receptor OS=Homo sapiens GN=MST1R PE=1 SV=2	sp|Q04912|RON_HUMAN	8.3	0.5	4.1296	0	4
EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2	sp|Q12805|FBLN3_HUMAN	8.3	0.5	4.1296	0	4
Zinc finger protein 609 OS=Homo sapiens GN=ZNF609 PE=1 SV=2	sp|O15014|ZN609_HUMAN	8.3	0.5	4.1296	0	4
Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2	sp|P35611|ADDA_HUMAN	8.3	0.5	4.1296	0	4
Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=1 SV=2	sp|Q8TD19|NEK9_HUMAN	8.3	0.5	4.1296	0	4

Neuronal pentraxin-1 OS=Homo sapiens GN=NPTX1 PE=2 SV=2	sp|Q15818|NPTX1_HUMAN	8.3	0.5	4.1296	0	4
Myomegalin OS=Homo sapiens GN=PDE4DIP PE=1 SV=1	sp|Q5VU43|MYOME_HUMAN	8.3	0.5	4.1296	0	4
NF-kappa-B essential modulator OS=Homo sapiens GN=IKBKG PE=1 SV=2	sp|Q9Y6K9|NEMO_HUMAN	8.3	0.5	4.1296	0	4
Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2	sp|P35658|NU214_HUMAN	8.3	0.5	4.1296	0	4
Lethal(2) giant larvae protein homolog 1 OS=Homo sapiens GN=LLGL1 PE=1 SV=3	sp|Q15334|L2GL1_HUMAN	8.3	0.5	4.1296	0	4
Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2	sp|Q15436|SC23A_HUMAN	8.3	0.5	4.1296	0	4
Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1	sp|A0AVT1|UBA6_HUMAN	8.3	0.5	4.1296	0	4
Mitochondrial amidoxime-reducing component 1 OS=Homo sapiens GN=MARC1 PE=1 SV=1	sp|Q5VT66|MARC1_HUMAN	8.3	0.5	4.1296	0	4
Lysine-specific demethylase 3B OS=Homo sapiens GN=KDM3B PE=1 SV=2	sp|Q7LBC6|KDM3B_HUMAN	8.3	0.5	4.1296	0	4
Molybdenum cofactor sulfurase OS=Homo sapiens GN=MOCOS PE=1 SV=2	sp|Q96EN8|MOCOS_HUMAN	8.3	0.5	4.1296	0	3
Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2	sp|A1L0T0|ILVBL_HUMAN	8.3	0.5	4.1296	0	4
Regulator of telomere elongation helicase 1 OS=Homo sapiens GN=RTEL1 PE=1 SV=2	sp|Q9NZ71|RTEL1_HUMAN	8.3	0.5	4.1296	0	4
Arachidonate 12-lipoxygenase, 12R-type OS=Homo sapiens GN=ALOX12B PE=1 SV=1	sp|O75342|LX12B_HUMAN	8.3	0.5	4.1296	0	4
IQ motif and SEC7 domain-containing protein 1 OS=Homo sapiens GN=IQSEC1 PE=1 SV=1	sp|Q6DN90|IQEC1_HUMAN	8.3	0.5	4.1296	0	4
Cystatin-SN OS=Homo sapiens GN=CST1 PE=1 SV=3	sp|P01037|CYTN_HUMAN	8.3	0.5	4.1296	0	4
DNA mismatch repair protein Mlh1 OS=Homo sapiens GN=MLH1 PE=1 SV=1	sp|P40692|MLH1_HUMAN	8.3	0.5	4.1296	0	4
Ras-related protein Rab-34 OS=Homo sapiens GN=RAB34 PE=1 SV=1	sp|Q9BZG1|RAB34_HUMAN	8.3	0.5	4.1296	0	4
Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	sp|Q99536|VAT1_HUMAN	8.3	0.5	4.1296	0	4
WD repeat and coiled-coil-containing protein C2orf44 OS=Homo sapiens GN=C2orf44 PE=1 SV=1	sp|Q9H6R7|CB044_HUMAN	8.3	0.5	4.1296	0	3
GPN-loop GTPase 1 OS=Homo sapiens GN=GPN1 PE=1 SV=1	sp|Q9HCN4|GPN1_HUMAN	8.3	0.5	4.1296	0	4
Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3	sp|P52565|GDIR1_HUMAN	8.3	0.5	4.1296	0	4
Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	sp|P56537|IF6_HUMAN	8.3	0.5	4.1296	0	3
Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	sp|P60900|PSA6_HUMAN	8.3	0.5	4.1296	0	4
28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=1 SV=2	sp|P82930|RT34_HUMAN	8.3	0.5	4.1296	0	4
Centrosomal protein of 97 kDa OS=Homo sapiens GN=CEP97 PE=1 SV=1	sp|Q8IW35|CEP97_HUMAN	8.3	0.5	4.1296	0	4
MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1	sp|Q9NX63|MIC19_HUMAN	8.3	0.5	4.1296	0	4
Sialidase-3 OS=Homo sapiens GN=NEU3 PE=1 SV=1	sp|Q9UQ49|NEUR3_HUMAN	8.3	0.5	4.1296	0	4
Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	sp|P32119|PRDX2_HUMAN	8.3	0.5	4.1296	0	2
Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6 PE=1 SV=2	sp|P46379|BAG6_HUMAN	7.3	7.7566	56.782	8	41
Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB	sp|P62714|PP2AB_HUMAN	6.7	2.9087	19.616	2	17
RAF proto-oncogene serine/threonine-protein kinase OS=Homo sapiens GN=RAF1 PE=1 SV=1	sp|P04049|RAF1_HUMAN	6.4	0.96958	6.1944	1	6
Transport and Golgi organization protein 6 homolog OS=Homo sapiens GN=TANGO6 PE=1 SV=2	sp|Q9C0B7|TNG6_HUMAN	6.4	0.96958	6.1944	1	6
Serine/threonine-protein kinase A-Raf OS=Homo sapiens GN=ARAF PE=1 SV=2	sp|P10398|ARAF_HUMAN	6.4	0.96958	6.1944	1	6
Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2	sp|O95486|SC24A_HUMAN	6.4	0.96958	6.1944	1	6
Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	sp|Q01469|FABP5_HUMAN	6.4	0.96958	6.1944	1	4
Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4	sp|Q16777|H2A2C_HUMAN (+1)	6.4	1.9392	12.389	1	5
Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3	sp|P19367|HXK1_HUMAN	6.2	0.5	3.0972	0	3
Schlafen family member 11 OS=Homo sapiens GN=SLFN11 PE=1 SV=2	sp|Q7Z7L1|SLN11_HUMAN	6.2	0.5	3.0972	0	3
Inositol polyphosphate 5-phosphatase OCRL-1 OS=Homo sapiens GN=OCRL PE=1 SV=3	sp|Q01968|OCRL_HUMAN	6.2	0.5	3.0972	0	3
Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4	sp|Q99439|CNN2_HUMAN	6.2	0.5	3.0972	0	2
ATP-dependent 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	sp|P17858|PFKAL_HUMAN	6.2	0.5	3.0972	0	3
Poly [ADP-ribose] polymerase 14 OS=Homo sapiens GN=PARP14 PE=1 SV=3	sp|Q460N5|PAR14_HUMAN	6.2	0.5	3.0972	0	3
Polyribonucleotide nucleotidyltransferase 1, mitochondrial OS=Homo sapiens GN=PNPT1 PE=1 SV=2	sp|Q8TCS8|PNPT1_HUMAN	6.2	0.5	3.0972	0	3
Tuberin OS=Homo sapiens GN=TSC2 PE=1 SV=2	sp|P49815|TSC2_HUMAN	6.2	0.5	3.0972	0	3
Serine/threonine-protein kinase 11-interacting protein OS=Homo sapiens GN=STK11IP PE=1 SV=3	sp|Q8N1F8|S11IP_HUMAN	6.2	0.5	3.0972	0	3
Protein unc-13 homolog B OS=Homo sapiens GN=UNC13B PE=1 SV=2	sp|O14795|UN13B_HUMAN	6.2	0.5	3.0972	0	3
Centrosomal protein of 192 kDa OS=Homo sapiens GN=CEP192 PE=1 SV=2	sp|Q8TEP8|CE192_HUMAN	6.2	0.5	3.0972	0	3
Tensin-1 OS=Homo sapiens GN=TNS1 PE=1 SV=2	sp|Q9HBL0|TENS1_HUMAN	6.2	0.5	3.0972	0	3
Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	sp|Q16555|DPYL2_HUMAN	6.2	0.5	3.0972	0	3
Gigaxonin OS=Homo sapiens GN=GAN PE=1 SV=1	sp|Q9H2C0|GAN_HUMAN	6.2	0.5	3.0972	0	3
Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2	sp|Q9NSE4|SYIM_HUMAN	6.2	0.5	3.0972	0	3
Amidophosphoribosyltransferase OS=Homo sapiens GN=PPAT PE=1 SV=1	sp|Q06203|PUR1_HUMAN	6.2	0.5	3.0972	0	3
NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2	sp|Q96RS6|NUDC1_HUMAN	6.2	0.5	3.0972	0	3
HEAT repeat-containing protein 6 OS=Homo sapiens GN=HEATR6 PE=1 SV=1	sp|Q6AI08|HEAT6_HUMAN	6.2	0.5	3.0972	0	3
WD repeat-containing protein 91 OS=Homo sapiens GN=WDR91 PE=1 SV=2	sp|A4D1P6|WDR91_HUMAN	6.2	0.5	3.0972	0	2
Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	sp|P04632|CPNS1_HUMAN	6.2	0.5	3.0972	0	3
Cystatin-S OS=Homo sapiens GN=CST4 PE=1 SV=3	sp|P01036|CYTS_HUMAN	6.2	0.5	3.0972	0	3
L-fucose kinase OS=Homo sapiens GN=FUK PE=2 SV=2	sp|Q8N0W3|FUK_HUMAN	6.2	0.5	3.0972	0	3
Protein NipSnap homolog 2 OS=Homo sapiens GN=GBAS PE=1 SV=1	sp|O75323|NIPS2_HUMAN	6.2	0.5	3.0972	0	3
Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	sp|Q9Y4K0|LOXL2_HUMAN	6.2	0.5	3.0972	0	3
MICOS complex subunit MIC27 OS=Homo sapiens GN=APOOL PE=1 SV=1	sp|Q6UXV4|MIC27_HUMAN	6.2	0.5	3.0972	0	3
CREB-regulated transcription coactivator 3 OS=Homo sapiens GN=CRTC3 PE=1 SV=2	sp|Q6UUV7|CRTC3_HUMAN	6.2	0.5	3.0972	0	3
Nuclear receptor-binding protein OS=Homo sapiens GN=NRBP1 PE=1 SV=1	sp|Q9UHY1|NRBP_HUMAN	6.2	0.5	3.0972	0	3
2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3	sp|Q9Y6K5|OAS3_HUMAN	6.2	0.5	3.0972	0	3
ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	sp|P08237|PFKAM_HUMAN	6.2	0.5	3.0972	0	3
Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	sp|Q9BR76|COR1B_HUMAN	6.2	0.5	3.0972	0	3
Dystrophia myotonica WD repeat-containing protein OS=Homo sapiens GN=DMWD PE=1 SV=3	sp|Q09019|DMWD_HUMAN	6.2	0.5	3.0972	0	3
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=	sp|P21912|SDHB_HUMAN	6.2	0.5	3.0972	0	3
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 4, mitochondrial OS=Homo sapiens GN=PDK	sp|Q16654|PDK4_HUMAN	6.2	0.5	3.0972	0	3
Kynureninase OS=Homo sapiens GN=KYNU PE=1 SV=1	sp|Q16719|KYNU_HUMAN	6.2	0.5	3.0972	0	3
Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2	sp|Q8NF37|PCAT1_HUMAN	6.2	0.5	3.0972	0	2
Protein SCO1 homolog, mitochondrial OS=Homo sapiens GN=SCO1 PE=1 SV=1	sp|O75880|SCO1_HUMAN	6.2	0.5	3.0972	0	3
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	sp|P62081|RS7_HUMAN	6.2	0.5	3.0972	0	3
Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 PE=1 SV=3	sp|Q86X55|CARM1_HUMAN	6.2	0.5	3.0972	0	3
Zinc finger HIT domain-containing protein 2 OS=Homo sapiens GN=ZNHIT2 PE=1 SV=1	sp|Q9UHR6|ZNHI2_HUMAN	6.2	0.5	3.0972	0	3
Testisin OS=Homo sapiens GN=PRSS21 PE=1 SV=1	sp|Q9Y6M0|TEST_HUMAN	6.2	0.5	3.0972	0	3
(Reversed) Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE	Reversed_sp|P16219|ACADS_HUMAN	6.2	0.5	3.0972	0	2
Acyl-coenzyme A thioesterase 8 OS=Homo sapiens GN=ACOT8 PE=1 SV=1	sp|O14734|ACOT8_HUMAN	6.2	0.5	3.0972	0	3
Centrosomal protein of 44 kDa OS=Homo sapiens GN=CEP44 PE=1 SV=2	sp|Q9C0F1|CEP44_HUMAN	6.2	0.5	3.0972	0	3
Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2	sp|Q92542|NICA_HUMAN	6.2	0.5	3.0972	0	3
C-terminal-binding protein 1 OS=Homo sapiens GN=CTBP1 PE=1 SV=2	sp|Q13363|CTBP1_HUMAN	6.2	0.5	3.0972	0	3
Serine/threonine-protein phosphatase CPPED1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3	sp|Q9BRF8|CPPED_HUMAN	6.2	0.5	3.0972	0	2
FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=1 SV=2	sp|Q96CU9|FXRD1_HUMAN	6.2	0.5	3.0972	0	3
Uncharacterized protein C19orf52 OS=Homo sapiens GN=C19orf52 PE=1 SV=2	sp|Q9BSF4|CS052_HUMAN	6.2	0.5	3.0972	0	3
Putative tRNA (cytidine(32)/guanosine(34)-2'-O)-methyltransferase OS=Homo sapiens GN=FTSJ1 PE=1 SV=	sp|Q9UET6|TRM7_HUMAN	6.2	0.5	3.0972	0	3
Glutamate-rich WD repeat-containing protein 1 OS=Homo sapiens GN=GRWD1 PE=1 SV=1	sp|Q9BQ67|GRWD1_HUMAN	6.2	0.5	3.0972	0	3
EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2	sp|Q9H4M9|EHD1_HUMAN	6.2	0.5	3.0972	0	3
Nuclear pore glycoprotein p62 OS=Homo sapiens GN=NUP62 PE=1 SV=3	sp|P37198|NUP62_HUMAN	6.2	0.5	3.0972	0	2
Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	sp|P34932|HSP74_HUMAN	5.8	31.996	186.86	26	100
Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3	sp|O95757|HS74L_HUMAN	5.5	19.392	107.37	17	65
Mitotic interactor and substrate of PLK1 OS=Homo sapiens GN=MISP PE=1 SV=1	sp|Q8IVT2|MISP_HUMAN	5.3	2.9087	15.486	3	13
Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	sp|P31151|S10A7_HUMAN	5.3	2.9087	15.486	2	8
Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L PE=1 SV=2	sp|Q9Y4W2|LAS1L_HUMAN	5.3	0.96958	5.162	1	5
WD repeat-containing protein 81 OS=Homo sapiens GN=WDR81 PE=1 SV=2	sp|Q562E7|WDR81_HUMAN	5.3	0.96958	5.162	1	5
CDK5 regulatory subunit-associated protein 2 OS=Homo sapiens GN=CDK5RAP2 PE=1 SV=5	sp|Q96SN8|CK5P2_HUMAN	5.3	0.96958	5.162	1	5
Armadillo repeat-containing protein 6 OS=Homo sapiens GN=ARMC6 PE=1 SV=2	sp|Q6NXE6|ARMC6_HUMAN	5.3	0.96958	5.162	1	4
Signal transducer and activator of transcription 5B OS=Homo sapiens GN=STAT5B PE=1 SV=2	sp|P51692|STA5B_HUMAN	5.3	0.96958	5.162	1	4
Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens GN=RRM2 PE=1 SV=1	sp|P31350|RIR2_HUMAN	5.3	0.96958	5.162	1	5
NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=	sp|O75306|NDUS2_HUMAN	5.3	0.96958	5.162	1	5
Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2 PE=1 SV=3	sp|O43488|ARK72_HUMAN	5.3	0.96958	5.162	1	4
Aurora kinase B OS=Homo sapiens GN=AURKB PE=1 SV=3	sp|Q96GD4|AURKB_HUMAN	5.3	0.96958	5.162	1	4
Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2	sp|Q9Y5P6|GMPPB_HUMAN	5.3	0.96958	5.162	1	5
Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1	sp|P15927|RFA2_HUMAN	5.3	0.96958	5.162	1	3
DmX-like protein 1 OS=Homo sapiens GN=DMXL1 PE=1 SV=3	sp|Q9Y485|DMXL1_HUMAN	5.3	1.9392	10.324	2	10
LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1	sp|Q9NS86|LANC2_HUMAN	5.3	1.9392	10.324	2	9

Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	sp|Q13162|PRDX4_HUMAN	5.3	1.9392	10.324	1	6
Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	sp|P29508|SPB3_HUMAN	4.9	4.8479	23.745	3	14
Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=4	sp|P50851|LRBA_HUMAN	4.8	1.9392	9.2916	2	9
Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=1 SV=4	sp|P22735|TGM1_HUMAN	4.8	1.9392	9.2916	2	9
ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2	sp|O43681|ASNA_HUMAN	4.8	1.9392	9.2916	2	9
Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=1 SV=2	sp|O75153|CLU_HUMAN	4.6	8.7262	40.263	9	36
Cell division cycle protein 123 homolog OS=Homo sapiens GN=CDC123 PE=1 SV=1	sp|O75794|CD123_HUMAN	4.3	2.9087	12.389	3	12
Breast cancer type 1 susceptibility protein OS=Homo sapiens GN=BRCA1 PE=1 SV=2	sp|P38398|BRCA1_HUMAN	4.3	0.96958	4.1296	1	2
Insulin-like growth factor 1 receptor OS=Homo sapiens GN=IGF1R PE=1 SV=1	sp|P08069|IGF1R_HUMAN	4.3	0.96958	4.1296	1	3
Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D PE=	sp|Q13557|KCC2D_HUMAN	4.3	0.96958	4.1296	1	4
Protein arginine N-methyltransferase 7 OS=Homo sapiens GN=PRMT7 PE=1 SV=1	sp|Q9NVM4|ANM7_HUMAN	4.3	0.96958	4.1296	1	4
Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens GN=HERC4 PE=1 SV=1	sp|Q5GLZ8|HERC4_HUMAN	4.3	0.96958	4.1296	1	4
Vacuolar protein sorting-associated protein 11 homolog OS=Homo sapiens GN=VPS11 PE=1 SV=1	sp|Q9H270|VPS11_HUMAN	4.3	0.96958	4.1296	1	4
NAD kinase 2, mitochondrial OS=Homo sapiens GN=NADK2 PE=1 SV=2	sp|Q4G0N4|NAKD2_HUMAN	4.3	0.96958	4.1296	1	4
Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	sp|O75874|IDHC_HUMAN	4.3	0.96958	4.1296	1	4
DDB1- and CUL4-associated factor 7 OS=Homo sapiens GN=DCAF7 PE=1 SV=1	sp|P61962|DCAF7_HUMAN	4.3	0.96958	4.1296	1	4
Ankycorbin OS=Homo sapiens GN=RAI14 PE=1 SV=2	sp|Q9P0K7|RAI14_HUMAN	4.3	0.96958	4.1296	1	4
WD repeat-containing protein 61 OS=Homo sapiens GN=WDR61 PE=1 SV=1	sp|Q9GZS3|WDR61_HUMAN	4.3	0.96958	4.1296	1	4
Bromodomain-containing protein 2 OS=Homo sapiens GN=BRD2 PE=1 SV=2	sp|P25440|BRD2_HUMAN	4.3	0.96958	4.1296	1	4
N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4	sp|Q9UJ70|NAGK_HUMAN	4.3	0.96958	4.1296	1	4
39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1	sp|P09001|RM03_HUMAN	4.3	0.96958	4.1296	1	2
2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial OS=Homo sapiens GN=GCAT PE=1 SV=1	sp|O75600|KBL_HUMAN	4.3	0.96958	4.1296	1	4
Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2	sp|Q969V3|NCLN_HUMAN	4.3	0.96958	4.1296	1	4
Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	sp|P35613|BASI_HUMAN	4.3	0.96958	4.1296	1	2
Suprabasin OS=Homo sapiens GN=SBSN PE=1 SV=2	sp|Q6UWP8|SBSN_HUMAN	4.3	0.96958	4.1296	1	3
Ancient ubiquitous protein 1 OS=Homo sapiens GN=AUP1 PE=1 SV=1	sp|Q9Y679|AUP1_HUMAN	4.3	0.96958	4.1296	1	4
Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2	sp|Q8IXI1|MIRO2_HUMAN	4.3	0.96958	4.1296	1	4
WD repeat-containing protein 6 OS=Homo sapiens GN=WDR6 PE=1 SV=1	sp|Q9NNW5|WDR6_HUMAN	4.3	3.8783	16.518	4	14
Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1	sp|P57740|NU107_HUMAN	4.3	1.9392	8.2592	2	8
Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens GN=EML4 PE=1 SV=3	sp|Q9HC35|EMAL4_HUMAN	4.3	1.9392	8.2592	2	8
Low-density lipoprotein receptor-related protein 2 OS=Homo sapiens GN=LRP2 PE=1 SV=3	sp|P98164|LRP2_HUMAN	4.1	0.5	2.0648	0	2
Dedicator of cytokinesis protein 8 OS=Homo sapiens GN=DOCK8 PE=1 SV=3	sp|Q8NF50|DOCK8_HUMAN	4.1	0.5	2.0648	0	2
(Reversed) Transforming acidic coiled-coil-containing protein 2 OS=Homo sapiens GN=TACC2 PE=1 SV=3	Reversed_sp|O95359|TACC2_HUMAN	4.1	0.5	2.0648	0	2
Protocadherin Fat 4 OS=Homo sapiens GN=FAT4 PE=1 SV=2	sp|Q6V0I7|FAT4_HUMAN	4.1	0.5	2.0648	0	2
Serine/threonine-protein kinase SIK3 OS=Homo sapiens GN=SIK3 PE=1 SV=3	sp|Q9Y2K2|SIK3_HUMAN	4.1	0.5	2.0648	0	2
Serine/threonine-protein kinase SIK2 OS=Homo sapiens GN=SIK2 PE=1 SV=1	sp|Q9H0K1|SIK2_HUMAN	4.1	0.5	2.0648	0	2
BAH and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=BAHCC1 PE=1 SV=3	sp|Q9P281|BAHC1_HUMAN	4.1	0.5	2.0648	0	2
Protein PRR14L OS=Homo sapiens GN=PRR14L PE=1 SV=1	sp|Q5THK1|PR14L_HUMAN	4.1	0.5	2.0648	0	2
Ubiquitin carboxyl-terminal hydrolase 19 OS=Homo sapiens GN=USP19 PE=1 SV=2	sp|O94966|UBP19_HUMAN	4.1	0.5	2.0648	0	2
Tyrosine-protein phosphatase non-receptor type 23 OS=Homo sapiens GN=PTPN23 PE=1 SV=1	sp|Q9H3S7|PTN23_HUMAN	4.1	0.5	2.0648	0	2
Mitogen-activated protein kinase 14 OS=Homo sapiens GN=MAPK14 PE=1 SV=3	sp|Q16539|MK14_HUMAN	4.1	0.5	2.0648	0	2
Tyrosine-protein kinase SgK223 OS=Homo sapiens GN=SGK223 PE=1 SV=4	sp|Q86YV5|SG223_HUMAN	4.1	0.5	2.0648	0	2
Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4	sp|Q8NCM8|DYHC2_HUMAN	4.1	0.5	2.0648	0	2
Rapamycin-insensitive companion of mTOR OS=Homo sapiens GN=RICTOR PE=1 SV=1	sp|Q6R327|RICTR_HUMAN	4.1	0.5	2.0648	0	2
Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4	sp|O60437|PEPL_HUMAN	4.1	0.5	2.0648	0	2
Mitotic checkpoint serine/threonine-protein kinase BUB1 OS=Homo sapiens GN=BUB1 PE=1 SV=1	sp|O43683|BUB1_HUMAN	4.1	0.5	2.0648	0	2
Intraflagellar transport protein 122 homolog OS=Homo sapiens GN=IFT122 PE=1 SV=2	sp|Q9HBG6|IF122_HUMAN	4.1	0.5	2.0648	0	2
Protocadherin-23 OS=Homo sapiens GN=DCHS2 PE=2 SV=1	sp|Q6V1P9|PCD23_HUMAN	4.1	0.5	2.0648	0	2
Putative ATP-dependent RNA helicase TDRD9 OS=Homo sapiens GN=TDRD9 PE=2 SV=3	sp|Q8NDG6|TDRD9_HUMAN	4.1	0.5	2.0648	0	2
Germinal-center associated nuclear protein OS=Homo sapiens GN=MCM3AP PE=1 SV=2	sp|O60318|GANP_HUMAN	4.1	0.5	2.0648	0	2
Synemin OS=Homo sapiens GN=SYNM PE=1 SV=2	sp|O15061|SYNEM_HUMAN	4.1	0.5	2.0648	0	2
Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	sp|P21266|GSTM3_HUMAN	4.1	0.5	2.0648	0	2
Insulin receptor substrate 2 OS=Homo sapiens GN=IRS2 PE=1 SV=2	sp|Q9Y4H2|IRS2_HUMAN	4.1	0.5	2.0648	0	2
Epidermal growth factor receptor substrate 15 OS=Homo sapiens GN=EPS15 PE=1 SV=2	sp|P42566|EPS15_HUMAN	4.1	0.5	2.0648	0	2
Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2	sp|Q66K74|MAP1S_HUMAN	4.1	0.5	2.0648	0	2
Fibronectin type III domain-containing protein 3B OS=Homo sapiens GN=FNDC3B PE=1 SV=2	sp|Q53EP0|FND3B_HUMAN	4.1	0.5	2.0648	0	2
Fibronectin type-III domain-containing protein 3A OS=Homo sapiens GN=FNDC3A PE=1 SV=4	sp|Q9Y2H6|FND3A_HUMAN	4.1	0.5	2.0648	0	2
Probable ATP-dependent RNA helicase DHX34 OS=Homo sapiens GN=DHX34 PE=1 SV=2	sp|Q14147|DHX34_HUMAN	4.1	0.5	2.0648	0	2
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Homo sapiens GN=PLCG1 PE=1	sp|P19174|PLCG1_HUMAN	4.1	0.5	2.0648	0	2
Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit beta OS=Homo sapiens GN=PIK3	sp|O00750|P3C2B_HUMAN	4.1	0.5	2.0648	0	2
Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	sp|P23142|FBLN1_HUMAN	4.1	0.5	2.0648	0	2
Rho guanine nucleotide exchange factor 1 OS=Homo sapiens GN=ARHGEF1 PE=1 SV=2	sp|Q92888|ARHG1_HUMAN	4.1	0.5	2.0648	0	2
Serine/threonine-protein kinase greatwall OS=Homo sapiens GN=MASTL PE=1 SV=1	sp|Q96GX5|GWL_HUMAN	4.1	0.5	2.0648	0	2
Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1	sp|Q9UN37|VPS4A_HUMAN	4.1	0.5	2.0648	0	2
WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	sp|O75083|WDR1_HUMAN	4.1	0.5	2.0648	0	2
COBW domain-containing protein 6 OS=Homo sapiens GN=CBWD6 PE=3 SV=1	sp|Q4V339|CBWD6_HUMAN (+2)	4.1	0.5	2.0648	0	2
Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=2	sp|P46736|BRCC3_HUMAN	4.1	0.5	2.0648	0	2
Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4	sp|Q00796|DHSO_HUMAN	4.1	0.5	2.0648	0	2
Cyclic AMP-dependent transcription factor ATF-6 beta OS=Homo sapiens GN=ATF6B PE=1 SV=2	sp|Q99941|ATF6B_HUMAN	4.1	0.5	2.0648	0	2
Cysteine desulfurase, mitochondrial OS=Homo sapiens GN=NFS1 PE=1 SV=3	sp|Q9Y697|NFS1_HUMAN	4.1	0.5	2.0648	0	2
Serine/threonine-protein kinase MRCK alpha OS=Homo sapiens GN=CDC42BPA PE=1 SV=1	sp|Q5VT25|MRCKA_HUMAN	4.1	0.5	2.0648	0	2
Protein CIP2A OS=Homo sapiens GN=KIAA1524 PE=1 SV=2	sp|Q8TCG1|CIP2A_HUMAN	4.1	0.5	2.0648	0	2
Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens GN=ELAC2 PE=1 SV=2	sp|Q9BQ52|RNZ2_HUMAN	4.1	0.5	2.0648	0	2
Leucine-rich repeat-containing protein 1 OS=Homo sapiens GN=LRRC1 PE=1 SV=1	sp|Q9BTT6|LRRC1_HUMAN	4.1	0.5	2.0648	0	2
CTTNBP2 N-terminal-like protein OS=Homo sapiens GN=CTTNBP2NL PE=1 SV=2	sp|Q9P2B4|CT2NL_HUMAN	4.1	0.5	2.0648	0	2
Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	sp|Q15437|SC23B_HUMAN	4.1	0.5	2.0648	0	2
RCC1 domain-containing protein 1 OS=Homo sapiens GN=RCCD1 PE=1 SV=1	sp|A6NED2|RCCD1_HUMAN	4.1	0.5	2.0648	0	2
Dihydropyrimidinase-related protein 4 OS=Homo sapiens GN=DPYSL4 PE=1 SV=2	sp|O14531|DPYL4_HUMAN	4.1	0.5	2.0648	0	2
Aryl hydrocarbon receptor OS=Homo sapiens GN=AHR PE=1 SV=2	sp|P35869|AHR_HUMAN	4.1	0.5	2.0648	0	2
E3 ubiquitin-protein ligase TRAF7 OS=Homo sapiens GN=TRAF7 PE=1 SV=1	sp|Q6Q0C0|TRAF7_HUMAN	4.1	0.5	2.0648	0	2
Methyltransferase-like protein 13 OS=Homo sapiens GN=METTL13 PE=1 SV=1	sp|Q8N6R0|MET13_HUMAN	4.1	0.5	2.0648	0	2
Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=	sp|P11166|GTR1_HUMAN	4.1	0.5	2.0648	0	2
Serine/threonine-protein kinase D3 OS=Homo sapiens GN=PRKD3 PE=1 SV=1	sp|O94806|KPCD3_HUMAN	4.1	0.5	2.0648	0	2
3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2	sp|P09110|THIK_HUMAN	4.1	0.5	2.0648	0	2
F-box only protein 3 OS=Homo sapiens GN=FBXO3 PE=1 SV=3	sp|Q9UK99|FBX3_HUMAN	4.1	0.5	2.0648	0	2
Ribonuclease H2 subunit A OS=Homo sapiens GN=RNASEH2A PE=1 SV=2	sp|O75792|RNH2A_HUMAN	4.1	0.5	2.0648	0	2
Ribosomal RNA small subunit methyltransferase NEP1 OS=Homo sapiens GN=EMG1 PE=1 SV=4	sp|Q92979|NEP1_HUMAN	4.1	0.5	2.0648	0	2
Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3	sp|P49023|PAXI_HUMAN	4.1	0.5	2.0648	0	2
Interleukin-1 receptor-associated kinase 1 OS=Homo sapiens GN=IRAK1 PE=1 SV=2	sp|P51617|IRAK1_HUMAN	4.1	0.5	2.0648	0	2
UPF0428 protein CXorf56 OS=Homo sapiens GN=CXorf56 PE=1 SV=1	sp|Q9H5V9|CX056_HUMAN	4.1	0.5	2.0648	0	2
Nucleoporin SEH1 OS=Homo sapiens GN=SEH1L PE=1 SV=3	sp|Q96EE3|SEH1_HUMAN	4.1	0.5	2.0648	0	2
Proteasomal ATPase-associated factor 1 OS=Homo sapiens GN=PAAF1 PE=1 SV=2	sp|Q9BRP4|PAAF1_HUMAN	4.1	0.5	2.0648	0	2
F-box only protein 6 OS=Homo sapiens GN=FBXO6 PE=1 SV=1	sp|Q9NRD1|FBX6_HUMAN	4.1	0.5	2.0648	0	2
Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1	sp|P27707|DCK_HUMAN	4.1	0.5	2.0648	0	2
Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2	sp|P48739|PIPNB_HUMAN	4.1	0.5	2.0648	0	2
Probable E3 ubiquitin-protein ligase TRIML2 OS=Homo sapiens GN=TRIML2 PE=2 SV=1	sp|Q8N7C3|TRIMM_HUMAN	4.1	0.5	2.0648	0	2
Chromosome transmission fidelity protein 18 homolog OS=Homo sapiens GN=CHTF18 PE=1 SV=1	sp|Q8WVB6|CTF18_HUMAN	4.1	0.5	2.0648	0	2
Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1	sp|Q96AY3|FKB10_HUMAN	4.1	0.5	2.0648	0	2
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	sp|P62826|RAN_HUMAN	4.1	0.5	2.0648	0	2
RNA-binding protein with multiple splicing OS=Homo sapiens GN=RBPMS PE=1 SV=1	sp|Q93062|RBPMS_HUMAN	4.1	0.5	2.0648	0	2
Protein angel homolog 1 OS=Homo sapiens GN=ANGEL1 PE=2 SV=1	sp|Q9UNK9|ANGE1_HUMAN	4.1	0.5	2.0648	0	2
Inositol polyphosphate 5-phosphatase K OS=Homo sapiens GN=INPP5K PE=1 SV=3	sp|Q9BT40|INP5K_HUMAN	4.1	0.5	2.0648	0	2
3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3	sp|P25325|THTM_HUMAN	4.1	0.5	2.0648	0	2
Enhancer of mRNA-decapping protein 3 OS=Homo sapiens GN=EDC3 PE=1 SV=1	sp|Q96F86|EDC3_HUMAN	4.1	0.5	2.0648	0	2
BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1	sp|Q96CX2|KCD12_HUMAN	4.1	0.5	2.0648	0	2

Mitochondrial ribosome-associated GTPase 2 OS=Homo sapiens GN=MTG2 PE=1 SV=1	sp|Q9H4K7|MTG2_HUMAN	4.1	0.5	2.0648	0	2
Autophagy-related protein 9A OS=Homo sapiens GN=ATG9A PE=1 SV=3	sp|Q7Z3C6|ATG9A_HUMAN	4.1	0.5	2.0648	0	2
Vitamin K-dependent gamma-carboxylase OS=Homo sapiens GN=GGCX PE=1 SV=2	sp|P38435|VKGC_HUMAN	4.1	0.5	2.0648	0	2
Spartin OS=Homo sapiens GN=SPG20 PE=1 SV=1	sp|Q8N0X7|SPG20_HUMAN	4.1	0.5	2.0648	0	2
Maspardin OS=Homo sapiens GN=SPG21 PE=1 SV=1	sp|Q9NZD8|SPG21_HUMAN	4.1	0.5	2.0648	0	2
Glutamine-rich protein 1 OS=Homo sapiens GN=QRICH1 PE=1 SV=1	sp|Q2TAL8|QRIC1_HUMAN	4.1	0.5	2.0648	0	2
Arfaptin-2 OS=Homo sapiens GN=ARFIP2 PE=1 SV=1	sp|P53365|ARFP2_HUMAN	4.1	0.5	2.0648	0	2
Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1	sp|O75934|SPF27_HUMAN	4.1	0.5	2.0648	0	2
Cyclin-dependent kinase 7 OS=Homo sapiens GN=CDK7 PE=1 SV=1	sp|P50613|CDK7_HUMAN	4.1	0.5	2.0648	0	2
60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	sp|P62913|RL11_HUMAN	4.1	0.5	2.0648	0	2
Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	sp|P00966|ASSY_HUMAN	4.1	0.5	2.0648	0	2
YEATS domain-containing protein 4 OS=Homo sapiens GN=YEATS4 PE=1 SV=1	sp|O95619|YETS4_HUMAN	4.1	0.5	2.0648	0	2
Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	sp|P29966|MARCS_HUMAN	4.1	0.5	2.0648	0	2
40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	sp|P08708|RS17_HUMAN	4.1	0.5	2.0648	0	2
Protein S100-A16 OS=Homo sapiens GN=S100A16 PE=1 SV=1	sp|Q96FQ6|S10AG_HUMAN	4.1	0.5	2.0648	0	2
Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	sp|P30048|PRDX3_HUMAN	4.1	0.5	2.0648	0	2
Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	sp|P49721|PSB2_HUMAN	4.1	0.5	2.0648	0	2
Queuine tRNA-ribosyltransferase subunit QTRTD1 OS=Homo sapiens GN=QTRTD1 PE=1 SV=1	sp|Q9H974|QTRD1_HUMAN	4.1	0.5	2.0648	0	2
Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1	sp|P40261|NNMT_HUMAN	4.1	0.5	2.0648		
Protein S100-A14 OS=Homo sapiens GN=S100A14 PE=1 SV=1	sp|Q9HCY8|S10AE_HUMAN	4.1	0.5	2.0648		
TRPM8 channel-associated factor 1 OS=Homo sapiens GN=TCAF1 PE=1 SV=3	sp|Q9Y4C2|TCAF1_HUMAN	4.0	4.8479	19.616	5	19
Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens GN=BIRC6 PE=1 SV=2	sp|Q9NR09|BIRC6_HUMAN	4.0	7.7566	30.972	7	26
Hsp70-binding protein 1 OS=Homo sapiens GN=HSPBP1 PE=1 SV=1	sp|Q9NZL4|HPBP1_HUMAN	3.9	5.8175	22.713	5	16
SH3 domain-binding protein 4 OS=Homo sapiens GN=SH3BP4 PE=1 SV=1	sp|Q9P0V3|SH3B4_HUMAN	3.9	2.9087	11.356	3	10
(CONTAMINANT) Ig gamma (C)	CONTAM_AAA31289.1	3.9	7.7566	29.939	2	3
Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	sp|Q08188|TGM3_HUMAN	3.8	4.8479	18.583	4	14
Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	sp|P12273|PIP_HUMAN	3.8	6.787	25.81	5	9
Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	sp|P04350|TBB4A_HUMAN	3.8	42.661	162.09	22	53
Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	sp|Q13509|TBB3_HUMAN	3.8	28.118	106.34	14	39
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE	sp|P31040|SDHA_HUMAN	3.7	3.8783	14.454	4	11
Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2	sp|Q14126|DSG2_HUMAN	3.7	1.9392	7.2268	2	6
Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2	sp|Q12965|MYO1E_HUMAN	3.7	1.9392	7.2268	2	7
Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	sp|P31944|CASPE_HUMAN	3.7	1.9392	7.2268	2	5
Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=GCDH PE=1 SV=1	sp|Q92947|GCDH_HUMAN	3.7	1.9392	7.2268	2	6
Chitobiosyldiphosphodolichol beta-mannosyltransferase OS=Homo sapiens GN=ALG1 PE=1 SV=2	sp|Q9BT22|ALG1_HUMAN	3.7	1.9392	7.2268	2	7
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	sp|P62851|RS25_HUMAN	3.7	1.9392	7.2268	2	4
45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1	sp|Q9BRK5|CAB45_HUMAN	3.7	1.9392	7.2268	2	7
Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	sp|Q13885|TBB2A_HUMAN	3.7	44.6	165.18	19	54
Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	sp|Q9BUF5|TBB6_HUMAN	3.7	24.239	88.786	12	37
Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1	sp|Q7KZF4|SND1_HUMAN	3.7	6.787	24.778	7	20
Retrotransposon-derived protein PEG10 OS=Homo sapiens GN=PEG10 PE=1 SV=2	sp|Q86TG7|PEG10_HUMAN	3.7	13.574	49.555	13	32
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	sp|P68371|TBB4B_HUMAN	3.6	52.357	190.99	24	61
MOB kinase activator 2 OS=Homo sapiens GN=MOB2 PE=1 SV=1	sp|Q70IA6|MOB2_HUMAN	3.5	2.9087	10.324	3	9
Peroxisome biogenesis factor 1 OS=Homo sapiens GN=PEX1 PE=1 SV=1	sp|O43933|PEX1_HUMAN	3.5	2.9087	10.324	3	10
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	sp|P10809|CH60_HUMAN	3.5	91.14	322.11	58	119
Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	sp|Q06323|PSME1_HUMAN	3.5	3.8783	13.421	4	10
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	sp|P62249|RS16_HUMAN	3.5	3.8783	13.421	2	5
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	sp|P07437|TBB5_HUMAN	3.4	56.235	193.06	26	61
ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1	sp|P61221|ABCE1_HUMAN	3.4	5.8175	19.616	6	17
Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	sp|P68431|H31_HUMAN (+3)	3.4	5.8175	19.616	3	5
Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4	sp|O15067|PUR4_HUMAN	3.3	7.7566	25.81	8	24
Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	sp|P05109|S10A8_HUMAN	3.3	7.7566	25.81	5	10
Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2	sp|P46734|MP2K3_HUMAN	3.3	8.7262	28.907	8	17
Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	sp|P06702|S10A9_HUMAN	3.3	8.7262	28.907	5	10
Mitochondrial glutamate carrier 1 OS=Homo sapiens GN=SLC25A22 PE=1 SV=1	sp|Q9H936|GHC1_HUMAN	3.2	3.8783	12.389	4	10
HCLS1-associated protein X-1 OS=Homo sapiens GN=HAX1 PE=1 SV=2	sp|O00165|HAX1_HUMAN	3.2	2.9087	9.2916	3	7
Tetratricopeptide repeat protein 37 OS=Homo sapiens GN=TTC37 PE=1 SV=1	sp|Q6PGP7|TTC37_HUMAN	3.2	2.9087	9.2916	3	9
Inositol-3-phosphate synthase 1 OS=Homo sapiens GN=ISYNA1 PE=1 SV=1	sp|Q9NPH2|INO1_HUMAN	3.2	2.9087	9.2916	2	8
Nodal modulator 1 OS=Homo sapiens GN=NOMO1 PE=1 SV=5	sp|Q15155|NOMO1_HUMAN	3.2	2.9087	9.2916	3	9
Chromosome-associated kinesin KIF4A OS=Homo sapiens GN=KIF4A PE=1 SV=3	sp|O95239|KIF4A_HUMAN	3.2	0.96958	3.0972	1	3
Serine/threonine-protein kinase Nek7 OS=Homo sapiens GN=NEK7 PE=1 SV=1	sp|Q8TDX7|NEK7_HUMAN	3.2	0.96958	3.0972	1	3
Ubiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens GN=USP47 PE=1 SV=3	sp|Q96K76|UBP47_HUMAN	3.2	0.96958	3.0972	1	3
Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	sp|Q29RF7|PDS5A_HUMAN	3.2	0.96958	3.0972	1	3
WASH complex subunit strumpellin OS=Homo sapiens GN=KIAA0196 PE=1 SV=1	sp|Q12768|STRUM_HUMAN	3.2	0.96958	3.0972	1	3
39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=1 SV=2	sp|Q9BRJ2|RM45_HUMAN	3.2	0.96958	3.0972	1	3
Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	sp|Q13867|BLMH_HUMAN	3.2	0.96958	3.0972	1	2
Next to BRCA1 gene 1 protein OS=Homo sapiens GN=NBR1 PE=1 SV=3	sp|Q14596|NBR1_HUMAN	3.2	0.96958	3.0972	1	3
Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 OS=Homo sapiens GN=CMTR1 PE=1 SV=1	sp|Q8N1G2|CMTR1_HUMAN	3.2	0.96958	3.0972	1	3
Rhophilin-2 OS=Homo sapiens GN=RHPN2 PE=1 SV=1	sp|Q8IUC4|RHPN2_HUMAN	3.2	0.96958	3.0972	1	3
COBW domain-containing protein 2 OS=Homo sapiens GN=CBWD2 PE=1 SV=1	sp|Q8IUF1|CBWD2_HUMAN	3.2	0.96958	3.0972	1	3
DTW domain-containing protein 2 OS=Homo sapiens GN=DTWD2 PE=1 SV=1	sp|Q8NBA8|DTWD2_HUMAN	3.2	0.96958	3.0972	1	3
Phosphorylase b kinase gamma catalytic chain, liver/testis isoform OS=Homo sapiens GN=PHKG2 PE=1 S	sp|P15735|PHKG2_HUMAN	3.2	0.96958	3.0972	1	3
Rac GTPase-activating protein 1 OS=Homo sapiens GN=RACGAP1 PE=1 SV=1	sp|Q9H0H5|RGAP1_HUMAN	3.2	0.96958	3.0972	1	3
Vacuolar protein sorting-associated protein 18 homolog OS=Homo sapiens GN=VPS18 PE=1 SV=2	sp|Q9P253|VPS18_HUMAN	3.2	0.96958	3.0972	1	3
Pleckstrin homology domain-containing family A member 2 OS=Homo sapiens GN=PLEKHA2 PE=1 SV=2	sp|Q9HB19|PKHA2_HUMAN	3.2	0.96958	3.0972	1	3
FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1	sp|Q08945|SSRP1_HUMAN	3.2	0.96958	3.0972	1	3
Peptidyl-prolyl cis-trans isomerase-like 4 OS=Homo sapiens GN=PPIL4 PE=1 SV=1	sp|Q8WUA2|PPIL4_HUMAN	3.2	0.96958	3.0972	1	3
L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase OS=Homo sapiens GN=AAS	sp|Q9NRN7|ADPPT_HUMAN	3.2	0.96958	3.0972	1	3
Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2	sp|P13674|P4HA1_HUMAN	3.2	0.96958	3.0972	1	3
Reticulocalbin-3 OS=Homo sapiens GN=RCN3 PE=1 SV=1	sp|Q96D15|RCN3_HUMAN	3.2	0.96958	3.0972	1	3
Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4	sp|P08243|ASNS_HUMAN	3.2	0.96958	3.0972	1	3
Probable tRNA pseudouridine synthase 2 OS=Homo sapiens GN=TRUB2 PE=1 SV=1	sp|O95900|TRUB2_HUMAN	3.2	0.96958	3.0972	1	3
Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3	sp|P49959|MRE11_HUMAN	3.2	0.96958	3.0972	1	3
Actin-related protein 10 OS=Homo sapiens GN=ACTR10 PE=1 SV=1	sp|Q9NZ32|ARP10_HUMAN	3.2	0.96958	3.0972	1	3
Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1	sp|Q96DG6|CMBL_HUMAN	3.2	0.96958	3.0972	1	2
Cleavage stimulation factor subunit 1 OS=Homo sapiens GN=CSTF1 PE=1 SV=1	sp|Q05048|CSTF1_HUMAN	3.2	6.787	21.68	6	14
Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2	sp|Q9NQW6|ANLN_HUMAN	3.2	1.9392	6.1944	2	6
Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2	sp|Q9BTE3|MCMBP_HUMAN	3.2	1.9392	6.1944	2	6
Casein kinase I isoform delta OS=Homo sapiens GN=CSNK1D PE=1 SV=2	sp|P48730|KC1D_HUMAN	3.2	1.9392	6.1944	2	6
Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	sp|Q6YN16|HSDL2_HUMAN	3.2	1.9392	6.1944	2	6
Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4	sp|Q9H9B4|SFXN1_HUMAN	3.2	1.9392	6.1944	2	5
Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	sp|P30101|PDIA3_HUMAN	3.2	1.9392	6.1944	2	6
Mitochondrial basic amino acids transporter OS=Homo sapiens GN=SLC25A29 PE=1 SV=2	sp|Q8N8R3|MCATL_HUMAN	3.2	1.9392	6.1944	2	5
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=	sp|P11310|ACADM_HUMAN	3.2	1.9392	6.1944	2	6
Mitochondrial thiamine pyrophosphate carrier OS=Homo sapiens GN=SLC25A19 PE=1 SV=1	sp|Q9HC21|TPC_HUMAN	3.2	1.9392	6.1944	2	6
Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=1 SV=2	sp|Q9BWM7|SFXN3_HUMAN	3.2	1.9392	6.1944	2	6
Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	sp|Q92598|HS105_HUMAN	3.2	41.692	132.15	33	75
60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	sp|P62750|RL23A_HUMAN	3.1	8.7262	26.842	8	13
Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	sp|Q8NC51|PAIRB_HUMAN	3.0	4.8479	14.454	4	11
C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3	sp|P11586|C1TC_HUMAN	3.0	14.544	43.361	15	40
60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	sp|P32969|RL9_HUMAN	2.9	6.787	19.616	6	12
Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3	sp|Q6ZRV2|FA83H_HUMAN	2.8	2.9087	8.2592	3	8
Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2	sp|Q14573|ITPR3_HUMAN	2.8	2.9087	8.2592	3	8
Cytosolic Fe-S cluster assembly factor NUBP2 OS=Homo sapiens GN=NUBP2 PE=1 SV=1	sp|Q9Y5Y2|NUBP2_HUMAN	2.8	2.9087	8.2592	3	7
Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	sp|P33176|KINH_HUMAN	2.8	10.665	29.939	11	28

Rho guanine nucleotide exchange factor 10 OS=Homo sapiens GN=ARHGEF10 PE=1 SV=4	sp|O15013|ARHGA_HUMAN	2.8	7.7566	21.68	8	15
60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	sp|P62906|RL10A_HUMAN	2.8	7.7566	21.68	7	13
Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=	sp|Q3ZCQ8|TIM50_HUMAN	2.8	4.8479	13.421	5	12
Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1	sp|P61289|PSME3_HUMAN	2.8	4.8479	13.421	4	9
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	sp|P04792|HSPB1_HUMAN	2.8	11.635	32.004	10	19
Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1	sp|Q96P63|SPB12_HUMAN	2.7	6.787	18.583	5	10
Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1	sp|Q6UB35|C1TM_HUMAN	2.7	6.787	18.583	7	17
Aurora kinase A OS=Homo sapiens GN=AURKA PE=1 SV=2	sp|O14965|AURKA_HUMAN	2.7	3.8783	10.324	4	9
DNA polymerase delta catalytic subunit OS=Homo sapiens GN=POLD1 PE=1 SV=2	sp|P28340|DPOD1_HUMAN	2.7	3.8783	10.324	3	9
Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	sp|P02452|CO1A1_HUMAN	2.7	1.9392	5.162	2	5
Protein RTF2 homolog OS=Homo sapiens GN=RTFDC1 PE=1 SV=3	sp|Q9BY42|RTF2_HUMAN	2.7	1.9392	5.162	2	4
UDP-glucose:glycoprotein glucosyltransferase 2 OS=Homo sapiens GN=UGGT2 PE=1 SV=4	sp|Q9NYU1|UGGG2_HUMAN	2.7	1.9392	5.162	2	5
Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3	sp|O60313|OPA1_HUMAN	2.7	1.9392	5.162	2	4
mRNA export factor OS=Homo sapiens GN=RAE1 PE=1 SV=1	sp|P78406|RAE1L_HUMAN	2.7	1.9392	5.162	2	5
Transducin beta-like protein 3 OS=Homo sapiens GN=TBL3 PE=1 SV=2	sp|Q12788|TBL3_HUMAN	2.7	1.9392	5.162	2	5
Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1	sp|Q15293|RCN1_HUMAN	2.7	1.9392	5.162	2	5
Striatin OS=Homo sapiens GN=STRN PE=1 SV=4	sp|O43815|STRN_HUMAN	2.7	1.9392	5.162	2	5
Pleckstrin homology-like domain family B member 2 OS=Homo sapiens GN=PHLDB2 PE=1 SV=2	sp|Q86SQ0|PHLB2_HUMAN	2.7	1.9392	5.162	2	4
Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3	sp|Q16881|TRXR1_HUMAN	2.7	1.9392	5.162	2	4
Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2	sp|P58876|H2B1D_HUMAN	2.6	14.544	38.199	5	7
Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2	sp|P31327|CPSM_HUMAN	2.6	54.296	139.37	47	94
Heat shock 70 kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=1 SV=1	sp|P0DMV8|HS71A_HUMAN (+1)	2.6	113.44	291.14	65	132
Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3	sp|Q12769|NU160_HUMAN	2.6	4.8479	12.389	5	10
Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2	sp|P40763|STAT3_HUMAN	2.6	4.8479	12.389	5	12
Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	sp|P26639|SYTC_HUMAN	2.6	4.8479	12.389	5	11
Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	sp|P22102|PUR2_HUMAN	2.5	12.604	32.004	12	26
Palladin OS=Homo sapiens GN=PALLD PE=1 SV=3	sp|Q8WX93|PALLD_HUMAN	2.5	7.7566	19.616	8	19
BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3	sp|O95817|BAG3_HUMAN	2.5	7.7566	19.616	7	16
DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1	sp|P30876|RPB2_HUMAN	2.5	15.513	39.231	16	34
Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB PE=1 SV=3	sp|Q93100|KPBB_HUMAN	2.5	2.9087	7.2268	3	7
Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2	sp|Q96FW1|OTUB1_HUMAN	2.5	2.9087	7.2268	3	7
H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens GN=GAR1 PE=1 SV=1	sp|Q9NY12|GAR1_HUMAN	2.5	2.9087	7.2268	3	5
Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=1 SV=1	sp|Q9BZX2|UCK2_HUMAN	2.5	2.9087	7.2268	3	7
Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=3	sp|Q07157|ZO1_HUMAN	2.4	6.787	16.518	7	16
S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	sp|P31153|METK2_HUMAN	2.4	44.6	107.37	33	52
Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	sp|P38646|GRP75_HUMAN	2.4	87.262	209.58	52	89
Small proline-rich protein 2D OS=Homo sapiens GN=SPRR2D PE=2 SV=2	sp|P22532|SPR2D_HUMAN	2.4	3.8783	9.2916	1	4
Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	sp|Q15019|SEPT2_HUMAN	2.4	3.8783	9.2916	4	8
Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2	sp|P35520|CBS_HUMAN	2.4	3.8783	9.2916	4	9
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	sp|P62277|RS13_HUMAN	2.4	3.8783	9.2916	4	6
Protein SGT1 homolog OS=Homo sapiens GN=SUGT1 PE=1 SV=3	sp|Q9Y2Z0|SGT1_HUMAN	2.4	3.8783	9.2916	4	9
Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	sp|Q13347|EIF3I_HUMAN	2.4	17.452	41.296	13	22
Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	sp|P33778|H2B1B_HUMAN	2.3	14.544	34.069	5	7
E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3	sp|Q63HN8|RN213_HUMAN	2.3	4.8479	11.356	5	11
DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens GN=POLR1C PE=1 SV=1	sp|O15160|RPAC1_HUMAN	2.3	4.8479	11.356	5	7
Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	sp|P21796|VDAC1_HUMAN	2.3	4.8479	11.356	5	10
CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	sp|P27708|PYR1_HUMAN	2.3	95.988	223	78	135
Inositol 1,4,5-trisphosphate receptor type 1 OS=Homo sapiens GN=ITPR1 PE=1 SV=3	sp|Q14643|ITPR1_HUMAN	2.3	5.8175	13.421	6	13
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=	sp|Q13155|AIMP2_HUMAN	2.2	8.7262	19.616	6	15
Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2	sp|O75746|CMC1_HUMAN	2.2	8.7262	19.616	9	16
Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1	sp|O75694|NU155_HUMAN	2.2	28.118	62.976	27	46
Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1	sp|Q7L2H7|EIF3M_HUMAN	2.2	9.6958	21.68	8	18
Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	sp|P17066|HSP76_HUMAN	2.2	42.661	94.98	22	40
Heat shock 70 kDa protein 1-like OS=Homo sapiens GN=HSPA1L PE=1 SV=2	sp|P34931|HS71L_HUMAN	2.2	64.962	144.54	34	61
Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1	sp|Q6P2E9|EDC4_HUMAN	2.2	12.604	27.875	13	27
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	sp|P11142|HSP7C_HUMAN	2.1	247.24	529.62	105	185
Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	sp|O95831|AIFM1_HUMAN	2.1	10.665	22.713	11	19
Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2	sp|P61619|S61A1_HUMAN	2.1	6.787	14.454	5	7
Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	sp|P54886|P5CS_HUMAN	2.1	6.787	14.454	7	13
60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	sp|P27635|RL10_HUMAN	2.1	12.604	26.842	7	12
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	sp|Q93008|USP9X_HUMAN	2.1	17.452	37.166	17	34
Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2	sp|P45974|UBP5_HUMAN	2.1	2.9087	6.1944	3	6
DNA-directed RNA polymerase I subunit RPA2 OS=Homo sapiens GN=POLR1B PE=1 SV=2	sp|Q9H9Y6|RPA2_HUMAN	2.1	2.9087	6.1944	3	5
Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=1 SV=2	sp|Q8WUM0|NU133_HUMAN	2.1	2.9087	6.1944	3	6
BRISC and BRCA1-A complex member 1 OS=Homo sapiens GN=BABAM1 PE=1 SV=1	sp|Q9NWV8|BABA1_HUMAN	2.1	2.9087	6.1944	3	5
Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3	sp|Q96KB5|TOPK_HUMAN	2.1	2.9087	6.1944	3	5
Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	sp|Q9Y6N5|SQRD_HUMAN	2.1	2.9087	6.1944	3	6
Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	sp|P11717|MPRI_HUMAN	2.1	5.8175	12.389	6	11
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=	sp|Q12904|AIMP1_HUMAN	2.1	11.635	24.778	10	14
Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2	sp|Q14694|UBP10_HUMAN	2.1	5.8175	12.389	6	12
TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1	sp|Q92804|RBP56_HUMAN	2.1	3.8783	8.2592	4	6
Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	sp|Q16543|CDC37_HUMAN	2.1	3.8783	8.2592	4	7
DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4	sp|P25685|DNJB1_HUMAN	2.1	3.8783	8.2592	4	6
Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	sp|Q8NBS9|TXND5_HUMAN	2.1	3.8783	8.2592	4	8
40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	sp|P62854|RS26_HUMAN	2.1	3.8783	8.2592	2	3
Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2	sp|Q99715|COCA1_HUMAN	2.1	0.96958	2.0648	1	2
Transcription factor 20 OS=Homo sapiens GN=TCF20 PE=1 SV=3	sp|Q9UGU0|TCF20_HUMAN	2.1	0.96958	2.0648	1	2
von Willebrand factor A domain-containing protein 8 OS=Homo sapiens GN=VWA8 PE=1 SV=2	sp|A3KMH1|VWA8_HUMAN	2.1	0.96958	2.0648	1	2
Dysferlin OS=Homo sapiens GN=DYSF PE=1 SV=1	sp|O75923|DYSF_HUMAN	2.1	0.96958	2.0648	1	2
Lon protease homolog 2, peroxisomal OS=Homo sapiens GN=LONP2 PE=1 SV=1	sp|Q86WA8|LONP2_HUMAN	2.1	0.96958	2.0648	1	2
Epithelial splicing regulatory protein 2 OS=Homo sapiens GN=ESRP2 PE=1 SV=1	sp|Q9H6T0|ESRP2_HUMAN	2.1	0.96958	2.0648	1	2
Spectrin beta chain, non-erythrocytic 4 OS=Homo sapiens GN=SPTBN4 PE=1 SV=2	sp|Q9H254|SPTN4_HUMAN	2.1	0.96958	2.0648	1	2
Protein misato homolog 1 OS=Homo sapiens GN=MSTO1 PE=1 SV=1	sp|Q9BUK6|MSTO1_HUMAN	2.1	0.96958	2.0648	1	2
DNA topoisomerase 3-beta-1 OS=Homo sapiens GN=TOP3B PE=1 SV=1	sp|O95985|TOP3B_HUMAN	2.1	0.96958	2.0648	1	2
Pleckstrin homology domain-containing family A member 7 OS=Homo sapiens GN=PLEKHA7 PE=1 SV=2	sp|Q6IQ23|PKHA7_HUMAN	2.1	0.96958	2.0648	1	2
LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2	sp|Q14847|LASP1_HUMAN	2.1	0.96958	2.0648	1	2
Melanoma-associated antigen 3 OS=Homo sapiens GN=MAGEA3 PE=1 SV=1	sp|P43357|MAGA3_HUMAN	2.1	0.96958	2.0648	1	2
cGMP-inhibited 3',5'-cyclic phosphodiesterase A OS=Homo sapiens GN=PDE3A PE=1 SV=3	sp|Q14432|PDE3A_HUMAN	2.1	0.96958	2.0648	1	2
WD repeat-containing protein 11 OS=Homo sapiens GN=WDR11 PE=1 SV=1	sp|Q9BZH6|WDR11_HUMAN	2.1	0.96958	2.0648	1	2
Serpin B8 OS=Homo sapiens GN=SERPINB8 PE=1 SV=2	sp|P50452|SPB8_HUMAN	2.1	0.96958	2.0648	1	2
A-kinase anchor protein 1, mitochondrial OS=Homo sapiens GN=AKAP1 PE=1 SV=1	sp|Q92667|AKAP1_HUMAN	2.1	0.96958	2.0648	1	2
Melanoma inhibitory activity protein 3 OS=Homo sapiens GN=MIA3 PE=1 SV=1	sp|Q5JRA6|MIA3_HUMAN	2.1	0.96958	2.0648	1	2
Serine/threonine-protein phosphatase 1 regulatory subunit 10 OS=Homo sapiens GN=PPP1R10 PE=1 SV=1	sp|Q96QC0|PP1RA_HUMAN	2.1	0.96958	2.0648	1	2
Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 PE=1 SV=2	sp|Q8NCE2|MTMRE_HUMAN	2.1	0.96958	2.0648	1	2
Huntingtin OS=Homo sapiens GN=HTT PE=1 SV=2	sp|P42858|HD_HUMAN	2.1	0.96958	2.0648	1	2
Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1 PE=1 SV=3	sp|P52306|GDS1_HUMAN	2.1	0.96958	2.0648	1	2
Probable ATP-dependent RNA helicase DDX60-like OS=Homo sapiens GN=DDX60L PE=2 SV=2	sp|Q5H9U9|DDX6L_HUMAN	2.1	0.96958	2.0648	1	2
Pleiotropic regulator 1 OS=Homo sapiens GN=PLRG1 PE=1 SV=1	sp|O43660|PLRG1_HUMAN	2.1	0.96958	2.0648	1	2
(Reversed) Transmembrane protein 141 OS=Homo sapiens GN=TMEM141 PE=1 SV=1	Reversed_sp|Q96I45|TM141_HUMAN	2.1	0.96958	2.0648	1	2
Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	sp|Q9NQC3|RTN4_HUMAN	2.1	0.96958	2.0648	1	2
TELO2-interacting protein 1 homolog OS=Homo sapiens GN=TTI1 PE=1 SV=3	sp|O43156|TTI1_HUMAN	2.1	0.96958	2.0648	1	2
Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens GN=PIP4K2C PE=1 SV=3	sp|Q8TBX8|PI42C_HUMAN	2.1	0.96958	2.0648	1	2
Forkhead box protein K1 OS=Homo sapiens GN=FOXK1 PE=1 SV=1	sp|P85037|FOXK1_HUMAN	2.1	0.96958	2.0648	1	2
(Reversed) Rho guanine nucleotide exchange factor 10 OS=Homo sapiens GN=ARHGEF10 PE=1 SV=4	Reversed_sp|O15013|ARHGA_HUMAN	2.1	0.96958	2.0648	1	2
LIM domain-containing protein 1 OS=Homo sapiens GN=LIMD1 PE=1 SV=1	sp|Q9UGP4|LIMD1_HUMAN	2.1	0.96958	2.0648	1	2

Tonsoku-like protein OS=Homo sapiens GN=TONSL PE=1 SV=2	sp|Q96HA7|TONSL_HUMAN	2.1	0.96958	2.0648	1	2
Pantothenate kinase 4 OS=Homo sapiens GN=PANK4 PE=1 SV=1	sp|Q9NVE7|PANK4_HUMAN	2.1	0.96958	2.0648	1	2
Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform OS=Homo sapiens GN=PHKA1 P	sp|P46020|KPB1_HUMAN	2.1	0.96958	2.0648	1	2
Protein FAM83B OS=Homo sapiens GN=FAM83B PE=1 SV=1	sp|Q5T0W9|FA83B_HUMAN	2.1	0.96958	2.0648	1	2
Cleft lip and palate transmembrane protein 1 OS=Homo sapiens GN=CLPTM1 PE=1 SV=1	sp|O96005|CLPT1_HUMAN	2.1	0.96958	2.0648	1	2
Integrator complex subunit 11 OS=Homo sapiens GN=CPSF3L PE=1 SV=2	sp|Q5TA45|INT11_HUMAN	2.1	0.96958	2.0648	1	2
ERC protein 2 OS=Homo sapiens GN=ERC2 PE=1 SV=3	sp|O15083|ERC2_HUMAN	2.1	0.96958	2.0648	1	2
Very-long-chain 3-oxoacyl-CoA reductase OS=Homo sapiens GN=HSD17B12 PE=1 SV=2	sp|Q53GQ0|DHB12_HUMAN	2.1	0.96958	2.0648	1	2
RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1	sp|Q01844|EWS_HUMAN	2.1	0.96958	2.0648	1	2
Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2	sp|P52888|THOP1_HUMAN	2.1	0.96958	2.0648	1	2
NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1	sp|P15559|NQO1_HUMAN	2.1	0.96958	2.0648	1	2
WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 PE=1 SV=2	sp|Q2M389|WASH7_HUMAN	2.1	0.96958	2.0648	1	2
Kinesin-like protein KIF2C OS=Homo sapiens GN=KIF2C PE=1 SV=2	sp|Q99661|KIF2C_HUMAN	2.1	0.96958	2.0648	1	2
Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3	sp|P17174|AATC_HUMAN	2.1	0.96958	2.0648	1	2
Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1	sp|P18754|RCC1_HUMAN	2.1	0.96958	2.0648	1	2
Unconventional prefoldin RPB5 interactor 1 OS=Homo sapiens GN=URI1 PE=1 SV=3	sp|O94763|RMP_HUMAN	2.1	0.96958	2.0648	1	2
Gasdermin-A OS=Homo sapiens GN=GSDMA PE=1 SV=4	sp|Q96QA5|GSDMA_HUMAN	2.1	0.96958	2.0648	1	2
Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	sp|P61626|LYSC_HUMAN	2.1	0.96958	2.0648	1	2
Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	sp|P49257|LMAN1_HUMAN	2.1	0.96958	2.0648	1	2
NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1	sp|Q13564|ULA1_HUMAN	2.1	0.96958	2.0648	1	2
Serine/threonine-protein phosphatase 6 regulatory subunit 2 OS=Homo sapiens GN=PPP6R2 PE=1 SV=2	sp|O75170|PP6R2_HUMAN	2.1	0.96958	2.0648	1	2
BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 3 OS=Homo sapiens G	sp|Q9H3F6|BACD3_HUMAN	2.1	0.96958	2.0648	1	2
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=N	sp|O95299|NDUAA_HUMAN	2.1	0.96958	2.0648	1	2
Inositol monophosphatase 2 OS=Homo sapiens GN=IMPA2 PE=1 SV=1	sp|O14732|IMPA2_HUMAN	2.1	0.96958	2.0648	1	2
Zinc finger protein basonuclin-2 OS=Homo sapiens GN=BNC2 PE=1 SV=1	sp|Q6ZN30|BNC2_HUMAN	2.1	0.96958	2.0648	1	2
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	sp|Q01105|SET_HUMAN	2.1	0.96958	2.0648	1	2
Guanine nucleotide-binding protein subunit beta-like protein 1 OS=Homo sapiens GN=GNB1L PE=1 SV=2	sp|Q9BYB4|GNB1L_HUMAN	2.1	0.96958	2.0648	1	2
60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2	sp|P61513|RL37A_HUMAN	2.1	0.96958	2.0648	1	2
V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4	sp|P21283|VATC1_HUMAN	2.1	0.96958	2.0648	1	2
V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1	sp|P36543|VATE1_HUMAN	2.1	0.96958	2.0648	1	2
Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2	sp|Q02750|MP2K1_HUMAN	2.1	0.96958	2.0648	1	2
Mothers against decapentaplegic homolog 2 OS=Homo sapiens GN=SMAD2 PE=1 SV=1	sp|Q15796|SMAD2_HUMAN	2.1	0.96958	2.0648	1	2
Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1	sp|Q9H479|FN3K_HUMAN	2.1	0.96958	2.0648	1	2
Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3	sp|P38117|ETFB_HUMAN	2.1	0.96958	2.0648	1	2
Protein SCO2 homolog, mitochondrial OS=Homo sapiens GN=SCO2 PE=1 SV=3	sp|O43819|SCO2_HUMAN	2.1	0.96958	2.0648	1	2
Cytochrome c oxidase assembly protein COX15 homolog OS=Homo sapiens GN=COX15 PE=1 SV=1	sp|Q7KZN9|COX15_HUMAN	2.1	0.96958	2.0648	1	2
Snurportin-1 OS=Homo sapiens GN=SNUPN PE=1 SV=1	sp|O95149|SPN1_HUMAN	2.1	0.96958	2.0648	1	2
Ubiquitin-like domain-containing CTD phosphatase 1 OS=Homo sapiens GN=UBLCP1 PE=1 SV=2	sp|Q8WVY7|UBCP1_HUMAN	2.1	0.96958	2.0648	1	2
Cleavage and polyadenylation specificity factor subunit 7 OS=Homo sapiens GN=CPSF7 PE=1 SV=1	sp|Q8N684|CPSF7_HUMAN	2.1	0.96958	2.0648	1	2
AH receptor-interacting protein OS=Homo sapiens GN=AIP PE=1 SV=2	sp|O00170|AIP_HUMAN	2.1	0.96958	2.0648	1	2
Activating signal cointegrator 1 complex subunit 1 OS=Homo sapiens GN=ASCC1 PE=1 SV=1	sp|Q8N9N2|ASCC1_HUMAN	2.1	0.96958	2.0648	1	2
Glycosyltransferase 8 domain-containing protein 1 OS=Homo sapiens GN=GLT8D1 PE=1 SV=2	sp|Q68CQ7|GL8D1_HUMAN	2.1	0.96958	2.0648	1	2
Rhomboid domain-containing protein 2 OS=Homo sapiens GN=RHBDD2 PE=2 SV=2	sp|Q6NTF9|RHBD2_HUMAN	2.1	0.96958	2.0648	1	2
Ras-related protein Rab-32 OS=Homo sapiens GN=RAB32 PE=1 SV=3	sp|Q13637|RAB32_HUMAN	2.1	0.96958	2.0648	1	2
Putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8 OS=Homo sapiens GN=IGH	sp|A6NJ16|IV4F8_HUMAN	2.1	0.96958	2.0648	1	2
Spindlin-2B OS=Homo sapiens GN=SPIN2B PE=2 SV=1	sp|Q9BPZ2|SPI2B_HUMAN	2.1	4.8479	10.324	4	6
Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=	sp|P14678|RSMB_HUMAN	2.1	4.8479	10.324	5	7
Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	sp|P25311|ZA2G_HUMAN	2.1	4.8479	10.324	2	8
Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3	sp|P28482|MK01_HUMAN	2.1	4.8479	10.324	5	9
Retinol dehydrogenase 10 OS=Homo sapiens GN=RDH10 PE=1 SV=1	sp|Q8IZV5|RDH10_HUMAN	2.1	4.8479	10.324	4	8
D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	sp|O43175|SERA_HUMAN	2.1	4.8479	10.324	5	10
Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1	sp|O94905|ERLN2_HUMAN	2.1	4.8479	10.324	5	9
Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2	sp|O75821|EIF3G_HUMAN	2.1	8.7262	18.583	8	13
Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3	sp|P46459|NSF_HUMAN	2.1	8.7262	18.583	9	18
Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=3	sp|O15027|SC16A_HUMAN	2.1	28.118	59.879	27	42
Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2	sp|P51610|HCFC1_HUMAN	2.1	7.7566	16.518	8	14
DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1	sp|Q9UBS4|DJB11_HUMAN	2.1	7.7566	16.518	6	13
Symplekin OS=Homo sapiens GN=SYMPK PE=1 SV=2	sp|Q92797|SYMPK_HUMAN	2.1	1.9392	4.1296	2	4
EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1	sp|Q96C19|EFHD2_HUMAN	2.1	1.9392	4.1296	2	4
GRIP and coiled-coil domain-containing protein 2 OS=Homo sapiens GN=GCC2 PE=1 SV=4	sp|Q8IWJ2|GCC2_HUMAN	2.1	1.9392	4.1296	1	3
Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2 PE=1 SV=2	sp|O95218|ZRAB2_HUMAN	2.1	1.9392	4.1296	2	4
Myosin phosphatase Rho-interacting protein OS=Homo sapiens GN=MPRIP PE=1 SV=3	sp|Q6WCQ1|MPRIP_HUMAN	2.1	1.9392	4.1296	2	3
Protein HEXIM1 OS=Homo sapiens GN=HEXIM1 PE=1 SV=1	sp|O94992|HEXI1_HUMAN	2.1	1.9392	4.1296	2	4
GTPase Era, mitochondrial OS=Homo sapiens GN=ERAL1 PE=1 SV=2	sp|O75616|ERAL1_HUMAN	2.1	1.9392	4.1296	2	4
Gamma-tubulin complex component 2 OS=Homo sapiens GN=TUBGCP2 PE=1 SV=2	sp|Q9BSJ2|GCP2_HUMAN	2.1	1.9392	4.1296	2	4
ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2	sp|Q7Z478|DHX29_HUMAN	2.1	1.9392	4.1296	2	2
Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3	sp|O15143|ARC1B_HUMAN	2.1	1.9392	4.1296	2	4
Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=2	sp|Q9UHD1|CHRD1_HUMAN	2.1	1.9392	4.1296	2	4
Gem-associated protein 2 OS=Homo sapiens GN=GEMIN2 PE=1 SV=1	sp|O14893|GEMI2_HUMAN	2.1	1.9392	4.1296	2	4
Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	sp|P00738|HPT_HUMAN	2.1	1.9392	4.1296	1	2
Myeloid leukemia factor 2 OS=Homo sapiens GN=MLF2 PE=1 SV=1	sp|Q15773|MLF2_HUMAN	2.1	1.9392	4.1296	2	3
Selenocysteine insertion sequence-binding protein 2-like OS=Homo sapiens GN=SECISBP2L PE=1 SV=3	sp|Q93073|SBP2L_HUMAN	2.1	1.9392	4.1296	2	4
Protein HGH1 homolog OS=Homo sapiens GN=HGH1 PE=1 SV=1	sp|Q9BTY7|HGH1_HUMAN	2.1	1.9392	4.1296	2	4
Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3	sp|O95292|VAPB_HUMAN	2.1	1.9392	4.1296	2	4
Ubiquitin-protein ligase E3C OS=Homo sapiens GN=UBE3C PE=1 SV=3	sp|Q15386|UBE3C_HUMAN	2.1	1.9392	4.1296	2	3
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3	sp|P46977|STT3A_HUMAN	2.1	1.9392	4.1296	1	3
60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1	sp|Q6DKI1|RL7L_HUMAN	2.1	1.9392	4.1296	2	4
Cell differentiation protein RCD1 homolog OS=Homo sapiens GN=RQCD1 PE=1 SV=1	sp|Q92600|RCD1_HUMAN	2.1	1.9392	4.1296	2	4
Notchless protein homolog 1 OS=Homo sapiens GN=NLE1 PE=1 SV=4	sp|Q9NVX2|NLE1_HUMAN	2.1	1.9392	4.1296	2	4
6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2	sp|O95336|6PGL_HUMAN	2.1	1.9392	4.1296	2	4
Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	sp|P54709|AT1B3_HUMAN	2.1	1.9392	4.1296	2	4
ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	sp|P12236|ADT3_HUMAN	2.1	44.6	92.916	28	37
Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	sp|P23526|SAHH_HUMAN	2.1	13.574	27.875	13	19
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	sp|P11021|GRP78_HUMAN	2.1	92.11	188.93	55	91
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	sp|P62280|RS11_HUMAN	2.0	12.604	25.81	9	13
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	sp|P62269|RS18_HUMAN	2.0	11.635	23.745	6	12
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	sp|P55884|EIF3B_HUMAN	2.0	36.844	74.333	32	48
Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4	sp|P11413|G6PD_HUMAN	2.0	7.7566	15.486	7	13
4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3	sp|P08195|4F2_HUMAN	2.0	21.331	42.328	13	26
Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	sp|Q8WUM4|PDC6I_HUMAN	2.0	6.787	13.421	6	12
Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=1 SV=2	sp|O60341|KDM1A_HUMAN	2.0	6.787	13.421	7	12
Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	sp|Q13242|SRSF9_HUMAN	2.0	6.787	13.421	6	10
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	sp|Q06830|PRDX1_HUMAN	2.0	6.787	13.421	4	8
Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	sp|P54652|HSP72_HUMAN	2.0	99.866	197.19	49	83
Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2	sp|Q9UJS0|CMC2_HUMAN	2.0	24.239	47.49	21	34
Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1 PE=1 SV=2	sp|Q86V48|LUZP1_HUMAN	2.0	5.8175	11.356	6	11
Protein MON2 homolog OS=Homo sapiens GN=MON2 PE=1 SV=3	sp|Q7Z3U7|MON2_HUMAN	2.0	5.8175	11.356	6	11
ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	sp|P05141|ADT2_HUMAN	1.9	56.235	109.43	32	42
Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	sp|P55786|PSA_HUMAN	1.9	10.665	20.648	10	20
Dedicator of cytokinesis protein 5 OS=Homo sapiens GN=DOCK5 PE=1 SV=3	sp|Q9H7D0|DOCK5_HUMAN	1.9	4.8479	9.2916	5	9
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	sp|P04083|ANXA1_HUMAN	1.9	4.8479	9.2916	5	7
Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1	sp|P51570|GALK1_HUMAN	1.9	4.8479	9.2916	5	8
BTB/POZ domain-containing protein KCTD5 OS=Homo sapiens GN=KCTD5 PE=1 SV=1	sp|Q9NXV2|KCTD5_HUMAN	1.9	31.996	60.911	21	28
Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens GN=USP11 PE=1 SV=3	sp|P51784|UBP11_HUMAN	1.9	7.7566	14.454	8	14
LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=4	sp|Q9UPQ0|LIMC1_HUMAN	1.9	3.8783	7.2268	4	7

Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	sp|O60610|DIAP1_HUMAN	1.9	3.8783	7.2268	4	7
A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L PE=1 SV=3	sp|Q9ULX6|AKP8L_HUMAN	1.9	3.8783	7.2268	2	6
Isochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3	sp|Q96CN7|ISOC1_HUMAN	1.9	3.8783	7.2268	4	6
Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1	sp|O15427|MOT4_HUMAN	1.9	3.8783	7.2268	4	6
Protein FAM46A OS=Homo sapiens GN=FAM46A PE=1 SV=2	sp|Q96IP4|FA46A_HUMAN	1.9	3.8783	7.2268	4	6
Dolichol-phosphate mannosyltransferase subunit 1 OS=Homo sapiens GN=DPM1 PE=1 SV=1	sp|O60762|DPM1_HUMAN	1.9	3.8783	7.2268	4	7
Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2	sp|P54819|KAD2_HUMAN	1.9	3.8783	7.2268	4	6
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	sp|Q86YZ3|HORN_HUMAN	1.8	16.483	29.939	7	8
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	sp|O43707|ACTN4_HUMAN	1.8	9.6958	17.551	10	16
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens G	sp|P63151|2ABA_HUMAN	1.8	12.604	22.713	12	18
Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2	sp|Q9UBX3|DIC_HUMAN	1.8	12.604	22.713	9	14
Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1	sp|O00303|EIF3F_HUMAN	1.8	12.604	22.713	11	16
14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	sp|P61981|1433G_HUMAN	1.8	15.513	27.875	12	17
Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	sp|P62805|H4_HUMAN	1.8	18.422	33.037	6	6
Acetyl-CoA carboxylase 2 OS=Homo sapiens GN=ACACB PE=1 SV=3	sp|O00763|ACACB_HUMAN	1.8	2.9087	5.162	3	5
Histone-lysine N-methyltransferase 2A OS=Homo sapiens GN=KMT2A PE=1 SV=5	sp|Q03164|KMT2A_HUMAN	1.8	2.9087	5.162	2	1
E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens GN=RNF40 PE=1 SV=4	sp|O75150|BRE1B_HUMAN	1.8	2.9087	5.162	3	5
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Homo sapiens GN=INPPL1 PE=1 SV=2	sp|O15357|SHIP2_HUMAN	1.8	2.9087	5.162	3	5
Pre-mRNA-splicing factor SYF1 OS=Homo sapiens GN=XAB2 PE=1 SV=2	sp|Q9HCS7|SYF1_HUMAN	1.8	2.9087	5.162	3	5
Casein kinase I isoform epsilon OS=Homo sapiens GN=CSNK1E PE=1 SV=1	sp|P49674|KC1E_HUMAN	1.8	2.9087	5.162	3	5
RING finger protein 219 OS=Homo sapiens GN=RNF219 PE=1 SV=1	sp|Q5W0B1|RN219_HUMAN	1.8	2.9087	5.162	3	5
Sperm-associated antigen 5 OS=Homo sapiens GN=SPAG5 PE=1 SV=2	sp|Q96R06|SPAG5_HUMAN	1.8	2.9087	5.162	3	5
SLIT and NTRK-like protein 5 OS=Homo sapiens GN=SLITRK5 PE=2 SV=2	sp|O94991|SLIK5_HUMAN	1.8	2.9087	5.162	3	4
Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 OS=Homo sapiens GN=DHX16 PE=	sp|O60231|DHX16_HUMAN	1.8	2.9087	5.162	2	4
Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1	sp|P04181|OAT_HUMAN	1.8	2.9087	5.162	3	5
Kinase D-interacting substrate of 220 kDa OS=Homo sapiens GN=KIDINS220 PE=1 SV=3	sp|Q9ULH0|KDIS_HUMAN	1.8	2.9087	5.162	3	4
tRNA (guanine(26)-N(2))-dimethyltransferase OS=Homo sapiens GN=TRMT1 PE=1 SV=1	sp|Q9NXH9|TRM1_HUMAN	1.8	2.9087	5.162	3	5
Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3	sp|Q9NPD3|EXOS4_HUMAN	1.8	2.9087	5.162	3	3
Thymidylate synthase OS=Homo sapiens GN=TYMS PE=1 SV=3	sp|P04818|TYSY_HUMAN	1.8	2.9087	5.162	3	5
DNA-directed RNA polymerase II subunit RPB3 OS=Homo sapiens GN=POLR2C PE=1 SV=2	sp|P19387|RPB3_HUMAN	1.8	2.9087	5.162	3	4
Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Homo sapiens GN=OSGEP PE=1 SV=1	sp|Q9NPF4|OSGEP_HUMAN	1.8	2.9087	5.162	3	5
Geranylgeranyl transferase type-2 subunit beta OS=Homo sapiens GN=RABGGTB PE=1 SV=2	sp|P53611|PGTB2_HUMAN	1.8	2.9087	5.162	3	4
Polyribonucleotide 5'-hydroxyl-kinase Clp1 OS=Homo sapiens GN=CLP1 PE=1 SV=1	sp|Q92989|CLP1_HUMAN	1.8	2.9087	5.162	3	5
Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	sp|Q9HB71|CYBP_HUMAN	1.8	2.9087	5.162	3	5
Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1	sp|P09496|CLCA_HUMAN	1.8	2.9087	5.162	3	4
Protein LAP2 OS=Homo sapiens GN=ERBB2IP PE=1 SV=2	sp|Q96RT1|LAP2_HUMAN	1.8	5.8175	10.324	6	10
RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	sp|P35637|FUS_HUMAN	1.8	5.8175	10.324	6	8
Glucose-induced degradation protein 8 homolog OS=Homo sapiens GN=GID8 PE=1 SV=1	sp|Q9NWU2|GID8_HUMAN	1.8	5.8175	10.324	6	8
ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4	sp|P12235|ADT1_HUMAN	1.8	42.661	75.365	26	33
Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2	sp|Q9NU22|MDN1_HUMAN	1.8	19.392	34.069	19	30
Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	sp|P56192|SYMC_HUMAN	1.8	19.392	34.069	19	26
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	sp|P13639|EF2_HUMAN	1.8	71.749	125.95	53	70
Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	sp|Q13263|TIF1B_HUMAN	1.7	13.574	23.745	13	19
Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	sp|O95163|ELP1_HUMAN	1.7	10.665	18.583	11	17
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	sp|P49327|FAS_HUMAN	1.7	73.688	128.02	60	91
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens G	sp|P30153|2AAA_HUMAN	1.7	18.422	32.004	15	22
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	sp|Q02413|DSG1_HUMAN	1.7	15.513	26.842	10	15
Tubulin alpha chain-like 3 OS=Homo sapiens GN=TUBAL3 PE=1 SV=2	sp|A6NHL2|TBAL3_HUMAN	1.7	7.7566	13.421	4	4
Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	sp|P07951|TPM2_HUMAN	1.7	7.7566	13.421	6	8
Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1	sp|O15371|EIF3D_HUMAN	1.7	7.7566	13.421	8	11
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	sp|P68104|EF1A1_HUMAN	1.7	115.38	197.19	46	74
Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=3	sp|Q14192|FHL2_HUMAN	1.7	4.8479	8.2592	3	5
Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA	sp|E9PAV3|NACAM_HUMAN	1.7	4.8479	8.2592	5	3
Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	sp|Q9BSJ8|ESYT1_HUMAN	1.7	4.8479	8.2592	5	7
Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3	sp|P08574|CY1_HUMAN	1.7	4.8479	8.2592	5	6
Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	sp|Q15181|IPYR_HUMAN	1.7	4.8479	8.2592	5	8
Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	sp|Q9UL46|PSME2_HUMAN	1.7	4.8479	8.2592	5	8
Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2	sp|P06753|TPM3_HUMAN	1.7	11.635	19.616	9	14
60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	sp|P18621|RL17_HUMAN	1.7	18.422	30.972	9	11
Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	sp|P22314|UBA1_HUMAN	1.7	18.422	30.972	16	24
BTB/POZ domain-containing protein KCTD2 OS=Homo sapiens GN=KCTD2 PE=1 SV=3	sp|Q14681|KCTD2_HUMAN	1.7	20.361	34.069	13	18
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	sp|P24534|EF1B_HUMAN	1.7	6.787	11.356	6	9
Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	sp|Q05639|EF1A2_HUMAN	1.7	66.901	111.5	27	38
DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5	sp|P33991|MCM4_HUMAN	1.7	8.7262	14.454	9	14
Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	sp|Q00325|MPCP_HUMAN	1.6	23.27	38.199	18	19
Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	sp|P29401|TKT_HUMAN	1.6	12.604	20.648	11	17
DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	sp|P43246|MSH2_HUMAN	1.6	12.604	20.648	13	19
Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	sp|P16152|CBR1_HUMAN	1.6	12.604	20.648	12	17
Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2	sp|Q14157|UBP2L_HUMAN	1.6	14.544	23.745	13	17
Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2	sp|Q10570|CPSF1_HUMAN	1.6	15.513	24.778	15	19
ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	sp|P53396|ACLY_HUMAN	1.6	17.452	27.875	18	24
Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	sp|P12814|ACTN1_HUMAN	1.6	7.7566	12.389	8	12
La-related protein 4B OS=Homo sapiens GN=LARP4B PE=1 SV=3	sp|Q92615|LAR4B_HUMAN	1.6	7.7566	12.389	8	12
Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4	sp|Q16643|DREB_HUMAN	1.6	7.7566	12.389	8	11
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	sp|P14923|PLAK_HUMAN	1.6	40.722	65.041	23	33
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1	sp|O60568|PLOD3_HUMAN	1.6	3.8783	6.1944	4	6
NUAK family SNF1-like kinase 2 OS=Homo sapiens GN=NUAK2 PE=1 SV=1	sp|Q9H093|NUAK2_HUMAN	1.6	3.8783	6.1944	2	2
Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1	sp|P19623|SPEE_HUMAN	1.6	3.8783	6.1944	4	6
BAG family molecular chaperone regulator 5 OS=Homo sapiens GN=BAG5 PE=1 SV=1	sp|Q9UL15|BAG5_HUMAN	1.6	3.8783	6.1944	4	5
Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3	sp|Q08379|GOGA2_HUMAN	1.6	3.8783	6.1944	4	6
Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3	sp|O14579|COPE_HUMAN	1.6	3.8783	6.1944	4	6
Ubiquitin thioesterase otulin OS=Homo sapiens GN=OTULIN PE=1 SV=3	sp|Q96BN8|OTUL_HUMAN	1.6	3.8783	6.1944	4	4
Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3	sp|Q9Y5M8|SRPRB_HUMAN	1.6	3.8783	6.1944	4	6
Cyclic AMP-dependent transcription factor ATF-6 alpha OS=Homo sapiens GN=ATF6 PE=1 SV=3	sp|P18850|ATF6A_HUMAN	1.6	3.8783	6.1944	4	6
Apolipoprotein L2 OS=Homo sapiens GN=APOL2 PE=1 SV=1	sp|Q9BQE5|APOL2_HUMAN	1.6	3.8783	6.1944	4	5
A-kinase anchor protein 9 OS=Homo sapiens GN=AKAP9 PE=1 SV=3	sp|Q99996|AKAP9_HUMAN	1.6	9.6958	15.486	10	15
182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	sp|Q9C0C2|TB182_HUMAN	1.6	9.6958	15.486	10	14
Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A OS=Homo sapiens GN=ANK	sp|O15084|ANR28_HUMAN	1.6	9.6958	15.486	10	13
Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1	sp|O14929|HAT1_HUMAN	1.6	5.8175	9.2916	6	9
Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1	sp|O75477|ERLN1_HUMAN	1.6	5.8175	9.2916	5	8
Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	sp|P28066|PSA5_HUMAN	1.6	5.8175	9.2916	4	7
Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1	sp|Q96IJ6|GMPPA_HUMAN	1.6	5.8175	9.2916	6	9
DnaJ homolog subfamily C member 7 OS=Homo sapiens GN=DNAJC7 PE=1 SV=2	sp|Q99615|DNJC7_HUMAN	1.6	11.635	18.583	11	17
Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2	sp|Q14571|ITPR2_HUMAN	1.6	1.9392	3.0972	2	3
UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	sp|Q9NYU2|UGGG1_HUMAN	1.6	1.9392	3.0972	2	3
Nuclear receptor corepressor 1 OS=Homo sapiens GN=NCOR1 PE=1 SV=2	sp|O75376|NCOR1_HUMAN	1.6	1.9392	3.0972	2	3
Protein FAM208B OS=Homo sapiens GN=FAM208B PE=1 SV=1	sp|Q5VWN6|F208B_HUMAN	1.6	1.9392	3.0972	2	3
YEATS domain-containing protein 2 OS=Homo sapiens GN=YEATS2 PE=1 SV=2	sp|Q9ULM3|YETS2_HUMAN	1.6	1.9392	3.0972	2	3
Phosphoinositide 3-kinase regulatory subunit 4 OS=Homo sapiens GN=PIK3R4 PE=1 SV=3	sp|Q99570|PI3R4_HUMAN	1.6	1.9392	3.0972	2	3
Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2	sp|Q16181|SEPT7_HUMAN	1.6	1.9392	3.0972	2	3
GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 S	sp|Q14C86|GAPD1_HUMAN	1.6	1.9392	3.0972	2	3
Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4	sp|P20810|ICAL_HUMAN	1.6	1.9392	3.0972	2	3
Mediator of RNA polymerase II transcription subunit 12 OS=Homo sapiens GN=MED12 PE=1 SV=4	sp|Q93074|MED12_HUMAN	1.6	1.9392	3.0972	2	3
Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens GN=RAB3GAP1 PE=1 SV=3	sp|Q15042|RB3GP_HUMAN	1.6	1.9392	3.0972	2	2
Zinc finger and BTB domain-containing protein 11 OS=Homo sapiens GN=ZBTB11 PE=1 SV=2	sp|O95625|ZBT11_HUMAN	1.6	1.9392	3.0972	2	2

RNA polymerase-associated protein RTF1 homolog OS=Homo sapiens GN=RTF1 PE=1 SV=4	sp|Q92541|RTF1_HUMAN	1.6	1.9392	3.0972	2	3
Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1	sp|P48507|GSH0_HUMAN	1.6	1.9392	3.0972	2	2
Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3	sp|Q9NSD9|SYFB_HUMAN	1.6	1.9392	3.0972	2	3
GPI-anchor transamidase OS=Homo sapiens GN=PIGK PE=1 SV=2	sp|Q92643|GPI8_HUMAN	1.6	1.9392	3.0972	2	2
Cancer/testis antigen family 45 member A6 OS=Homo sapiens GN=CT45A6 PE=2 SV=1	sp|P0DMU7|CT456_HUMAN (+4)	1.6	1.9392	3.0972	2	3
Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1	sp|Q99961|SH3G1_HUMAN	1.6	1.9392	3.0972	2	3
Elongator complex protein 3 OS=Homo sapiens GN=ELP3 PE=1 SV=2	sp|Q9H9T3|ELP3_HUMAN	1.6	1.9392	3.0972	2	3
Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=1 SV=3	sp|O94979|SC31A_HUMAN	1.6	1.9392	3.0972	2	3
Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1	sp|P46109|CRKL_HUMAN	1.6	1.9392	3.0972	2	3
Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C OS=Homo sapiens GN=ANKRD5	sp|Q8NB46|ANR52_HUMAN	1.6	1.9392	3.0972	2	3
V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3	sp|Q93050|VPP1_HUMAN	1.6	1.9392	3.0972	2	3
39S ribosomal protein L46, mitochondrial OS=Homo sapiens GN=MRPL46 PE=1 SV=1	sp|Q9H2W6|RM46_HUMAN	1.6	1.9392	3.0972	2	3
Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	sp|Q9Y6C9|MTCH2_HUMAN	1.6	1.9392	3.0972	1	2
Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	sp|O76003|GLRX3_HUMAN	1.6	1.9392	3.0972	2	3
Protein FAM207A OS=Homo sapiens GN=FAM207A PE=1 SV=2	sp|Q9NSI2|F207A_HUMAN	1.6	1.9392	3.0972	2	3
Zinc transporter SLC39A7 OS=Homo sapiens GN=SLC39A7 PE=1 SV=2	sp|Q92504|S39A7_HUMAN	1.6	1.9392	3.0972	2	3
Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2	sp|Q14517|FAT1_HUMAN	1.6	34.905	54.717	35	51
CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2	sp|P17812|PYRG1_HUMAN	1.6	14.544	22.713	13	19
DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	sp|P31689|DNJA1_HUMAN	1.6	39.753	61.944	28	36
F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	sp|P47756|CAPZB_HUMAN	1.6	12.604	19.616	10	16
Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1	sp|O00743|PPP6_HUMAN	1.5	10.665	16.518	7	11
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	sp|P05023|AT1A1_HUMAN	1.5	36.844	56.782	29	38
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN	sp|P30154|2AAB_HUMAN	1.5	8.7262	13.421	8	9
ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2	sp|O00148|DX39A_HUMAN	1.5	8.7262	13.421	7	9
Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1	sp|Q9NZ01|TECR_HUMAN	1.5	8.7262	13.421	6	10
CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	sp|A5YKK6|CNOT1_HUMAN	1.5	15.513	23.745	14	23
Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	sp|P49411|EFTU_HUMAN	1.5	53.327	81.559	30	41
Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	sp|Q13085|ACACA_HUMAN	1.5	22.3	34.069	23	32
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens G	sp|P08559|ODPA_HUMAN	1.5	6.787	10.324	7	10
Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	sp|P50416|CPT1A_HUMAN	1.5	6.787	10.324	7	10
Kanadaptin OS=Homo sapiens GN=SLC4A1AP PE=1 SV=1	sp|Q9BWU0|NADAP_HUMAN	1.5	6.787	10.324	7	9
Guanine deaminase OS=Homo sapiens GN=GDA PE=1 SV=1	sp|Q9Y2T3|GUAD_HUMAN	1.5	6.787	10.324	7	9
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	sp|P07900|HS90A_HUMAN	1.5	39.753	59.879	27	33
Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	sp|P22234|PUR6_HUMAN	1.5	16.483	24.778	14	21
Histone deacetylase 6 OS=Homo sapiens GN=HDAC6 PE=1 SV=2	sp|Q9UBN7|HDAC6_HUMAN	1.5	9.6958	14.454	9	11
Cyclin-dependent kinase 4 OS=Homo sapiens GN=CDK4 PE=1 SV=2	sp|P11802|CDK4_HUMAN	1.5	4.8479	7.2268	2	5
Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	sp|Q7L576|CYFP1_HUMAN	1.5	4.8479	7.2268	5	7
Triple functional domain protein OS=Homo sapiens GN=TRIO PE=1 SV=2	sp|O75962|TRIO_HUMAN	1.5	4.8479	7.2268	5	7
F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	sp|P47755|CAZA2_HUMAN	1.5	4.8479	7.2268	4	7
Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=2	sp|P48729|KC1A_HUMAN	1.5	4.8479	7.2268	5	7
DnaJ homolog subfamily B member 6 OS=Homo sapiens GN=DNAJB6 PE=1 SV=2	sp|O75190|DNJB6_HUMAN	1.5	4.8479	7.2268	5	7
Mitochondrial inner membrane protein OXA1L OS=Homo sapiens GN=OXA1L PE=1 SV=3	sp|Q15070|OXA1L_HUMAN	1.5	4.8479	7.2268	5	5
Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens GN=HSP90AB3P PE=5 SV=1	sp|Q58FF7|H90B3_HUMAN	1.5	22.3	33.037	17	20
Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1	sp|Q9UBB4|ATX10_HUMAN	1.5	17.452	25.81	17	20
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	sp|Q14697|GANAB_HUMAN	1.5	12.604	18.583	12	16
Transcription factor E2F7 OS=Homo sapiens GN=E2F7 PE=1 SV=3	sp|Q96AV8|E2F7_HUMAN	1.5	20.361	29.939	19	23
Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1	sp|Q9H3U1|UN45A_HUMAN	1.5	7.7566	11.356	7	10
Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	sp|P53007|TXTP_HUMAN	1.5	7.7566	11.356	6	9
Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	sp|P63244|GBLP_HUMAN	1.5	21.331	30.972	19	20
Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	sp|P51659|DHB4_HUMAN	1.4	19.392	27.875	16	19
DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2	sp|P24928|RPB1_HUMAN	1.4	8.7262	12.389	9	11
F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	sp|P52907|CAZA1_HUMAN	1.4	8.7262	12.389	7	10
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	sp|P22695|QCR2_HUMAN	1.4	8.7262	12.389	9	10
Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1	sp|Q15084|PDIA6_HUMAN	1.4	8.7262	12.389	8	11
YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=3	sp|P49750|YLPM1_HUMAN	1.4	2.9087	4.1296	3	4
Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens GN=MDC1 PE=1 SV=3	sp|Q14676|MDC1_HUMAN	1.4	2.9087	4.1296	3	4
Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2	sp|Q27J81|INF2_HUMAN	1.4	2.9087	4.1296	3	4
Eukaryotic peptide chain release factor GTP-binding subunit ERF3B OS=Homo sapiens GN=GSPT2 PE=	sp|Q8IYD1|ERF3B_HUMAN	1.4	2.9087	4.1296	3	3
Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2	sp|Q9ULW0|TPX2_HUMAN	1.4	2.9087	4.1296	3	4
Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1	sp|P01605|KV113_HUMAN	1.4	2.9087	4.1296	1	2
Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	sp|P80723|BASP1_HUMAN	1.4	2.9087	4.1296	2	4
Mitogen-activated protein kinase 6 OS=Homo sapiens GN=MAPK6 PE=1 SV=1	sp|Q16659|MK06_HUMAN	1.4	2.9087	4.1296	3	4
Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=1 SV=1	sp|Q9H078|CLPB_HUMAN	1.4	2.9087	4.1296	3	4
Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2	sp|Q9HA64|KT3K_HUMAN	1.4	2.9087	4.1296	3	3
Phosphoglycolate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1	sp|A6NDG6|PGP_HUMAN	1.4	2.9087	4.1296	3	3
Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1	sp|P12277|KCRB_HUMAN	1.4	2.9087	4.1296	3	4
Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2	sp|P49588|SYAC_HUMAN	1.4	2.9087	4.1296	3	4
Programmed cell death protein 2-like OS=Homo sapiens GN=PDCD2L PE=1 SV=1	sp|Q9BRP1|PDD2L_HUMAN	1.4	2.9087	4.1296	3	4
V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1	sp|P61421|VA0D1_HUMAN	1.4	2.9087	4.1296	3	4
Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3	sp|P43307|SSRA_HUMAN	1.4	2.9087	4.1296	3	3
Cyclin-dependent-like kinase 5 OS=Homo sapiens GN=CDK5 PE=1 SV=3	sp|Q00535|CDK5_HUMAN	1.4	5.8175	8.2592	3	7
Ubiquitin-associated protein 2 OS=Homo sapiens GN=UBAP2 PE=1 SV=1	sp|Q5T6F2|UBAP2_HUMAN	1.4	5.8175	8.2592	4	8
Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	sp|P23258|TBG1_HUMAN	1.4	5.8175	8.2592	6	6
KN motif and ankyrin repeat domain-containing protein 2 OS=Homo sapiens GN=KANK2 PE=1 SV=1	sp|Q63ZY3|KANK2_HUMAN	1.4	5.8175	8.2592	6	8
Coordinator of PRMT5 and differentiation stimulator OS=Homo sapiens GN=COPRS PE=1 SV=3	sp|Q9NQ92|COPRS_HUMAN	1.4	11.635	16.518	7	7
Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	sp|Q71U36|TBA1A_HUMAN	1.4	88.231	124.92	43	39
Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4	sp|O75116|ROCK2_HUMAN	1.4	21.331	29.939	21	25
Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	sp|P68366|TBA4A_HUMAN	1.4	89.201	124.92	40	41
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	sp|Q9BQE3|TBA1C_HUMAN	1.4	91.14	126.98	40	39
Breast cancer type 2 susceptibility protein OS=Homo sapiens GN=BRCA2 PE=1 SV=3	sp|P51587|BRCA2_HUMAN	1.4	9.6958	13.421	10	13
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	sp|P08238|HS90B_HUMAN	1.4	60.114	82.592	39	45
Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3	sp|P35237|SPB6_HUMAN	1.4	6.787	9.2916	7	8
Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1	sp|O43684|BUB3_HUMAN	1.4	6.787	9.2916	7	8
40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	sp|P62266|RS23_HUMAN	1.4	6.787	9.2916	4	6
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	sp|P07355|ANXA2_HUMAN	1.4	61.083	83.624	37	42
Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1	sp|Q16576|RBBP7_HUMAN	1.4	13.574	18.583	11	12
Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	sp|Q9UMS4|PRP19_HUMAN	1.4	13.574	18.583	12	13
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	sp|P50990|TCPQ_HUMAN	1.4	34.905	47.49	30	34
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	sp|P15924|DESP_HUMAN	1.4	241.42	326.24	175	180
La-related protein 4 OS=Homo sapiens GN=LARP4 PE=1 SV=3	sp|Q71RC2|LARP4_HUMAN	1.3	14.544	19.616	13	15
Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3	sp|Q15046|SYK_HUMAN	1.3	14.544	19.616	15	17
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 OS=Homo sapiens GN=PFKFB2 PE=1 SV=2	sp|O60825|F262_HUMAN	1.3	58.175	78.462	32	46
Sodium/potassium-transporting ATPase subunit alpha-2 OS=Homo sapiens GN=ATP1A2 PE=1 SV=1	sp|P50993|AT1A2_HUMAN	1.3	15.513	20.648	11	13
Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=1 SV=1	sp|O60282|KIF5C_HUMAN	1.3	3.8783	5.162	4	5
Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=1 SV=4	sp|Q14766|LTBP1_HUMAN	1.3	3.8783	5.162	4	5
Kinesin-like protein KIF23 OS=Homo sapiens GN=KIF23 PE=1 SV=3	sp|Q02241|KIF23_HUMAN	1.3	3.8783	5.162	4	5
DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2	sp|P49916|DNLI3_HUMAN	1.3	3.8783	5.162	4	5
A-kinase anchor protein 8 OS=Homo sapiens GN=AKAP8 PE=1 SV=1	sp|O43823|AKAP8_HUMAN	1.3	7.7566	10.324	8	9
Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	sp|P41250|SYG_HUMAN	1.3	7.7566	10.324	6	9
THO complex subunit 3 OS=Homo sapiens GN=THOC3 PE=1 SV=1	sp|Q96J01|THOC3_HUMAN	1.3	3.8783	5.162	4	4
Kelch-like ECH-associated protein 1 OS=Homo sapiens GN=KEAP1 PE=1 SV=2	sp|Q14145|KEAP1_HUMAN	1.3	3.8783	5.162	4	5
Dimethyladenosine transferase 2, mitochondrial OS=Homo sapiens GN=TFB2M PE=1 SV=1	sp|Q9H5Q4|TFB2M_HUMAN	1.3	3.8783	5.162	4	5
Non-receptor tyrosine-protein kinase TYK2 OS=Homo sapiens GN=TYK2 PE=1 SV=3	sp|P29597|TYK2_HUMAN	1.3	3.8783	5.162	3	4
Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3	sp|Q8TEM1|PO210_HUMAN	1.3	3.8783	5.162	4	5
Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3	sp|Q15024|EXOS7_HUMAN	1.3	3.8783	5.162	3	3

Angiopoietin-related protein 4 OS=Homo sapiens GN=ANGPTL4 PE=1 SV=2	sp|Q9BY76|ANGL4_HUMAN	1.3	3.8783	5.162	3	5
Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2	sp|Q7L0Y3|MRRP1_HUMAN	1.3	3.8783	5.162	4	4
60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3	sp|Q969Q0|RL36L_HUMAN	1.3	3.8783	5.162	3	3
Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3	sp|Q9Y6G9|DC1L1_HUMAN	1.3	3.8783	5.162	4	5
Twinfilin-1 OS=Homo sapiens GN=TWF1 PE=1 SV=3	sp|Q12792|TWF1_HUMAN	1.3	3.8783	5.162	4	5
Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2	sp|Q99426|TBCB_HUMAN	1.3	3.8783	5.162	4	4
Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 PE=1 SV=3	sp|Q9Y4E8|UBP15_HUMAN	1.3	61.083	80.527	49	55
DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	sp|P33992|MCM5_HUMAN	1.3	20.361	26.842	19	23
Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	sp|P41252|SYIC_HUMAN	1.3	41.692	54.717	37	43
Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 SV=	sp|Q14558|KPRA_HUMAN	1.3	12.604	16.518	11	14
Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1	sp|Q9NY65|TBA8_HUMAN	1.3	55.266	72.268	24	21
T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	sp|Q99832|TCPH_HUMAN	1.3	30.057	39.231	27	31
Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	sp|O15020|SPTN2_HUMAN	1.3	8.7262	11.356	8	8
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens GN=ND	sp|Q16795|NDUA9_HUMAN	1.3	8.7262	11.356	9	8
Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2	sp|Q99623|PHB2_HUMAN	1.3	8.7262	11.356	8	9
Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	sp|P17931|LEG3_HUMAN	1.3	44.6	57.814	22	26
rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2	sp|P22087|FBRL_HUMAN	1.3	22.3	28.907	15	15
RNA-binding protein 5 OS=Homo sapiens GN=RBM5 PE=1 SV=2	sp|P52756|RBM5_HUMAN	1.3	13.574	17.551	11	12
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	sp|P00338|LDHA_HUMAN	1.3	18.422	23.745	16	18
Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	sp|P14625|ENPL_HUMAN	1.3	23.27	29.939	21	25
Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2	sp|Q9P2J5|SYLC_HUMAN	1.3	23.27	29.939	23	28
Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	sp|P47897|SYQ_HUMAN	1.3	24.239	30.972	23	26
Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1	sp|O95433|AHSA1_HUMAN	1.3	4.8479	6.1944	5	6
PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1	sp|Q6Y7W6|PERQ2_HUMAN	1.3	4.8479	6.1944	4	5
Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1	sp|P23921|RIR1_HUMAN	1.3	4.8479	6.1944	5	6
7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	sp|Q9UBM7|DHCR7_HUMAN	1.3	4.8479	6.1944	5	5
FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1	sp|Q9Y5B9|SP16H_HUMAN	1.3	4.8479	6.1944	5	6
Cullin-4A OS=Homo sapiens GN=CUL4A PE=1 SV=3	sp|Q13619|CUL4A_HUMAN	1.3	4.8479	6.1944	4	5
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	sp|P63104|1433Z_HUMAN	1.3	19.392	24.778	12	15
Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	sp|P54136|SYRC_HUMAN	1.3	19.392	24.778	16	20
Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2	sp|Q14978|NOLC1_HUMAN	1.3	14.544	18.583	13	15
Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	sp|P60891|PRPS1_HUMAN	1.3	20.361	25.81	15	16
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	sp|P62258|1433E_HUMAN	1.3	15.513	19.616	12	13
Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	sp|Q5D862|FILA2_HUMAN	1.3	15.513	19.616	5	11
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	sp|P22626|ROA2_HUMAN	1.3	57.205	72.268	30	31
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN	sp|O15294|OGT1_HUMAN	1.3	47.509	59.879	41	48
EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2	sp|Q9NZN4|EHD2_HUMAN	1.3	10.665	13.421	10	12
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	sp|P49368|TCPG_HUMAN	1.3	42.661	53.685	33	36
Rabankyrin-5 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2	sp|Q9P2R3|ANFY1_HUMAN	1.3	48.479	60.911	44	51
60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	sp|P61254|RL26_HUMAN	1.3	32.966	41.296	10	13
Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=1 SV=1	sp|P54105|ICLN_HUMAN	1.2	72.718	90.851	19	23
POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2	sp|A5A3E0|POTEF_HUMAN	1.2	39.753	49.555	15	24
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	sp|P10515|ODP2_HUMAN	1.2	11.635	14.454	11	11
Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2	sp|Q9UDY2|ZO2_HUMAN	1.2	5.8175	7.2268	5	7
Protein AAR2 homolog OS=Homo sapiens GN=AAR2 PE=1 SV=2	sp|Q9Y312|AAR2_HUMAN	1.2	5.8175	7.2268	6	7
THO complex subunit 6 homolog OS=Homo sapiens GN=THOC6 PE=1 SV=1	sp|Q86W42|THOC6_HUMAN	1.2	5.8175	7.2268	3	6
Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=1 SV=2	sp|Q53H12|AGK_HUMAN	1.2	5.8175	7.2268	6	7
Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	sp|P68133|ACTS_HUMAN	1.2	66.901	82.592	26	30
Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	sp|P12004|PCNA_HUMAN	1.2	12.604	15.486	11	12
116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1	sp|Q15029|U5S1_HUMAN	1.2	37.813	46.458	30	34
14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	sp|P31946|1433B_HUMAN	1.2	19.392	23.745	12	14
Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	sp|O14980|XPO1_HUMAN	1.2	19.392	23.745	19	19
ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2	sp|Q15717|ELAV1_HUMAN	1.2	19.392	23.745	14	18
T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	sp|P40227|TCPZ_HUMAN	1.2	26.179	32.004	21	24
(CONTAMINANT) trypsinogen anionic precursor [Bos taurus]	CONTAM_CAA38513.1	1.2	6.787	8.2592	2	2
14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	sp|P31947|1433S_HUMAN	1.2	6.787	8.2592	4	5
L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	sp|P07195|LDHB_HUMAN	1.2	6.787	8.2592	7	7
Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	sp|P35221|CTNA1_HUMAN	1.2	6.787	8.2592	6	7
Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1	sp|Q13838|DX39B_HUMAN	1.2	6.787	8.2592	6	7
Nucleolar protein 6 OS=Homo sapiens GN=NOL6 PE=1 SV=2	sp|Q9H6R4|NOL6_HUMAN	1.2	6.787	8.2592	7	7
Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	sp|O43852|CALU_HUMAN	1.2	6.787	8.2592	6	6
Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1	sp|Q8NBJ5|GT251_HUMAN	1.2	6.787	8.2592	7	8
Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	sp|P61160|ARP2_HUMAN	1.2	6.787	8.2592	7	8
Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	sp|P35606|COPB2_HUMAN	1.2	13.574	16.518	14	16
Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	sp|P41091|IF2G_HUMAN	1.2	13.574	16.518	13	12
Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2	sp|P35030|TRY3_HUMAN	1.2	35.874	43.361	13	11
60S ribosomal protein L26-like 1 OS=Homo sapiens GN=RPL26L1 PE=1 SV=1	sp|Q9UNX3|RL26L_HUMAN	1.2	30.057	36.134	9	13
Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	sp|P67936|TPM4_HUMAN	1.2	15.513	18.583	13	13
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	sp|Q14247|SRC8_HUMAN	1.2	15.513	18.583	15	16
Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	sp|P50454|SERPH_HUMAN	1.2	15.513	18.583	12	14
Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1	sp|P63267|ACTH_HUMAN	1.2	69.809	83.624	27	30
Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1	sp|Q9UJZ1|STML2_HUMAN	1.2	7.7566	9.2916	8	7
Serum paraoxonase/arylesterase 2 OS=Homo sapiens GN=PON2 PE=1 SV=3	sp|Q15165|PON2_HUMAN	1.2	7.7566	9.2916	6	5
Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1	sp|Q15942|ZYX_HUMAN	1.2	7.7566	9.2916	8	8
Alkaline phosphatase, placental type OS=Homo sapiens GN=ALPP PE=1 SV=2	sp|P05187|PPB1_HUMAN	1.2	24.239	28.907	19	22
Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	sp|P63261|ACTG_HUMAN	1.2	146.41	174.47	55	70
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	sp|P23396|RS3_HUMAN	1.2	57.205	68.138	35	35
Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	sp|P23246|SFPQ_HUMAN	1.2	16.483	19.616	14	16
cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens GN=PRKAR1A PE=1	sp|P10644|KAP0_HUMAN	1.2	16.483	19.616	16	17
Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	sp|P25789|PSA4_HUMAN	1.2	43.631	51.62	29	27
Nardilysin OS=Homo sapiens GN=NRD1 PE=1 SV=2	sp|O43847|NRDC_HUMAN	1.2	8.7262	10.324	9	10
Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2	sp|Q9UQE7|SMC3_HUMAN	1.2	8.7262	10.324	9	10
Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=1 SV=2	sp|O43432|IF4G3_HUMAN	1.2	8.7262	10.324	7	7
Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	sp|P07814|SYEP_HUMAN	1.2	65.931	77.43	56	58
DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	sp|Q14566|MCM6_HUMAN	1.2	9.6958	11.356	10	11
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 OS=Homo sapiens GN=TAB1 PE=1 SV=1	sp|Q15750|TAB1_HUMAN	1.2	41.692	48.523	30	25
Alstrom syndrome protein 1 OS=Homo sapiens GN=ALMS1 PE=1 SV=3	sp|Q8TCU4|ALMS1_HUMAN	1.2	10.665	12.389	11	12
Very large A-kinase anchor protein OS=Homo sapiens GN=CRYBG3 PE=1 SV=3	sp|Q68DQ2|CRBG3_HUMAN	1.2	10.665	12.389	11	12
pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2	sp|Q9C0J8|WDR33_HUMAN	1.2	10.665	12.389	10	11
Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=2	sp|Q99700|ATX2_HUMAN	1.2	10.665	12.389	10	11
Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	sp|P45880|VDAC2_HUMAN	1.2	10.665	12.389	9	10
Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	sp|P35232|PHB_HUMAN	1.2	10.665	12.389	10	11
Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	sp|Q14203|DCTN1_HUMAN	1.2	21.331	24.778	21	22
Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2	sp|P23458|JAK1_HUMAN	1.2	99.866	115.63	71	74
Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	sp|Q9UPQ9|TNR6B_HUMAN	1.2	22.3	25.81	22	23
14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	sp|Q04917|1433F_HUMAN	1.2	11.635	13.421	9	9
Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	sp|Q14444|CAPR1_HUMAN	1.2	23.27	26.842	20	20
Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3	sp|Q9Y285|SYFA_HUMAN	1.2	11.635	13.421	11	10
Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5	sp|Q9UPN7|PP6R1_HUMAN	1.2	11.635	13.421	12	12
T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	sp|P17987|TCPA_HUMAN	1.2	34.905	40.263	29	27
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	sp|P60709|ACTB_HUMAN	1.1	147.38	169.31	55	68
Proline and serine-rich protein 1 OS=Homo sapiens GN=PROSER1 PE=1 SV=2	sp|Q86XN7|PRSR1_HUMAN	1.1	12.604	14.454	11	13
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	sp|P02545|LMNA_HUMAN	1.1	37.813	43.361	34	32
Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	sp|O75369|FLNB_HUMAN	1.1	102.77	117.69	86	92
Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	sp|P61163|ACTZ_HUMAN	1.1	13.574	15.486	11	14

Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	sp|Q9NZM1|MYOF_HUMAN	1.1	41.692	47.49	40	42
Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	sp|P53618|COPB_HUMAN	1.1	29.087	33.037	23	25
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	sp|P27348|1433T_HUMAN	1.1	30.057	34.069	18	18
HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3	sp|Q9H583|HEAT1_HUMAN	1.1	15.513	17.551	12	17
Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	sp|Q15645|PCH2_HUMAN	1.1	15.513	17.551	12	14
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	sp|P55072|TERA_HUMAN	1.1	46.54	52.652	36	43
Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	sp|Q13045|FLII_HUMAN	1.1	16.483	18.583	16	17
BTB/POZ domain-containing protein KCTD17 OS=Homo sapiens GN=KCTD17 PE=1 SV=3	sp|Q8N5Z5|KCD17_HUMAN	1.1	33.935	38.199	16	18
(CONTAMINANT) Trypsin precursor	CONTAM_TRYP_PIG	1.1	382.98	430.51	73	80
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	sp|P62847|RS24_HUMAN	1.1	17.452	19.616	5	5
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	sp|P46781|RS9_HUMAN	1.1	35.874	40.263	15	17
Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	sp|Q562R1|ACTBL_HUMAN	1.1	39.753	44.393	21	22
Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2	sp|P11908|PRPS2_HUMAN	1.1	20.361	22.713	16	13
Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	sp|P01859|IGHG2_HUMAN	1.1	131.86	146.6	11	13
Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2	sp|Q8N163|CCAR2_HUMAN	1.1	23.27	25.81	22	24
POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	sp|Q6S8J3|POTEE_HUMAN	1.1	48.479	53.685	20	26
DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	sp|O60884|DNJA2_HUMAN	1.1	25.209	27.875	20	19
Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 OS=Homo sapiens GN=DHX38 PE=1 SV=2	sp|Q92620|PRP16_HUMAN	1.1	29.087	32.004	25	28
Spindlin-1 OS=Homo sapiens GN=SPIN1 PE=1 SV=3	sp|Q9Y657|SPIN1_HUMAN	1.1	34.905	38.199	18	18
Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2	sp|Q14254|FLOT2_HUMAN	1.1	34.905	38.199	27	25
DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	sp|P25205|MCM3_HUMAN	1.1	37.813	41.296	34	31
Protein phosphatase 1A OS=Homo sapiens GN=PPM1A PE=1 SV=1	sp|P35813|PPM1A_HUMAN	1.1	39.753	43.361	21	21
Ig kappa chain V-II region GM607 (Fragment) OS=Homo sapiens PE=4 SV=1	sp|P06309|KV205_HUMAN	1.1	46.54	50.587	8	9
Ig kappa chain V-II region RPMI 6410 OS=Homo sapiens PE=4 SV=1	sp|P06310|KV206_HUMAN	1.1	46.54	50.587	8	9
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	sp|P08670|VIME_HUMAN	1.1	70.779	76.397	44	43
60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	sp|P84098|RL19_HUMAN	1.1	13.574	14.454	6	4
Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	sp|P25788|PSA3_HUMAN	1.1	12.604	13.421	10	10
RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	sp|Q9Y230|RUVB2_HUMAN	1.1	12.604	13.421	13	13
Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1	sp|O15372|EIF3H_HUMAN	1.1	12.604	13.421	12	10
Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3	sp|Q02978|M2OM_HUMAN	1.1	12.604	13.421	12	12
SLAIN motif-containing protein 2 OS=Homo sapiens GN=SLAIN2 PE=1 SV=2	sp|Q9P270|SLAI2_HUMAN	1.1	18.422	19.616	19	19
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	sp|P29692|EF1D_HUMAN	1.1	24.239	25.81	12	14
Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2	sp|P12268|IMDH2_HUMAN	1.1	17.452	18.583	12	15
Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=2	sp|Q08043|ACTN3_HUMAN	1.1	2.9087	3.0972	3	3
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	sp|P06733|ENOA_HUMAN	1.1	29.087	30.972	24	21
Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	sp|P04114|APOB_HUMAN	1.1	2.9087	3.0972	3	3
Testin OS=Homo sapiens GN=TES PE=1 SV=1	sp|Q9UGI8|TES_HUMAN	1.1	2.9087	3.0972	3	3
Tetratricopeptide repeat protein 28 OS=Homo sapiens GN=TTC28 PE=1 SV=4	sp|Q96AY4|TTC28_HUMAN	1.1	2.9087	3.0972	3	3
Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	sp|P30740|ILEU_HUMAN	1.1	2.9087	3.0972	3	3
AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2	sp|Q9Y4W6|AFG32_HUMAN	1.1	2.9087	3.0972	3	3
Transportin-3 OS=Homo sapiens GN=TNPO3 PE=1 SV=3	sp|Q9Y5L0|TNPO3_HUMAN	1.1	2.9087	3.0972	3	3
ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1	sp|P28288|ABCD3_HUMAN	1.1	2.9087	3.0972	3	3
Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2	sp|O00767|ACOD_HUMAN	1.1	2.9087	3.0972	3	2
Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1	sp|Q9BPW8|NIPS1_HUMAN	1.1	2.9087	3.0972	3	2
Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2	sp|Q99816|TS101_HUMAN	1.1	2.9087	3.0972	3	3
Transcription elongation factor SPT5 OS=Homo sapiens GN=SUPT5H PE=1 SV=1	sp|O00267|SPT5H_HUMAN	1.1	2.9087	3.0972	3	3
Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1	sp|P36507|MP2K2_HUMAN	1.1	2.9087	3.0972	3	3
Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4	sp|Q14160|SCRIB_HUMAN	1.1	11.635	12.389	12	12
WD repeat-containing protein 5 OS=Homo sapiens GN=WDR5 PE=1 SV=1	sp|P61964|WDR5_HUMAN	1.1	11.635	12.389	8	8
Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	sp|P20700|LMNB1_HUMAN	1.1	11.635	12.389	11	10
Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens GN=PRPSAP2 PE=1 SV=	sp|O60256|KPRB_HUMAN	1.1	11.635	12.389	10	9
Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=1	sp|Q5T750|XP32_HUMAN	1.1	6.787	7.2268	3	5
Polymerase delta-interacting protein 2 OS=Homo sapiens GN=POLDIP2 PE=1 SV=1	sp|Q9Y2S7|PDIP2_HUMAN	1.1	6.787	7.2268	7	5
Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1	sp|O15269|SPTC1_HUMAN	1.1	6.787	7.2268	7	7
Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1	sp|Q8WXF1|PSPC1_HUMAN	1.1	6.787	7.2268	7	7
F-box only protein 2 OS=Homo sapiens GN=FBXO2 PE=1 SV=2	sp|Q9UK22|FBX2_HUMAN	1.1	6.787	7.2268	7	7
U2 small nuclear ribonucleoprotein B'' OS=Homo sapiens GN=SNRPB2 PE=1 SV=1	sp|P08579|RU2B_HUMAN	1.1	6.787	7.2268	6	7
Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	sp|Q09028|RBBP4_HUMAN	1.1	7.7566	8.2592	7	7
Catenin alpha-2 OS=Homo sapiens GN=CTNNA2 PE=1 SV=5	sp|P26232|CTNA2_HUMAN	1.1	3.8783	4.1296	3	4
Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2	sp|Q5VYK3|ECM29_HUMAN	1.1	3.8783	4.1296	4	4
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	sp|P62899|RL31_HUMAN	1.1	7.7566	8.2592	6	6
Activity-dependent neuroprotector homeobox protein OS=Homo sapiens GN=ADNP PE=1 SV=1	sp|Q9H2P0|ADNP_HUMAN	1.1	3.8783	4.1296	4	4
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN	sp|P13995|MTDC_HUMAN	1.1	7.7566	8.2592	8	7
DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4	sp|P49736|MCM2_HUMAN	1.1	3.8783	4.1296	4	4
Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1	sp|Q9UKF6|CPSF3_HUMAN	1.1	3.8783	4.1296	4	4
Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	sp|B9A064|IGLL5_HUMAN	1.1	3.8783	4.1296	2	2
GDP-mannose 4,6 dehydratase OS=Homo sapiens GN=GMDS PE=1 SV=1	sp|O60547|GMDS_HUMAN	1.1	3.8783	4.1296	4	4
Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	sp|Q9BS26|ERP44_HUMAN	1.1	3.8783	4.1296	4	4
Tetratricopeptide repeat protein 25 OS=Homo sapiens GN=TTC25 PE=1 SV=2	sp|Q96NG3|TTC25_HUMAN	1.1	3.8783	4.1296	2	1
Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2	sp|P53004|BIEA_HUMAN	1.1	3.8783	4.1296	4	4
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	sp|P50991|TCPD_HUMAN	1.1	38.783	41.296	23	25
Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	sp|P06493|CDK1_HUMAN	1.1	16.483	17.551	12	14
RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3	sp|P49756|RBM25_HUMAN	1.1	16.483	17.551	16	14
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	sp|P83731|RL24_HUMAN	1.1	16.483	17.551	7	6
Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2	sp|Q8N1F7|NUP93_HUMAN	1.1	8.7262	9.2916	9	8
U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=1 SV=3	sp|P09012|SNRPA_HUMAN	1.1	8.7262	9.2916	9	6
Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens GN=CPSF2 PE=1 SV=2	sp|Q9P2I0|CPSF2_HUMAN	1.1	10.665	11.356	10	8
Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	sp|Q00610|CLH1_HUMAN	1.1	96.958	103.24	80	76
E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1	sp|P19474|RO52_HUMAN	1.1	96.958	103.24	53	56
HLA class I histocompatibility antigen, B-47 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1	sp|P30485|1B47_HUMAN	1.1	4.8479	5.162	5	5
Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	sp|P08123|CO1A2_HUMAN	1.1	4.8479	5.162	2	3
DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2	sp|P26358|DNMT1_HUMAN	1.1	4.8479	5.162	5	5
Putative RNA-binding protein Luc7-like 1 OS=Homo sapiens GN=LUC7L PE=1 SV=1	sp|Q9NQ29|LUC7L_HUMAN	1.1	4.8479	5.162	2	3
Fanconi anemia group I protein OS=Homo sapiens GN=FANCI PE=1 SV=4	sp|Q9NVI1|FANCI_HUMAN	1.1	9.6958	10.324	10	10
Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	sp|Q9Y266|NUDC_HUMAN	1.1	9.6958	10.324	9	10
Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2	sp|Q32MZ4|LRRF1_HUMAN	1.1	4.8479	5.162	5	5
U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1	sp|Q9BVJ6|UT14A_HUMAN	1.1	4.8479	5.162	5	5
Condensin-2 complex subunit G2 OS=Homo sapiens GN=NCAPG2 PE=1 SV=1	sp|Q86XI2|CNDG2_HUMAN	1.1	4.8479	5.162	5	5
WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1	sp|Q8NI36|WDR36_HUMAN	1.1	4.8479	5.162	5	5
ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2	sp|Q01813|PFKAP_HUMAN	1.1	4.8479	5.162	5	5
SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1	sp|Q6P3W7|SCYL2_HUMAN	1.1	4.8479	5.162	5	5
TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1	sp|Q13148|TADBP_HUMAN	1.1	4.8479	5.162	3	3
Unconventional myosin-Ia OS=Homo sapiens GN=MYO1A PE=1 SV=1	sp|Q9UBC5|MYO1A_HUMAN	1.1	4.8479	5.162	5	5
Exosome complex component RRP4 OS=Homo sapiens GN=EXOSC2 PE=1 SV=2	sp|Q13868|EXOS2_HUMAN	1.1	4.8479	5.162	5	5
PCI domain-containing protein 2 OS=Homo sapiens GN=PCID2 PE=1 SV=2	sp|Q5JVF3|PCID2_HUMAN	1.1	4.8479	5.162	5	5
NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3	sp|P00387|NB5R3_HUMAN	1.1	4.8479	5.162	5	4
Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	sp|P04040|CATA_HUMAN	1.1	4.8479	5.162	4	3
39S ribosomal protein L4, mitochondrial OS=Homo sapiens GN=MRPL4 PE=1 SV=1	sp|Q9BYD3|RM04_HUMAN	1.1	4.8479	5.162	4	4
DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	sp|P33993|MCM7_HUMAN	1.1	21.331	22.713	20	21
Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	sp|O14818|PSA7_HUMAN	1.1	21.331	22.713	17	17
Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1	sp|Q9BPX3|CND3_HUMAN	1.1	5.8175	6.1944	6	5
Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3	sp|Q9P0L0|VAPA_HUMAN	1.1	5.8175	6.1944	6	4
DNA-directed RNA polymerase III subunit RPC2 OS=Homo sapiens GN=POLR3B PE=1 SV=2	sp|Q9NW08|RPC2_HUMAN	1.1	5.8175	6.1944	6	6
Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3	sp|P53985|MOT1_HUMAN	1.1	5.8175	6.1944	5	4
DnaJ homolog subfamily C member 10 OS=Homo sapiens GN=DNAJC10 PE=1 SV=2	sp|Q8IXB1|DJC10_HUMAN	1.1	5.8175	6.1944	6	6

DnaJ homolog subfamily B member 4 OS=Homo sapiens GN=DNAJB4 PE=1 SV=1	sp|Q9UDY4|DNJB4_HUMAN	1.1	5.8175	6.1944	5	6
Tyrosine-protein kinase CSK OS=Homo sapiens GN=CSK PE=1 SV=1	sp|P41240|CSK_HUMAN	1.1	5.8175	6.1944	6	6
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	sp|P04406|G3P_HUMAN	1.1	36.844	39.231	14	17
Myopalladin OS=Homo sapiens GN=MYPN PE=1 SV=2	sp|Q86TC9|MYPN_HUMAN	1.1	15.513	16.518	15	14
Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	sp|Q14103|HNRPD_HUMAN	1.1	15.513	16.518	13	13
Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	sp|Q15365|PCBP1_HUMAN	1.1	30.057	32.004	18	18
Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4	sp|P55265|DSRAD_HUMAN	1.1	19.392	20.648	19	19
26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2	sp|P48556|PSMD8_HUMAN	1.1	19.392	20.648	17	16
2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3	sp|Q02218|ODO1_HUMAN	1.1	14.544	15.486	15	13
Retinoic acid-induced protein 3 OS=Homo sapiens GN=GPRC5A PE=1 SV=2	sp|Q8NFJ5|RAI3_HUMAN	1.1	14.544	15.486	4	6
TATA-binding protein-associated factor 172 OS=Homo sapiens GN=BTAF1 PE=1 SV=2	sp|O14981|BTAF1_HUMAN	1.1	1.9392	2.0648	2	2
LINE-1 retrotransposable element ORF1 protein OS=Homo sapiens GN=L1RE1 PE=1 SV=1	sp|Q9UN81|LORF1_HUMAN	1.1	1.9392	2.0648	2	2
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	sp|P10909|CLUS_HUMAN	1.1	1.9392	2.0648	1	2
Nck-associated protein 5-like OS=Homo sapiens GN=NCKAP5L PE=1 SV=2	sp|Q9HCH0|NCK5L_HUMAN	1.1	1.9392	2.0648	2	1
Serine/threonine-protein kinase mTOR OS=Homo sapiens GN=MTOR PE=1 SV=1	sp|P42345|MTOR_HUMAN	1.1	1.9392	2.0648	2	2
Elongator complex protein 2 OS=Homo sapiens GN=ELP2 PE=1 SV=2	sp|Q6IA86|ELP2_HUMAN	1.1	1.9392	2.0648	2	1
Golgin subfamily A member 4 OS=Homo sapiens GN=GOLGA4 PE=1 SV=1	sp|Q13439|GOGA4_HUMAN	1.1	1.9392	2.0648	2	2
Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3	sp|P35573|GDE_HUMAN	1.1	1.9392	2.0648	2	2
Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2	sp|P49790|NU153_HUMAN	1.1	1.9392	2.0648	2	2
Gamma-tubulin complex component 3 OS=Homo sapiens GN=TUBGCP3 PE=1 SV=2	sp|Q96CW5|GCP3_HUMAN	1.1	1.9392	2.0648	2	2
F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens GN=TBL1XR1 PE=1 SV=1	sp|Q9BZK7|TBL1R_HUMAN	1.1	1.9392	2.0648	2	2
Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1	sp|Q9UJW0|DCTN4_HUMAN	1.1	1.9392	2.0648	2	2
E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2	sp|Q5VTR2|BRE1A_HUMAN	1.1	1.9392	2.0648	2	2
GPN-loop GTPase 3 OS=Homo sapiens GN=GPN3 PE=1 SV=2	sp|Q9UHW5|GPN3_HUMAN	1.1	1.9392	2.0648	1	2
Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1	sp|Q99829|CPNE1_HUMAN	1.1	1.9392	2.0648	2	2
Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1	sp|P01040|CYTA_HUMAN	1.1	1.9392	2.0648	1	2
Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6	sp|P17655|CAN2_HUMAN	1.1	1.9392	2.0648	2	2
TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2	sp|O75663|TIPRL_HUMAN	1.1	1.9392	2.0648	2	2
CCR4-NOT transcription complex subunit 7 OS=Homo sapiens GN=CNOT7 PE=1 SV=3	sp|Q9UIV1|CNOT7_HUMAN	1.1	1.9392	2.0648	2	2
Ribonuclease P protein subunit p38 OS=Homo sapiens GN=RPP38 PE=1 SV=2	sp|P78345|RPP38_HUMAN	1.1	1.9392	2.0648	2	2
Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	sp|Q9NZT1|CALL5_HUMAN	1.1	1.9392	2.0648	2	2
Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1	sp|Q96A33|CCD47_HUMAN	1.1	1.9392	2.0648	2	2
Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	sp|P78417|GSTO1_HUMAN	1.1	1.9392	2.0648	2	2
Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3	sp|O00154|BACH_HUMAN	1.1	1.9392	2.0648	2	2
Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3	sp|Q15691|MARE1_HUMAN	1.1	1.9392	2.0648	2	2
WD repeat-containing protein 41 OS=Homo sapiens GN=WDR41 PE=2 SV=3	sp|Q9HAD4|WDR41_HUMAN	1.1	1.9392	2.0648	2	2
Transcription termination factor 3, mitochondrial OS=Homo sapiens GN=MTERF3 PE=1 SV=2	sp|Q96E29|MTEF3_HUMAN	1.1	1.9392	2.0648	2	2
General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2	sp|O60763|USO1_HUMAN	1.1	1.9392	2.0648	2	2
Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens GN=ERGIC1 PE=1 SV	sp|Q969X5|ERGI1_HUMAN	1.1	1.9392	2.0648	2	2
PIH1 domain-containing protein 1 OS=Homo sapiens GN=PIH1D1 PE=1 SV=1	sp|Q9NWS0|PIHD1_HUMAN	1.1	1.9392	2.0648	2	2
Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=1 SV=2	sp|Q14318|FKBP8_HUMAN	1.1	1.9392	2.0648	2	2
Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=	sp|P39687|AN32A_HUMAN	1.1	1.9392	2.0648	2	2
C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1	sp|P56545|CTBP2_HUMAN	1.1	1.9392	2.0648	2	2
Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1	sp|Q7L1Q6|BZW1_HUMAN	1.1	1.9392	2.0648	2	2
RNA-binding protein 7 OS=Homo sapiens GN=RBM7 PE=1 SV=1	sp|Q9Y580|RBM7_HUMAN	1.1	1.9392	2.0648	2	2
EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1	sp|Q9H223|EHD4_HUMAN	1.1	1.9392	2.0648	2	2
RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3	sp|P98175|RBM10_HUMAN	1.1	163.86	173.44	96	97
Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2	sp|P23588|IF4B_HUMAN	1.1	176.46	185.83	85	80

APPENDIX B

HYDROPHILIC METABOLITES IN BROWN ADIPOSE TISSUE

		ApoL6-BAT RT				
Sample	11010-tissue-pos-qc-1	11010-tissue-pos–1	11010-tissue-pos–2	11010-tissue-pos–3	11010-tissue-pos–4	11010-tissue-pos–5
Sample		11010-tissue-pos–1	11010-tissue-pos–2	11010-tissue-pos–3	11010-tissue-pos–4	11010-tissue-pos–5
Acq. Date-Time	11/ 10/ 2018 10:45	11/ 10/ 2018 11:16	11/ 10/ 2018 11:47	11/ 10/ 2018 12:17	11/ 10/ 2018 12:48	11/ 10/ 2018 13:19
Phenylbutazone Results	1123.14012	3147.108966	1141.023172	1742.39548	1791.148547	1914.404728
3-hydroxykynurenine Results	5946.967042	19818.11799	12312.38168	21248.53411	15950.82971	12320.65387
NAD Results						
dTMP Results	2194.270059	4423.298573	2839.881866	5768.532133	5191.492385	3617.819218
N,N-Dicyclohexylurea Results	650.1260289	14825.20383	1259.857408	14892.38199	10194.71039	3558.496671
4-Pyridoxic acid Results	14414.92774	17962.42678	24567.77275	24951.8955	26495.63429	19480.48101
Melatonin Results	445.8477846	4561.817151	509.6321772	6295.507938	4575.032194	4431.846073
Urate Results	3738.421807	14078.16971	3637.347778	16365.78259	9602.502545	5728.645641
Caffeine Results	266.9906649	2633.870481	530.6881977	3508.347145	2370.370587	1950.562877
Folinic acid Results	132.7878556	440.3968329	128.837668	98.19693032	588.421416	603.2822395
lenalidomide Results	29.63853245	549.5005104	474.9184387	27.33152451	39.06418794	535.6405106
Tetracaine Results	168.8730297	83.32748864	28.0314399	218.2180687	1452.09839	235.0365389
3-Indolepropionic acid Results	174.4670483	11.86910284	461.4003211	114.5685318	85.60096931	352.2631078
Anthranilic acid Results	10732.49531	6354.25633	1676.071255	5677.000498	42011.39764	6820.338607
2-Pyrrolidinone Results	9722.845546	37388.42905	9612.809067	43191.86847	45504.42682	41207.225
Phosphocreatine Results	187941.231	515564.0203	266352.9383	504384.1158	629238.2892	567782.1273
Dihydroxyacetone Results	36068.64946	27438.30495	1525.212198	21128.41582	41047.02315	32881.35363
Nicotinamide Results	14855759.7	2311061.236	14759656.47	3679999.432	4923008.19	3093131.115
Imidazole Results	16973.85604	87062.04741	43258.91322	124360.0724	144166.0397	93030.02205
N-Acetylethanolamine Results	8195.599857	17932.43382	6247.736242	15434.40838	15394.35526	19728.77569
Allopurinol Results	96.1448282	698.044854	361.3258069	1760.075141	1959.336093	1831.989499
Xanthurenic acid Results	86.2823077	169.8941395	28.87674264	361.5464447	188.2182495	142.6178488
2-Deoxyuridine Results	576.0285729	44.3399365	257.9001738	1386.124571	328.5160936	493.9001586
Pyridoxine Results	247.4076867	30.93977732	53.06111777	134.1834244	163.0989637	74.56611097
Decanoylcarnitine Results	0	13663.51734	30525.16895	9043.640157	8257.708786	11405.82957
Kynurenic acid Results	264.8760997	240.3963572	68.70746603	223.1688594	142.7541538	54.15092535
Hippuric acid Results	0	107.1550749	26.91597629	18.29595294	386.0597231	27.0614354
Propranolol Results	226.3000866	1477.97177	90.38204049	448.1436819	1620.520226	1109.306608
2-Phenylglycinol Results	292.0553925	1526.502854	0	1206.660146	1602.127344	2559.823125
Acetylcysteine Results	1118.378967	1540.084883	4267.732711	757.3047542	256.9347761	1741.684932
2-Deoxyadenosine Results	0	1953.663726	940.292375	3138.38246	1117.009604	3085.524077
Adenine Results	189061.0036	70671.76151	223850.5212	82908.864	60748.94064	61673.64716
Isovalerylglycine Results	1141.862836	1202.655266	1551.913873	667.0992208	686.2416911	898.3093029
Hypoxanthine Results	285173.2965	51980.0644	283863.9387	57726.82022	71229.8795	49338.82674
Uridine Results	34951.16106	10593.71658	86881.19758	10957.53257	18267.36315	12442.50317
Creatinine Results	6719853.749	1423538.933	2689281.094	2004077.18	2662073.306	555997.8551
Adenosine Results	1392821.024	239104.9205	2260698.755	384152.2617	324792.7344	256973.5173
Xanthine Results	9606.851604	1445.016236	25701.85221	1807.907631	2462.38411	2078.555353
Tryptamine Results	280.2675942	186.3991638	394.4151993	67.48195003	299.0065357	368.9964676
Acetylcholine Results	226673.5243	653.4671562	134229.7392	1545.058581	1601.553712	1231.898384
Cytosine Results	167146.9053	28277.1668	131329.4947	37541.59974	10144.28555	20436.69888
2-Deoxycytidine Results	76092.52207	5089.083544	48243.04179	17060.19773	7037.049634	4651.22846
Nicotinic acid Results	6115.984943	2900.870648	2747.533972	5274.459782	2887.398933	10622.49553
Inosine Results	2456638.167	1478764.374	1785366.701	1711672.983	1850569.461	669905.955
5-Methylcytidine Results	6211.079352	5106.882012	3338.037311	6322.424223	9182.825081	6302.592467
Biotin Results	0	22216.52075	846.6037577	6674.105194	21598.26053	4513.845083
Metanephrine Results	0	1944.391259	814.3986773	3386.281266	3217.730222	3234.947665
2-deoxyguanosine Results	9858.133346	5315.705185	273.3895405	32663.83996	40900.28539	10804.14639
Guanine Results	63288.05306	74081.00431	91938.27719	132838.7249	110864.9322	81750.32366
Dopamine Results	532.7440153	1524.948324	1540.635662	1682.04048	779.1333979	531.9892875
6-Methyl-DL-Tryptophan Results	3930.202504	2740.565018	8958.644919	2458.692381	2424.396019	2612.578211
Pantothenic acid Results	1634183.562	1496456.339	1096675.201	1288701.586	2844610.041	2423601.449
Amiloride Results	18882.51819	13318.15659	17239.53107	18542.70682	24534.51328	10756.29675
Cytidine Results	335326.2426	320653.4673	258233.9755	306245.5288	471137.8635	330402.6786
Nicotinuric acid Results	0	1808.120464	1605.580362	716.9121391	4908.978867	686.7241057
Serotonin Results	165.6316917	363.5454713	735.5960426	968.0037996	1178.255289	261.892648
Acetylglycine Results	219.4252943	34.40349838	47.00060504	178.7349794	115.3509703	46.63642873
Phenylalanine Results	1948348.287	1420029.638	1608039.291	1746224.446	1774247.711	1633895.462
N-Acetyl-D-galactosamine Results	0	10871.05208	6220.314499	6994.47384	15651.82974	12023.32269
Tryptophan Results	234126.6139	95120.0227	225539.9263	56776.21099	89613.33675	123047.2316
Urocanic acid Results	24025.61733	31218.6363	29177.87967	40274.34127	71683.65755	63912.256
Indole-3-lactic acid Results	11604.86831	5988.857706	8118.042189	4921.545593	8472.920663	6991.425532
Normetanephrine Results	13930.98077	13788.04127	11174.67914	21871.03562	15848.68924	12910.83228
isoleucine/ Leucine/ Norleucine Re	6677345.338	3789309.564	4211287.167	8534802.611	6719523.816	5053602.916
Kynurenine Results	330.9756531	302.3602177	394.8271052	388.1595734	392.0117497	245.0341139
N-Acetyl-D-Glucosamine Results						
Acetylglucosamine Results	2142.410404	1249.533394	2265.018439	1227.653479	3316.812382	1665.167651
HIAA Results	0	468.2660594	3250.207194	2674.602427	603.012748	
6-Hydroxynicotinic acid Results	1421.842823	2041.369623	226.3087188	10416.60471	2622.026604	14220.808
Guanosine Results	121058.2254	150899.5487	193310.8058	253056.3775	224735.9237	155737.3691
Pyroglutamic acid Results	134637.6671	89612.43738	94332.2162	94241.29534	118973.6755	117823.3903
Isoleucine Results	6743766.872	3791948.204	4154931.326	8555379.51	6609469.073	5061965.48
Betaine Results	55091520.13	50950540.03	50652172.43	62206824.51	56435909	60790145.6
3-Nitrotyrosine Results	108.4728504	166.7852499	849.3745053	131.3014605	1519.991129	
Xanthosine Results	7983.990467	8410.894423	11628.53351	13440.6812	14580.17669	9211.367209
Acetyl-L-glutamine Results	1245.154442	1059.210747	772.5633277	1893.111334	2450.881421	1616.233773
Methylhistamine Results	83961.06496	92279.01271	82670.20639	90247.58627	89813.49825	84752.44553

Methionine Results	62699.63798	2285.245555	170568.5227	5562.073139	1353.533839	7825.254223			
Norvaline Results	1406703.304	768195.5047	1000737.736	1334936.969	1084702.11	846501.7399			
Acetamide Results		619466.8322		2422466.73	469772.5395	1625854.111			
cGMP Results	837.6016218	1362.501838	635.0349891	260.288861	1741.675859	659.9120797			
4-Aminophenol Results	1468.513366	851.8145048		742.9309485	914.7679662	983.9394508			
Taurine Results	5201253.619	6304142.281	4856005.942	5922014.522	6715058.396	6262608.43			
Valine Results	1429562.255	823941.9238	1003861.236	1373560.044	1161461.068	967110.0624			
5-Hydroxytryptophan Results	176.3233032	111.3172639	92.58113181	223.7017194	814.5652075	129.9961753			
Quinolinic acid Results	934.9401654	4944.798918	1564.224999	4840.365031	2306.618627	2539.337883			
Tyrosine Results	162260.3485	86593.98805	67972.28465	89359.86501	103190.4001	80679.87441			
inoisobutyric acid/ Dimethylglycine	228079.8179	9431992.297	110902.502	11059321.06	17146239.92	13676482.56			
Picolinic acid Results	2684.652086	2009.961165	2061.860858	2138.784588	2368.015746	1504.662312			
Epinephrine Results	1259.809574	3070.755672	1181.054612	6205.919057	10765.79725	2752.607865			
Acetylcarnitine Results	95781538.05	88562387.23	95730215.07	90583665.07	62166361.07	70405982.17			
Indole Results	2484.725659	7673.740613	13698.13887	4105.490236	4638.896308	6501.929396			
Pipecolinic acid Results	828104.0341	854647.8782	848240.1317	820288.9029	1372791.855	1138426.017			
Proline Results	4528564.471	3162894.582	3773677.94	5298164.304	3808677.923	3404084.171			
4-Imidazoleacetic acid Results	1330.501799	1576.326401	1622.741776	971.9582273	3494.626141	2402.606604			
Neopterin Results	354.0178215	106.4933451	62.77540727	60.01846658	275.6695089	113.7694274			
2-Aminobutyric acid Results	217193.0985	9260820.822	111376.3736	11148654.58	17264117.61	6773033.183			
Methylguanidine Results	118836.8674	6999.50423	36462.40602	12863.52415	8741.310614	8597.579011			
DOPA Results	3925.351115	812.5300386	3178.501752	427.5466789	857.2694857	1408.861266			
Sarcosine Results	1885376.166	2895003.248	2479919.84	1821361.781	2615078.551	2339334.59			
3-Aminobutyric acid Results	3792.945882	36899.51642	3077.71145	239599.2308	53875.96204	79323.14354			
Choline Results	0	18655519.85	1318752.465	23283446.06		11130652.4			
Hydroxyproline Results	1403362.465	1751443.382	1238784.956	1030014.602	1763871.737	1344448.416			
Putrescine Results	2206.821027	662.8024302	497.3408854	814.1350679	679.2705545	479.7328857			
Alanine Results	1693537.979	2540672.627	2197594.485	1682531.533	2286925.997	2129008.577			
TMAO Results	3523852.108	4802535.355	5582629.669	1845340.42	2655904.344	2707826.564			
Indole-3-acetic acid Results	5659.19477	22946.28721	3557.971511	12347.599	12632.45013	13961.1331			
Creatine Results	41413677.82	38338189.36	42303947.51	33843079.74	45824433.67	29662138.33			
Acetohydroxamic acid Results	10268.852	15560.95438	17955.26119	5858.556664	10067.35622	10541.95316			
Carnitine Results	52131433.04	56887422.38	59829965.14	61305436.18	64731139.87	61357938.27			
Homoserine/ Threonine Results	296992.3507	298907.0691	403403.4189	352054.2352	246909.9145	281540.6925			
Glycocyamine Results	198646.2481	1404183.643	45844.30592	1792047.557	946481.7285	1613109.167			
N-Acetylneuraminic acid Results	2801.565645	12856.2145	1223.884395	5204.822232	35217.70778	20012.60653			
1-Methyladenosine Results	161273.4405	148400.694	220345.0779	376418.8085	464234.5923	279617.2947			
Spermidine Results	976.784035	1125.75801	109.4224314	1089.019749	723.9244284	1597.711228			
Cadaverine Results	0	14715.36394	1013.829991	7927.834291	10184.66416	12356.02373			
5-Aminolevulinic acid Results	17753.06763	70016.96939	21259.19412	77849.04922	111819.786	77197.20238			
4-Aminobutyric acid Results	3971.361363	60345.59365	9671.303087	101916.6326	122946.5091	131963.1193			
Glycine Results	37746.69221	127481.9015	35107.5658	40379.90204	43151.97675	35335.99958			
13C5-15N-Glutamic acid Results	0	17591.29672	4650.225359	3822.449407	4425.023066	10552.42978			
Glutamic acid Results	34299.61794	107607.2366	63872.96037	175960.8933	200979.3688	166376.016			
Glutamine Results	2930046.767	8167702.215	4429188.343	10869050.8	13472534.68	11513409.75			
Glycylproline Results	107.9352115	127.3099694	83.82521677	70.21044895	1653.69447	398.4764081			
Acetylornithine Results	2525.274276	2364.540341	3065.488268	2157.405225	2747.952522	1652.572023			
Dihydrofolic acid Results	16.65308187	43.40365437	59.70572248	29.06029202	6.505700011	21.76908059			
Glucosamine Results	14076.42467	24722.50984	1672.600275	648.4961796	1880.645617	1583.173125			
Folic acid Results	12.24482618	41.66188704	43.3607197	19.39283378	31.64117473	17.36848299			
Asparagine Results	37179.99487	42632.5352	46010.6906	68754.3837	43882.03199	40451.32332			
Amino valerate Results	3115.993988	2047.623962	973.1408412	1237.315652	1474.778764	1686.716823			
Glutathione reduced Results	2851.9937	7605.2305	4181.010193	10686.72274	19828.05488	16320.21877			
Serine Results	120503.7733	155600.0234	136531.523	233255.693	184546.0513	191968.2496			
2-Aminoadipic acid Results	306.8952888	310.7343807	281.7767466	334.3968851	595.8431383	2417.554482			
Adenosyl-L-homocysteine Results	31772.43365	1604.949437	23292.07496	7892.596226	1861.644439	19506.54114			
Aspartate Results	0	1686.449469	2486.415234	3745.043047	2140.655574	17626.89579			
Agmatine Results	40950.33432	20120.96179	41685.44536	38521.35415	37963.31007	35819.24019			
1-Methylhistidine Results	17753.9096	3636.713835	3665.584715	3099.996381	2810.82447	2840.005111			
Siacar Results	148.1102315	171.5506139	9.390696038	58.66461592	86.1782775	187.9272015			
Hydroxybutyryl coenzyme A Result	13987.01019	12730.32528	8338.291267	6287.689055	31153.69057	20262.7335			
Isobutyryl-CoA Results		2608.936557		2628.464182	3661.499506	1605.942679			
UDP-GlcNAc Results	400.6994275	39.16561898	321.7521425	74.23859098	547.9851349	86.51142135			
Citrulline Results	428066.2762	86364.92121	106749.6574	67943.0754	112503.0181	124096.5545			
Histidine Results	0	18817.80301	30278.75628	23016.39884	10174.39821	12828.82102			
Acetyl-CoA Results									
Carnosine Results	152986.2622	260463.6399	5831.104013	172644.3306	501765.4849	150328.7727			
Glutathione oxidized Results	0	204492.207	186357.0431	360512.8878	339907.8807	538621.3908			
Adenylosuccinate Results	2574.99796	42408.13447	2771.080196	5010.893637	2553.284614	3945.816524			
GDP Results	0	115414.9458	18822.71594	81942.15835	86145.63005	104306.9346			
dUTP Results	362.0271539	1181.296432	478.9168228	1860.186195	1634.616855	1029.003934			
DCTP Results	32.38747589	56.93072599	39.27658186	80.04452509	78.23768503	93.85326173			
Homocysteine Results	358.1248577	516.4595637	843.575103	445.0141856	177.2193926	621.2462892			
ATP Results	11366.93569	30581.91257	15930.39264	64051.25217	107653.331				
Histamine Results		29835.23739			19802.16941	17105.23506			
Uracil Results									
Cystine Results	6079.830471	8918.163854	432.0308066	1078.786383	15718.81204				
Cystamine Results	31.99618055	375.9171478	99.56827661	178.7681459	196.5107723	318.9403841			
Glucosamine 6-phosphate Results		164.3299279			975.5370348				
Dimethylarginine Results	119.8663551	45.98687732	50.6057314	229.7303618	75.2417331	24.41723166			
ADP Results									

DCDP Results			203.9663644			
Ornithine Results	0	747.4748633	15493.06892	23562.62737	16994.38068	16619.78953
Arginine Results	173.4152432	795.7700774	322.0547389	166.6327159	197.3858163	805.1912318
Lysine Results	161.3660998	107.6369463	415.9194296	494.557453	1375.512779	38.53918711
Indole-3-pyruvic acid Results	1117.123753	309.0765295	1731.443151	298.4860575	237.9356543	1045.018946
Cysteine Results	920.2037568	1354.270999	853.4507134	580.6900883	427.1023704	1494.421031
3-hydroxyanthranilic acid Results	258.9429479	61.0691552	150.9120803	80.41152379	112.4043223	247.4978621
Sample	11010-tissue-neg-qc-1	11010-tissue-neg-1	11010-tissue-neg-2	11010-tissue-neg-3	11010-tissue-neg-4	11010-tissue-neg-5
Acq. Date-Time	11/11/2018 5:41	11/11/2018 6:12	11/11/2018 6:43	11/11/2018 7:14	11/11/2018 7:45	11/11/2018 8:15
pregnenolone sulfate Results	2373.178607	4071.586577	1419.561075	653.0438821	770.9894584	4941.046621
2,3-Dihydroxybenzoic acid Results	222.6053551	40.93628909	605.5385021	22.67570738	72.68591099	280.8513964
Nonadecanoic acid Results	100014.4255	99390.15388	46048.40412	63643.2287	34562.54942	73597.18266
Stearic acid Results	687103.8134	414870.7414	316408.0607	289408.609	671358.8305	250802.8305
Heptadecanoic acid Results	61956.35038	174677.1278	39763.20346	123217.1571	117398.8128	163354.5211
9-Octadecynoic acid Results	3397990.721	554801.5879	883242.7983	426204.0786	708939.6807	1210905.753
Myristic acid Results	155805.4051	210386.1352	179934.0651	152699.3223	79103.44968	98776.32527
Palmitic acid Results	715784.0782	327839.1276	482174.7262	527385.1254	355388.0414	394377.1146
Pentadecanoic acid Results	92654.25669	87675.34325	58876.30692	76548.16215	69467.40181	96035.1786
2-Hydroxybenzoic acid Results	679.1019237	1539.888538	2122.958307	1199.038645	788.5592104	1491.778654
Lauric acid Results	32275.82866	132338.5848	28949.41085	101291.9715	72720.32518	150444.0293
Capric acid Results	24688.6585	324833.0089	46364.91189	378357.4757	137824.5892	329934.59
-Hydroxyphenylpyruvic acid Result	479.2174018	937.2255951	397.5839984	1562.205635	451.9487046	1692.556677
Phenylpyruvic acid Results	87.16429738	697.3217465	72.90921255	238.6078946	200.9363821	465.7840686
ylacetic acid/ 3-Hydroxyphenylacet	545.334501	2473.817548	1033.637534	1916.804233	897.6839071	2514.65001
4-Hydroxybenzaldehyde Results	1119.675475	1992.643283	1840.333167	2793.886456	815.0185298	1392.57445
Phenylglyoxylic acid Results	87.47017784	483.3716597	28.20054708	279.2495456	263.2044399	429.0203601
Caprylic acid Results	24308.31034	21087.85457	50389.63793	26798.59759	10028.16587	23725.5417
3-Methyl-2-oxovaleric acid Results	6507.778918	24927.39728	10853.58281	23941.36851	14540.40508	26721.62423
GA3P Results						106.1401932
Naproxen Results	55.42125096	70.38083689	5.498641205	2.327213947	24.87777401	24.75868939
entanoic acid/ Ketoleucine/ Ketoisc	3487.587134	8813.747455	10004.67299	5145.785112	2057.717895	7376.999141
Gentisic acid Results	14.44853386	58.1557569	34.61072874	62.97592271	122.0680658	5.567801075
-Ketoisovaleric acid/ Maleic acid R	6081.326635	59740.47473	16714.37157	38907.552	12444.98319	47905.94399
PGE2 Results	351.1048775	239.5919476	212.7866935	442.1490971	18.58114944	165.8323366
Benzoic acid Results	7395.740445	14246.89013	11295.13708	11557.51037	2198.813993	10638.01149
Citraconic acid Results	2769.359715	5831.070371	3301.292397	4195.767391	1794.923473	3091.844436
2-Ketobutyric acid Results	24.43047135	116.817696	66.79173092	149.176801	133.634873	19.14485564
Myoinositol Results	481.8880944	1407.831071	478.9104364	294.9590112	138.7332926	900.3447225
3-Phenyllactic acid Results	281.9286095	224.6938674	54.50029248	129.5157592		166.0537339
-Methoxyphenylacetic acid Result	3.243098477	129.7941194	28.78732746	14.43334007	57.93925396	30.21862792
m-Coumaric acid Results	7762.749933	49851.42389	1142.432426	62077.53433	24578.0019	56514.24315
lacetic acid/ 4-Ethylbenzoic acid R	6470.684822	14957.86314	7209.734193	17722.70559	4844.061821	13871.67453
Phenylacetic acid Results	6106.393799	17739.93913	18333.00283	16859.87643	3955.025252	14888.36051
ethylvaleric acid/ Hexanoic acid Re	18899.04299	60203.60248	67248.25854	48017.72733	22874.3956	42491.10839
Ferulic acid Results	39.33011023	92.13719234	0.497025183	57.93344087	54.15025768	78.81511827
Gibberellic acid Results	52.63251794	89.73374481	46.90226345	121.9302757	44.05867538	14.22811844
ethylbutyric acid/ Valeric acid Res	4537.163687	22743.89284	4656.485633	22242.65135	7180.220745	19548.42107
Protocatechuic acid Results	301.9037827	164.609586	253.8565865	110.3053859	96.54484546	59.28515856
2-Furoic acid Results	76.0346284	6.792527769	20.42170366	39.2831937	28.65806858	49.25387586
p-Coumaric acid Results	7763.240264	49926.05957	1140.208594	62079.52864	24636.75855	56476.10652
xyphenylacetic acid/ Mandelic acid	87.75228	373.410872	256.5777534	177.5555043	62.99847984	162.4113899
Hydroxy-3-methylbenzoic acid Resu	46.28186708	39.61918465	343.2748199	43.15900082	57.21564843	41.31373888
Isobutyric acid Results	4146.518816	243.0403267	157.8815917	743.8575554	91.39036131	701.3911496
Leucic acid Results	78.06039004	31.77859088	50.585731	74.17882904	81.85522129	118.2792065
Vanillic acid Results	69.74639308	87.47715887	65.2979181	161.763928	57.22263702	23.4419717
Methyl succinate Results	886.8249396	199.5474691	1469.300638	537.651146	363.8475979	284.6641206
Pyruvate Results	8.269304734	66.3019415	73.84120062	46.81783478	15.03765051	18.9997001
elta-Hydroxyisovaleric acid Result	54.59810218	61.16538791	53.15950188	110.8952094	33.96872307	91.8003594
Acetoacetate Results		222.1000093				
Homovanillic acid Results	60.12090518	54.46496027	29.1110361	94.34492744	33.75173754	56.16267287
4-Hydroxybenzoic acid Results	527.3597731	612.786493	804.8567192	115.9850176	90.63802756	400.2970839
Phthalic acid Results	2990.752086	4755.831551	333.6709868	6413.12454	10255.75121	3795.910905
L-Ascorbic acid Results	290.501127				112.8228649	76.2029478
Methyl-D-mannopyranoside Results	78.90631729	557.9151569	130.4112851	115.6431824	79.76860927	121.1362158
Ribose Results	1619.029719	856.9511181	2556.581384	1026.6754	1377.308152	40.89236165
Levulinic acid Results	16184.10709	23342.74115	19834.35623	16678.55755	36935.60236	16332.33186
Ethylmalonic acid Results	306.0342705	28.90829588	175.146741	388.2532209	85.66956432	740.7406677
Sebacic acid Results	150.8270346	692.8705343	305.8547832	174.5710756	111.0595755	154.1325875
N-Acetylmuramic Acid Results	38.46308107	38.2725539	95.95456156	13.22811607	50.21600275	31.37841593
Azelaic acid Results	3141.203624	1704.63434	2888.747871	1758.38424	51.53039111	1359.498268
Lactate Results	120676.1052	96155.35696	154365.9619	57915.54253	238.0233733	42315.13996
Adonitol Results	18.83359625	365.4684163	162.0829336	255.0684087	85.13826079	155.7999814
3-hydroxybutyric acid Results	161.5375273	54.98623807	60.57538323	471.3347591	36.77261376	645.9957907
droxybutyric acid/ Malonic acid Re	0	1780.608092	505.8599553	19016.47866	363.2119059	11993.44485
thyl alpha-D-glucopyranoside Resu	41.93205062	39.32138725	76.8442054	33.27811045	46.25037155	94.19405746
Xylose Results	113.7120526	974.1692733	352.3194657	433.3604301	360.6296209	423.3490343
13C3-Lactate Results	0	337899.5476	319006.5827	241819.9573		253104.7411
L-(-)-Arabitol Results	630.3137051	516.4915501	534.2336799	151.0575686	591.3140461	738.1884246
Xylitol Results	158.7545679	282.0102366	844.8349335	230.5703045	308.7907452	214.4187888
Erythrose Results	1.297917328	58.34050834	60.06259077	30.5961368	2.901642233	55.26022258
Methylmalonic acid Results	818294.5595	450833.9204	1079884.294	207127.4945	173834.2688	409581.0489

Fructose/ Galactose Results	19076.00072	18536.59193	7366.241196	13410.70455	10240.1038	12904.18512
Glutaconic acid Results	8540.928032	6211.351911	9841.164112	4374.952507	296.0457225	6181.307977
Glyceric acid Results	60.03522421	56.45596567	979.6005867	88.76928662	326.6665301	606.1119039
Suberic acid Results	126.2838487	1101.038846	1859.611391	753.0334005	15.88125165	1122.607019
Glyoxylic acid Results	178.7424076	36.51646697	26.32718815	34.66264671	64.61195583	107.7507042
D-Mannitol Results	67.65002739	6395.228488	1026.479813	334.2745861	130.6769878	231.0522709
)-Xylonic Acid (Lithium Salt) Result	21597.2948	58139.13171	4237.684472	5423.144379	20468.68679	5904.501176
Sorbitol Results	237.9839884	13328.18231	1412.462624	232.4354849	508.415863	535.9859983
Dulcitol Results	187.8111241	16104.76016	1632.182243	389.0718871	616.2853267	208.2469572
Glycolic acid Results	72.20867176	26.72186917	29.26705504	42.5064345	13.23210608	21.65918809
Mannose Results	6468.448072	4768.219632	2631.883238	5377.80358	2863.376104	3985.389532
Glucose Results	19148.74381	18582.37439	7115.08039	14012.95136	9597.645789	11935.50245
Fumaric Acid Results	13845.59073	17040.26447	26168.586	10678.8706	4777.571156	11589.76848
3-Methyladipic acid Results	21.38668573	45.31311198	76.50018653	41.15513044	113.9270642	21.09678174
2-Methylglutaric acid Results	0	6350.212477	8822.201631	6902.114028	3586.254211	249.9206103
Muconic acid Results	27.11629305	49.32599388	38.59183728	136.1122912	67.42166547	117.7613537
Homogentisic acid Results	85.99351124		94.07740567		58.86400403	
Shikimic acid Results	12.86373056	42.72927121	35.50594753	75.47117281	25.36679363	5.58906723
alpha-KG/ Adipic acid Results	9432.201053	9607.111967	11606.0105	7488.002428	5456.550364	5513.507745
L-(+)-Arabinose Results	38.957437	155.1590724	175.5234929	130.2738583	148.0649347	25.19733111
3-Hexenedioic acid Results	701.1147644	590.1460265	1276.04769	421.5499806	1772.390884	32.02082751
Succinate Results	5515.379022	10963.84159	4165.124677	2965.179888	5821.900917	8132.375757
Isovaleric acid Results	0	984.6871755	1262.38032		975.1852152	523.4157617
Fumarate Results	388.8883333	278.6839309	9079.014498	221.5864901	145.9062485	408.0632977
Glutaric acid Results	147.9415311	639.0080953	193.85761	400.9893043	253.2976792	136.2324169
Aconitic acid Results	2468.834919	2962.431448	4072.150302	85.1897994	1552.622279	115.1475568
Sucrose Results	33.93112541	1169.611921	70.08622881	89.55068885	47.2492412	
Glucuronic acid Results	842.5345697	598.9766272	1079.661432	48.80959857	516.0678585	107.7103636
R5P Results	38128.61461	33218.45073	58697.7189	31793.59202	20128.41179	24208.22281
D-Galacturonic acid Results	21.29694873	15.03701816	21.62310164	28.84454282	70.34253238	27.96455065
2HG Results						
Oxaloacetic acid Results	82.96291951	121.9895668	1673.038526	1329.30182	740.8184223	46.71724429
Galactonic acid Results	397.0786287	850.2206596	533.3067918	298.2988396	94.63789493	234.8869866
D-(+)-Cellobiose Results	1838.962436	1538.290766	688.6451004	28.91695403	41.65473167	33.21805808
Gluconic acid Results	55.90414016	32.81067766	44.6052781	25.36382316	84.59727085	74.85094126
3-Phosphoglyceric acid Results	0	1552.342295	3482.157462	25644.7071	1135.727835	2061.034003
Trehalose Results	165.8973598	37.19074025	60.29702671	40.87509082	19.15328085	63.32539421
Lactose Results	745.7213287	1447.013691	146.1482738	30.40712342	62.74841071	33.93890144
Mucic acid Results	209.283249	1275.280187	160.5437978	428.6645673	18.2523174	88.31411149
e 6-Phosphate (disodium salt hydra	61147.62913	160977.9069	64687.2639	46791.13976	82052.95871	69903.41805
DUMP Results	119.2254864	11.84817055	26.00777115	60.79420769	37.63959154	16.94284262
Raffinose Results	275.7639958	623.7573128	1888.336752	434.9259731	277.5460536	753.230114
F6P/ G6P Results	17569.23936		2462.995505	15988.44337		
G1P Results				2641.591546		
Galactinol Dihydrate Results	382.0827826	87.77696557	771.3421377	29.38774817	62.23649259	26.54899359
F16BP Results	638.430034	1037.174617	468.6639236	292.0359451	596.235047	1176.571096
G16BP Results	123.0526625	591.8505438	442.7800462	403.3493047	3031.490691	228.1743728
PEP Results						
eHydrate (from Stachyse Tuberifer	22.66785774	37.77004382	9.355754146	0.512166212	32.00039214	7.174200491
UDP Results						
Malate Results						
X5P Results						
Citrate Results						
meso-Tartaric acid Results						
Tartaric acid Results					45.83095046	
Thymol Results						
IsoCitrate Results						
6-Phosphogluconic acid Results	63.89624937	141.2517091	66.84891839	61.29409018	115.1683221	168.4214122

	Wild-Type RT					
Sample	11010-tissue-pos–6	11010-tissue-pos–7	11010-tissue-pos–8	11010-tissue-pos-qc-	11010-tissue-pos–9	11010-tissue-pos–10
Sample	11010-tissue-pos–6	11010-tissue-pos–7	11010-tissue-pos–8		11010-tissue-pos–9	11010-tissue-pos–10
Acq. Date-Time	11/ 10/ 2018 13:49	11/ 10/ 2018 14:20	11/ 10/ 2018 14:51	11/ 10/ 2018 15:52	11/ 10/ 2018 16:23	11/ 10/ 2018 16:53
Phenylbutazone Results	1307.615907	1692.112238	2303.465993	1140.124049	2233.105343	2650.624811
3-hydroxykynurenine Results	22455.87715	18673.95649	20560.45176	7424.23344	25818.48912	20985.21335
NAD Results						
dTMP Results	5635.099236	5240.902841	5122.680982	2987.788894	4229.937091	6397.909249
N,N-Dicyclohexylurea Results	14739.13904	12161.34039	12885.10111	1553.923776	17419.57651	17422.8154
4-Pyridoxic acid Results	32878.50706	21745.94704	21805.46887	17407.27261	26994.83547	22092.74458
Melatonin Results	4918.553306	4970.86025	3377.464712	443.1275581	6414.87704	4157.429639
Urate Results	12029.86694	8887.939009	12982.85601	4196.594926	12340.01836	10228.25223
Caffeine Results	3132.645169	2573.630686	2167.438888	507.3266197	1881.855895	2499.455553
Folinic acid Results	313.2422165	699.1262571	1035.516589	411.2188533	362.3538011	182.2794301
lenalidomide Results	97.47133456	162.1194278	71.29597528	16.83880227	51.53284143	111.7804296
Tetracaine Results	291.4354024	153.4224281	59.21364655	101.2628252	116.274617	1142.920539
3-Indolepropionic acid Results	274.1055861	447.4860626	2054.3807	475.9133909	191.2260997	237.7786255
Anthranilic acid Results	7518.511374	10338.81198	3814.030677	14146.68543	15717.39607	2673.303878
2-Pyrrolidinone Results	57719.99971	32789.20431	25622.52437	10105.12968	38953.08726	34022.82207
Phosphocreatine Results	586635.133	502730.0491	531123.1899	207741.5211	536540.2941	491430.0045
Dihydroxyacetone Results	41845.29358	50879.27181	60924.12252	42725.15499	51246.91855	47598.29039
Nicotinamide Results	8677918.747	7559293.245	3405457.213	15482949.16	4745612.687	6467878.229

Imidazole Results	122454.1027	130181.5514	85745.15968	17110.82216	109345.8469	79149.52605
N-Acetylethanolamine Results	14698.35393	14849.83764	16940.34669	10067.22781	15696.66721	14399.33954
Allopurinol Results	2819.187024	768.9845183	351.0599298	514.2407837	863.7749419	214.4438974
Xanthurenic acid Results		480.4778473	102.5797194	75.8390547	483.4128037	88.56612027
2-Deoxyuridine Results	187.8108339	3099.686118	663.4211906	434.3760376	5884.798552	864.4460455
Pyridoxine Results	121.5277842	682.7015699	154.8500467	527.2635683	559.3988124	811.9324816
Decanoylcarnitine Results	11618.30157	30650.81378	12627.46021	0	8396.67943	25290.2487
Kynurenic acid Results	130.5878815	163.5725628	60.64350179	0	168.7220413	176.5640777
Hippuric acid Results	221.5196871	12408.86312	31.53594143	0	2486.602142	716.8868522
Propranolol Results	1189.240162	1071.693107	2093.055616	263.5833486	1299.440463	1369.332215
2-Phenylglycinol Results	1711.553364	645.0566984	1170.149743	364.1424898	1501.919741	2608.537996
Acetylcysteine Results		455.9492294	350.5107191	391.2326162	388.9704598	
2-Deoxyadenosine Results	4399.686975	2913.518475	2124.401886	0	2798.567071	4264.381957
Adenine Results	64312.25597	61496.1189	53609.10748	185741.0077	74875.47246	69169.30337
Isovalerylglycine Results	1674.402701	532.6907531	1136.190991	579.9000263	1774.534036	950.0530156
Hypoxanthine Results	169020.4666	187718.4908	112603.848	320297.7259	76473.96406	211987.2782
Uridine Results	26242.33479	24467.88665	13449.86851	33534.17808	11108.53208	27112.99468
Creatinine Results	647408.2759	981505.8763	3236386.047	7809230.396	1012727.996	645499.0936
Adenosine Results	534138.633	870696.7222	365809.1784	1364901.173	298484.4865	665023.8755
Xanthine Results	3744.210439	3112.227138	3115.065209	14248.05118	1698.4303	3671.274492
Tryptamine Results	166.2000291	194.4747652	108.2166804	4303.743265	171.6009494	463.9471842
Acetylcholine Results	1447.836437	1934.286089	1034.602015	0	1525.916793	317.7750335
Cytosine Results	8882.035178	19393.49238	9983.799766	189177.5333	14993.23137	14964.33016
2-Deoxycytidine Results	2967.721911	6083.677949	3091.916721	72447.33899	5857.263747	7421.953147
Nicotinic acid Results	4979.761986	5366.219238	3770.522722	0	1850.006184	2589.962762
Inosine Results	1578419.776	2350151.391	1877027.057	2620719.625	1558695.286	2254808.885
5-Methylcytidine Results	10928.75864	13264.79177	11395.20489	5233.273783	8656.395458	12995.8409
Biotin Results	28102.37353	21380.59593	2113.109685	0	21684.4244	4164.286335
Metanephrine Results	2463.819694	6006.051765	7202.077868	0	3268.656206	8476.364335
2-deoxyguanosine Results	17441.21728	8356.84308	9462.778155	8684.202514	9546.407617	14933.21755
Guanine Results	80929.35804	101939.3695	63941.47638	86650.08451	65918.47686	111006.2793
Dopamine Results	1467.49557	2050.043276	674.5362805	286.5611251	954.0822385	481.495172
6-Methyl-DL-Tryptophan Results	7898.384138	7478.62281	5825.031913	4525.195056	4500.026078	15507.52548
Pantothenic acid Results	1829300.433	1911904.395	1510266.944	0	1032617.468	1318731.009
Amiloride Results	26392.51291	46646.15616	29040.10484	16531.00907	25922.84132	35201.69282
Cytidine Results	737355.2194	710816.4619	454670.7575	460580.3717	488526.212	633122.1746
Nicotinuric acid Results	2732.611518	3783.464241	1601.22465	0	8771.982255	5089.570484
Serotonin Results	2339.45779	516.4903792	1218.599223	930.9645212	634.7514293	1742.304301
Acetylglycine Results	22.03985293	50.38624496	53.08476416	86.8627718	118.8442853	144.8061741
Phenylalanine Results	2754332.668	3515739.782	3626264.244	1916629.739	2029501.454	3236265.987
N-Acetyl-D-galactosamine Results	11833.44914	18845.94783	12491.01772	0	11573.74923	18438.14732
Tryptophan Results	300239.5764	479483.5081	433935.7599	221107.8445	180874.9774	528500.1729
Urocanic acid Results	9135.737671	11502.25088	25753.5501	30282.43405	25115.82352	25132.13358
Indole-3-lactic acid Results	16388.05902	21950.92123	18516.86208	10939.6388	10170.39451	21371.607
Normetanephrine Results	16670.79328	24610.01279	18870.4145	9942.864352	21516.90897	19968.34264
isoleucine/ Leucine/ Norleucine Re	9477214.864	17104104.37	15592927.76	7202373.924	7544803.043	13770829.49
Kynurenine Results	305.9594462	3486.719761	4417.031134	497.8124316	587.3695923	4433.353034
N-Acetyl-D-Glucosamine Results						
Acetylglucosamine Results	2992.097742	3798.1435	2474.279081	2459.739897	2113.066066	3763.411578
HIAA Results	1048.532854	1909.577577	2225.660806	0	2911.805995	4545.167284
6-Hydroxynicotinic acid Results	7697.366061	4853.414237	14266.86183	1321.416259	2085.216119	13476.40754
Guanosine Results	112194.3672	185874.2848	95378.96819	119204.4629	122523.4303	184689.5938
Pyroglutamic acid Results	177118.2533	186988.401	142400.2578	129357.0029	111687.666	167769.586
Isoleucine Results	9477214.864	17004746.57	15606263.84	7262658.144	7522043.839	14182602.94
Betaine Results	74613189.79	75063398.41	73596073.59	57292980.62	73203791.52	78803844.03
3-Nitrotyrosine Results	539.996568	1002.191867	1642.464682	0	265.6113993	831.9050471
Xanthosine Results	8183.155303	11037.31816	6369.467809	7820.353077	9650.170051	9910.798707
Acetyl-L-glutamine Results	2885.708065	2286.290796	2071.012172	1469.246057	1302.581675	1767.434828
Methylhistamine Results	92967.58358	98305.68069	90833.95766	83296.57868	96155.69836	92275.13512
Methionine Results	21480.93003	23701.40587	28843.32192	65575.56176	2743.055962	129523.9386
Norvaline Results	1479438.12	1623625.965	2452561.306	1396103.372	1301142.39	1667464.928
Acetamide Results	525409.636	1460327.266	542984.3343		812067.8043	974669.6344
cGMP Results	919.7316357	790.6158715	230.9614139	2325.718138	1830.375186	758.7215721
4-Aminophenol Results	942.6141176	1683.873139	1750.824734	1121.142217	1389.334598	1325.382988
Taurine Results	6098901.906	5985930.382	5879109.277	5289313.876	5294081.477	5540980.192
Valine Results	1538494.931	1808559.315	2570946.751	1432385.673	1390393.105	1922889.459
5-Hydroxytryptophan Results	1774.221662	541.9633204	143.3788201	81.94939366	41.1547011	221.5811428
Quinolinic acid Results	2459.450122	4612.384063	5729.363371	0	5126.636798	5226.504808
Tyrosine Results	114896.368	119098.7748	190426.866	143343.7483	119848.5334	157748.2335
inoisobutyric acid/ Dimethylglycine	16595029.41	15688609.87	11969427.41	217413.3865	12793490.36	12166010.92
Picolinic acid Results	2057.275652	3251.468772	3442.368183	3356.575757	2842.376258	2605.626505
Epinephrine Results	8446.771644	7273.442728	3426.321039	0	3344.008468	1870.296697
Acetylcarnitine Results	69758963.13	81494872.38	85716104.77	92140575.71	68375252.14	90615257.61
Indole Results	6012.223097	979.0857328	3333.570333	0	13404.58406	3088.184032
Pipecolinic acid Results	1891070.078	1383254.866	1278595.711	861235.1643	1041342.248	1405083.21
Proline Results	5457653.761	6090727.307	5319837.363	4468629.249	4783003.805	6868803.065
4-Imidazoleacetic acid Results	2927.560842	2553.303447	2074.575574	1780.290737	2183.791813	1798.505787
Neopterin Results	211.1396538	37.94825633	42.41666672	25.50415132	371.6723276	47.6484352
2-Aminobutyric acid Results	16596844.91	15657910.87	5799083.933	203147.1497	12858307.1	12226608.33
Methylguanidine Results	14122.38187	14223.14165	6947.88554	110969.9015	10175.07455	14926.66236
DOPA Results	1670.548457	1290.597873		2260.596388	1865.458389	3366.767459

Sarcosine Results	3338572.641	3183414.549	3484626.11	1989169.577	2725145.124	2996433.224
3-Aminobutyric acid Results	71443.56337	41356.68362	61525.04375	3637.147086	107243.5065	76029.24492
Choline Results		27736243.89		0	3723113.527	21253853.97
Hydroxyproline Results	1223947.031	1754541.384	2464079.317	1407392.982	1296782.142	1364085.583
Putrescine Results	546.1203803	140.8990754	754.5026452	0	1110.660989	778.1689136
Alanine Results	3035759.522	3136439.194	3239755.266	1589899.334	2391535.297	2588172.555
TMAO Results	2765155.94	2340963.802	3682143.465	3553760.543	2100754.672	2159447.11
Indole-3-acetic acid Results	15880.41174	12297.69243	11354.5649	5076.27554	20000.4768	14846.70494
Creatine Results	25599051.49	39694168.84	51444745.99	41989264.58	26637129.96	32539604.88
Acetohydroxamic acid Results	7686.355021	6579.693532	14002.81605	11904.38378	7427.338128	6087.633254
Carnitine Results	67912213.95	67952775.32	69005724.84	54324228.64	68870120.25	70650827.75
Homoserine/ Threonine Results	414349.7343	332676.1674	357763.7689	292710.7694	377953.5676	439557.5638
Glycocyamine Results	1623767.391	890020.7076	890072.3501	198611.0001	1891418.776	1538279.4
N-Acetylneuraminic acid Results	24978.34197	13758.98947	12482.92322	3968.340996	7079.378939	11987.37941
1-Methyladenosine Results	504503.9842	536281.6322	507262.4844	145268.944	338712.2108	475710.1534
Spermidine Results	778.1026805	3594.132375	533.0044877		775.2603526	4313.330437
Cadaverine Results	6352.619445	6598.413344	4945.705982	0	9455.559554	1368.111993
5-Aminolevulinic acid Results	60601.05713	90162.81396	150685.218	0	74960.5418	47718.8233
4-Aminobutyric acid Results	93160.35669	82982.5268	87921.08291	2749.536369	117125.7813	51215.7899
Glycine Results	30729.29068	30432.90197	49692.00406	36122.96148	29076.12844	24001.32697
13C5-15N-Glutamic acid Results	10918.50763		3653.010634		4368.18127	7524.474713
Glutamic acid Results	203798.0856	194028.1662	206162.8101	34394.97036	164085.5944	135473.1913
Glutamine Results	14599688.62	11567364.69	14347976.59	3006159.911	11161980.22	8688989.275
Glycylproline Results	92.53410507	155.9890887	56.16561731	68.68918249	164.9024341	1743.5699
Acetylornithine Results	2966.240523	2334.557488	3866.438007	2505.525252	2903.327755	3092.463178
Dihydrofolic acid Results	19.23158948	112.1185711	61.67083701	37.60012865	41.90686105	32.34434257
Glucosamine Results	1726.984705	2591.575689	1801.878155	1843.282597	1020.273167	276.6235427
Folic acid Results	51.44064628	55.7319688	31.61530071	37.21462878	41.82032455	44.19455021
Asparagine Results	58109.5768	70465.34988	72953.82452	32976.36836	63804.21721	56709.41264
Amino valerate Results	1163.788347	2571.505451	3970.484558	2430.573484	1178.157389	1135.318756
Glutathione reduced Results	59766.37554	81738.51872	32677.80674	3815.129631	11473.31521	38913.64417
Serine Results	250770.2163	238668.1571	295108.0716	118993.9765	229781.656	228610.5948
2-Aminoadipic acid Results	836.5338547	764.8736626	2793.363468	285.6112917	250.5264627	549.8824278
Adenosyl-L-homocysteine Results	48244.27967	59538.17041	28442.39322	33033.07543	11340.71209	72255.35562
Aspartate Results	1216.14709	2423.585858	739.2802984	0	2832.18967	2644.953752
Agmatine Results	28207.12507	26587.75659	37033.05519	0	30116.85957	21357.54719
1-Methylhistidine Results	5994.518527	7126.883311	5404.623865	22799.63512	3547.361624	7784.688242
Siacar Results	267.3728086	90.83911842	77.55739783	123.3244476	10.09471623	74.51281866
Hydroxybutyryl coenzyme A Results	42767.04547	47605.01467	30741.44099	0	9574.122191	21534.82834
Isobutyryl-CoA Results				4061.7086	2371.6645	
UDP-GlcNAc Results	225.9053064	67.70703273	94.42480739	277.0432204	84.83594094	69.1990429
Citrulline Results	186483.8796	206750.1027	284284.0293	355127.7032	144823.0462	190060.392
Histidine Results	23900.28162	65180.48256	48604.39409	0	16074.61788	135580.292
Acetyl-CoA Results						
Carnosine Results	34616.13846	221966.806	927091.8541	165715.9853	150022.046	83240.26542
Glutathione oxidized Results	558154.2206	652618.5099	530116.7085	0	375530.3697	628554.091
Adenylosuccinate Results	11286.73264	24726.39372	9849.313497	0	4573.891778	36438.22182
GDP Results	6539.254295	5808.738105	101542.2255	0	131427.8756	126026.1942
dUTP Results	1603.322543	777.6169111	865.2919169	383.9357167	192.9529071	1192.551701
DCTP Results	84.12616442	456.1812927	57.08552649	45.66370858	53.5860123	146.006231
Homocysteine Results	1934.909316	299.4331633	245.9635069	361.3424663	612.3443208	1397.061441
ATP Results	131963.0519	29160.03623	93491.54814	24711.45432	58704.18535	
Histamine Results		33343.32767	25998.05138			50285.37683
Uracil Results						
Cystine Results			23530.69402	7033.260846	16983.66121	
Cystamine Results	219.1173773	158.3052352	186.8692454	83.97974999	235.2924844	122.7854854
Glucosamine 6-phosphate Results			154.3571666			
Dimethylarginine Results	45.14262983	463.3364287	200.6429929	311.8064735	110.8607421	77.73463848
ADP Results						
DCDP Results		143.9655223				
Ornithine Results	35567.6264	53779.04823	81878.59079	0	1318.16968	41604.70979
Arginine Results	323.8334531	2772.515433	171.1218277	51.7757461	297.1412721	412.5194948
Lysine Results	121.3540838	382.458634	98.22573276	355.8891755	919.8250536	150.6331839
Indole-3-pyruvic acid Results	270.9584756	160.6835786	218.23128	181.0061048	442.8633931	434.3411947
Cysteine Results		1873.473406	442.2441692		836.3941307	
3-hydroxyanthranilic acid Results	40.37757628	376.6499231	349.0620107	348.7175529	63.27536438	331.1220498
Sample	11010-tissue-neg-6	11010-tissue-neg-7	11010-tissue-neg-8	11010-tissue-neg-qc	11010-tissue-neg-9	11010-tissue-neg-10
Acq. Date-Time	11/ 11/ 2018 8:46	11/ 11/ 2018 9:17	11/ 11/ 2018 9:48	11/ 11/ 2018 10:50	11/ 11/ 2018 11:20	11/ 11/ 2018 11:51
pregnenolone sulfate Results	1545.82303	1673.036033	861.7895891	1260.353336	638.7502232	1232.755703
2,3-Dihydroxybenzoic acid Results	124.3208662	40.81030274	17.38206259	109.6672257	56.49534175	54.22670126
Nonadecanoic acid Results	59082.32286	62442.62301	73323.20926	66048.45263	53338.33006	63247.00615
Stearic acid Results	462923.0629	285696.3811	281863.6615	379817.7572	264380.5267	132689.4869
Heptadecanoic acid Results	121766.1892	103686.3882	132346.3709	33165.63721	114571.3349	116130.8064
9-Octadecynoic acid Results	1183086.244	1113632.01	1177448.441	1462603.671	684845.1739	635857.9897
Myristic acid Results	106492.6964	96017.97972	101300.9102	75751.26003	72327.6448	94173.46663
Palmitic acid Results	487693.4449	590360.3172	434274.7568	319437.3539	403363.5058	202350.5206
Pentadecanoic acid Results	121613.5375	95753.55152	89356.42718	43613.68705	76671.07734	66634.13444
2-Hydroxybenzoic acid Results	1996.690656	1745.741436	1763.188711	673.8538434	2533.484404	1218.004546
Lauric acid Results	132504.1475	85814.65983	103100.7482	16467.04044	89014.73747	79557.77275
Capric acid Results	350720.6348	282588.1385	264612.2503	17453.25307	297908.9386	201721.6861
-Hydroxyphenylpyruvic acid Result	1228.147462	1467.787255	1907.926461	321.6921798	3367.991385	820.4799963

Phenylpyruvic acid Results	376.7482948	363.8808977	400.8046263	130.3664726	339.3111599	262.3228471
ylacetic acid/ 3-Hydroxyphenylacet	863.0022902	1980.859856	2551.967472	368.3540229	1461.19449	1307.260271
4-Hydroxybenzaldehyde Results	2720.451838	2248.742111	1122.259993	948.4595202	1488.932742	1549.596326
Phenylglyoxylic acid Results	322.2046705	627.5363509	146.0953306	60.39842702	161.872347	474.823
Caprylic acid Results	22885.05951	19205.76388	15923.59058	17803.9153	14844.88288	18007.20143
3-Methyl-2-oxovaleric acid Results	32799.23903	18947.86265	19227.88896	2666.153982	21812.09597	14566.08382
GA3P Results				83.73240221	84.36982214	
Naproxen Results	27.79019443	63.17949347	32.91917828	8.078066474	23.85724153	0.434798793
entanoic acid/ Ketoleucine/ Ketoisc	2236.499089	946.0529345	2386.01325	1983.4109	2161.747427	473.1819732
Gentisic acid Results	56.88750233	104.816913	35.82879731	68.76423357	66.99332279	26.90500082
-Ketoisovaleric acid/ Maleic acid R	35584.4413	39974.57743	35260.9432	2714.89627	35557.16771	32897.41864
PGE2 Results	746.1463529	523.207414	194.2586868	138.5123019	441.4704323	120.6105454
Benzoic acid Results	9707.960455	8987.114246	7746.681115	3488.886976	8263.291085	6716.901478
Citraconic acid Results	4886.749721	2444.860131	2503.986671	1598.460442	4339.166429	2791.775298
2-Ketobutyric acid Results	124.6387971	43.87365669	54.34870985	9.467257691	75.78560842	15.92494431
Myoinositol Results	1297.094309	1068.66786	540.0145761	113.2574469	3367.991385	915.8862016
3-Phenyllactic acid Results	36.78975028	31.17733197	26.58141682	116.5402216	21.50232652	34.47362707
-Methoxyphenylacetic acid Result	31.19377552	3.92829105	32.8478294	4.452527489	3.987262566	17.65848432
m-Coumaric acid Results	60102.37846	44400.60594	56161.95535	3763.252088	52987.1413	48031.65263
lacetic acid/ 4-Ethylbenzoic acid R	13591.45579	8256.746935	9182.071857	3042.337792	7733.179518	7328.124932
Phenylacetic acid Results	14913.98962	10305.05054	11979.87091	3586.284078	8184.70685	8959.78917
ethylvaleric acid/ Hexanoic acid Re	35546.88314	30825.70005	36863.93834	11855.80706	27480.58852	29960.17446
Ferulic acid Results	34.84505957	5.322777015	84.94143022	2.915873678		141.8901432
Gibberellic acid Results	56.41392353	68.03520034	37.63226303	37.97222346	28.5556894	17.27695295
lethylbutyric acid/ Valeric acid Res	27757.95868	18651.79424	19046.81865	3707.692256	17510.87614	15220.88522
Protocatechuic acid Results	103.8019414	56.90795984	231.471095	188.7902067	204.6204992	105.4031783
2-Furoic acid Results	92.91227163	76.62209838	36.84083781	24.67729752	41.92165119	20.66816221
p-Coumaric acid Results	60096.03373	44399.51385	56162.81957	3736.412374	53015.25993	48034.29447
xyphenylacetic acid/ Mandelic acid	466.8528394	352.1199548	151.7438816	45.61871938	233.516107	115.4917437
Hydroxy-3-methylbenzoic acid Resu	85.17852352	978.8321637	25.37367232	62.31554818	53.13785347	26.48389798
Isobutyric acid Results	238.8924101	105.9863093	195.3863867	252.1107285	176.3963394	429.6325952
Leucic acid Results	129.3897505	176.518673	131.7389876	14.63633004	41.40384359	39.58375063
Vanillic acid Results	159.1163502	50.81300765	393.8461583	52.54334949	178.9632552	65.80786945
Methyl succinate Results	161.5443056	309.4875106	266.6096477	150.5888152	277.097298	433.4953321
Pyruvate Results	30.74783362	77.30524891	18.94878135	32.00819322	29.84613429	53.38264493
belta-Hydroxyisovaleric acid Result	61.08709142	59.6151488	49.81406624	85.44773448	86.14904338	70.29888157
Acetoacetate Results	183.3192933					
Homovanillic acid Results	75.20315015	84.2675271	58.26279312	13.98612956	26.99438966	49.57942224
4-Hydroxybenzoic acid Results	3527.969742	341.5972634	192.6527853	90.0583348	614.6206553	243.284295
Phthalic acid Results	9125.768508	7088.174159	8006.101919	0	6138.578535	2319.200493
L-Ascorbic acid Results				329.1886172	120.0694433	
Methyl-D-mannopyranoside Results	112.0154068	79.84170284	199.574211	17.77387961	74.32075198	91.02399503
Ribose Results	981.8251329	1349.34803	576.4458135	43.23581907	520.2289399	593.2549865
Levulinic acid Results	13743.71584	18124.44418	15492.03824	0	14057.07867	9828.813083
Ethylmalonic acid Results	38.47430613	53.96587754	711.2918021	216.9331079	33.69369317	477.004385
Sebacic acid Results	177.5294279	163.9388649	459.9988045	63.43696497	90.7972279	105.9157699
N-Acetylmuramic Acid Results	83.11277944	59.42955143	33.83561029	46.89717472	47.40532777	160.5570667
Azelaic acid Results	2561.071677	3201.803648	2865.886119	2429.694257	1599.719882	1844.554387
Lactate Results	79300.02136	104761.1401	71021.14832	59001.94927	36448.00641	51079.3215
Adonitol Results	67.20708012	255.9504423	48.15193275	39.41805603	37.02013439	151.8616783
3-hydroxybutyric acid Results	607.2350118	157.9423083	54.80332559	58.97353155	55.44002847	212.8430773
droxybutyric acid/ Malonic acid Re	29354.959	4669.59937	1391.433862	0	19229.38028	1873.018697
ethyl alpha-D-glucopyranoside Resu	33.29921711	146.8375169	13.00209859	28.36913544	29.94461918	15.55113534
Xylose Results	356.5128554	100.9407843	106.6414255	85.73092351	396.3742922	123.1438098
13C3-Lactate Results	271696.3198	252861.6319	251095.4445	0	226234.8758	164023.6944
L-(-)-Arabitol Results	133.3412547	121.7746267	616.0865532	506.2876354	340.7424663	44.88535042
Xylitol Results	269.2927725	373.4666094	105.7517061	187.4448437	49.17866545	87.22381849
Erythrose Results	27.11935485	53.66885214	139.3510056	18.02452409	29.04907164	15.55530722
Methylmalonic acid Results	1053744.022	2681565.095	990009.302	426481.1936	731432.2649	1008054.143
Fructose/ Galactose Results	19669.08543	11606.49588	16213.77296	11831.40381	11046.53323	10168.57347
Glutaconic acid Results	7580.614144	13952.00371	6256.787375	4208.788667	5436.523451	6248.375187
Glyceric acid Results	77.84003518	3025.325102	34.28790703	55.69318215	628.273552	651.419754
Suberic acid Results	1409.226797	1680.549972	1264.337787	101.6765072	170.0733728	694.953454
Glyoxylic acid Results	141.2305257	160.3290173	104.0127729	120.0997444	93.34143568	110.3884131
D-Mannitol Results	224.4485171	275.3016399	462.0748417	34.12227772	42.15088269	187.5350689
)-Xylonic Acid (Lithium Salt) Result	5446.268647	4259.517058	5382.299089	13458.64488	16124.96154	2348.015338
Sorbitol Results	203.9792459	102.346074	82.02596612	107.1651451	80.14516952	64.34271521
Dulcitol Results	367.150763	80.60932166	96.97007651	135.0729274	122.601405	272.1748742
Glycolic acid Results	53.26282216	45.7903496	4.419304323	55.80777221	65.32811353	65.26453067
Mannose Results	6651.365254	4921.364247	4050.208424	3270.318283	3633.913193	3508.191117
Glucose Results	19665.8855	11604.51855	15559.48845	11844.75922	11086.31033	10391.75463
Fumaric Acid Results	22462.78414	40973.37961	19186.76401	10790.90715	12805.8464	25919.62044
3-Methyladipic acid Results	35.34179246	89.44794428	38.1759069	6.617417613	55.63650661	24.80820361
2-Methylglutaric acid Results	9362.592938	601.4835307	565.4843267	0	2720.241654	5346.043485
Muconic acid Results	49.27421511	82.06451161	43.33515697	88.6252797	34.652183	85.09312491
Homogentisic acid Results	52.6378806		94.74585421	37.89810123		
Shikimic acid Results	35.37137449	36.95339037	35.63539736	7.717554687	25.24453121	24.93384822
alpha-KG/ Adipic acid Results	11354.39123	10831.38282	11783.39324	5711.389187	5177.861357	8546.433635
L-(+)-Arabinose Results	549.5213326	52.67305925	59.04034889	28.25685686	16.58526322	85.54135871
3-Hexenedioic acid Results	60.16763506	840.7808732	418.9356089	685.4949445	46.68682255	20.74456247
Succinate Results	4260.8825	13299.15301	3033.167064	2560.096524	3287.48253	5035.799972

Isovaleric acid Results	1352.511019	7073.916698	1149.81086	0	1426.913525	1051.564694
Fumarate Results	6806.725199	816.3199409	299.3082035	156.2533031	4476.096315	8311.370397
Glutaric acid Results	264.7503653	238.8093484	378.3127361	140.4615533	104.2449553	94.66744527
Aconitic acid Results	3611.425425	5743.798036	2652.199927	76.80919067	156.6266906	3070.736462
Sucrose Results		79.84965776	83.55763141	30.78000735	116.5818076	65.40961601
Glucuronic acid Results	817.882622	102.2570418	67.43814862	112.763243	38.67885643	642.4456781
R5P Results	52770.61892	51259.9023	53510.5033	19781.45036	20208.32932	43035.29476
D-Galacturonic acid Results	6.649689943	25.71879521	47.02941476	56.38929643	17.18727093	18.39786405
2HG Results		12737.28603				
Oxaloacetic acid Results	631.7270816	63.62098075	47.54753507	80.68704337	399.8425447	37.8925719
Galactonic acid Results	214.804104	33.72028001	242.6123993	98.83238736	259.4115669	1050.411083
D-(+)-Cellobiose Results	941.895886	736.9384471	72.1166188	1016.566606	180.9255869	821.2976423
Gluconic acid Results	68.40563521	35.44183575	27.05059574	35.94230776	78.97326056	58.45353108
3-Phosphoglyceric acid Results	40503.65235	2297.457456	14764.18165	0	18103.87464	905.4848473
Trehalose Results	76.3411416	42.06291291	97.16805898	58.52975442	143.2362592	87.23945441
Lactose Results	598.1590827	32.1616402	73.46650085	50.65944915	15.20660801	526.8687203
Mucic acid Results	143.4620783	140.2532981	56.5676142	73.23735241	996.6850292	37.36434798
e 6-Phosphate (disodium salt hydra	49412.19326	58817.87746	46834.95801	32831.36165	43711.27489	40088.48431
DUMP Results	45.54922462	51.53339461	13.65058079	105.4475063	8.215229964	33.10510574
Raffinose Results	358.9909044	930.4628289	864.9538897	344.5842712	719.3175969	364.5136763
F6P/ G6P Results				7473.799377	3055.740074	7012.412003
G1P Results		2355.889169				
Galactinol Dihydrate Results	412.1255873	49.0362666	382.9269742	151.5042044	35.12779326	22.02412456
F16BP Results	433.1356467	335.659133	142.7298325	252.3234057	82.70953564	100.0292572
G16BP Results	407.6784142	536.4439095	212.2729314	549.7990271	181.4035598	187.0511159
PEP Results						
eHydrate (from Stachyse Tuberifera	3.932977241	1.313469244	23.01219257	18.66813171		40.61293465
UDP Results						
Malate Results						
X5P Results						
Citrate Results						
meso-Tartaric acid Results						
Tartaric acid Results						
Thymol Results						
IsoCitrate Results						
6-Phosphogluconic acid Results		68.94905923	122.2249637	31.86831245	49.01137579	84.67037849

	ApoL6-BAT cold							
Sample	11010-tissue-pos--11	11010-tissue-pos--12	11010-tissue-pos--13	11010-tissue-pos--14	11010-tissue-pos--15	11010-tissue-pos--16	11010-tissue-pos-qc-	11010-tissue-pos--17
Sample	11010-tissue-pos--11	11010-tissue-pos--12	11010-tissue-pos--13	11010-tissue-pos--14	11010-tissue-pos--15	11010-tissue-pos--16		11010-tissue-pos--17
Acq. Date-Time	11/ 10/ 2018 17:24	11/ 10/ 2018 17:55	11/ 10/ 2018 18:25	11/ 10/ 2018 18:56	11/ 10/ 2018 19:27	11/ 10/ 2018 19:57	11/ 10/ 2018 20:59	11/ 10/ 2018 21:29
Phenylbutazone Results	1484.631207	1226.680524	1546.131714	1236.559056	1862.847558	1795.693979	1046.502333	2977.313906
3-hydroxykynurenine Results	17683.30314	10447.08052	24616.21977	23750.22029	22972.79485	17999.94267	12034.34761	15506.77812
NAD Results								
dTMP Results	5799.872433	4621.93377	4426.20325	3616.055418	5423.059538	4243.593025	3181.565782	4763.41002
N,N-Dicyclohexylurea Results	12358.67853	2973.776991	14236.17636	1720.347341	12535.19492	13099.86842	1089.842623	8420.534747
4-Pyridoxic acid Results	18903.95789	32851.15939	24484.00201	83427.09439	25200.94667	24816.67108	17102.05902	25679.537
Melatonin Results	5119.546604	4253.941768	3641.783937	482.3677691	5002.260974	4619.395928	550.2174266	3105.074592
Urate Results	8520.422983	5188.912312	9370.342595	6160.87005	10096.82078	8965.946492	4213.68609	8586.445199
Caffeine Results	2224.546847	1411.135015	1881.228629	855.1018063	2062.908746	2098.086986	361.4895168	2805.81991
Folinic acid Results	564.5441473	306.987639	415.4770723		396.8681801	394.0884902	152.7468484	785.7301243
lenalidomide Results	447.8174474	80.11535847	427.4771628	28.25809117	267.0353726	169.9081194	20.73318999	71.26010918
Tetracaine Results	109.4888202	138.8943714	775.4219171	214.7500922	146.7960438	31.37163137	93.09268581	658.0612565
3-Indolepropionic acid Results	194.580955	212.7569932	2062.449937	30.69495831	313.7165689	164.9284931	302.0080867	1256.476149
Anthranilic acid Results	4651.983636	2397.109625	3725.534898	10688.89349	1796.896566	34385.00683	10413.20101	13320.32585
2-Pyrrolidinone Results	44299.32152	34649.9986	33020.76058	8246.249193	27513.32441	43552.45627	12040.84054	27719.72891
Phosphocreatine Results	480273.04	521900.7465	305776.4529	230988.4966	430295.9189	411597.3321	230003.9557	512001.2176
Dihydroxyacetone Results	30496.69003	29696.3791	15452.19868	1841.139637	54472.93994	42345.37336	44344.47144	28266.47449
Nicotinamide Results	3703595.431	5378259.064	1135671.033	19190030.22	5875500.972	1893012.449	17964498.31	7377535.091
Imidazole Results	95469.03372	152421.2075	67577.28402	111162.6731	79149.11791	59745.02448	24964.44531	81311.08763
N-Acetylethanolamine Results	12291.9195	13821.68925	5878.665149	17031.21058	12472.10025	12254.91055	9145.741989	13235.01951
Allopurinol Results	402.3086794	1919.417804	617.6371134		585.2128691	901.8682423	702.2253535	290.399085
Xanthurenic acid Results	229.3145674	74.99000743	61.24763953	211.0182567	182.8024277	153.5616223	52.59884682	342.897919
2-Deoxyuridine Results	344.6005875	491.29871	97.67817617	277.2609336	587.8383817	2111.955648	1110.375348	213.0187764
Pyridoxine Results	489.1237954	1489.657512	35.00449434	18.61732342	305.671973	184.9701885	351.1286977	541.740256
Decanoylcarnitine Results	45299.32447	30180.07242	5709.683037	14378.26676	33943.2539	29818.70527	0	45452.85348
Kynurenic acid Results	126.1743314	2271.085577	120.2053154	101.2499553	835.9740549	230.5337958	0	440.2774681
Hippuric acid Results	686.793524	237.1711678	31.56169052	246.1668744	39.54582436	1058.911446	0	104.7421756
Propranolol Results	877.3323305	1350.765017	1090.420492	120.7311633	1886.211052	1248.674024	74.64885532	1331.46692
2-Phenylglycinol Results	2486.971769	1556.266689	922.1544435	0	1590.106647	1296.199941	189.8343205	1562.243171
Acetylcysteine Results				1060.422489				
2-Deoxyadenosine Results	2804.826159	2319.710299	1666.09848	1187.442767	1786.083981	3390.459839	0	3425.573691
Adenine Results	45309.96235	43033.91547	96278.83088	78084.11211	78550.96224	69183.88478	157065.0693	73998.87393
Isovalerylglycine Results	1245.571373	1918.352166	982.9808121	0	798.7597799	172.1862988	1504.051999	2467.011974
Hypoxanthine Results	87262.77638	224798.6858	17914.14453	240896.496	311076.3562	44989.65423	276269.2422	219545.2098
Uridine Results	5521.922984	21648.68546	4828.011691	28439.81517	37983.77366	11503.38131	31612.61193	31427.71818
Creatinine Results	792211.0535	1178605.168	940689.4474	1331942.823	2563519.87	7829916.864	7979336.025	1285023.33
Adenosine Results	218903.8421	459612.2431	179886.6502	558811.1891	697260.8607	374183.2957	1471313.738	592733.8336
Xanthine Results	1295.119492	4011.5972	557.5643739	3598.741929	9324.716305	1418.589869	11056.3417	3866.794806
Tryptamine Results	223.5804774	221.896749	147.7276884	62.63037901	116.3997668	355.6306376	200.5861052	502.455159
Acetylcholine Results	1406.233909	1523.520226	848.4860889	938.687981	994.5158002	621.5342724	0	3614.885959

Cytosine Results	17964.60104	15864.62728	64415.53725	35418.79497	11374.33957	77379.54441	169805.1688	16426.98836
2-Deoxycytidine Results	4833.65341	7564.540938	23145.62233	6098.265055	9527.445013	34415.21863	59814.0329	7751.005839
Nicotinic acid Results	5790.044927	2782.800178	1727.099	1098.661944	3942.430033	2781.147696	0	4582.818909
Inosine Results	1150109.741	2110153.656	425314.1952	6210909.612	3201175.905	1087874.762	2214693.843	2924313.391
5-Methylcytidine Results	4952.147306	10001.54514	1658.01609	10821.46587	7949.550314	3969.057447	6828.330744	13151.34677
Biotin Results	2803.082475	21032.2887	1286.188815	844.4763975	19073.03214	2393.594855	0	1414.170611
Metanephrine Results	1494.529128	7936.207576	6448.101814	684.9501589	2959.904274	3692.085862	0	4795.116405
2-deoxyguanosine Results	7179.693292	4610.721717	4214.237295	2724.170621	6264.290975	37588.21922	8702.138408	10299.61752
Guanine Results	61523.97911	83682.35365	24245.05451	174567.849	164802.9558	60810.68791	72757.62717	199030.8067
Dopamine Results	828.7202338	219.0861245	271.076529	1227.61542	851.8488677	5494.991063		2166.81485
6-Methyl-DL-Tryptophan Results	5025.482184	13922.148	805.8016423	5999.59071	14676.18528	3987.975801	4702.311418	3171.75994
Pantothenic acid Results	4099879.231	1899302.254	686903.1175	2317403.655	2548327.571	1222901.004	0	4340997.233
Amiloride Results	41085.0055	24960.93529	4449.179198	28182.10913	24386.45057	23754.75138	16888.92195	29815.31613
Cytidine Results	134106.2391	623313.4652	96290.62975	840970.9433	794415.1788	197984.7873	429625.0632	810265.4618
Nicotinuric acid Results	516.530732	380.3931478	1853.74748	2384.039198	1230.626932	1256.182207	0	4862.652438
Serotonin Results	637.2427589	2903.941953	223.2844386	314.7990941	1514.858506	384.2750132	465.6915042	
Acetylglycine Results	35.78097291	20.77084404	35.10709664	191.0683319		63.06762983	134.1985147	111.5248061
Phenylalanine Results	2130636.703	3030400.457	493032.375	3183102.592	3088479.706	1141078.139	2013257.116	3469792.237
N-Acetyl-D-galactosamine Results	9734.284722	17329.82252	1501.416546	890.0137516	13396.55989	1720.800466	0	17450.34323
Tryptophan Results	133983.79	395794.2506	30226.76219	252546.6527	266850.4276	54697.93419	210320.0549	257676.6819
Urocanic acid Results	49697.33119	21168.17944	39703.99764	14774.38178	31632.88665	39627.74013	25687.03643	50837.39953
Indole-3-lactic acid Results	4778.401237	22239.43493	1586.466486	15295.30124	9172.818451	5683.41092	12659.38287	14286.80215
Normetanephrine Results	13061.42519	24319.69714	6164.16357	21049.2421	14923.19186	23301.9911	12746.53532	27534.30274
isoleucine/ Leucine/ Norleucine Re	6178047.594	14638852.57	1507302.959	12945261.87	7969726.18	5421383.039	7108929.314	11990547.93
Kynurenine Results	4628.70449	2267.42234	179.2678562	827.9878665	411.8033687	2101.013691	324.5127415	4088.256074
N-Acetyl-D-Glucosamine Results								
Acetylglucosamine Results	3785.113962	3878.79927	1746.984943	3044.004002	3494.768076	3457.463144	2335.399707	2883.172268
HIAA Results	372.8747491	6714.596153	803.8214835	4816.893071	14164.44542	626.3000566	0	3779.087112
6-Hydroxynicotinic acid Results	16133.37406	1375.735947	3800.750285	1106.132529	16561.91599	3758.755743	264.0193998	3768.764329
Guanosine Results	112266.785	101361.2266	49978.64914	296185.993	279747.5072	114135.5116	151564.031	330813.8459
Pyroglutamic acid Results	223160.9273	177469.7319	42809.46492	143012.1197	194374.974	111787.0633	116760.7767	186613.8741
Isoleucine Results	6191267.279	14534007.73	1475661.519	12912303.65	7895738.534	5432743.684	7157385.728	11828134.77
Betaine Results	82864119.03	74517858.28	44725686.13	67794846.21	74277842.16	51296984.02	60858669.11	71895681.63
3-Nitrotyrosine Results	2440.357532	439.164608	153.7382832	1413.765183	437.8159954	1436.057812	0	3664.639751
Xanthosine Results	7173.69835	7059.129712	3927.793302	19735.27244	15622.80282	6790.336861	8626.877703	17564.75304
Acetyl-L-glutamine Results	2424.552951	1627.134325	562.0924125	948.6141134	1855.812796	1435.284044	750.7329667	2994.625225
Methylhistamine Results	72261.06556	93584.87658	80516.77964	93361.15011	102532.7673	81771.35223	84213.48412	94587.51089
Methionine Results	10280.19724	186793.5354	2113.736848	5984.993076	274752.6716	388.5704091	57325.57375	9072.56505
Norvaline Results	954848.727	2040201.244	398508.9195	1672246.738	964323.7886	930720.4565	1325232.73	1665644.989
Acetamide Results	1326070.91	1334063.994	126392.8223	1208732.502	712371.5382	1428347.285		1137338.109
cGMP Results	522.6362372	742.2852342	222.0018786	448.6008772	444.8959643	940.5943105	339.1665901	416.1702005
4-Aminophenol Results	998.2692546	611.9446989	1225.684588	1375.722162	1627.049009	1042.391168	2789.51728	1238.361403
Taurine Results	4814793.022	6158287.573	4483457.228	6597221.48	6339030.747	5613175.611	6067453.582	6241749.773
Valine Results	1318624.178	1913653.665	412762.4652	1664751.436	1218493.625	958273.1432	1327250.825	1671080.434
5-Hydroxytryptophan Results	761.9637623	328.9252809	155.604623	203.0160349	694.8576969	302.6801735	648.814379	137.1416229
Quinolinic acid Results	3692.955446	2852.493301	4767.176951	13490.73379	1187.412757	1992.226438	0	1453.437451
Tyrosine Results	185398.7397	131937.5803	28331.42288	138372.6368	166452.841	86388.26706	156491.7482	154298.5064
inoisobutyric acid/ Dimethylglycine	3264948.656	14511952.35	45579.75287	25241608.28	17572903.55	143289.3414	220592.6222	20377708.58
Picolinic acid Results	4373.478056	2573.345712	956.1099321	4734.619146	3964.127285	3452.234264	3469.802827	3208.877518
Epinephrine Results	3311.515956	8705.938585	6964.326503	22746.45095	9796.295544	9313.562968	0	6692.784578
Acetylcarnitine Results	99294489.19	76517306.94	67204165.95	39057137.74	83099182.13	104945019.9	94264883.38	80281925.51
Indole Results	3665.842971	1827.943597	13053.81644	18715.4634	4038.861602	13940.74004		4014.860519
Pipecolinic acid Results	773202.5304	1552914.44	306729.4884	1554914.525	1111385.758	697476.3172	896945.5557	1778669.433
Proline Results	5493346.009	6418406.564	937493.6892	6458153.535	6508555.129	4081060.324	3952480.692	8104681.247
4-Imidazoleacetic acid Results	3345.26508	1759.542786	909.5731918	1687.259297	3721.662684	1818.740081	1222.343481	3571.322041
Neopterin Results	396.5981112	103.701063	36.78996191	59.17404266	78.047169	20.03734572	38.67126142	650.6067789
2-Aminobutyric acid Results	3252920.261	14663219.69	46331.46545	25278451.4	17652111.18	136853.1617	189271.7057	20566635.64
Methylguanidine Results	7218.997907	9225.422298	4563.687854	14071.54955	14483.00899	12619.39375	123685.4654	11826.15398
DOPA Results	2128.23818	3132.153403	538.6055954	1695.294676		443.0870744	1536.211533	3037.416088
Sarcosine Results	2010200.707	2994947.212	629229.3708	5492311.668	3287353.714	464655.4721	1768887.677	3067104.885
3-Aminobutyric acid Results	117771.0943	66125.17375	1771.903041	1649.632384	54503.43392	4668.07931	2804.253056	33878.5947
Choline Results	5629986.096	24436420.07	1714914.191	39764102.68	34037912.36	14336691.07	0	37401317.72
Hydroxyproline Results	970771.8446	1780047.877	332728.3064	2648484.124	1571944.087	1049186.03	1571123.62	1869069.267
Putrescine Results	982.8069285	3953.699283	3525.064905	952.3308712	3247.550974	1118.661452	0	457.6003785
Alanine Results	1863201.922	3006957.026	647635.5072	5145964.588	3062264.049	1200398.337	1752441.427	3038452.06
TMAO Results	1516277.462	2289075.728	2277494.574	1495093.634	2047768.211	2536550.73	3526377.791	3323556.872
Indole-3-acetic acid Results	17403.14492	12640.8121	13578.29468	2037.480676	15832.64073	11137.89866	6226.794092	12175.15372
Creatine Results	25457916.15	40172933.53	13692300.08	66719827.66	38714917.05	44652329.48	44492622.94	41031096.3
Acetohydroxamic acid Results	5721.03349	6804.353354	7345.675694	3686.351716	5774.161476	7457.993175	9811.23436	11788.97358
Carnitine Results	66378108.23	69118103.32	45483467.4	74400488.31	70641227.89	58571210.62	49027008.75	72587903.23
Homoserine/ Threonine Results	276554.8767	346412.2315	139871.6984	363536.9895	365928.6413	180588.8225	284242.1856	317603.8507
Glycocyamine Results	1579815.453	999494.4005	902641.7024	22898.30471	1229638.679	705570.2187	138737.4695	1162434.742
N-Acetylneuraminic acid Results	54817.73692	12840.51808	2419.346234	9389.769756	4913.520868	16779.35798	3049.931852	35097.93554
1-Methyladenosine Results	225350.6667	550956.1638	43151.90454	283070.8517	719726.0574	429539.5539	172250.638	491271.2056
Spermidine Results	1611.121214	5211.988312	2874.74451	535.7669228	795.7630168	626.0297115	371.9359849	885.6224503
Cadaverine Results	5829.965424	6415.652733	11703.28719	2382.865927	6503.679231	2331.697814	0	6724.783243
5-Aminolevulinic acid Results	84791.5425	92235.53994	60614.34744	78032.84103	66812.2842	45781.3113	0	18139.66081
4-Aminobutyric acid Results	257230.7716	67117.39028	241718.8321	51603.54766	59364.00672	76184.608	2523.230799	72774.80541
Glycine Results	21432.45911	33723.88176	55281.04856	33986.27834	39084.98566	52643.24346	38884.99536	36196.47225
13C5-15N-Glutamic acid Results	6941.388311	3664.935851	4120.373647	5748.271635	3611.072795		0	4035.721174
Glutamic acid Results	170335.2828	173633.0154	133865.4906	182920.1639	141827.4684	198736.7852	42442.4244	161017.8361

Glutamine Results	12260782.69	11252070	9820332.758	12856615.85	9915506.361	13307000.96	2962423.283	10737453.77
Glycylproline Results	154.7815217	1435.384794	39.4949786	804.8270049	104.7392467	1572.099689	1137.446697	213.4863124
Acetylornithine Results	3187.065527	3690.020358	1164.04962	2470.651631	1295.12107	2125.097557	2525.595087	2362.193566
Dihydrofolic acid Results	93.63871488	58.4886205	57.21059304	1.559163227	31.56787168	66.13531981	19.67493144	24.80525101
Glucosamine Results	6968.321229	3047.053034	691.6613866	588.4276287	155.8197173	6067.12999	1121.642713	7626.886237
Folic acid Results	22.30951625	30.42783768	105.8629085	1.161607809	2.269856036	9.299811049	23.16905591	45.12415919
Asparagine Results	70439.66335	57297.72261	25381.88687	36948.80462	39421.04144	77361.73165	33922.18578	57254.42749
Amino valerate Results	2884.043939	1155.9944	751.3198088	492.4299846	1673.966581	1961.220591	3318.592574	2237.324004
Glutathione reduced Results	12424.21836	61296.48433	927.2789037	42213.64912	42123.73548	12551.47293	2982.939018	27115.75352
Serine Results	193037.6562	221530.6767	124849.481	248939.6932	211836.708	244372.1661	121449.4345	224996.0455
2-Aminoadipic acid Results	145.8509626	781.2058906	1889.274826	209.5501003	409.6924135	2834.031704	227.0139108	169.5980247
Adenosyl-L-homocysteine Results	26271.23585	81638.6285	1688.137384	4895.874964	49907.92853	1432.832419	36614.20387	20782.75962
Aspartate Results	2815.986832	11826.78887	28057.70719	1084.096843	10952.52401	1417.051933	0	18463.11637
Agmatine Results	31230.77397	28529.19078	39222.20912	20283.5979	21277.50439	37750.76254	0	22282.96422
1-Methylhistidine Results	11743.85752	8312.766403	538.9840215	2019.70573	4405.88061	4702.366075	25304.51367	4309.65584
Siacar Results	122.2641535	75.99953477	72.84244771	163.6348643	60.29864712	62.27689316	146.2326399	88.80353236
Hydroxybutyryl coenzyme A Results	11153.18099	25576.53306	953.393902	14659.51727	29220.0928	38475.22914	0	19742.1753
Isobutyryl-CoA Results			5247.296647			5877.669257	2688.601059	
UDP-GlcNAc Results	95.92036195	236.2450351	22.99173768	130.1014536	57.11745844	128.4136837	114.4083905	280.0777574
Citrulline Results	122327.6542	236102.7468	23186.49523	102744.4886	130721.5536	191405.0947	380485.1313	165989.0169
Histidine Results	19310.54279	146212.7582	4941.253408	41640.73101	96759.30629	10659.97148	0	50470.35593
Acetyl-CoA Results								
Carnosine Results	74403.13747	282227.647	9762.717009	128412.1408	216719.3929	272404.4407	150860.0073	244622.604
Glutathione oxidized Results	348280.3796	603460.5956	73033.48696	548559.4054	585812.7918	347370.4838	0	505266.7692
Adenylosuccinate Results	31459.51549	18637.88534	3642.06086	15071.65079	6399.357216	65276.40755	0	21632.89821
GDP Results	152410.7775	15285.08964	38728.10572	166915.2035	143296.7491	89293.70705	0	168467.3263
dUTP Results	204.770236	2099.883046	227.8336575	218.1530356	315.5518853	373.6148118	241.6015577	2522.119473
DCTP Results	38.58233162	252.2199364	18.14378159	36.5838973	51.96370495	720.1846878	41.28240947	39.4900584
Homocysteine Results	671.5089497	320.163537	516.7963326	735.3280468	714.8299629	696.5191113	52.44861115	261.0372839
ATP Results	13036.00199	38158.16536	12028.21433	60091.61481	133844.3649			69216.99016
Histamine Results		48402.61736	10530.05855	57512.83279	54638.69274	22845.45983		62871.01878
Uracil Results								
Cystine Results	1536.083573	1449.228645	192.2647955	15311.8596		2392.504413	8181.392948	17638.06164
Cystamine Results	503.473516	665.8015731	190.2155307	330.062957	100.5853234	180.584833	138.846556	305.6716
Glucosamine 6-phosphate Results			72.0953415	171.0994967		1003.334534		
Dimethylarginine Results	86.13197381	36.32940966	98.52538354	191.6565616	278.5071848	13.40321503	168.6428207	54.98545076
ADP Results								
DCDP Results								
Ornithine Results	26885.96975	36399.46534	360.477456	1528.330834	25327.56971	25950.16935	0	27167.97621
Arginine Results	602.580856	204.0608844	578.9916734	195.3847002	141.4765454	62.54495094	878.569444	128.1558718
Lysine Results	121.2038861	114.9700812	1166.296888	97.81984076	765.8352741	173.9370317	237.1664234	67.07694326
Indole-3-pyruvic acid Results	418.761287	361.4211355	158.3516264	370.8068324	595.4997329	178.6714127	190.7740222	362.971649
Cysteine Results	332.4658734	591.2059442	161.9390571	1107.856843	609.1698154	513.1121093	858.4755992	924.9947016
3-hydroxyanthranilic acid Results	310.0264837	58.43761232	96.2175379	95.63070222	182.2166089	46.99675612	83.72813099	120.1640174
Sample	11010-tissue-neg-11	11010-tissue-neg-12	11010-tissue-neg-13	11010-tissue-neg-14	11010-tissue-neg-15	11010-tissue-neg-16	11010-tissue-neg-qc	11010-tissue-neg-17
Acq. Date-Time	11/ 11/ 2018 12:22	11/ 11/ 2018 12:53	11/ 11/ 2018 13:24	11/ 11/ 2018 13:55	11/ 11/ 2018 14:26	11/ 11/ 2018 14:56	11/ 11/ 2018 15:58	11/ 11/ 2018 16:29
pregnenolone sulfate Results	624.2878912	727.3980931	554.8207183	362.9209108	863.772878	1240.225014	904.288891	1483.949748
2,3-Dihydroxybenzoic acid Results	312.5500119	43.11427369	241.3697751	16.93719944	103.5674072	134.9071444	222.3049935	11.15377445
Nonadecanoic acid Results	67968.25078	53521.76763	45058.86581	35712.20687	29550.0349	51257.20803	40991.03284	34698.28224
Stearic acid Results	199094.9781	314689.5298	299008.5839	99727.75078	156201.3296	228391.7961	267175.6924	238459.6432
Heptadecanoic acid Results	88091.65089	137856.8935	66159.85926	18047.71225	115190.726	79859.63224	25359.36498	105261.8911
9-Octadecynoic acid Results	802178.2863	467456.8317	499712.6855	567935.5168	456102.1215	433179.9251	1200424.803	595375.6531
Myristic acid Results	89250.06224	83688.95302	52420.54722	96857.67699	85499.09483	63345.37953	63107.26733	57618.9891
Palmitic acid Results	311736.4404	275300.1351	317199.8432	428491.1403	199788.0115	225409.2809	243547.4085	245258.6331
Pentadecanoic acid Results	77958.68354	57007.4339	56431.86843	35004.40872	58473.06421	59935.8361	27026.28865	66682.01887
2-Hydroxybenzoic acid Results	1274.871079	677.5118277	675.9957903	1369.588702	965.2488937	1630.666292	313.1521219	1077.310829
Lauric acid Results	87286.0991	61642.74031	64010.04641	14411.5781	65059.18954	70341.43698	16393.48332	69848.42618
Capric acid Results	194613.4275	188425.6469	148261.228	13123.36615	204479.8672	238663.5924	12579.88816	191669.2284
-Hydroxyphenylpyruvic acid Result	1516.650288	1068.049984	1160.357268	320.4767735	961.7290864	473.1573279	113.3200511	312.4492137
Phenylpyruvic acid Results	432.8032966	194.9447005	238.3971744	23.70040451	258.7889569	206.0687949	53.03229453	263.5072857
ylacetic acid/ 3-Hydroxyphenylacet	2361.864089	1348.853871	241.8395269	193.7453443	626.7262102	696.5400163	56.44475368	1536.368473
4-Hydroxybenzaldehyde Results	1034.27959	1069.241614	1299.336468	839.0108044	1034.783065	2600.227326	597.4498952	1150.633109
Phenylglyoxylic acid Results	453.0240747	328.9400905	536.7531047	77.0406293	288.5110677	167.3867907	40.14270529	150.3649874
Caprylic acid Results	13433.10075	13777.8439	11230.60853	21631.28524	11738.39591	12967.11971	10655.86215	13522.28868
3-Methyl-2-oxovaleric acid Results	18299.62796	12999.78479	10989.19838	4751.757897	10401.34361	13611.95101	2371.005195	16120.52476
GA3P Results			40.32213777					29.50184646
Naproxen Results	17.09977439	12.36734371	12.49026139	0.523084546		6.914677776	2.580429902	27.90695598
entanoic acid/ Ketoleucine/ Ketoisc	1022.970592	2346.911501	978.96211	2244.512623	89.73787811	4260.937762	513.2159833	2234.063292
Gentisic acid Results	21.22950868	28.04258828	4.081256902	144.1738981	22.94354912	23.64562167	58.5213372	48.1748207
-Ketoisovaleric acid/ Maleic acid R	23638.00178	38888.10671	13055.99516	17795.53074	36921.2684	29101.9369	2870.387614	33427.9043
PGE2 Results	281.0545684	209.1523035	52.10348179	56.20179625	63.55997742	549.7855659	66.49719744	354.8359476
Benzoic acid Results	7341.172018	6651.842457	2415.914131	5987.411373	4880.74187	5382.541982	2726.655207	7756.352377
Citraconic acid Results	3253.706902	2713.631051	1451.281349	936.1402559	2960.344776	1926.962901	866.9069172	1841.737405
2-Ketobutyric acid Results	148.4598847	7.168495347	177.92894	44.37568837	8.05552082	5.787377507	52.11835434	80.41704685
Myoinositol Results	780.2953776	314.7852107	121.6298565	353.8057695	509.0051885	722.5189794	66.98388037	742.337758
3-Phenyllactic acid Results	36.91077736	56.58630448	26.81804139	33.32189533	219.9507466	66.5208051	27.10663715	59.55541891
-Methoxyphenylacetic acid Result	55.0145099	62.51290232	25.68081161		4.081205855	6.810583183	2.692670422	2.400047337
m-Coumaric acid Results	33857.25923	24202.30715	27708.99663	742.751664	35099.28491	41448.66811	2854.778432	31366.02302
lacetic acid/ 4-Ethylbenzoic acid R	5999.663034	6619.298622	3779.578075	5133.065383	6616.924854	5815.68889	3021.716109	8197.052713
Phenylacetic acid Results	8534.444154	7771.40848	3583.312097	8863.612743	6753.511857	5691.841291	2453.580254	9597.520161
ethylvaleric acid/ Hexanoic acid Re	31752.95584	29604.93768	21406.85125	56276.81515	33762.05646	26766.1345	8606.700852	30137.52814

Ferulic acid Results	7.362961069	58.76041933	97.95731297	2.238329346	1.313844108	60.60540065	30.45130073	23.1916192
Gibberellic acid Results	14.4894152	85.2213725	37.43660499	17.22738696	30.60836305	114.7543605	35.18599515	25.76802919
lethylbutyric acid/ Valeric acid Res	15036.27244	14489.11558	8320.941388	3416.718647	15657.56011	11175.78243	2883.908745	12420.63182
Protocatechuic acid Results	86.7122768	170.8135616	84.99128307	30.74590108	258.7335723	205.5183809	56.79033375	133.4552588
2-Furoic acid Results	24.12377996	31.02691828	36.26563734	40.62642125	36.51032887	26.72526257	24.55492518	49.7164741
p-Coumaric acid Results	33850.33013	24202.8542	27715.73899	943.5838688	35160.86042	41442.55879	2943.903491	31362.21591
xyphenylacetic acid/ Mandelic acid	137.1770584	1352.073563	111.071811	26.03761391	146.1242117	214.9487907	54.04276278	119.3512252
Hydroxy-3-methylbenzoic acid Resu	183.0092098	31.65260257	42.16091619	79.6190067	38.8969369	32.67820542	47.90836507	34.58375711
Isobutyric acid Results	320.6846713	151.8705523	522.1292005	387.8723747	278.6541788	137.9612437	461.2551388	252.7943841
Leucic acid Results	41.51186994	76.92308977	51.10524892	13.31558788	13.58122019	55.10186216	401.8668933	101.52411
Vanillic acid Results	43.13479766	100.4743596	35.16073797	32.62293526	102.6194543	84.91579123	20.13638909	55.73556837
Methyl succinate Results	646.8795968	114.595658	131.5537024	422.1634326	968.0335784	97.90533024	213.6641634	233.6547947
Pyruvate Results	22.48793686	31.88154646	33.83623125	3.163445398	32.65312302	59.19319964	60.13817985	52.18693904
belta-Hydroxyisovaleric acid Result	154.5289725	113.4386737	35.34270252	89.82426756	54.16883437	28.98186531	170.1679764	39.16614322
Acetoacetate Results	314.5614894		171.803508	112.1293913	189.7973058			
Homovanillic acid Results	43.7175976	28.71694077	38.30797808	10.37336179	69.12225298	17.34878041	37.08136685	29.8265588
4-Hydroxybenzoic acid Results	884.0449141	293.0216862	166.4042135	78.60131166	90.24735656	579.7640573	91.77893957	2008.939953
Phthalic acid Results	1696.656593	1059.710579	2382.406291	84.55633205	4688.486216	5595.527472	0	1162.88265
L-Ascorbic acid Results		70.44050113	41.09854482		67.76075866		126.3528599	57.48798055
Methyl-D-mannopyranoside Results	133.3662649	40.18527226	29.53797779	284.6658014	98.77706507	73.47492926	17.79719057	121.832645
Ribose Results	559.8367681	669.2140535	421.1849707	1077.107994	852.116007	808.678053	546.6339996	616.0058788
Levulinic acid Results	26023.76626	10313.06927	7542.581148	5731.376275	6996.688658	8898.546927	0	6497.109714
Ethylmalonic acid Results	654.3097789	165.5933583	352.0702654	22.64797416	240.7614608	355.0153069	252.8107062	851.6221677
Sebacic acid Results	140.4503832	132.5536773	62.03684398	97.03264952	81.64892144	223.0624958	411.6157984	108.3171246
N-Acetylmuramic Acid Results	25.4102547	54.99618265	104.5112032	73.26183424	49.28925273	36.83037512	44.57258137	101.3180273
Azelaic acid Results	1170.62462	3072.438924	263.8573749	2408.356381	1789.2986	1767.025101	1020.138872	1645.309002
Lactate Results	17141.90886	49238.56404	11517.78239	80967.67956	58962.70224	59900.41885	51988.63186	43268.25979
Adonitol Results	60.32072191	87.09031343	45.34367376	94.22873571	80.61217556	177.4933368	12.79601466	265.6093038
3-hydroxybutyric acid Results	44.08643009	51.9421033	46.44678604	75.55660187	254.9511145	271.5959179	64.46913496	52.24667654
droxybutyric acid/ Malonic acid Re	2729.748242	21740.8544	806.0789829	1532.788903	13552.87025	9417.403342	0	735.2106861
thyl alpha-D-glucopyranoside Resu	6.90219554	50.31249726	46.72135587	18.10002569	138.7430707	13.13815897	40.18342557	29.60158009
Xylose Results	187.3679586	35.9949441	169.9464522	219.6393674	159.8532901	722.7390095	151.1406436	196.8163212
13C3-Lactate Results	166711.9923	172669.0054	64673.0921	173432.8747	156959.5021	173593.9116	0	166796.1042
L-(-)-Arabitol Results	46.1332465	40.01094943	80.56965739	86.80692209	453.7458869	76.76460722	264.9992807	543.0049569
Xylitol Results	129.9295549	121.0034231	67.66887622	77.52798168	74.75705411	97.64656748	164.300996	174.0334308
Erythrose Results	10.50269647	19.00733939	30.12215708	21.70227176	19.67234357	17.39344636		84.12320738
Methylmalonic acid Results	488975.0851	806387.7539	100380.7132	592650.1371	455187.7337	361103.3643	363571.662	448840.3932
Fructose/ Galactose Results	31093.84645	7525.085684	2135.437467	11356.62361	11465.25807	7841.616021	7643.455411	15286.05457
Glutaconic acid Results	10736.1138	6047.454627	662.0422775	3672.919528	3902.484282	3905.267317	2523.824214	5287.928083
Glyceric acid Results	37.76712135	2896.636607	61.43290819	361.1411445	309.9131637	29.07783295	210.1629296	678.8339147
Suberic acid Results	2016.887086	911.4855673	228.3777653	1138.79188	666.3810766	950.5065084	1183.265336	783.4099935
Glyoxylic acid Results	119.8216465	93.95678065	18.67676704	260.9311803	18.64430002	53.11382789	20.57374256	47.29795985
D-Mannitol Results	133.3061978	201.8980654	276.3960727	122.0588664	228.1371353	272.6218225	305.0654634	168.2985051
)-Xylonic Acid (Lithium Salt) Result	2910.270633	2212.566225	1515.283181	29748.42415	1710.330315	46766.62304	9831.63212	22345.8907
Sorbitol Results	377.7250327	586.9736715	1029.739334	252.6007912	215.031865	139.7749807	56.49454386	41.50101892
Dulcitol Results	39.90964728	239.4953279	1243.19947	175.7123741	129.6988459	172.50139	41.26352637	92.66818937
Glycolic acid Results	89.81818	28.40889118	45.57806607	31.61986016	68.71243862	24.26377574	9.017504381	44.43122547
Mannose Results	9979.663046	2431.55694	835.6534232	3930.275365	4023.138406	2968.540848	2773.992512	4717.706015
Glucose Results	30865.21751	7453.256889	2080.211876	11453.73712	10784.85279	8170.462376	7611.680708	15078.93611
Fumaric Acid Results	21474.46515	19519.07554	2836.050661	15433.07873	12928.99336	10771.1192	8357.153113	15371.20653
3-Methyladipic acid Results	21.60654835	67.78574025	17.66468834	38.63613465	41.56042937	67.71863297	1.373308625	18.09691575
2-Methylglutaric acid Results	196.2044223	558.3638755	123.3572681	251.8561709	321.0153643	5704.558359	0	262.421406
Muconic acid Results	124.8564064	48.52754873	49.1934946	13.14915819	171.6997288	89.41914486	89.03086969	54.0244908
Homogentisic acid Results		47.75523362		3.170662942				
Shikimic acid Results	0.740349845	4.166928576	21.50368255	28.20247566	63.61864502	53.63277922	40.32800878	28.94726261
alpha-KG/ Adipic acid Results	4684.27055	6189.159753	1104.3341	2989.555503	3451.737283	6810.326813	3816.850451	6511.095037
L-(+)-Arabinose Results	31.01240388	15.53961589	12.80102033	54.42765265	21.11281527	47.24763104	16.30956547	32.94010911
3-Hexenedioic acid Results	215.8415663	19.56813574	1262.92693	123.0695337	69.74905347	187.142163	270.9636617	181.3479852
Succinate Results	4709.951352	4126.472021	688.5281749	11905.28321	1424.045088	7137.993381	2786.581375	14408.82508
Isovaleric acid Results	527.379877	661.6696245	965.2736997	763.4186982	1431.651932	522.0607554	0	452.6129306
Fumarate Results	362.4625614	5592.982699	133.2038811	327.2108628	4284.122865	493.3906881	296.4874826	678.2387517
Glutaric acid Results	122.285243	276.4462345	44.34332856	197.9771847	86.48632527	106.8066192	225.693225	1092.768279
Aconitic acid Results	148.6991369	2144.018951	50.51929637	2001.267006	3216.932964	182.8022049	27.03287079	1020.18287
Sucrose Results	32.38331982	43.85004118	400.8264749	53.47631404	407.2951215	275.0172661	33.13908498	38.49051463
Glucuronic acid Results	138.2186386	55.12897139	87.07772295	90.08725368	288.843507	446.1192815	15.59138572	51.21170534
R5P Results	21228.76496	44523.55846	6703.249301	38648.01037	54205.47005	16001.05224	18385.38919	48236.62524
D-Galacturonic acid Results	31.73831724	80.96804824	66.75490494	4.98870625	35.39121473	32.93896842	10.44981205	19.52085888
2HG Results				3839.586749				7528.875278
Oxaloacetic acid Results	664.3543946	36.397611	18.51969432	338.3977713	68.98525113	39.62226181	870.8714827	732.4457722
Galactonic acid Results	310.7642565	294.468413	388.7398306	110.1216073	864.8143151	261.3020801	239.6779937	427.0987105
D-(+)-Cellobiose Results	385.2068234	809.8540823	526.5621903	606.3965393	223.5903221	108.3932961	932.2220184	366.8896837
Gluconic acid Results	2.308927114	2.412190175	62.85599174	1.696460283	37.87767059	24.20947484	48.96040594	2.932886246
3-Phosphoglyceric acid Results	490.6268032	10269.85634	429.7218152	765.9101462	1086.570732	1721.654009	0	1247.982503
Trehalose Results	47.79709162	37.86123636	21.28682254	29.48507981	33.56513517	34.07033571	93.68016441	127.808777
Lactose Results	13.69798141	810.5076937	4.576533398	610.3420243	160.6689578	25.00093749	725.5260313	37.71987509
Mucic acid Results	53.722017	96.96744393	43.93467838	84.77116037	1046.359466	74.90247571	39.64548402	68.78225961
e 6-Phosphate (disodium salt hydra	26165.56477	37903.73956	8350.762998	40342.24814	40256.2903	97359.19669	29981.25966	40315.94481
DUMP Results	23.33778428	47.06075888	2.974843812	28.44674545	31.74720441	31.98339982	69.86245808	24.62023791
Raffinose Results	362.8910496	1308.159863	451.7137054	932.5808091	1017.925551	11468.92765	398.196929	246.4765261
F6P/ G6P Results		9595.355685					9859.112025	
G1P Results	1647.384418							

Galactinol Dihydrate Results	39.35778914	328.5132866	29.80421211	37.82739924	193.7086614	121.5045908	124.8792443	344.3660416
F16BP Results	218.7854163	99.06718319	356.8729043	33.91002886	267.6145724	411.1962458	420.7997889	163.3789174
G16BP Results	141.7687566	367.2130811	135.0120025	165.6329436	446.3614656	174.7920023	155.984099	160.0318215
PEP Results								
eHydrate (from Stachyse Tuberifera	16.68611733	27.23629034	0.91680485	38.04027901	2.713362119	1.99958924	0.205129378	19.79769154
UDP Results			784.747995	1180.858389	1011.661221			
Malate Results								
X5P Results								
Citrate Results								
meso-Tartaric acid Results								
Tartaric acid Results								
Thymol Results							40.81336609	
IsoCitrate Results								
6-Phosphogluconic acid Results	78.91416568	75.01195169	30.08329244	49.10600291	77.0102355	186.2150273	54.17313667	55.77373733

	Wild-Type cold							
Sample	11010-tissue-pos–18	11010-tissue-pos–19	11010-tissue-pos–20	11010-tissue-pos–21	11010-tissue-pos–22	11010-tissue-pos–23	11010-tissue-pos–24	11010-tissue-pos-qc-4
Sample	11010-tissue-pos–18	11010-tissue-pos–19	11010-tissue-pos–20	11010-tissue-pos–21	11010-tissue-pos–22	11010-tissue-pos–23	11010-tissue-pos–24	
Acq. Date-Time	11/10/2018 22:00	11/10/2018 22:31	11/10/2018 23:01	11/10/2018 23:32	11/11/2018 0:03	11/11/2018 0:33	11/11/2018 1:04	11/11/2018 2:05
Phenylbutazone Results	1609.473657	1047.789087	1067.986416	3253.106834	1105.064759	1414.104318	1415.899745	957.3685277
3-hydroxykynurenine Results	22966.09195	12332.36939	16613.29355	22326.12216	15439.29486	13211.97721	18008.78036	22795.22087
NAD Results								
dTMP Results	4601.473896	3451.5613	4098.309635	5913.861909	3369.121324	3630.547163	5626.626647	2022.504299
N,N-Dicyclohexylurea Results	12392.37531	4954.517199	9282.165153	11874.52176	5624.533448	11438.92536	14634.54977	944.0389323
4-Pyridoxic acid Results	24266.37286	36638.03488	42253.3014	31188.65988	17284.0167	17071.74524	27087.10176	17215.6593
Melatonin Results	5683.919307	1487.115963	3868.109676	3801.762989	2814.573859	6259.322151	4454.176538	589.337698
Urate Results	11040.97754	3590.839037	10010.2178	10670.348	3531.287224	7716.411877	9823.935148	3525.650144
Caffeine Results	1844.868322	1075.448086	1986.216219	1687.058279	804.7072665	2510.295687	2567.03232	482.1653815
Folinic acid Results	307.1004476			126.2544912	248.0398095	280.9689558	419.1172199	117.0722322
lenalidomide Results	75.57669366	15.57452496	67.33010483	268.4371013	40.3756265	253.3660573	174.6007716	126.9333026
Tetracaine Results	138.5496603	221.5584499	160.9166437	52.61524545	328.9150665	646.3882051	123.7345037	230.5314615
3-Indolepropionic acid Results	267.5332763	153.5404886	265.2686188	167.340514	230.7096336	593.5838437	2740.648466	232.6139164
Anthranilic acid Results	2210.228315	29920.96314	17609.74321	2159.329586	8527.292287	647.9504102	3571.155608	11977.13444
2-Pyrrolidinone Results	44162.09517	45143.08917	33596.6088	27304.15999	31589.46809	30264.58869	28851.81256	10476.17567
Phosphocreatine Results	379317.8255	412645.4654	547591.8482	481723.0062	430638.4107	214980.3388	481006.9966	187222.7503
Dihydroxyacetone Results	33127.00903	29703.98698	45854.77491	43189.58266	26590.14887	31481.7293	75527.60044	9886.229156
Nicotinamide Results	1868011.285	3383752.381	6779790.525	6696094.472	5588624.887	1542750.959	4859865.202	14227845.91
Imidazole Results	63754.28732	30680.60219	76257.06331	82345.3178	27684.30594	34424.72002	82555.75526	22101.12558
N-Acetylethanolamine Results	6766.881267	5772.588809	14748.2952	12561.00065	4078.836908	10368.67408	14738.6286	9773.777682
Allopurinol Results		153.4949003					483.0434184	
Xanthurenic acid Results	474.13103	470.2931541	244.9308105	140.0845114	106.0868419	142.4180443	594.9034498	96.73901191
2-Deoxyuridine Results	1057.819195	502.8164676	2083.800639	514.7447123	476.7215686	5420.902051	159.6198381	395.3913062
Pyridoxine Results	313.7957541	261.3139211	55.80900352	281.6561121	738.3019715	343.4063384	869.1636884	84.73403452
Decanoylcamitine Results	44516.30472	63225.82179	7792.471066	28495.97502	0	0	0	0
Kynurenic acid Results	269.8914112	7646.975106	141.6314809	167.6829841	22127.3516	116.2708023	255.4768776	0
Hippuric acid Results	20.95395315	1157.79462	501.0836322	401.4354384	160.6911531	60.66448178	0	0
Propranolol Results	983.6649321	320.6620098	1095.455889	1067.23965	1086.163013	1460.174392	1737.5273	227.4816074
2-Phenylglycinol Results	1165.2214	1554.918175	825.8017728	1604.253817	2249.14593	1814.431384	1877.810596	145.819572
Acetylcysteine Results	502.8668294					621.2484719	587.7908934	
2-Deoxyadenosine Results	5377.798365	2844.844678	2125.546019	2131.137253	5344.879436	0	0	0
Adenine Results	118162.4478	154335.5698	56509.10936	57269.91208	165009.5918	74533.48898	62547.33175	193303.8919
Isovalerylglycine Results	14629.11974	8464.811994	1198.714067	1772.067229	9121.090953	616.074535	796.1568453	2015.836913
Hypoxanthine Results	101678.3561	184458.2454	1974928.002	174037.4651	274365.8026	110632.8698	323176.5913	249995.3561
Uridine Results	13071.86413	33333.44511	36593.16331	29256.53976	38451.00993	17771.29141	26491.46267	34852.71102
Creatinine Results	11239598.77	8994952.309	2493461.73	1801771.076	6359601.515	2600003.473	1334995.147	7668296.872
Adenosine Results	1059274.137	1628940.887	118869.5405	560282.8216	2153085.275	849096.3857	605497.4586	1373678.904
Xanthine Results	1640.930969	4116.472073	11781.93438	3883.379011	7263.3629	1930.022993	4671.014418	6733.807316
Tryptamine Results	78.42162168	110.8603859	321.6840332	69.49039879	230.0000408	52.49500402	289.1205734	357.3142688
Acetylcholine Results	378.8353961	357.9289622	804.9031966	632.1056638	8219.176272	447.6723862	1079.326364	0
Cytosine Results	158029.1995	203882.9838	14375.94755	19129.26456	152313.2805	97487.55595	23919.09427	183823.8937
2-Deoxycytidine Results	51326.77786	77735.26327	6142.083711	9978.612555	50565.91336	47866.00546	12467.51134	60676.69851
Nicotinic acid Results	3499.172427	5839.289017	9107.458175	6928.360093	4582.421325	3341.89561	7858.234083	0
Inosine Results	1813167.862	2035941.797	6483991.812	2057699.159	1826381.992	1288439.929	3546904.954	2355828.676
5-Methylcytidine Results	5221.521573	15615.28701	13486.00141	12382.76339	5862.373471	6649.156553	12403.90011	7401.781399
Biotin Results	17310.3405	30882.02059	8705.581819	16586.32804	4589.936267	19498.59031	6351.233029	0
Metanephrine Results	8344.914011	5318.349426	3618.365066	1956.229751	4918.084594	0	0	0
2-deoxyguanosine Results	4992.027658	15645.16107	15066.74816	7353.347369	9830.218335	11168.71201	5462.534823	7223.241764
Guanine Results	51988.77046	79233.82159	91615.13374	97279.92574	45748.42343	56674.80324	136078.7557	87684.25118
Dopamine Results	1555.162107	509.4280875	1023.21003	2903.593683	891.9820789	611.0435856	1586.391091	
6-Methyl-DL-Tryptophan Results	4009.866245	3670.082179	3233.362236	9099.13688	3951.963558	6050.484985	3296.346195	5817.531456
Pantothenic acid Results	516026.4139	1694432.221	1360627.961	2908202.15	583993.3012	1103260.011	2030767.226	0
Amiloride Results	13837.94322	25719.26784	31277.72441	25788.49471	34043.38289	20110.47951	30872.03682	17774.67151
Cytidine Results	155269.8742	309244.5263	791398.922	644379.9339	175101.811	229447.5737	655911.7139	402340.5714
Nicotinuric acid Results	2813.495287	2278.412966	7626.695042	2176.118586	1439.666521	557.6070769	3476.175295	0
Serotonin Results	2358.534132	1160.021523	205.6853004	2257.59646	750.9916246	616.432638	6726.560192	329.6648779
Acetylglycine Results	51.3865516	61.91702793	65.35464317	53.95138692	182.9425049	84.0140073	32.71210021	14.68138605
Phenylalanine Results	1524538.183	2107970.105	4580180.145	3926263.465	1524631.012	1498860.023	2803617.394	2053425.339
N-Acetyl-D-galactosamine Results	7132.944242	2621.942482	18523.80039	13434.26198	2911.019261	7055.657467	13137.25393	0
Tryptophan Results	190338.839	307928.6053	395988.5011	395067.439	220292.6206	215852.2358	543540.1739	203992.9091
Urocanic acid Results	29646.4342	22794.45363	25160.52173	30598.23257	28090.01572	9691.17362	29153.15074	30193.17176
Indole-3-lactic acid Results	9817.463982	15724.39066	25195.6393	18691.32675	12542.57069	8844.779244	25332.07689	9081.938367

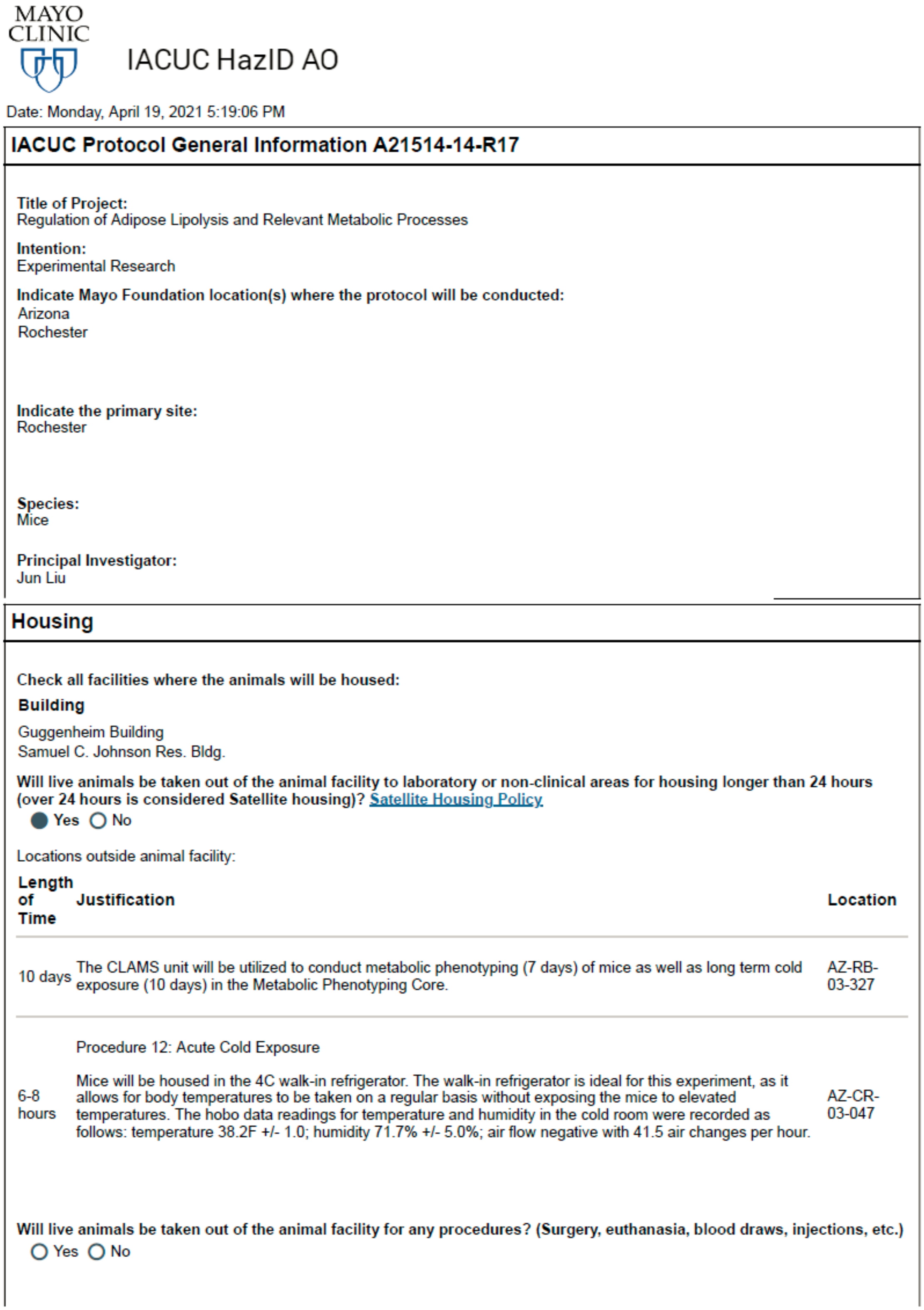
Normetanephrine Results	12132.56501	23863.3731	20777.25388	24421.56769	20350.06446	17193.80591	26300.51204	12492.79092
isoleucine/ Leucine/ Norleucine Re	7083842.544	11076965.4	18565162.37	14239080.54	8021532.069	8069279.302	14156266.14	6857685.366
Kynurenine Results	1874.195744	495.9818439	7089.51604	3613.348007	4514.339132	488.1636809	1680.221735	852.6476824
N-Acetyl-D-Glucosamine Results								
Acetylglucosamine Results	3651.372027	2464.701369	2764.278053	2702.571254	2647.180671	2423.460062	2852.579225	2102.607863
HIAA Results	2486.203982	1684.840052	852.8037909	2541.749216	3642.280729	446.7296747	2838.346054	0
6-Hydroxynicotinic acid Results	2871.904059	424.0078964	5302.183425	4988.491901	3953.928681	929.8154517	3612.790364	826.3762424
Guanosine Results	111576.1106	124325.6504	126232.7062	178042.8868	83260.13586	78288.08448	161013.3863	125759.9096
Pyroglutamic acid Results	99739.29031	167728.0115	140312.9281	249732.3146	126472.1879	100493.1723	224206.4805	104627.1584
Isoleucine Results	7038695.135	11019475.13	18395628.51	14147767.92	8101419.343	8008759.431	14375077.23	6925038.171
Betaine Results	57695385.6	68796529.55	76396518.1	77068832.84	62652197.32	75196677.13	74473729.95	67558617.02
3-Nitrotyrosine Results	408.7868038	536.9483957	503.6267684	2332.750226	303.8572589	126.3431512	1463.405057	0
Xanthosine Results	5978.41746	8738.243619	9257.743353	8254.286591	5359.386211	7160.258554	11635.12709	8262.557589
Acetyl-L-glutamine Results	913.0883857	1611.937971	2340.720905	2631.273386	1655.545195	1044.033741	1206.120082	552.8895393
Methylhistamine Results	89153.56491	81843.37891	89922.28277	82899.56722	81376.91333	81451.99295	99663.98193	81006.56865
Methionine Results	27513.54211	17573.17812	11713.04247	226334.759	29377.77511	112072.6612	287047.5133	58598.39818
Norvaline Results	1575153.015	1804706.502	2259611.805	1415931.81	1491431.631	1476790.946	1539952.624	1439907.932
Acetamide Results			819736.6554	881287.5056	404932.9726	1504529.373	1189997.943	
cGMP Results	715.6917073	1408.532454	763.6993549	668.9143323	184.1585115		684.8654985	653.5530502
4-Aminophenol Results	997.9315676	980.4277049	815.3631671	2115.073033	500.31091	438.2125355	1219.302821	688.2819976
Taurine Results	5686584.012	6084426.199	6631402.082	5622196.305	5562118.815	5320090.248	5959579.704	4895897.282
Valine Results	1571479.626	1836227.624	2609105.159	1890380.495	1503078.956	1608890.861	2024907.7	1450032.372
5-Hydroxytryptophan Results	408.4794238	278.2017209	560.530652	844.3151744	255.261857	70.70760797	63.18222768	128.6633813
Quinolinic acid Results	4175.226576	1821.697103	1644.225287	9938.912974	1228.520563	3195.396054	7331.816061	0
Tyrosine Results	117794.5079	132659.9852	234735.1446	189144.6304	121792.2244	146442.2634	131881.7482	155813.8166
inoisobutyric acid/ Dimethylglycine	243705.9137	385089.5158	14597007.14	15815515.15	229662.574	261120.5393	13295230.41	212583.242
Picolinic acid Results	3677.905189	3960.755173	4975.95934	4703.528171	3247.441269	3072.257285	1830.610707	3204.11686
Epinephrine Results	5037.953625	4549.158473	6291.512807	7354.052124	5417.63461	6858.469552	3446.607061	0
Acetylcarnitine Results	90000542.08	111517293.6	97847640.06	89340563.02	101886467.9	96959914.8	104543844.9	94034300.3
Indole Results	5042.996904	6193.402181	3870.031081	3785.756231	2607.922956	7075.696521	1555.078149	0
Pipecolinic acid Results	648050.7298	1115330.099	1198043.949	1539684.611	903015.3891	926783.0496	1589862.607	872399.8397
Proline Results	3695346.177	6105352.209	7039919.067	8605725.168	4163884.461	3850119.683	5989661.233	4281746.45
4-Imidazoleacetic acid Results	2001.880602	1308.209661	3031.913728	1591.647663	1698.106738	1067.615383	2896.639821	1084.736405
Neopterin Results	212.9331372	185.0533072	66.8122361	649.0864145	39.40147068	66.55210904	61.23735903	438.7062313
2-Aminobutyric acid Results	243705.9137	397762.4439	14731785.69	15717551.23	243312.2369	339358.6409	13016454.13	212144.7359
Methylguanidine Results	188743.4124	154347.3125	7576.800792	7797.050885	104883.0998	10320.34941	10424.59719	99588.24025
DOPA Results	3348.39503	2096.532778	1724.611059	2937.876144	2300.399919			3076.784715
Sarcosine Results	1378855.248	2158037.202	3279193.598	3130745.223	1512461.605	1096043.689	2744852.682	1878412.168
3-Aminobutyric acid Results	5007.693709	4503.848778	75463.42213	40494.52814	1412.453407	3545.963343	23777.49561	3053.816617
Choline Results	2176507.751	7940609.654	24794206.83	25626462.54	8318011.813	1892971.225	28892880.73	0
Hydroxyproline Results	1715009.905	1578014.118	1831586.715	2287515.799	1283101.96	572816.949	1857909.315	1424322.078
Putrescine Results	2292.68576	1466.322382	4005.336438	809.4141828	1261.608397	1772.009016	556.9224869	0
Alanine Results	1379582.85	1938885.144	2891858.986	2950705.345	1410799.44	1070530.345	2272311.526	1636239.683
TMAO Results	5004344.227	3599917.128	2015222.689	6457203.797	3713944.35	1694522.845	3649035.309	3634121.565
Indole-3-acetic acid Results	13528.4406	12316.4626	14171.92145	11332.55065	12048.22686	12870.80285	8834.716597	6353.779558
Creatine Results	49976601.96	40816306.98	36467866.2	48810438.13	36675480.67	17549391.23	49279340.68	49605356.99
Acetohydroxamic acid Results	14979.95795	9572.339504	7554.014633	19849.28958	11139.20733	4682.648045	9674.185856	11560.42235
Carnitine Results	39008479.4	56783577.82	69579005.13	65965067.16	52309035.81	71645424.36	71130435.28	51997267.24
Homoserine/ Threonine Results	194488.0047	311609.5923	360957.3513	265186.1061	311049.0674	338091.5685	302562.3034	277493.5324
Glycocyamine Results	549255.1641	644182.9819	976542.0669	775093.1102	896845.3387	867513.5363	833447.1391	174756.2191
N-Acetylneuraminic acid Results	8370.251343	13593.48101	12216.10094	77783.24685	6305.834251	5982.69264	21772.05512	3844.540961
1-Methyladenosine Results	267320.0122	304438.3849	330161.5662	512987.5335	225215.5434	260449.1036	859019.2845	181886.0156
Spermidine Results	508.0751869	533.0255343	879.4403514	988.6104839	357.7858554	1452.882318	699.9150907	109.0252354
Cadaverine Results	3553.738875	1156.417742	1403.309756	2365.496854	872.5803872	6983.659212	5657.626236	0
5-Aminolevulinic acid Results	83404.99307	39149.15477	38383.62165	94898.68959	12252.39652	59414.51727	72213.4393	0
4-Aminobutyric acid Results	53090.02796	18389.61918	82711.83948	58751.32516	3897.785859	79989.62941	63416.72406	2811.123808
Glycine Results	36468.59955	31981.55575	33835.41911	42152.56463	31388.13834	30937.90231	32006.55821	35807.96347
13C5-15N-Glutamic acid Results	8112.886538	2348.72735	5868.741703	1388.128486	2958.450543	6795.842831	4729.406549	0
Glutamic acid Results	153341.086	83820.99571	159575.9757	216542.7276	45472.93326	175174.4439	207413.5642	33003.55296
Glutamine Results	9621727.48	6269805.075	12542919.82	14711101.79	3260083.399	13291556.62	12470236.62	2813388.269
Glycylproline Results	2237.955422	603.4188446	297.8252971	2857.278146	138.4247672	2941.2057	2547.396291	469.2205948
Acetylornithine Results	1882.156558	1035.077807	2454.44431	3347.015281	1815.898459	1431.504993	2982.322469	4508.443103
Dihydrofolic acid Results	22.57038106	2.820901982	36.69276693	1.996210294	66.32077126	49.25161107	57.65211549	54.11475954
Glucosamine Results	1989.698771	234.2798764	4351.62858	5363.749782	4182.491748	1550.524942	4069.003433	791.3169482
Folic acid Results	73.06031097	13.86243262	112.0272945	1.120639817	42.47631555	1.541749406	20.26989091	18.47717857
Asparagine Results	100667.8702	79565.93162	119831.7578	78019.22032	40370.83016	69186.74157	82694.16482	34338.71061
Amino valerate Results	8662.11732	3581.439806	2461.570377	3180.606822	1726.305426	4038.977632	2765.701331	2143.143818
Glutathione reduced Results	6573.333365	19332.09333	17081.79198	43943.04597	9054.370159	9272.154172	40317.69762	3398.322015
Serine Results	201150.9344	210753.9304	344257.9189	256623.7042	135765.7707	192736.2238	247338.5992	124529.5564
2-Aminoadipic acid Results	552.5806062	187.1706254	536.0128022	2577.103646	1017.865869	3110.942159	335.9251582	432.7537413
Adenosyl-L-homocysteine Results	58633.07106	21070.40124	16924.08148	134508.3758	62448.71396	126137.6988	156255.3546	34001.43346
Aspartate Results	4400.123488	0	0	0	0	13925.09682	0	0
Agmatine Results	51556.37675	35846.22024	30304.03015	26731.77411	39911.4658	52325.19686	24442.57175	0
1-Methylhistidine Results	10738.9252	6358.244256	8731.565868	8870.147097	9384.682261	12499.21666	14414.47444	34430.40546
Siacar Results	71.44570518	19.42479231	138.3554361	94.65886746	29.13451569	38.52779134	63.07264823	54.00660432
Hydroxybutyryl coenzyme A Results	14466.40556	11374.01226	14990.55396	64104.84304	21119.83226	11288.40826	41400.23337	0
Isobutyryl-CoA Results	2606.314501		2465.807352				92797.57809	2780.749178
UDP-GlcNAc Results	59.12344589	127.665196	51.22702062	182.1728718	142.159867	39.76857453	191.2179346	75.64977391
Citrulline Results	236040.3984	198150.6417	276691.4447	260682.0657	193751.043	289211.0575	205268.1189	614955.1639
Histidine Results	48126.59665	24327.06546	28292.98644	180105.7815	47986.83409	25936.07234	248037.3881	0
Acetyl-CoA Results								

Carnosine Results	672728.3629	382177.2431	299579.1436	525366.5537	239667.6076	15815.87496	495246.0267	142752.5403
Glutathione oxidized Results	213424.8698	325370.7817	364007.8335	491358.9949	256472.0052	310122.1998	504973.5132	0
Adenylosuccinate Results	6581.798513	5895.387312	545179.3167	12674.10845	3954.136175	6707.301783	8342.771723	0
GDP Results	3514.408	130216.5409	74195.24475	137085.1748	3493.335608	0	0	0
dUTP Results	1017.272929	862.9935556	346.4167821	2343.358802	646.4517018	327.0573289	742.1789167	771.8206044
DCTP Results	74.08927351	482.473419	46.54277589	16.87819952	52.01874655	23.38752728	94.57295433	45.05432939
Homocysteine Results	238.177791	1376.014309	293.7185764	7260.308384	806.5076345	362.6530615	664.1015455	425.1210602
ATP Results	37394.47581	55028.89069			28125.57533	18621.17125	123542.0897	15428.66138
Histamine Results		43932.8755		72631.22334	37112.42851		110572.6487	
Uracil Results								
Cystine Results	10247.47158	13563.22			11432.43192	9081.333137	6756.338275	6102.547809
Cystamine Results	313.610773	75.93959575	440.2073897	349.1901557	236.5638467	292.2602697	52.1772591	39.34199503
Glucosamine 6-phosphate Results		209.6500906	378.675577		176.0169533			
Dimethylarginine Results	44.04795172	358.6653318	92.2692401	465.0254178	484.8765819	65.75309302	238.3645223	109.4541566
ADP Results								
DCDP Results		109.4649599						
Ornithine Results	30075.47989	42693.5001	49706.86893	59274.23562	26519.02964	20249.51836	0	0
Arginine Results	267.0597611	321.8153932	129.4525257	397.0590349	842.7361711	515.122992	664.2684909	1364.510296
Lysine Results	173.048497	355.1927775	394.7596422	473.8396818	203.9555595	174.0746384	280.8203509	260.2845406
Indole-3-pyruvic acid Results	629.7946508	615.6868066	424.1579632	274.9980186	1728.533986	390.3641112	153.1298633	785.1102075
Cysteine Results	568.6037119			984.1545584	1292.623782	1016.482299		1352.010388
3-hydroxyanthranilic acid Results	67.30921336	276.3886105	160.2364173	218.0297097	128.7248671	185.346679	191.808601	306.5689204
Sample	11010-tissue-neg-18	11010-tissue-neg-19	11010-tissue-neg-20	11010-tissue-neg-21	11010-tissue-neg-22	11010-tissue-neg-23	11010-tissue-neg-24	11010-tissue-neg-qc-4
Acq. Date-Time	11/11/2018 17:00	11/11/2018 17:31	11/11/2018 18:01	11/11/2018 18:32	11/11/2018 19:03	11/11/2018 19:34	11/11/2018 20:05	11/11/2018 21:06
pregnenolone sulfate Results	332.5411318	674.2492056	1248.14492	1122.550063	630.4584826	1380.74557	139.5420441	679.6764033
2,3-Dihydroxybenzoic acid Results	16.41255207	249.9424189	117.3382075	336.4145698	108.9732655	13.46516593	94.519498	77.89073888
Nonadecanoic acid Results	45869.73991	47109.85566	37517.20266	36465.78665	43417.81453	38740.74016	20010.23104	45258.44701
Stearic acid Results	210866.4366	201172.5346	203986.4274	146831.641	194109.4938	141073.0609	257466.7496	193308.3648
Heptadecanoic acid Results	71153.80969	91703.57036	91043.18611	116871.4871	117823.4612	59639.56115	24299.99767	22913.65147
9-Octadecynoic acid Results	1150008.315	562333.9402	1544151.374	1057707.146	485843.9857	649236.7302	425382.4091	1048924.398
Myristic acid Results	49172.54292	60627.40732	57104.68892	55224.58085	64698.68723	64353.45413	28901.40844	43015.68642
Palmitic acid Results	323261.5466	288422.9469	258525.6859	379687.7631	186365.3861	236205.7096	300955.6975	265397.5597
Pentadecanoic acid Results	53890.02663	68663.12941	69756.69725	61984.07671	58978.68335	42554.34631	32847.25469	27446.39206
2-Hydroxybenzoic acid Results	1055.837412	472.6098236	760.7299273	1410.232445	1290.615519	857.8572192	354.4890529	476.405326
Lauric acid Results	49217.04179	99807.78984	81826.84015	76163.30681	61673.53088	60155.07977	29531.10603	8446.509858
Capric acid Results	127719.0524	200039.7475	194809.8282	217372.1854	145847.0164	172868.9695	83320.02354	12373.65675
-Hydroxyphenylpyruvic acid Result	438.9517001	1733.893934	240.9216315	2048.433781	621.1912102	848.0610005	358.8126481	177.1286399
Phenylpyruvic acid Results	148.5463547	192.0961624	289.116407	359.9057849	308.5116829	200.9291758	219.1160334	58.05627128
ylacetic acid/ 3-Hydroxyphenylacet	1019.211471	1908.50819	1440.612287	151.778863	1822.90887	1362.964911	160.7317249	52.04182936
4-Hydroxybenzaldehyde Results	2025.820507	617.7703485	1135.341347	1273.251011	1247.031721	1149.796845	754.9262862	436.2770358
Phenylglyoxylic acid Results	21.93475457	384.5828228	121.7078988	284.6374453	160.3277462	41.5222262	273.2246722	12.16648834
Caprylic acid Results	11879.68698	14318.93245	12758.91351	11732.3683	13687.62962	13580.61651	5624.129416	11098.16079
3-Methyl-2-oxovaleric acid Results	11229.67471	15983.61303	10624.20454	15511.43093	11560.44159	9540.824333	5595.767307	1665.114889
GA3P Results							33.95085156	
Naproxen Results	1.325976519	26.18810111	2.06222335	38.22845444	30.75330247	1.909256707	1.31029663	0.804540366
entanoic acid/ Ketoleucine/ Ketoisc	1690.459333	1925.265828	2255.145717	1318.30189	1599.368228	1349.812811	396.6742792	690.8679629
Gentisic acid Results	31.86398909	33.93618356	55.04398486	27.84555747	9.302851053	34.65382965	3.96342782	43.743355
-Ketoisovaleric acid/ Maleic acid R	22636.52216	29612.13163	39837.15635	39305.92441	29009.33767	10727.96379	7217.780331	2527.222614
PGE2 Results	139.4172232	334.6158411	201.7937891	173.7756245	215.3968645	79.73189135	137.7942466	32.29739995
Benzoic acid Results	2687.4292	6881.651625	6511.715969	5113.114186	6290.048911	5090.793793	1767.708487	2478.761297
Citraconic acid Results	0	0	0	0	2455.403013	2008.934007	1586.965049	1017.032727
2-Ketobutyric acid Results	25.12252458	72.99582899	4.94993759	29.76428194	70.40292562	15.43535489	16.85488596	30.64758541
Myoinositol Results	158.6643811	1734.542746	280.2100692	2048.921092	284.1251313	848.2029179	33.28712703	71.22035951
3-Phenyllactic acid Results	56.70688042	38.35920556	44.6149755	212.3196746	12.17685496	27.5060431	105.100208	24.17012208
-Methoxyphenylacetic acid Results	10.39225753	20.87025511	1.039786323	2.455291322	36.37375108	24.61704037	45.20085012	0.594333075
m-Coumaric acid Results	29280.83795	37261.98082	39067.9674	31163.09255	25935.11158	29059.39337	17965.75677	3045.546129
lacetic acid/ 4-Ethylbenzoic acid R	5229.165237	7684.246996	7518.354129	6376.724476	4127.03119	5097.776339	2936.532437	1763.825821
Phenylacetic acid Results	4997.530121	9038.342695	7471.778749	8466.386218	5094.513351	5988.321935	2853.492915	1922.659979
ethylvaleric acid/ Hexanoic acid Re	18192.27249	26556.99771	30902.71955	29306.83265	34646.22888	22096.52394	5213.346053	7315.327445
Ferulic acid Results	2.409038377	28.83351176	28.89257607	59.58557874	1.79768861	2.928094096	18.0228351	17.0947377
Gibberellic acid Results	68.81389348	28.75361105	3.808034464	16.54625392	34.54772096	56.39008067	37.16367539	5.053875703
lethylbutyric acid/ Valeric acid Res	8981.726938	13829.37518	13578.25258	10935.73269	11686.1044	10417.34937	5960.425833	2397.081019
Protocatechuic acid Results	261.3332958	115.588726	174.4885482	145.1530671	72.38564588	220.8139286	55.59207968	111.5892138
2-Furoic acid Results	21.05785985	28.29793961	50.78464969	39.51586089	26.35032254	51.4534041	32.90153194	39.39082097
p-Coumaric acid Results	29272.8015	37342.43541	39075.4068	31470.53478	25935.23342	29060.90951	17960.602	3045.167419
xyphenylacetic acid/ Mandelic acid	131.8619434	159.4336857	125.5793396	63.71482967	158.9841426	131.7258614	32.11767887	59.77771944
Hydroxy-3-methylbenzoic acid Resu	29.5683871	36.26933076	40.59017601	88.83888461	59.25775336	30.03995106	26.32377379	60.54794151
Isobutyric acid Results	277.9540682	293.6444061	21.34552465	507.5680575	130.1186503	266.495931	442.0752577	294.5991008
Leucic acid Results	67.91254948	113.3621878	34.52423375	72.66023484	64.27521942	44.52686426	108.5053104	10.1637547
Vanillic acid Results	15.48181703	74.07713734	44.95635868	63.72699668	52.37446842	82.58075051	56.88260362	27.62705286
Methyl succinate Results	24.8639499	187.2734755	207.0782871	299.0676778	96.58543656	310.9790965	363.519354	305.1300906
Pyruvate Results	48.91723234	42.72864682	64.65532936	12.38221243	29.96072674	28.77348692	72.33662768	29.06080921
elta-Hydroxyisovaleric acid Results	35.09718377	40.19786701	54.77983231	28.24118548	72.26815348	29.39793539	32.60309487	41.52913669
Acetoacetate Results	149.7965855	238.5237611					114.7000202	
Homovanillic acid Results	35.46163814	25.88746989	66.31417596	31.9325711	24.35881493	42.58960114	39.44701664	7.492395107
4-Hydroxybenzoic acid Results	330.3791167	709.6905067	616.2264656	2466.901945	1221.191768	655.1052367	257.2317965	25.08271198
Phthalic acid Results	10703.94663	6167.145556	3435.490374	3162.341236	2574.097312	2397.916884	21784.70825	0
L-Ascorbic acid Results	35.56032784	64.28685048	63.3597073		54.27551437		52.3587206	40.9751932
Methyl-D-mannopyranoside Results	68.30375668	36.60110069	44.04051554	29.95424092	138.0914655	54.54355463	138.140904	108.8036047
Ribose Results	435.7828386	1060.123592	820.8641923	621.3434129	596.5464849	302.4776805	30.39226502	635.4671615
Levulinic acid Results	14779.21268	10556.74523	13736.32395	8000.186245	10133.0242	10901.41495	28565.61655	0

Ethylmalonic acid Results	301.1216042	32.56912115	49.35995575	30.07534769	42.95411962	63.03069522	372.5520291	43.46822492	
Sebacic acid Results	60.94551651	105.9499954	274.0043848	1091.863217	89.21069822	143.3148697	55.8300539	27.29308494	
N-Acetylmuramic Acid Results	26.63250313	96.29340335	58.07574717	2.618158787	14.09718909	2.813757235	78.08327312	35.87401351	
Azelaic acid Results	385.3148212	2898.872925	1565.627414	1813.092468	2446.556251	1243.068012	30.38118716	1247.483402	
Lactate Results	52525.26367	63133.89224	53844.06736	56422.40717	53197.49218	24723.83671	469.3042799	35840.54115	
Adonitol Results	204.6151377	29.30209771	244.4904338	63.53656039	20.20691894	65.44227949	29.74676564	90.97467699	
3-hydroxybutyric acid Results	40.92059812	566.8092153	39.15718206	412.698692	47.33036612	85.36501863	61.29703353	81.31242717	
droxybutyric acid/ Malonic acid Re	946.1561114	22555.24747	1800.137843	13219.25912	1005.401841	12806.13097	246.2124796	0	
thyl alpha-D-glucopyranoside Res	7.111415494	39.8090627	16.84624947	104.6766779	21.07705899	40.24886134	42.54325929	33.07531307	
Xylose Results	66.76208434	213.7177038	396.887265	39.97577074	89.13485464	36.38143064	8.410278614	87.68003202	
13C3-Lactate Results	150694.4338	157642.0817	154897.7108	140667.3685	142033.4088	168012.5	1629.021285	0	
L-(-)-Arabitol Results	10.2122983	648.7946588	88.77696207	250.2335481	50.51433767	17.91889217	15.15599124	54.1504612	
Xylitol Results	28.13238716	347.7356288	135.0475558	201.6179411	217.4873292	117.185009	51.01553229	144.8342411	
Erythrose Results	5.735231675	73.25220943	10.43485201	49.5525391	6.413350505	60.1690046	24.41555374	40.77449847	
Methylmalonic acid Results	257965.2613	798964.2885	147866.1591	857640.7291	587143.7755	429137.5138	225305.0962	300808.0305	
Fructose/ Galactose Results	6440.853845	6990.330371	8321.742261	25412.91291	8672.490032	7433.450866	4087.372134	6777.1451	
Glutaconic acid Results	2883.212557	8563.737688	7887.842493	4856.136544	5425.66415	3919.032966	38.09942411	2877.084732	
Glyceric acid Results	30.71216261	493.3572859	88.10404514	431.6498134	395.4062464	22.23534954	377.0835662	28.54354798	
Suberic acid Results	57.0276138	1653.413001	1114.509026	879.9755825	977.6653914	951.5556855	72.36248846	725.181477	
Glyoxylic acid Results	23.3100286	112.7275915	36.50466287	118.8351806	49.42805631	40.85212267	107.7961004	33.39886835	
D-Mannitol Results	413.0794766	275.4835616	38.30583564	242.1111249	306.3552158	93.66295824	53.26283599	196.0269774	
-Xylonic Acid (Lithium Salt) Result	1775.390429	5356.423562	21919.83723	5044.102597	2410.108057	1224.084533	1185.299387	8497.222798	
Sorbitol Results	114.5541757	38.25945276	914.6586534	143.8495662	147.6179761	31.27922799	89.48356257	79.20817559	
Dulcitol Results	189.9688331	95.64000927	104.4814093	155.8063308	90.95341112	71.19331991	89.91469771	177.2938655	
Glycolic acid Results	46.63272982	16.51511539	46.23985863	14.43020345	14.17180814	65.97591365	52.17674753	17.68139009	
Mannose Results	2338.120329	2579.919401	3300.662645	8661.942265	2544.237169	1654.447111	1283.009177	2448.48305	
Glucose Results	6299.721659	7287.636658	8376.529297	25011.61553	8671.141849	7272.487428	4113.853915	6837.866346	
Fumaric Acid Results	8365.774771	16147.06419	12472.89723	18363.09943	16460.88364	12855.55195	4639.82236	7357.820401	
3-Methyladipic acid Results	22.44437791	49.04196213	52.06046684	49.22994154	93.44071965	65.62500064	13.3844665	26.47713115	
2-Methylglutaric acid Results	2800.056849	4662.922992	3851.764659	1538.461115	3327.156104	220.1186766	1926.137842	0	
Muconic acid Results	50.14221293	38.52253074	60.00732025	55.23853366	28.37033634	29.5498715	24.50483153	49.16574746	
Homogentisic acid Results		31.81385026	14.96038331		19.91260557				
Shikimic acid Results	54.72125317	51.41721183	1.17442889	42.35923378	34.97494736	57.69694205	11.69673606	24.90917956	
alpha-KG/ Adipic acid Results	4447.958517	4270.315307	5751.255197	7519.32876	4233.086746	3722.920086	1537.393831	3902.585897	
L-(+)-Arabinose Results	52.90408419	38.10892716	43.09848592	71.02485467	24.05210295	34.06617507	32.74227991	98.0515789	
3-Hexenedioic acid Results	188.9209653	172.839983	105.4515273	70.03762059	49.84254719	372.5496956	128.3986767	157.1473139	
Succinate Results	1667.692907	8966.576107	2800.433834	2714.769037	4722.470764	1200.239729	753.3179844	1839.28834	
Isovaleric acid Results	970.5300665	1105.31353	1281.660695	1199.720932	233.6315363	90.33921197	2004.631466	0	
Fumarate Results	186.6854824	320.0410038	214.171339	289.3593227	4177.120149	3975.87386	132.6964162	111.2379533	
Glutaric acid Results	50.91621673	65.41050125	39.58419844	219.0057478	244.3374519	159.3271113	68.88949333	220.8079575	
Aconitic acid Results	51.42945011	124.9911421	2633.762332	2677.517123	1921.815856	117.8992458	85.5496673	512.2711587	
Sucrose Results	168.9393158	134.6722103		17.02615759	43.92536937	105.9830336	37.33850572	135.7839606	
Glucuronic acid Results	27.04554525	659.4351364	58.28239589	28.16350068	596.9427357	96.30298335	136.424835	22.24611386	
R5P Results	16257.51698	31843.08779	26031.08887	38390.10884	26160.57572	22127.67294	8998.457883	13766.97852	
D-Galacturonic acid Results	33.04102966	3.461810489	90.69664529	55.33455102	1.709313099	1.561099067	28.24759897	43.82329056	
2HG Results		9880.46893	3244.117374	11542.72897					
Oxaloacetic acid Results	773.791582	20.22221815	1020.850489	837.218504	352.619129	301.7790987	35.51165717	482.0550309	
Galactonic acid Results	172.5582733	166.5092458	263.4821383	403.6448342	86.04558374	202.4612606	138.9560518	295.777727	
D-(+)-Cellobiose Results	758.5592425	46.88821819	13.62955236	1014.235502	227.1270993	45.80619017	67.36500911	881.9347715	
Gluconic acid Results	55.55122076	35.97426205	2.724858858	67.74576172	65.54644281	3.703477156	3.541090679	1.906925075	
3-Phosphoglyceric acid Results	6769.713731	664.5067649	506.0205753	19899.84214	9815.453894	0	0	0	
Trehalose Results	66.15497774	37.83561846	37.64534484	72.81440611	37.71020932	29.77347589	143.7538669	17.54397679	
Lactose Results	64.56021236	341.780105	8.132690053	1030.314516	247.4953978	44.06822345	1326.402063	877.5397944	
Mucic acid Results	70.54028393	63.15842556	52.82375969	313.7065931	63.23434076	34.41026263	40.78121822	57.30109186	
e 6-Phosphate (disodium salt hydra	19764.55607	32650.90735	27188.60386	43987.04358	37858.19058	23362.62049	12647.80215	25407.67758	
DUMP Results	51.65174674	75.93586101	39.62905708	6.980940346	49.90482391	3.571349229	18.15383386	48.96491591	
Raffinose Results	237.0987914	132.503512	131.0832011	1147.051905	230.8725143	125.3424096	150.8832047	127.3238925	
F6P/ G6P Results	1111.967336	7385.943996		2595.769886	5992.339576	3225.382495	3542.664758	5597.612995	
G1P Results			1237.058867						
Galactinol Dihydrate Results	59.02760738	336.5282591	30.30022738	49.82341045	89.93070065	252.8198042	102.6534914	116.4904503	
F16BP Results	431.3173861	42.43216854	100.9158598	86.5496106	46.7069285	129.6556169	110.0619591	107.6781024	
G16BP Results	123.7939875	130.0800492	206.9802947	116.6209335	138.0444712	345.5279171	51.08099768	51.085562	
PEP Results	174.6491348								
eHydrate (from Stachyse Tuberifera	32.95961562	26.96224122	7.755148426	34.6595153		11.51355707	1.772618872		
UDP Results								287.3714633	
Malate Results									
X5P Results									
Citrate Results									
meso-Tartaric acid Results									
Tartaric acid Results		52.49740058							
Thymol Results			47.97224755				47.76772664		
IsoCitrate Results				418.3414413					
6-Phosphogluconic acid Results	74.70151157	69.35500119	65.33858537	97.34802009	75.47970833	50.22447478	21.63780921	60.78702446	

APPENDIX C

IACUC PROTOCOL A21514-14-R17



MAYO CLINIC

IACUC HazID AO

Date: Monday, April 19, 2021 5:19:06 PM

IACUC Protocol General Information A21514-14-R17

Title of Project:
Regulation of Adipose Lipolysis and Relevant Metabolic Processes

Intention:
Experimental Research

Indicate Mayo Foundation location(s) where the protocol will be conducted:
Arizona
Rochester

Indicate the primary site:
Rochester

Species:
Mice

Principal Investigator:
Jun Liu

Housing

Check all facilities where the animals will be housed:

Building

Guggenheim Building
Samuel C. Johnson Res. Bldg.

Will live animals be taken out of the animal facility to laboratory or non-clinical areas for housing longer than 24 hours (over 24 hours is considered Satellite housing)? Satellite Housing Policy

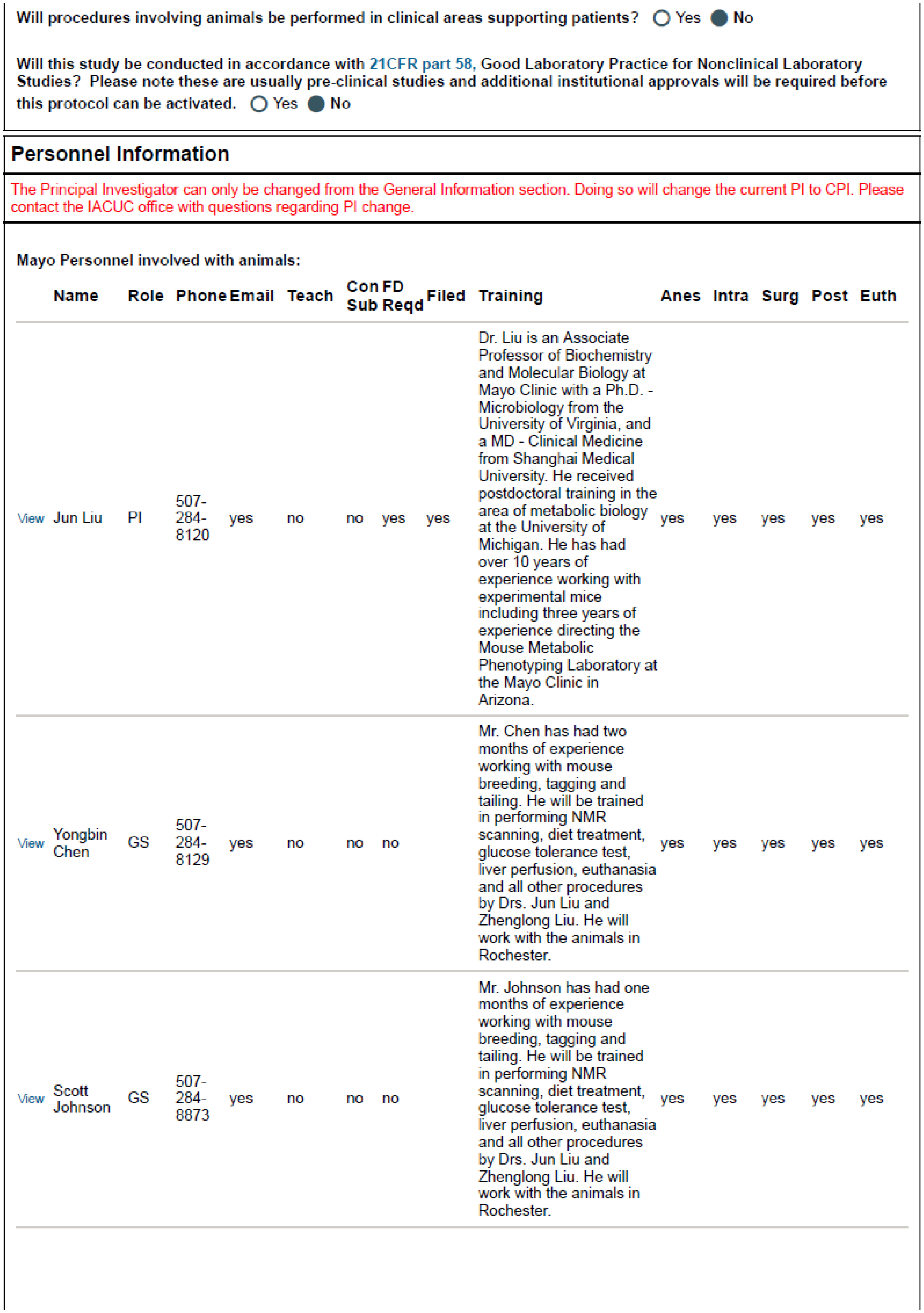
● Yes ○ No

Locations outside animal facility:

Length of Time	Justification	Location
10 days	The CLAMS unit will be utilized to conduct metabolic phenotyping (7 days) of mice as well as long term cold exposure (10 days) in the Metabolic Phenotyping Core.	AZ-RB-03-327
6-8 hours	Procedure 12: Acute Cold Exposure Mice will be housed in the 4C walk-in refrigerator. The walk-in refrigerator is ideal for this experiment, as it allows for body temperatures to be taken on a regular basis without exposing the mice to elevated temperatures. The hobo data readings for temperature and humidity in the cold room were recorded as follows: temperature 38.2F +/- 1.0; humidity 71.7% +/- 5.0%; air flow negative with 41.5 air changes per hour.	AZ-CR-03-047

Will live animals be taken out of the animal facility for any procedures? (Surgery, euthanasia, blood draws, injections, etc.)

○ Yes ○ No



Will procedures involving animals be performed in clinical areas supporting patients? ○ Yes ● No

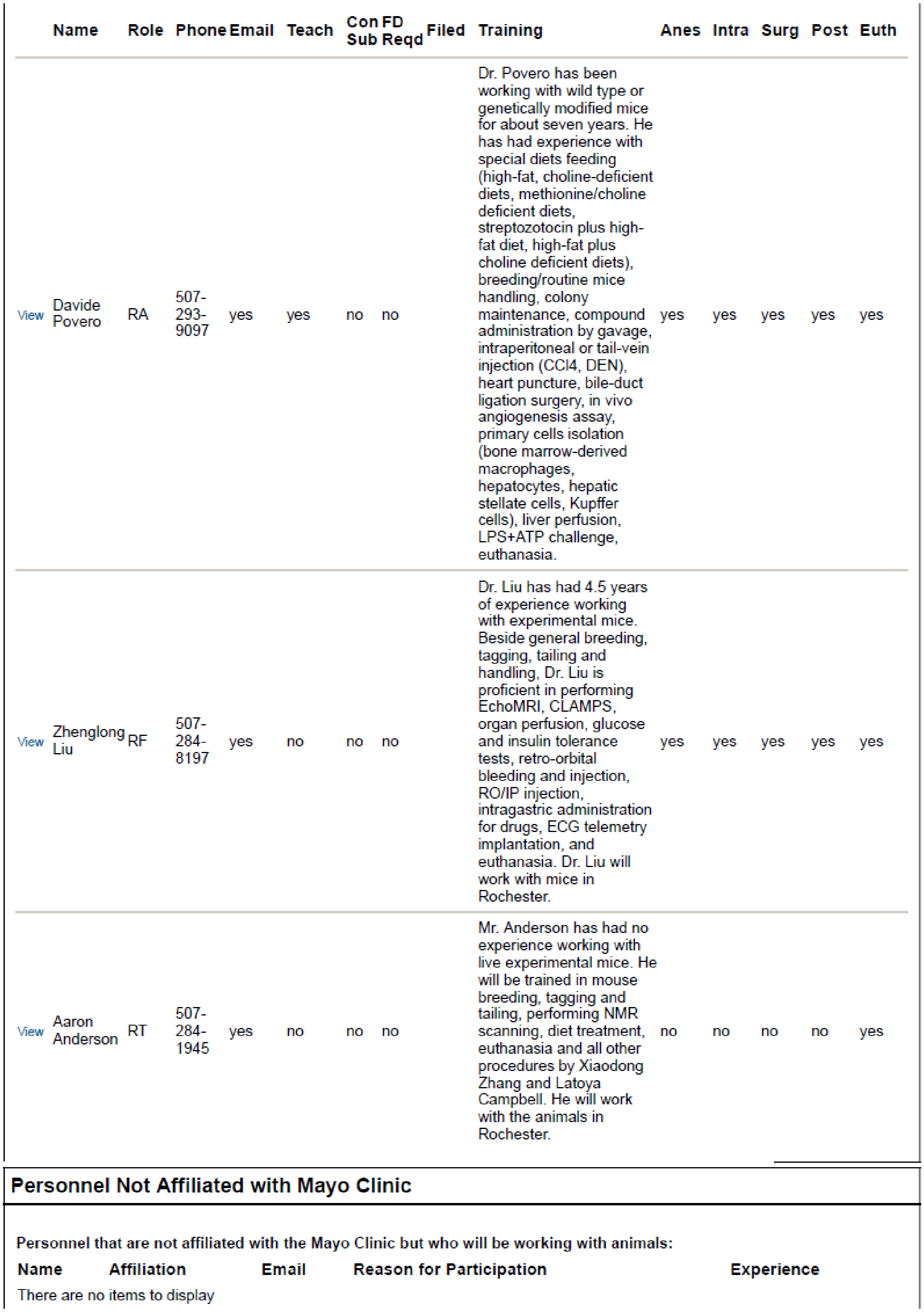
Will this study be conducted in accordance with 21CFR part 58, **Good Laboratory Practice for Nonclinical Laboratory Studies? Please note these are usually pre-clinical studies and additional institutional approvals will be required before this protocol can be activated.** ○ Yes ● No

Personnel Information

The Principal Investigator can only be changed from the General Information section. Doing so will change the current PI to CPI. Please contact the IACUC office with questions regarding PI change.

Mayo Personnel involved with animals:

	Name	Role	Phone	Email	Teach	Con Sub	FD Reqd	Filed	Training	Anes	Intra	Surg	Post	Euth
View	Jun Liu	PI	507-284-8120	yes	no	no	yes	yes	Dr. Liu is an Associate Professor of Biochemistry and Molecular Biology at Mayo Clinic with a Ph.D. - Microbiology from the University of Virginia, and a MD - Clinical Medicine from Shanghai Medical University. He received postdoctoral training in the area of metabolic biology at the University of Michigan. He has had over 10 years of experience working with experimental mice including three years of experience directing the Mouse Metabolic Phenotyping Laboratory at the Mayo Clinic in Arizona.	yes	yes	yes	yes	yes
View	Yongbin Chen	GS	507-284-8129	yes	no	no	no		Mr. Chen has had two months of experience working with mouse breeding, tagging and tailing. He will be trained in performing NMR scanning, diet treatment, glucose tolerance test, liver perfusion, euthanasia and all other procedures by Drs. Jun Liu and Zhenglong Liu. He will work with the animals in Rochester.	yes	yes	yes	yes	yes
View	Scott Johnson	GS	507-284-8873	yes	no	no	no		Mr. Johnson has had one months of experience working with mouse breeding, tagging and tailing. He will be trained in performing NMR scanning, diet treatment, glucose tolerance test, liver perfusion, euthanasia and all other procedures by Drs. Jun Liu and Zhenglong Liu. He will work with the animals in Rochester.	yes	yes	yes	yes	yes



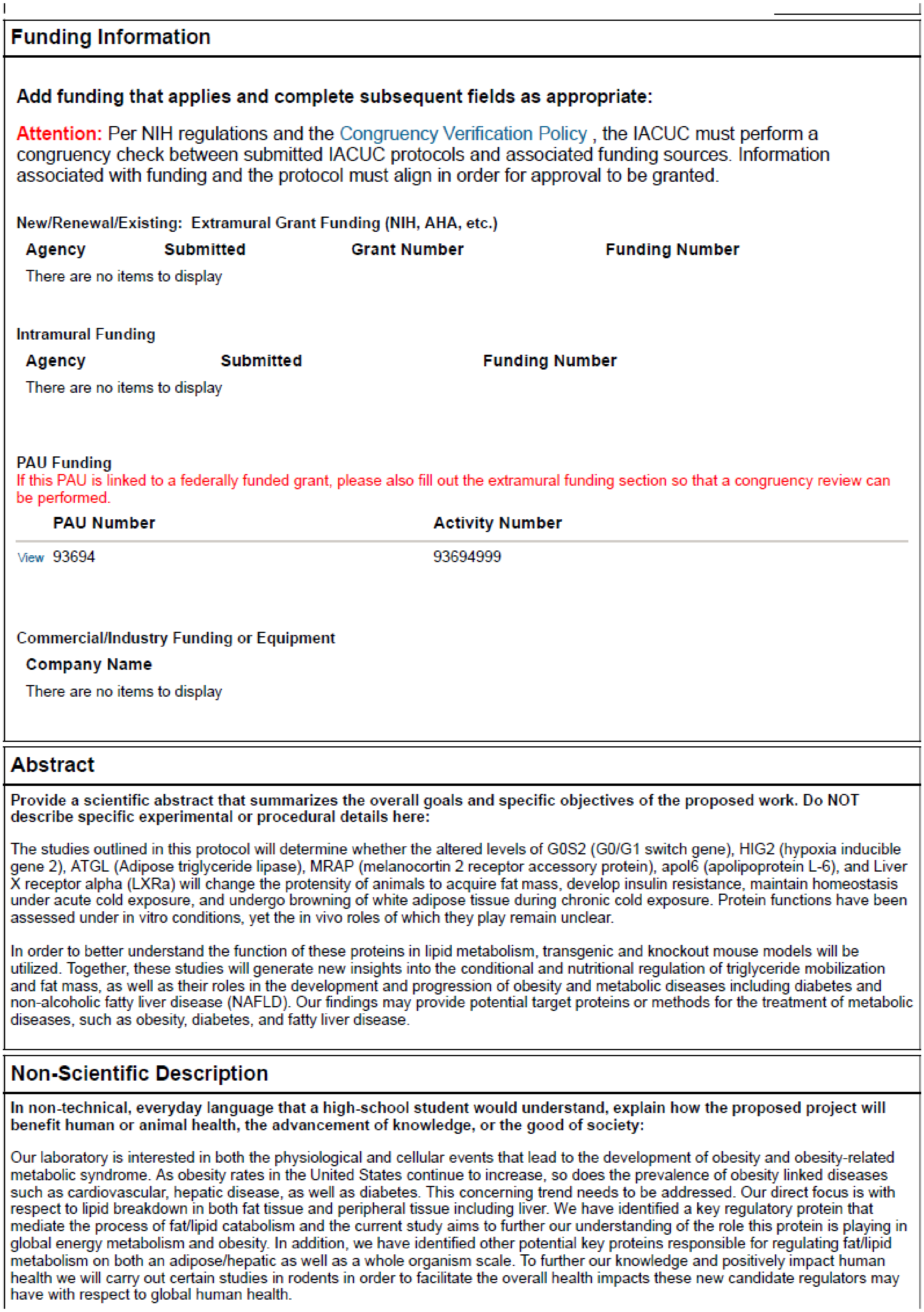
	Name	**Role**	**Phone**	**Email**	**Teach**	**Con Sub**	**FD Reqd**	**Filed**	**Training**	**Anes**	**Intra**	**Surg**	**Post**	**Euth**
View	Davide Povero	RA	507-293-9097	yes	yes	no	no		Dr. Povero has been working with wild type or genetically modified mice for about seven years. He has had experience with special diets feeding (high-fat, choline-deficient diets, methionine/choline deficient diets, streptozotocin plus high-fat diet, high-fat plus choline deficient diets), breeding/routine mice handling, colony maintenance, compound administration by gavage, intraperitoneal or tail-vein injection (CCl4, DEN), heart puncture, bile-duct ligation surgery, in vivo angiogenesis assay, primary cells isolation (bone marrow-derived macrophages, hepatocytes, hepatic stellate cells, Kupffer cells), liver perfusion, LPS+ATP challenge, euthanasia.	yes	yes	yes	yes	yes
View	Zhenglong Liu	RF	507-284-8197	yes	no	no	no		Dr. Liu has had 4.5 years of experience working with experimental mice. Beside general breeding, tagging, tailing and handling, Dr. Liu is proficient in performing EchoMRI, CLAMPS, organ perfusion, glucose and insulin tolerance tests, retro-orbital bleeding and injection, RO/IP injection, intragastric administration for drugs, ECG telemetry implantation, and euthanasia. Dr. Liu will work with mice in Rochester.	yes	yes	yes	yes	yes
View	Aaron Anderson	RT	507-284-1945	yes	no	no	no		Mr. Anderson has had no experience working with live experimental mice. He will be trained in mouse breeding, tagging and tailing, performing NMR scanning, diet treatment, euthanasia and all other procedures by Xiaodong Zhang and Latoya Campbell. He will work with the animals in Rochester.	no	no	no	no	yes

Personnel Not Affiliated with Mayo Clinic

Personnel that are not affiliated with the Mayo Clinic but who will be working with animals:

Name	**Affiliation**	**Email**	**Reason for Participation**	**Experience**

There are no items to display



Funding Information

Add funding that applies and complete subsequent fields as appropriate:

Attention: Per NIH regulations and the Congruency Verification Policy , the IACUC must perform a congruency check between submitted IACUC protocols and associated funding sources. Information associated with funding and the protocol must align in order for approval to be granted.

New/Renewal/Existing: Extramural Grant Funding (NIH, AHA, etc.)

Agency	Submitted	Grant Number	Funding Number
There are no items to display			

Intramural Funding

Agency	Submitted	Funding Number
There are no items to display		

PAU Funding

If this PAU is linked to a federally funded grant, please also fill out the extramural funding section so that a congruency review can be performed.

	PAU Number	Activity Number
View	93694	93694999

Commercial/Industry Funding or Equipment

Company Name
There are no items to display

Abstract

Provide a scientific abstract that summarizes the overall goals and specific objectives of the proposed work. Do NOT describe specific experimental or procedural details here:

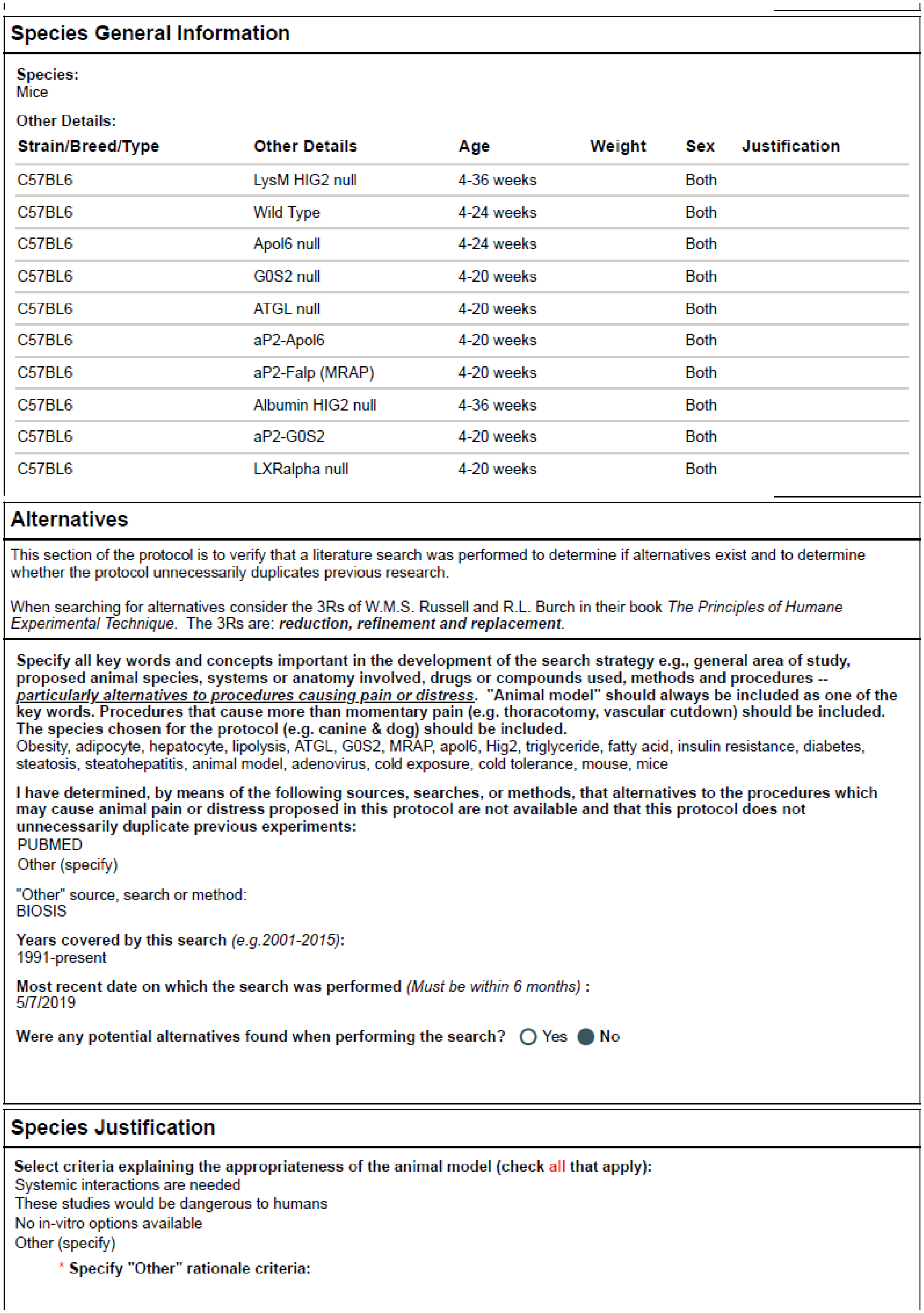
The studies outlined in this protocol will determine whether the altered levels of G0S2 (G0/G1 switch gene), HIG2 (hypoxia inducible gene 2), ATGL (Adipose triglyceride lipase), MRAP (melanocortin 2 receptor accessory protein), apol6 (apolipoprotein L-6), and Liver X receptor alpha (LXRa) will change the protensity of animals to acquire fat mass, develop insulin resistance, maintain homeostasis under acute cold exposure, and undergo browning of white adipose tissue during chronic cold exposure. Protein functions have been assessed under in vitro conditions, yet the in vivo roles of which they play remain unclear.

In order to better understand the function of these proteins in lipid metabolism, transgenic and knockout mouse models will be utilized. Together, these studies will generate new insights into the conditional and nutritional regulation of triglyceride mobilization and fat mass, as well as their roles in the development and progression of obesity and metabolic diseases including diabetes and non-alcoholic fatty liver disease (NAFLD). Our findings may provide potential target proteins or methods for the treatment of metabolic diseases, such as obesity, diabetes, and fatty liver disease.

Non-Scientific Description

In non-technical, everyday language that a high-school student would understand, explain how the proposed project will benefit human or animal health, the advancement of knowledge, or the good of society:

Our laboratory is interested in both the physiological and cellular events that lead to the development of obesity and obesity-related metabolic syndrome. As obesity rates in the United States continue to increase, so does the prevalence of obesity linked diseases such as cardiovascular, hepatic disease, as well as diabetes. This concerning trend needs to be addressed. Our direct focus is with respect to lipid breakdown in both fat tissue and peripheral tissue including liver. We have identified a key regulatory protein that mediate the process of fat/lipid catabolism and the current study aims to further our understanding of the role this protein is playing in global energy metabolism and obesity. In addition, we have identified other potential key proteins responsible for regulating fat/lipid metabolism on both an adipose/hepatic as well as a whole organism scale. To further our knowledge and positively impact human health we will carry out certain studies in rodents in order to facilitate the overall health impacts these new candidate regulators may have with respect to global human health.



Species General Information

Species:
Mice

Other Details:

Strain/Breed/Type	**Other Details**	**Age**	**Weight**	**Sex**	**Justification**
C57BL6	LysM HIG2 null	4-36 weeks		Both	
C57BL6	Wild Type	4-24 weeks		Both	
C57BL6	Apol6 null	4-24 weeks		Both	
C57BL6	G0S2 null	4-20 weeks		Both	
C57BL6	ATGL null	4-20 weeks		Both	
C57BL6	aP2-Apol6	4-20 weeks		Both	
C57BL6	aP2-Falp (MRAP)	4-20 weeks		Both	
C57BL6	Albumin HIG2 null	4-36 weeks		Both	
C57BL6	aP2-G0S2	4-20 weeks		Both	
C57BL6	LXRalpha null	4-20 weeks		Both	

Alternatives

This section of the protocol is to verify that a literature search was performed to determine if alternatives exist and to determine whether the protocol unnecessarily duplicates previous research.

When searching for alternatives consider the 3Rs of W.M.S. Russell and R.L. Burch in their book *The Principles of Humane Experimental Technique*. The 3Rs are: ***reduction, refinement and replacement***.

Specify all key words and concepts important in the development of the search strategy e.g., general area of study, proposed animal species, systems or anatomy involved, drugs or compounds used, methods and procedures -- *particularly alternatives to procedures causing pain or distress*. "Animal model" should always be included as one of the key words. Procedures that cause more than momentary pain (e.g. thoracotomy, vascular cutdown) should be included. The species chosen for the protocol (e.g. canine & dog) should be included.
Obesity, adipocyte, hepatocyte, lipolysis, ATGL, G0S2, MRAP, apol6, Hig2, triglyceride, fatty acid, insulin resistance, diabetes, steatosis, steatohepatitis, animal model, adenovirus, cold exposure, cold tolerance, mouse, mice

I have determined, by means of the following sources, searches, or methods, that alternatives to the procedures which may cause animal pain or distress proposed in this protocol are not available and that this protocol does not unnecessarily duplicate previous experiments:
PUBMED
Other (specify)

"Other" source, search or method:
BIOSIS

Years covered by this search *(e.g.2001-2015)*:
1991-present

Most recent date on which the search was performed *(Must be within 6 months)* **:**
5/7/2019

Were any potential alternatives found when performing the search? ○ Yes ● **No**

Species Justification

Select criteria explaining the appropriateness of the animal model (check all that apply):
Systemic interactions are needed
These studies would be dangerous to humans
No in-vitro options available
Other (specify)

* **Specify "Other" rationale criteria:**

The nature of the scientific issues involved precludes the use of non-animal alternatives. We will study how the loss and/or gain of G0S2, HIG2, MRAP, ATGL, LXRa and apol6 proteins affects the propensity of mice to become obese and to develop fatty liver on a high fat diet. A cell or computer model does not exist that accurately mimics the elaborate control mechanisms that exist in vivo. Mouse models are the least sentient model that allows genetic manipulations and sill has energy metabolic regulation relatively similar to humans.

Procedures

Check all procedures to be performed:

- ☐ Behavior Studies/Testing
- ☑ **Breeding**
- ☐ Food and Water Restriction (over 12 hours)
- ☑ **Food and Water Restriction**
- ☑ **Genotyping Rodents or Fish**
- ☑ **Hypo/Hyperthermia**
- ☐ Immunization
- ☐ Organ System Failure or Dysfunction will be Experimentally Induced
- ☐ Paralysis Experimentally Induced
- ☐ Prolonged Physical Restraint or Restriction of Movement with Mechanical Devices (over 2 hours)
- ☑ **Radiation Exposure/Imaging**
- ☑ **Rodent Identification**
- ☐ Sepsis
- ☑ **Special Housing and Husbandry**
- ☑ **Specimens (tissue and/or body fluids) will be collected from live animals**
- ☑ **Substances/Agents will be administered to live animals**
- ☐ Surgery-Survival (Single or Multiple)
- ☑ **Surgery-Terminal Non-Survival**
- ☐ Tumor Growth/Inoculation with Biological Products
- ☑ **Other: study procedure not described/listed**
- ☐ No Procedure

Breeding

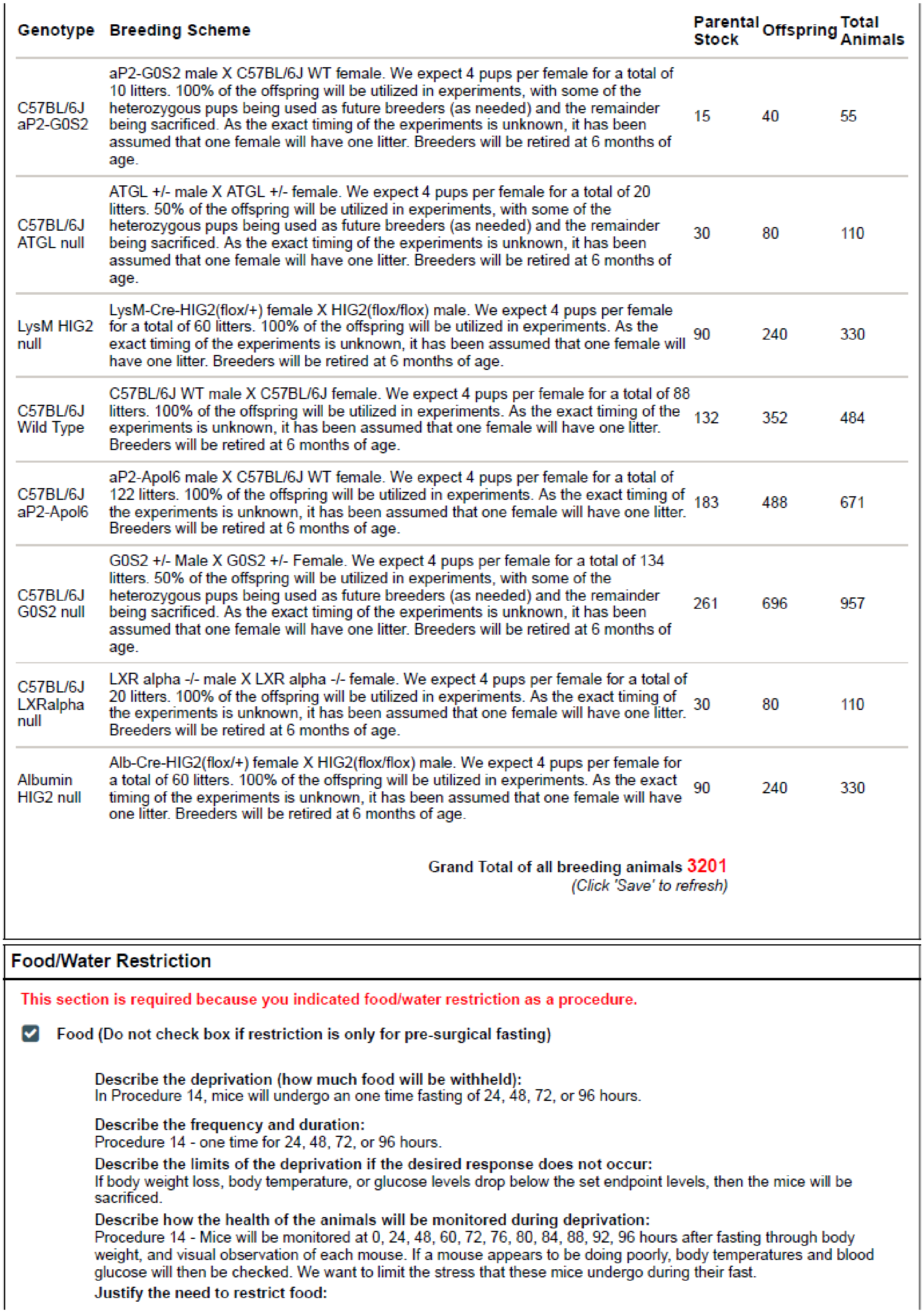
This section is required because you indicated breeding as a procedure.

Justification for Breeding (check all that apply):
Breeding is required to generate experimental animals

Breeding Method (check all that apply):
Trio or harem, where pregnant dams are separated prior to giving birth

Description of Breeding Scheme and Justification of Number of Breeding Animals:

Genotype	**Breeding Scheme**	**Parental Stock**	**Offspring**	**Total Animals**
C57BL/6J aP2-Falp (MRAP) Homozygous	aP2-MRAP male +/- X aP2-MRAP female +/-. We expect 4 pups per female for a total of 8 litters. 25% of the offspring will be utilized as breeders for a homozygous transgenic line. The remainder of the pups will be sacrificed. This breeding will occur once, and breeders will be sacrificed once the homozygous status of pups has been confirmed through genotyping.	12	32	44
C57BL/6J aP2-Falp (MRAP) Homozygous	aP2-MRAP male homozygous X aP2-MRAP female homozygous. We expect 4 pups per female for a total of 20 litters. 100% of the offspring will be utilized in experiments. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	30	80	110



Genotype	Breeding Scheme	Parental Stock	Offspring	Total Animals
C57BL/6J aP2-G0S2	aP2-G0S2 male X C57BL/6J WT female. We expect 4 pups per female for a total of 10 litters. 100% of the offspring will be utilized in experiments, with some of the heterozygous pups being used as future breeders (as needed) and the remainder being sacrificed. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	15	40	55
C57BL/6J ATGL null	ATGL +/- male X ATGL +/- female. We expect 4 pups per female for a total of 20 litters. 50% of the offspring will be utilized in experiments, with some of the heterozygous pups being used as future breeders (as needed) and the remainder being sacrificed. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	30	80	110
LysM HIG2 null	LysM-Cre-HIG2(flox/+) female X HIG2(flox/flox) male. We expect 4 pups per female for a total of 60 litters. 100% of the offspring will be utilized in experiments. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	90	240	330
C57BL/6J Wild Type	C57BL/6J WT male X C57BL/6J female. We expect 4 pups per female for a total of 88 litters. 100% of the offspring will be utilized in experiments. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	132	352	484
C57BL/6J aP2-Apol6	aP2-Apol6 male X C57BL/6J WT female. We expect 4 pups per female for a total of 122 litters. 100% of the offspring will be utilized in experiments. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	183	488	671
C57BL/6J G0S2 null	G0S2 +/- Male X G0S2 +/- Female. We expect 4 pups per female for a total of 134 litters. 50% of the offspring will be utilized in experiments, with some of the heterozygous pups being used as future breeders (as needed) and the remainder being sacrificed. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	261	696	957
C57BL/6J LXRalpha null	LXR alpha -/- male X LXR alpha -/- female. We expect 4 pups per female for a total of 20 litters. 100% of the offspring will be utilized in experiments. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	30	80	110
Albumin HIG2 null	Alb-Cre-HIG2(flox/+) female X HIG2(flox/flox) male. We expect 4 pups per female for a total of 60 litters. 100% of the offspring will be utilized in experiments. As the exact timing of the experiments is unknown, it has been assumed that one female will have one litter. Breeders will be retired at 6 months of age.	90	240	330

Grand Total of all breeding animals **3201**
(Click 'Save' to refresh)

Food/Water Restriction

This section is required because you indicated food/water restriction as a procedure.

☑ **Food (Do not check box if restriction is only for pre-surgical fasting)**

Describe the deprivation (how much food will be withheld):
In Procedure 14, mice will undergo an one time fasting of 24, 48, 72, or 96 hours.

Describe the frequency and duration:
Procedure 14 - one time for 24, 48, 72, or 96 hours.

Describe the limits of the deprivation if the desired response does not occur:
If body weight loss, body temperature, or glucose levels drop below the set endpoint levels, then the mice will be sacrificed.

Describe how the health of the animals will be monitored during deprivation:
Procedure 14 - Mice will be monitored at 0, 24, 48, 60, 72, 76, 80, 84, 88, 92, 96 hours after fasting through body weight, and visual observation of each mouse. If a mouse appears to be doing poorly, body temperatures and blood glucose will then be checked. We want to limit the stress that these mice undergo during their fast.

Justify the need to restrict food:

Procedure 14 - The purpose of fasting mice for this length of time is to completely deplete their fat stores, so that the metabolic effects on the liver can be assessed in our different metabolic mouse strains. 96 hour fasting has been used to induce to induce fatty liver (5).

References:
1. Faggioni R, Moser A, Feingold KR, Grunfeld C. Reduced leptin levels in starvation increase susceptibility to endotoxic shock. Am J Pathol (2000) 156:1781–710.1016/S0002-9440(10)65049-3
2. Flynn, J., Meadows, E., Fiorotto, M. and Klein, W. Myogenin Regulates Exercise Capacity and Skeletal Muscle Metabolism in the Adult Mouse. PLoS ONE (2010) 5(10), p.e13535.
3. Hashimoto, T. Defect in Peroxisome Proliferator-activated Receptor alpha -inducible Fatty Acid Oxidation Determines the Severity of Hepatic Steatosis in Response to Fasting. Journal of Biological Chemistry (2000) 275(37), pp.28918-28928.
4. Jensen, T., Kiersgaard, M., Sorensen, D. and Mikkelsen, L. Fasting of mice: a review. Laboratory Animals (2013) 47(4), pp.225-240.

5. Songtao Yu, Kimihiko Matsusue, Papreddy Kashireddy, Wen-Qing Cao, Vaishalee Yeldandi, Anjana V. Yeldandi, M. Sambasiva Rao, Frank J. Gonzalez, and Janardan K. Reddy. Adipocyte-specific Gene Expression and Adipogenic Steatosis in the Mouse Liver Due to Peroxisome Proliferator-activated Receptor γ1 (PPARγ1) Overexpression J. Biol. Chem. 2003 278: 498-505. First Published on October 24, 2002, doi:10.1074/jbc.M210062200

☐ **Water**

Genotyping Rodents or Fish

This section is required because you indicated either rodents or fish would have genotyping.

Check all methods that will be used :

☐ **Ear Punch/Ear Notch**

☑ **Tail Clipping will be performed on or before 21 days of age** *(Topical Anesthesia Recommended)*

☑ **Tail Clipping will be performed after 21 days of age** *(Anesthesia Required)*

List anesthetic agent(s) that will be administered:

Agent	Dose (mg/kg or mg/kg/hr)	Route
Isoflurane-vaporizer	2.5%	Inhalation

☐ **Toe Clipping will be performed before 7 days of age** *(Topical Anesthesia Recommended)*

☐ **Toe Clipping will be performed after 7 days of age** *(Anesthesia Required)*

☐ **Other** (e.g. Fin Clipping)

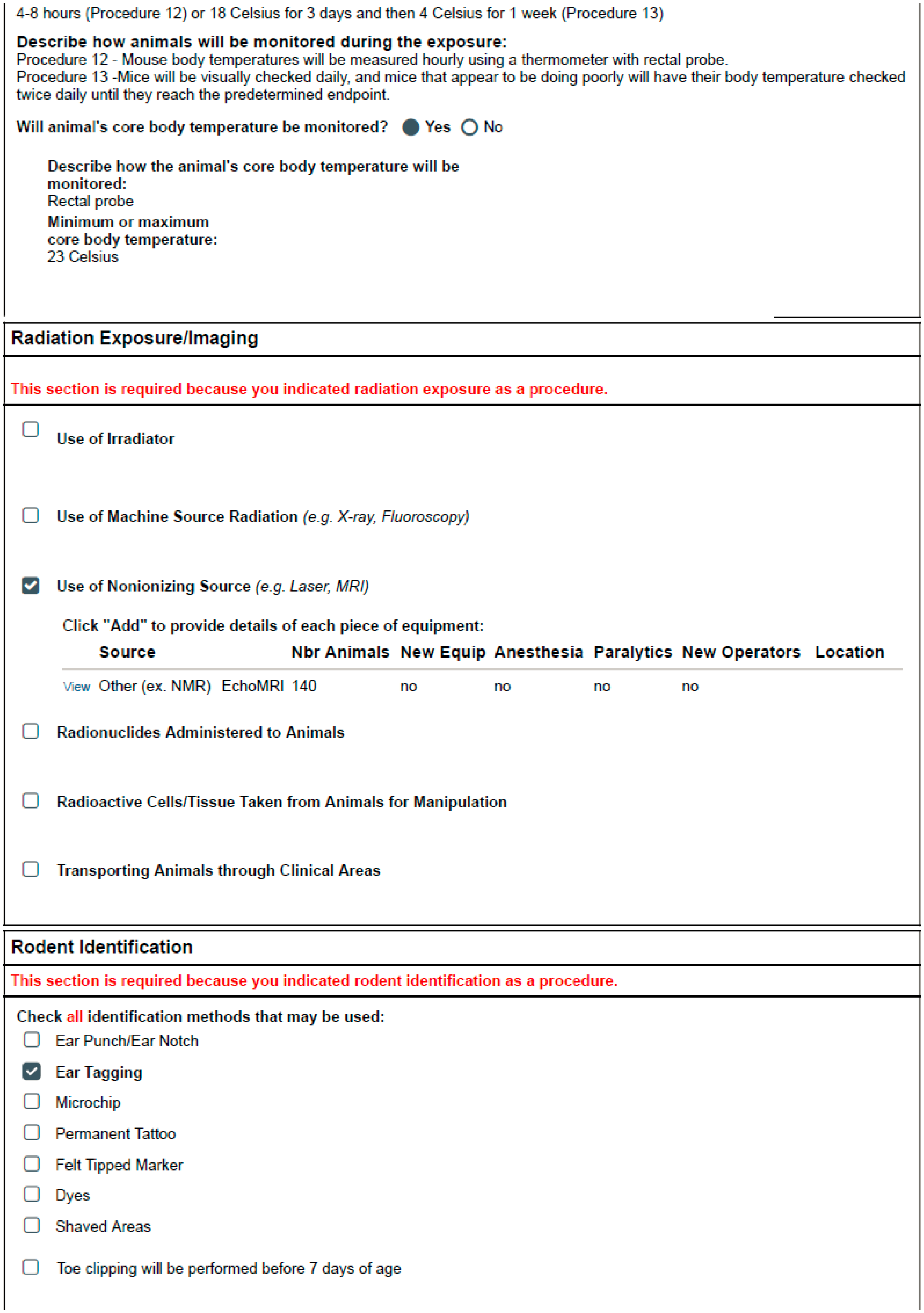
Hypo/Hyperthermia

This section is required because you indicated hypo/hyperthermia as a procedure.

Describe the rationale/justification for inducing hypo/hyperthermia and the method(s) that will be used to achieve this:
Procedure 12: The acute cold exposure will measure a strain's ability to maintain their temperature homeostasis when challenged with an acute cold exposure. Mice will be caged individually and fasted for 2 hours at room temperature prior to the cold room. Mice will be in a cage with water; but will not have access to bedding or food while in the cold room. Fasting will continue throughout the cold exposure. Mouse body temperatures will be measured hourly using a thermometer with rectal probe. At the conclusion of this procedure the mice will be euthanized and tissues harvested for biochemical analysis.
Procedure 14: The long term cold exposure will induce a metabolic response to maintain temperature homeostasis. We will look at the differences in the metabolic response that occur between the different mouse strains. Mice between the ages of 12-16 weeks will be housed in the CLAMS unit, located in Johnson 325/327, and will have ad libitum access to food and water. Mice will be housed individually in experimental cages and will be acclimated to a temperature of 18°C for 3 days. The temperature in the CLAMS unit will then be reduced to 4°C for 1 weeks.

Temperature exposed to:
4 Celsius

Duration of exposed temperature:



4-8 hours (Procedure 12) or 18 Celsius for 3 days and then 4 Celsius for 1 week (Procedure 13)

Describe how animals will be monitored during the exposure:
Procedure 12 - Mouse body temperatures will be measured hourly using a thermometer with rectal probe.
Procedure 13 -Mice will be visually checked daily, and mice that appear to be doing poorly will have their body temperature checked twice daily until they reach the predetermined endpoint.

Will animal's core body temperature be monitored? ● Yes ○ No

Describe how the animal's core body temperature will be monitored:
Rectal probe

Minimum or maximum core body temperature:
23 Celsius

Radiation Exposure/Imaging

This section is required because you indicated radiation exposure as a procedure.

☐ **Use of Irradiator**

☐ **Use of Machine Source Radiation** *(e.g. X-ray, Fluoroscopy)*

☑ **Use of Nonionizing Source** *(e.g. Laser, MRI)*

Click "Add" to provide details of each piece of equipment:

	Source	Nbr Animals	New Equip	Anesthesia	Paralytics	New Operators	Location
View	Other (ex. NMR) EchoMRI	140	no	no	no	no	

☐ **Radionuclides Administered to Animals**

☐ **Radioactive Cells/Tissue Taken from Animals for Manipulation**

☐ **Transporting Animals through Clinical Areas**

Rodent Identification

This section is required because you indicated rodent identification as a procedure.

Check all identification methods that may be used:

☐ Ear Punch/Ear Notch
☑ **Ear Tagging**
☐ Microchip
☐ Permanent Tattoo
☐ Felt Tipped Marker
☐ Dyes
☐ Shaved Areas

☐ Toe clipping will be performed before 7 days of age

☐ Other identification method

Special Housing and Husbandry

This section is required because you indicated special housing and husbandry.

Medicated Water ○ Yes ● **No**

Special Diet ● **Yes** ○ No

List diet: Custom Rodent Diets must be irradiated by manufacturer before use in Mayo Clinic facilities. For questions, contact DCM at (77) 4-1050
Mice will be started on a diet at 6 weeks of age from Research Diets Inc.: (1) standard chow diet (Purina 5008); (2) 60% very high fat diet (D12492); (3) 45% high fat diet (D12451); (4) high carbohydrate diet (D12450B); (5) high trans-fat/fructose diet (HTF-C diet, D09100301); and (6) high cholesterol diet (Harlan TD.94059). The mice will receive diet treatment for 12-16 weeks. Alternately, to induce non-alcoholic steatohepatitis (NASH), mice will be fed with (1) a methionine/choline-deficient diet (MCD; MP Biomedicals; 0296043910) for 2 weeks; (2) a fast food diet with 40% energy as fat, 12% saturated fatty acids and 2% cholesterol (Western Diet; Test Diet; AIN-76) for 25 weeks. For triglyceride secretion, mice will be placed on (1) fat-free/62% sucrose diet (Harlan TD.03314) for 5-6 hours.
List person(s) feeding the diet (*include pager/phone number(s)*): NOTE: DCM staff will not feed special diet
Lab staff
Where will the special diet be stored?
45% HFD will be stored in Guggenheim 14-05 at room temperature, per manufacturers instructions. All remaining diets are stored in MCCRB 14-05 at -20C.

Metabolic Cages ● **Yes** ○ No

Explain:
Procedure 5: Measurement of food intake, water intake, and indirect calorimetry will be taken by housing mice in CLAMS unit located in Johnson 325/327. For acclimation, mice will be transferred to Johnson 325/327. Individual mice will be transferred to experimental cages containing specialized lids for water and food delivery, and inlet/outlet airflow. The level of food, water, airflow through the system, mice, and computer software measurements will be checked twice daily (morning and afternoon). Measurements will be recorded over 5 days including a 24 h fast period between day 2 and day 3. Extended fasting is implemented to deplete glycogen storage in the liver and muscle thereby inducing triglyceride mobilization in adipose tissue. The procedure is designed for studying the animals' capability to switch energy substrates from glucose to fatty acids during the times of metabolic needs. The procedure has been commonly used in the studies of adipose triglyceride turnover (lipolysis) and its impact on whole-body energy homeostasis. At the end of recording, mice will either be euthanized according to individual study or housed individually in the step down room (C-029H) until study termination.
Procedure 13: Mice between the ages of 12-16 weeks will be housed in the CLAMS unit, located in Johnson 325/327, and will have ad libitum access to food and water. Mice will be housed individually in experimental cages and will be acclimated to a temperature of 18°C for 3 days. The temperature in the CLAMS unit will then be reduced to 4°C for 1 weeks. Wild-type mice have been shown to live up to 6 months at 4°C. Mice will be visually checked daily, and mice that appear to be doing poorly will have their body temperature checked twice daily until they reach a predetermined endpoint. A control group of wild-type mice will be house in the animal facility and will be sacrificed at the end of the study. At the end of the 2 week cold exposure, prior to sacrifice, 100ul of blood will be collected. The groups of mice that are injected with adenovirus will be injected in the ABBSL2-level animal facility and will be transported in accordance to Procedure 9. Mice will be transported back down the ABBSL2 facility (utilizing the same transport method) to be re-injected with adenovirus 6-7 days after initial injection to ensure continuous levels of protein expression.

Will DCM metabolic caging be used for collection? ○ Yes ● **No**

Experimental devices added to caging (e.g. running wheels) ○ Yes ● **No**

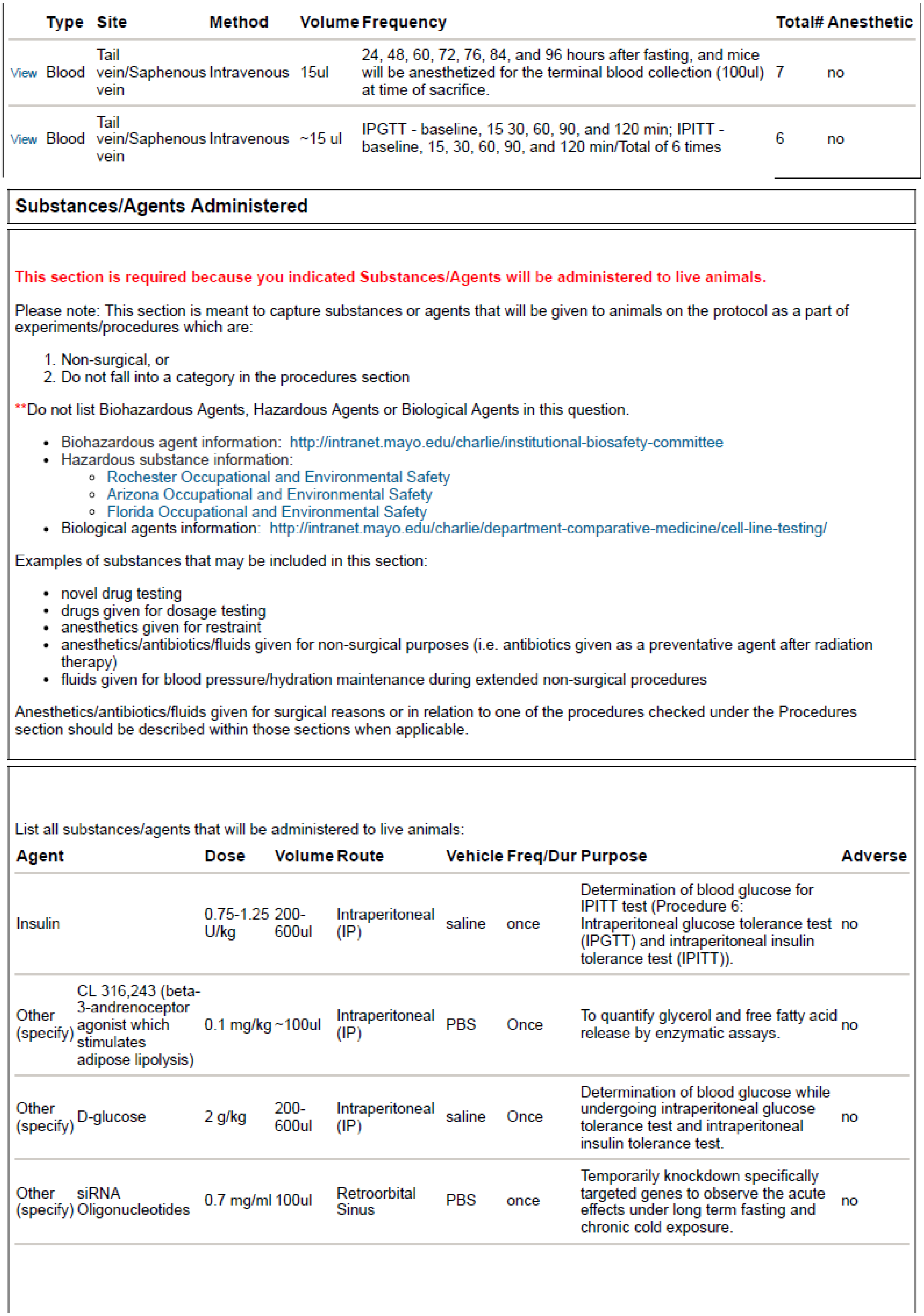
Other ○ Yes ● **No**

Specimens Collected

This section is required because you indicated specimens (tissue and/or body fluids) will be collected from live animals.

Specimens to be collected:

	Type	Site	Method	Volume	Frequency	Total#	Anesthetic
View	Blood	retroorbital venous plexus	Retroorbital Sinus	15-100ul	Lipolysis - 0, 30, 60 and 120 min post injection; TG Secretion - 0, 30, 60, and 120 min post injection	4	yes



	Type	Site	Method	Volume	Frequency	Total#	Anesthetic
View	Blood	Tail vein/Saphenous vein	Intravenous	15ul	24, 48, 60, 72, 76, 84, and 96 hours after fasting, and mice will be anesthetized for the terminal blood collection (100ul) at time of sacrifice.	7	no
View	Blood	Tail vein/Saphenous vein	Intravenous	~15 ul	IPGTT - baseline, 15 30, 60, 90, and 120 min; IPITT - baseline, 15, 30, 60, 90, and 120 min/Total of 6 times	6	no

Substances/Agents Administered

This section is required because you indicated Substances/Agents will be administered to live animals.

Please note: This section is meant to capture substances or agents that will be given to animals on the protocol as a part of experiments/procedures which are:

1. Non-surgical, or
2. Do not fall into a category in the procedures section

**Do not list Biohazardous Agents, Hazardous Agents or Biological Agents in this question.

- Biohazardous agent information: http://intranet.mayo.edu/charlie/institutional-biosafety-committee
- Hazardous substance information:
    - Rochester Occupational and Environmental Safety
    - Arizona Occupational and Environmental Safety
    - Florida Occupational and Environmental Safety
- Biological agents information: http://intranet.mayo.edu/charlie/department-comparative-medicine/cell-line-testing/

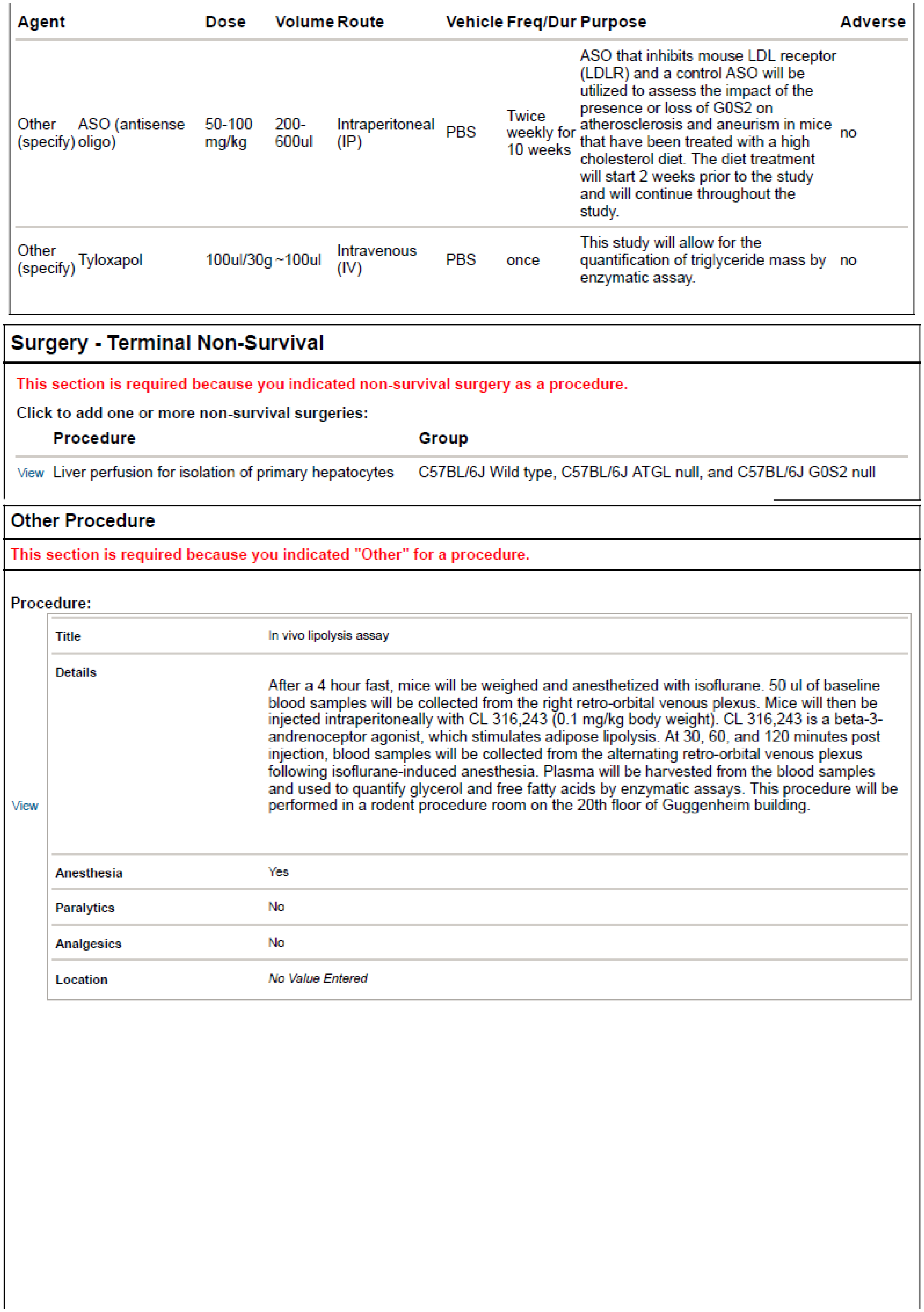
Examples of substances that may be included in this section:

- novel drug testing
- drugs given for dosage testing
- anesthetics given for restraint
- anesthetics/antibiotics/fluids given for non-surgical purposes (i.e. antibiotics given as a preventative agent after radiation therapy)
- fluids given for blood pressure/hydration maintenance during extended non-surgical procedures

Anesthetics/antibiotics/fluids given for surgical reasons or in relation to one of the procedures checked under the Procedures section should be described within those sections when applicable.

List all substances/agents that will be administered to live animals:

Agent		Dose	Volume	Route	Vehicle	Freq/Dur	Purpose	Adverse
Insulin		0.75-1.25 U/kg	200-600ul	Intraperitoneal (IP)	saline	once	Determination of blood glucose for IPITT test (Procedure 6: Intraperitoneal glucose tolerance test (IPGTT) and intraperitoneal insulin tolerance test (IPITT)).	no
Other (specify)	CL 316,243 (beta-3-andrenoceptor agonist which stimulates adipose lipolysis)	0.1 mg/kg	~100ul	Intraperitoneal (IP)	PBS	Once	To quantify glycerol and free fatty acid release by enzymatic assays.	no
Other (specify)	D-glucose	2 g/kg	200-600ul	Intraperitoneal (IP)	saline	Once	Determination of blood glucose while undergoing intraperitoneal glucose tolerance test and intraperitoneal insulin tolerance test.	no
Other (specify)	siRNA Oligonucleotides	0.7 mg/ml	100ul	Retroorbital Sinus	PBS	once	Temporarily knockdown specifically targeted genes to observe the acute effects under long term fasting and chronic cold exposure.	no



Agent		**Dose**	**Volume**	**Route**	**Vehicle**	**Freq/Dur**	**Purpose**	**Adverse**
Other (specify)	ASO (antisense oligo)	50-100 mg/kg	200-600ul	Intraperitoneal (IP)	PBS	Twice weekly for 10 weeks	ASO that inhibits mouse LDL receptor (LDLR) and a control ASO will be utilized to assess the impact of the presence or loss of G0S2 on atherosclerosis and aneurism in mice that have been treated with a high cholesterol diet. The diet treatment will start 2 weeks prior to the study and will continue throughout the study.	no
Other (specify)	Tyloxapol	100ul/30g	~100ul	Intravenous (IV)	PBS	once	This study will allow for the quantification of triglyceride mass by enzymatic assay.	no

Surgery - Terminal Non-Survival

This section is required because you indicated non-survival surgery as a procedure.

Click to add one or more non-survival surgeries:

	Procedure	**Group**
View	Liver perfusion for isolation of primary hepatocytes	C57BL/6J Wild type, C57BL/6J ATGL null, and C57BL/6J G0S2 null

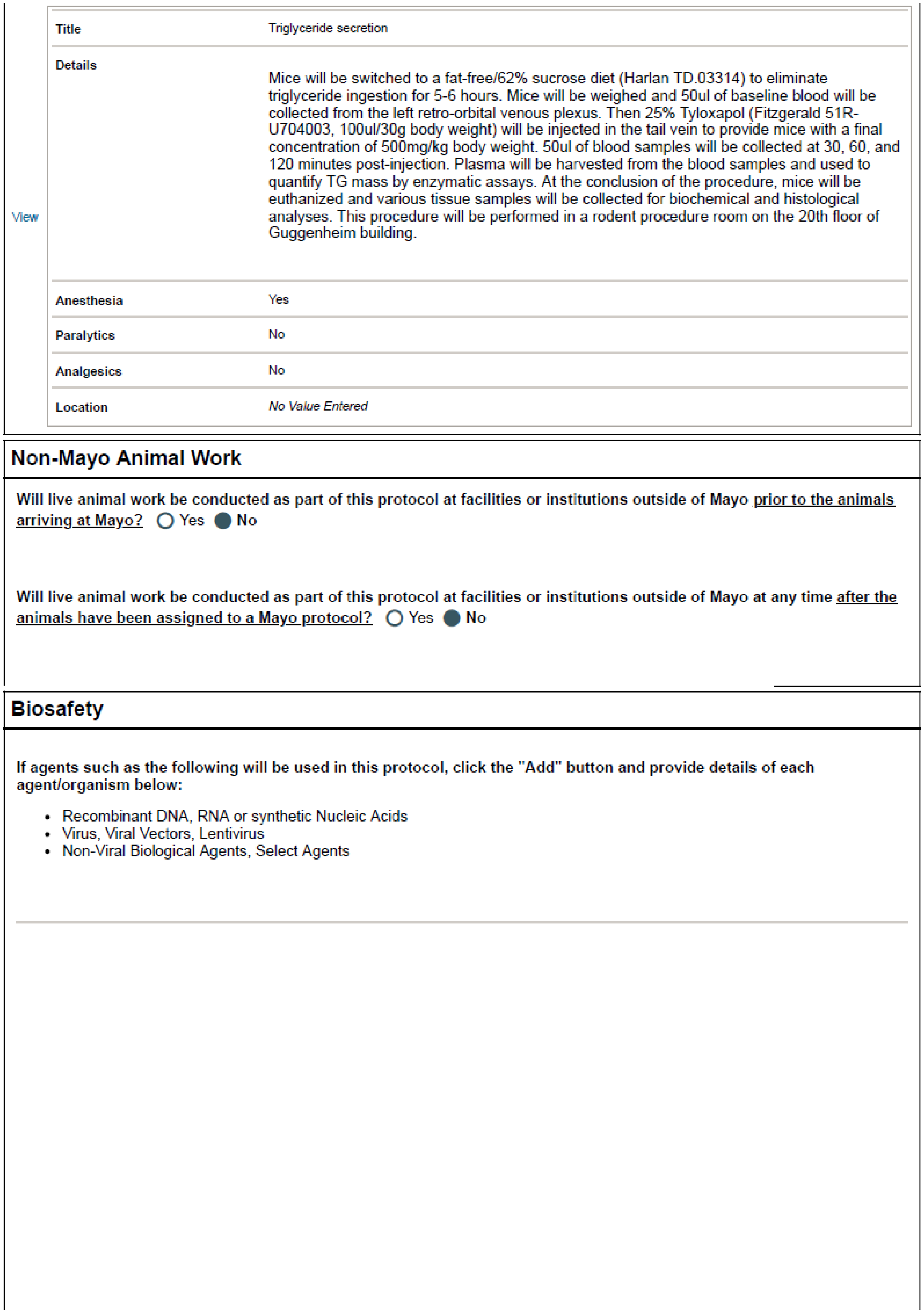
Other Procedure

This section is required because you indicated "Other" for a procedure.

Procedure:

View

Title	In vivo lipolysis assay
Details	After a 4 hour fast, mice will be weighed and anesthetized with isoflurane. 50 ul of baseline blood samples will be collected from the right retro-orbital venous plexus. Mice will then be injected intraperitoneally with CL 316,243 (0.1 mg/kg body weight). CL 316,243 is a beta-3-andrenoceptor agonist, which stimulates adipose lipolysis. At 30, 60, and 120 minutes post injection, blood samples will be collected from the alternating retro-orbital venous plexus following isoflurane-induced anesthesia. Plasma will be harvested from the blood samples and used to quantify glycerol and free fatty acids by enzymatic assays. This procedure will be performed in a rodent procedure room on the 20th floor of Guggenheim building.
Anesthesia	Yes
Paralytics	No
Analgesics	No
Location	*No Value Entered*



Title	Triglyceride secretion
Details	Mice will be switched to a fat-free/62% sucrose diet (Harlan TD.03314) to eliminate triglyceride ingestion for 5-6 hours. Mice will be weighed and 50ul of baseline blood will be collected from the left retro-orbital venous plexus. Then 25% Tyloxapol (Fitzgerald 51R-U704003, 100ul/30g body weight) will be injected in the tail vein to provide mice with a final concentration of 500mg/kg body weight. 50ul of blood samples will be collected at 30, 60, and 120 minutes post-injection. Plasma will be harvested from the blood samples and used to quantify TG mass by enzymatic assays. At the conclusion of the procedure, mice will be euthanized and various tissue samples will be collected for biochemical and histological analyses. This procedure will be performed in a rodent procedure room on the 20th floor of Guggenheim building.
Anesthesia	Yes
Paralytics	No
Analgesics	No
Location	*No Value Entered*

Non-Mayo Animal Work

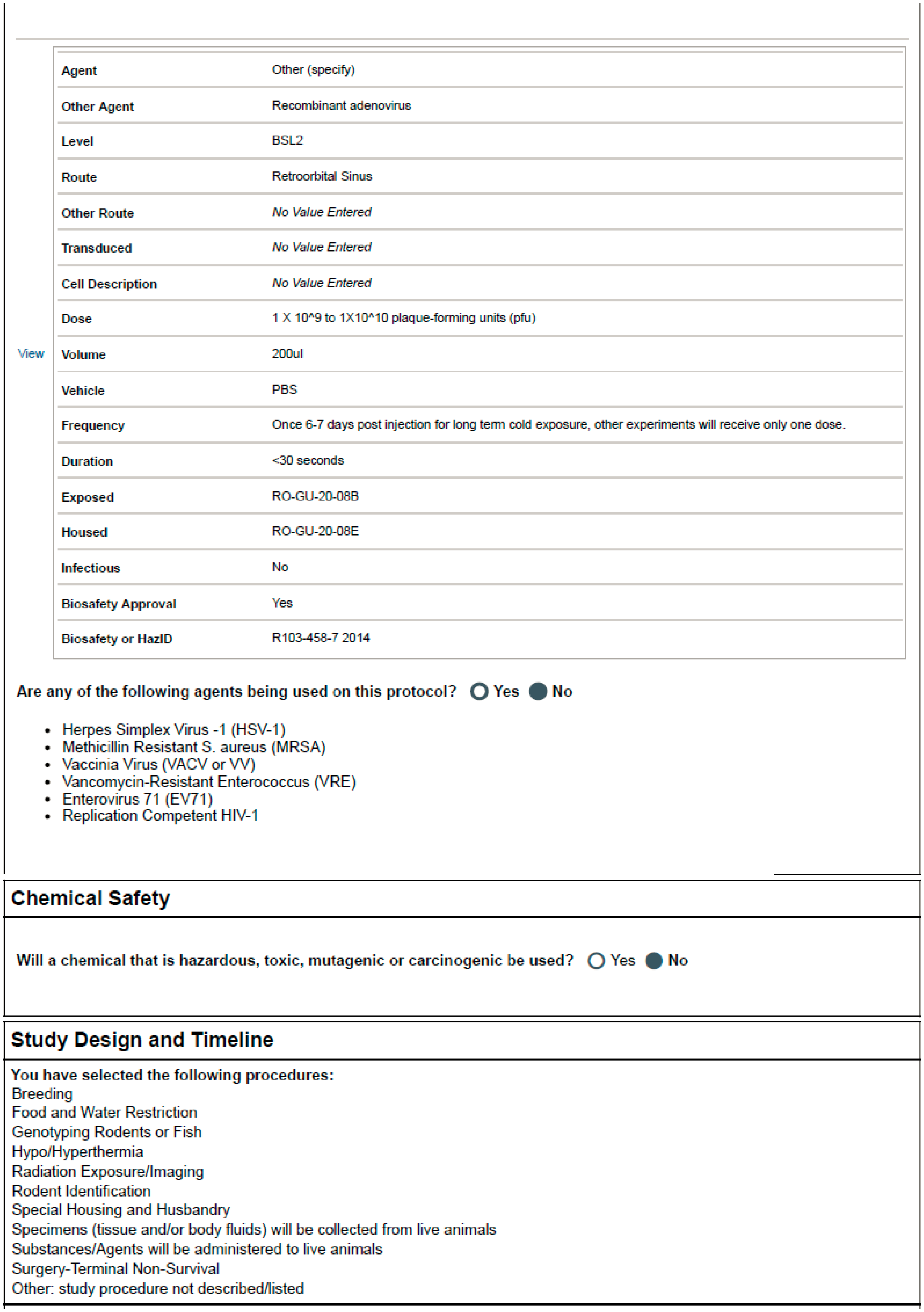
Will live animal work be conducted as part of this protocol at facilities or institutions outside of Mayo prior to the animals arriving at Mayo? ○ Yes ● **No**

Will live animal work be conducted as part of this protocol at facilities or institutions outside of Mayo at any time after the animals have been assigned to a Mayo protocol? ○ Yes ● **No**

Biosafety

If agents such as the following will be used in this protocol, click the "Add" button and provide details of each agent/organism below:

- Recombinant DNA, RNA or synthetic Nucleic Acids
- Virus, Viral Vectors, Lentivirus
- Non-Viral Biological Agents, Select Agents



View

Agent	Other (specify)
Other Agent	Recombinant adenovirus
Level	BSL2
Route	Retroorbital Sinus
Other Route	*No Value Entered*
Transduced	*No Value Entered*
Cell Description	*No Value Entered*
Dose	1 X 10^9 to 1X10^10 plaque-forming units (pfu)
Volume	200ul
Vehicle	PBS
Frequency	Once 6-7 days post injection for long term cold exposure, other experiments will receive only one dose.
Duration	<30 seconds
Exposed	RO-GU-20-08B
Housed	RO-GU-20-08E
Infectious	No
Biosafety Approval	Yes
Biosafety or HazID	R103-458-7 2014

Are any of the following agents being used on this protocol? ○ **Yes** ● **No**

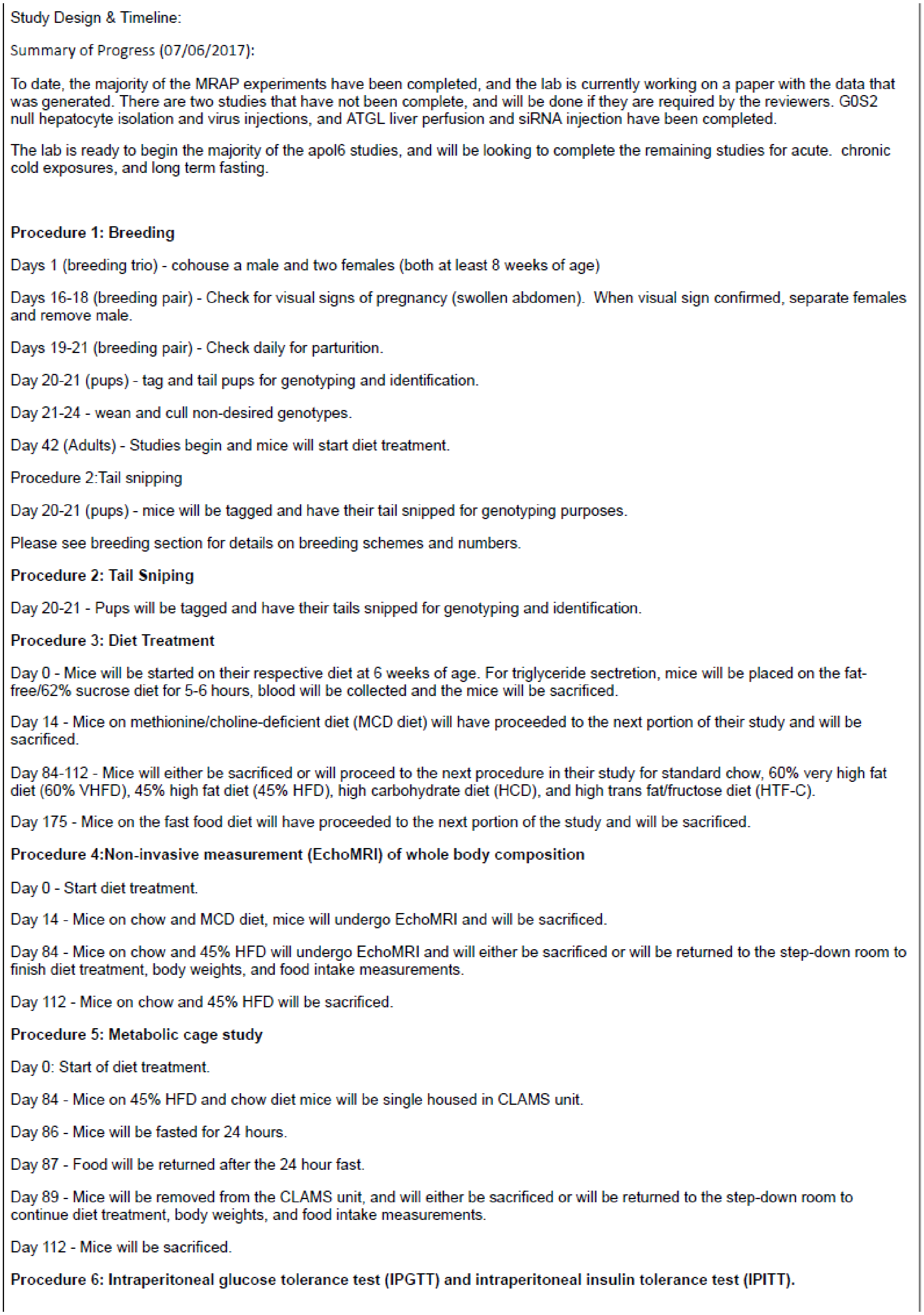
- Herpes Simplex Virus -1 (HSV-1)
- Methicillin Resistant S. aureus (MRSA)
- Vaccinia Virus (VACV or VV)
- Vancomycin-Resistant Enterococcus (VRE)
- Enterovirus 71 (EV71)
- Replication Competent HIV-1

Chemical Safety

Will a chemical that is hazardous, toxic, mutagenic or carcinogenic be used? ○ Yes ● **No**

Study Design and Timeline

You have selected the following procedures:
Breeding
Food and Water Restriction
Genotyping Rodents or Fish
Hypo/Hyperthermia
Radiation Exposure/Imaging
Rodent Identification
Special Housing and Husbandry
Specimens (tissue and/or body fluids) will be collected from live animals
Substances/Agents will be administered to live animals
Surgery-Terminal Non-Survival
Other: study procedure not described/listed



Study Design & Timeline:

Summary of Progress (07/06/2017):

To date, the majority of the MRAP experiments have been completed, and the lab is currently working on a paper with the data that was generated. There are two studies that have not been complete, and will be done if they are required by the reviewers. G0S2 null hepatocyte isolation and virus injections, and ATGL liver perfusion and siRNA injection have been completed.

The lab is ready to begin the majority of the apol6 studies, and will be looking to complete the remaining studies for acute. chronic cold exposures, and long term fasting.

Procedure 1: Breeding

Days 1 (breeding trio) - cohouse a male and two females (both at least 8 weeks of age)

Days 16-18 (breeding pair) - Check for visual signs of pregnancy (swollen abdomen). When visual sign confirmed, separate females and remove male.

Days 19-21 (breeding pair) - Check daily for parturition.

Day 20-21 (pups) - tag and tail pups for genotyping and identification.

Day 21-24 - wean and cull non-desired genotypes.

Day 42 (Adults) - Studies begin and mice will start diet treatment.

Procedure 2:Tail snipping

Day 20-21 (pups) - mice will be tagged and have their tail snipped for genotyping purposes.

Please see breeding section for details on breeding schemes and numbers.

Procedure 2: Tail Sniping

Day 20-21 - Pups will be tagged and have their tails snipped for genotyping and identification.

Procedure 3: Diet Treatment

Day 0 - Mice will be started on their respective diet at 6 weeks of age. For triglyceride sectretion, mice will be placed on the fat-free/62% sucrose diet for 5-6 hours, blood will be collected and the mice will be sacrificed.

Day 14 - Mice on methionine/choline-deficient diet (MCD diet) will have proceeded to the next portion of their study and will be sacrificed.

Day 84-112 - Mice will either be sacrificed or will proceed to the next procedure in their study for standard chow, 60% very high fat diet (60% VHFD), 45% high fat diet (45% HFD), high carbohydrate diet (HCD), and high trans fat/fructose diet (HTF-C).

Day 175 - Mice on the fast food diet will have proceeded to the next portion of the study and will be sacrificed.

Procedure 4:Non-invasive measurement (EchoMRI) of whole body composition

Day 0 - Start diet treatment.

Day 14 - Mice on chow and MCD diet, mice will undergo EchoMRI and will be sacrificed.

Day 84 - Mice on chow and 45% HFD will undergo EchoMRI and will either be sacrificed or will be returned to the step-down room to finish diet treatment, body weights, and food intake measurements.

Day 112 - Mice on chow and 45% HFD will be sacrificed.

Procedure 5: Metabolic cage study

Day 0: Start of diet treatment.

Day 84 - Mice on 45% HFD and chow diet mice will be single housed in CLAMS unit.

Day 86 - Mice will be fasted for 24 hours.

Day 87 - Food will be returned after the 24 hour fast.

Day 89 - Mice will be removed from the CLAMS unit, and will either be sacrificed or will be returned to the step-down room to continue diet treatment, body weights, and food intake measurements.

Day 112 - Mice will be sacrificed.

Procedure 6: Intraperitoneal glucose tolerance test (IPGTT) and intraperitoneal insulin tolerance test (IPITT).

Day 0 - Mice will begin diet treatment

Day 84 - Mice on 45% HFD and chow diet will undergo IPGTT.

Day 98 - Mice will undergo IPITT.

Day 112 - Mice will be sacrificed.

Procedure 7: In vivo lipolysis assay

Day 0 - Mice will begin diet treatment

Day 84 - Mice on 60% VHFD, 45% HFD, and chow diet will undergo 4 hour fasting, will be injected with CL 316,243, and blood will be collected. Mice will then be sacrificed.

Procedure 8: Liver perfusion for isolation of primary hepatocytes

Age: 42-56 days, mice on chow diet will undergo liver perfusion.

Procedure 9: In vivo gene transfer mediated by recombinant adenovirus

Day 0 - Mice on chow diet will be transferred to the ABSL2 facility and will be anesthetized and receive a retro-orbital injection.

Day 6-8 - Mice will be transported to the MCA metabolic phenotyping laboratory following required transport procedure.

Day 8 - Mice will be sacrificed.

Procedure 10: Retro-Orbital Injection of siRNA Oligonucleotides in Mice

Day 0 - Mice will begin diet treatment.

Day 84 - Mice on 60% VHFD and chow diet will be anesthetized and receive a retro-orbital injection.

Day 87-91 - Mice will undergo Triglyceride Secretion and will be sacrificed.

Procedure 11: Triglyceride Secretion

Day 87-91 of procedure 10, mice will be switched to fat-free/62% diet for 5-6 hours. Blood will be collected, mouse will receive tail vein injection, and 3 more blood collections. Following this procedure, mice will be sacrificed.

Procedure 12: Acute Cold Exposure

Day 0 - Mice will begin diet treatment.

Day 84 - Mice will be single housed and fasted for two hours. They will undergo cold exposure at 4C for 4-8 hours with body temperature monitored hourly. Mice will be sacrificed following the procedure.

Procedure 13: Chronic Cold Exposure

Day 0 - Groups designated for adenovirus injection will be anesthetized and receive their RO injection in the ABSL2 facility prior to transport to CLAMS unit. Mice in siRNA groups will be anesthetized and receive their injection prior to transfer to the CLAMS unit. Mice will be single housed in CLAMS unit. Reduce temperature to 18C for 3 days. Mice observed daily.

Day 3 - Temperature in CLAMS will be reduced to 4C.

Day 6-7 - Mice will be re-injected with siRNA and adenovirus. Mice in the adenovirus group will be transferred back to the ABSL2 facility for injection and returned to the CLAMS unit.

Day 10 - Mice will have blood collected and will be sacrificed.

Procedure 14: Long-term fasting

Day 0 - EchoMRI, transfer to step-down room, and single house mice.

Day 1 - Bodyweights and visual observations for all, EchoMRI measurement for 24 hour fasted group and sacrifice.

Day 2 - Bodyweights and visual observations for all, EchoMRI measurement for 48 hour fasted group and sacrifice.

Day 3 - Bodyweights and visual observations for all, EchoMRI measurement for 72 hour fasted group and sacrifice.

Day 4 - Bodyweights and visual observations for all, EchoMRI measurement for 96 hour fasted group and chow fed group, and sacrifice remaining mice.

Procedure 15: ASO injections

Day 0 - Mice will begin high cholesterol diet treatment.

Day 14 - Start of ASO treatment 2x weekly for 10 weeks. Mice continue on high cholesterol diet.

Day 84 - Mice are euthanized and tissue is collected for histological analysis of atherosclerosis and aneurism.

Numbers Justification

This section is required because you indicated Experimental Research as an intention.

Ensuring proper justification of animals requested is a critical charge of the IACUC. Please provide adequate statistical justification for the animal numbers requested.

- Justify the number of animals required for the 3-year duration of the IACUC protocol.
- Each group size and the total number of animals must be justified.
- The total number of animals requested must be justified on the basis of the experimental design.

Please use the categories below as a guide.

Check all that apply and provide the requested information:

☑ **Hypothesis driven research**

List numbers in each group Total (Sum of numbers needed for all groups):

These numbers are based on our best estimate (power analysis, experience, and published studies) of the number of subjects required to attain statistical significance in both the in vivo studies and analyses of the tissues. The study proposed for the effects of standard rodent chow versus different diets are organized in a 22 factorial design (a complete between-subject design where Factor A = 2 and Factor B = 2). For statistical comparisons, a separate analysis of variance (ANOVA) will be done for each of the dependent variables. Triplicate measurements of each dependent variable will be taken from each mouse and the average value of these measurements will be used as data in the separate ANOVAs. Significant main (donor type and diet) and interaction effects will be evaluated using linear contrasts. To ensure that the probability of incorrectly rejecting the transgenic hypothesis for any of the mean comparisons does not exceed the significance level (a), multiple comparison methods that control the error rate will be used. Mean comparisons may be tested using Tukey-Kramer tests. The Tukey-Kramer test is an extension of the Tukey test, a method for controlling the probability of Type I error (rejecting the transgenic hypothesis when it is true) to unequal replicates (by chance alone different numbers of mice are expected to be lost from subgroups). To further reduce the potential of Type 1 errors, statistical significance in these experiments will be assessed using a = 0.01. The planned number of mice (replicates) to be assigned to each unique AB treatment combination (at least 4 unique groups) is 10, for a study total of 40 mice. 1 to 3 mice are estimated to be lost from each treatment group. Therefore, given the projected sample size of 7 mice in each AB unique treatment combination, the study will be >90% powered (with a = 0.01) to detect a minimum effect size of 1.1 in contrasting the levels of Factor A (diet) and the levels of Factor B (donor type) and an effect size of 1.7 in the contrasting the levels of AxB.

Studies on whole-body lipid metabolism

Procedure 3. Diet treatment alone

20 groups, 10 mice/group. Total: 200 mice.

Procedure 4. EchoMRI body composition measurement

24 groups, 10 mice/group. Total: 240 mice.

Procedure 5. Metabolic Cage Study

13 groups, 6 mice/group. Total 78 mice. CLAMs unit only has room for 12 mice, so the group size has been reduced to 6 mice/group in order to be able to house 2 groups at a time.

Procedure 6. Intraperitoneal glucose tolerance test (IPGTT) and intraperitoneal insulin tolerance test (IPITT)

16 groups, 10 mice/group. Total: 160 mice.

Procedure 7. In vivo lipolysis assay

22 groups, 10 mice/group. Total: 220 mice.

Procedure 8. Liver perfusion for isolation of primary hepatocytes

15 groups, 10 mice/group. Total: 150 mice.

Procedure 9. In vivo gene transfer meditation by recombinant adenovirus

10 groups, 10 mice/group. Total: 100 mice.

Procedure 10. Retro-orbital injection of siRNA oligonucleotides

12 groups, 10 mice/group. Total: 120 mice.

Procedure 11. Triglyceride secretion

8 groups, 10 mice/group. Total mice: 80 mice.

Procedure 12. Acute cold exposure

18 groups, 10 mice/group. Total mice: 180 mice.

Procedure 13. Chronic cold exposure

28 groups, 6 mice/group. Total: 168 mice. CLAMs unit only has room for 12 mice, so the group size has been reduced to 6 mice/group in order to be able to house 2 groups at a time.

Procedure 14. Long term fasting

30 groups, 10 mice/group. Total: 300 mice.

Procedure 15. ASO injection

12 groups, 10 mice/group. Total: 120 mice.

☐ **The procedures are technically difficult and extra animals will be needed to replace failures of the experiment**

☐ **The experiment is a feasibility study to develop or learn a new procedure**

☐ **The experiment is a pre-clinical study (e.g. device testing, therapeutic intervention testing)**

☐ **The experiment requires a specific amount of tissue or number of cells for work in vitro**

☐ **Other experimental design or justification**

Animal Numbers

Provide total number of animals required for this protocol (include any animal numbers calculated in the breeding procedure section): 3201

Will any animals experience procedures that will cause significant pain, (more than just momentary) or distress for which anesthetics, analgesics and/or tranquilizers will be withheld? ● **Yes** ○ No

Provide the number of animals:
348

Provide scientific rationale for withholding anesthetics and/or analgesics:

Acute Cold Exposure

Mice will be studied over a range of 4-8 hr lengths of clold exposure at 4°C. The procedure will be performed in a cold room (CRB 3-047) that is adjacent to the investigator's main laboratory. The hobo data reedings for temperature and humidity in the cold room were recorded as follows: temperature 38.2°F ± 1.0; humidity 71.7% ± 5.0%; air flow negative with 41.5 air changes per hour. Mice will be caged individually and fasted for 2 hrs at room temperature prior to the transfer to the cold room. Mouse body temperature will be measured hourly using a thermometer with rectal probe. At the conclusion of this procedure the mice will be euthanized and tissues harvested for biochemical analyses.

Chronic cold exposure

Mice between the ages of 12-16 weeks will be housed in the CLAMS unit, located in Johnson 325/327, and will have *ad libitum* access to food and water. Mice will be housed individually in experimental cages and will be acclimated to a temperature of 18°C for 3 days. The temperature in the CLAMS unit will then be reduced to 4°C for 2 weeks. Wild-type mice have been shown to live up to 6 months at 4°C[1]. Mice will be visually checked daily, and mice that appear to be doing poorly will have their body temperature checked twice daily until they reach the predetermined endpoint. A control group of wild-type mice will be house in the animal facility and will be sacrificed at the end of the study. At the end of the 2 week cold exposure, prior to sacrifice, 100ul of blood will be collected. The groups of mice that are injected with adenovirus will be injected in the ABBSL2-level animal facility and will be transported in accordance to Procedure 9. Mice will be transported back down the

ABBSL2 facility (utilizing the same transport method) to be re-injected with adenovirus every 6-7 days to ensure continuous levels of protein expression.

References:

1. Golozoubova, V., Hohtola, E., Matthias, A., Jacobsson, A., Cannon, B., & Nedergaard, J. (2001). Only UCP1 can mediate adaptive nonshivering thermogenesis in the cold. *Faseb Journal*. doi:10.1096/fj.00-0536fje

2. Mulligan, J. D., Gonzalez, A. A., Stewart, A. M., Carey, H. V., & Saupe, K. W. (2007). Upregulation of AMPK during cold exposure occurs via distinct mechanisms in brown and white adipose tissue of the mouse. *The Journal of Physiology*. 580(Pt 2): 677–684. doi: 10.1113/jphysiol.2007.128652

3. Shabalina, I. G., Petrovic, N., De Jong, J. M., Kalinovich, A. V., Cannon, B., & Nedergaard, J. (2013). UCP1 in Brite/Beige Adipose Tissue Mitochondria is Functionally Thermogenic. *Cell Report*, 10(044). doi:10.1016/j.celrep.2013.10.044

4. Wang, Q. A., Tao, C., Gupta, R. K., & Scherer, P. E. (2013). Tracking adipogenesis during white adipose tissue development, expansion and regeneration. *Nature Medicine*. 1338–1344 (2013) doi:10.1038/nm.3324

Long-term fasting

300 mice will be fasted for 24, 48, 72, and 96 hours. Mice have been observed to survive fasting periods of 6 days.[2] It has been shown in rodents that fasting for 24 hours can produce a analgesic response.[1,3,4] Mice will be monitored at 24, 48, 60, 72, 84, 96 hours after fasting through body weight, blood glucose, body temperature, and visual observation of each mouse. If a mouse looks to be doing poorly prior to reaching a pre-established endpoint, they will be monitored more closely (ex. every 4-6 hours).
References:

1.de los Santos-Arteaga M, Sierra-Domínguez SA, Fontanella GH, Delgado-García JM, Carrión AM. Analgesia induced by dietary restriction is mediated by the kappa-opioid system. J Neurosci. 2003 Dec 3;23(35):11120-6.

2. Faggioni R, Moser A, Feingold KR, Grunfeld C. Reduced leptin levels in starvation increase susceptibility to endotoxic shock. Am J Pathol (2000) 156:1781–710.1016/S0002-9440(10)65049-3

3. Hamm RJ, Knisely JS, Watson A, Lyeth BG, Bossut DF. Hormonal mediation of the analgesia produced by food deprivation. Physiol Behav. 1985 Dec;35(6):879-82.

4. Kulkarni SK and Robert RK. Studies on Starvation and Dehydration-induced Analgesia in Rats. Ind. J. Physiol Pharmac. (1982) Vol. 26 (4) 321-324.

Complications

Describe the most commonly recognized complications or side effects of the specific drug, device and/or procedures that the animals may experience as a result of these experiments.

Intraperitoneal injections may result in intraperitoneal hemorrhage.

Breeding: Dytocia, cannibalism, and malocclusion.

Acute cold exposure: lethargy, hypothermia

Chronic cold exposure: weight loss, hypothermia,

Long term fasting: weight loss, lethargy

How often will the animal be observed to detect complications or side effects?

Intraperitoneal injections: Mice will be monitored following injection, a couple hours post-injection, and the following day.

Gravid females will be visibly observed 1-2 days prior to parturition and one day post parturition to monitor for dystocia.

Litters will observed at 3 days of age to observe if females have cannibalized the litter. This is to avoid disturbing the mother with her new litter, and inadvertently stress her leading her to cannibalize her litter.

Malocclusion - pups will be checks at the time of weaning. Further monitoring will be based on weight loss.

Acute cold exposure: hourly.

Chronic cold exposure: twice daily

Long term fasting: Mice will be monitored at 0, 24, 48, 60, 72, 76, 80, 84, 88, 92, 96 hours after fasting.

Describe how each complication or side effect will be reduced or alleviated.

Personnel are all trained/will be trained in the correct injection techniques to minimize the possibility of complications to the procedure.

Females that experience dystocia will be sacrificed.

Females that cannibalize a litter will be sacrificed.

Mice that are observed with malocclusion will be sacrificed and the breeding pair will not be bred again.

Acute cold exposure: mice will be sacrificed if body temperatures drops below 23C.

Chronic cold exposure: mice will be sacrificed if body temperature drops below 23C or if body weight loss is equal to or greater than 20%.

Long term fasting: mice will be sacrificed if body temperature drops below 23C, body weight loss is equal to or greater than 30%, or if their blood glucose levels drop below 30mg/dl.

Humane Endpoints

Early removal (before the planned experimental endpoint) of an animal from the study must occur based on humane endpoints.

List the specific clinical or behavioral signs that indicate a humane endpoint. When these signs are observed, animals must be removed from studies and euthanized. **The Principal Investigator (PI) and laboratory staff is responsible for monitoring, documenting, and euthanizing animals when an animal has reached humane endpoint criteria.** Animals must be monitored in accordance with the monitoring plan outlined in the investigator's IACUC protocol.

NOTE: Death is not an acceptable end point. Every effort to recognize endpoints predictive of death so that animals can be humanely euthanized prior to death must be made to avoid death as an endpoint.

Note: The following are institutional policy endpoints that must be observed for all studies:

- Weight loss greater than or equal to 20% of body weight
- Inability to ambulate
- Inability to reach food and/or water
- Tumors greater than or equal to 10% body weight
- Tumors that have ulcerated
- A body condition score of 1 or less using the IACUC approved scoring system

Provide additional humane endpoints not already listed above that will be observed:

Activity level: Hypoactivity (abnormally low-lethargic), hyperactivity, restlessness.

Behavior: Vocalization, self-trauma, aggressiveness, ataxia.

Appearance: Unkempt fur, porphyrin staining around the eyes and nostrils, hunched posture, cyanosis, pale mucous membranes, soiled genital area.

Vital Signs: Respiratory Distress.

Weight Loss: Mice will be weighed weekly for the duration of the study, mice will be sacrificed if an individual has weight loss that is ≥20%

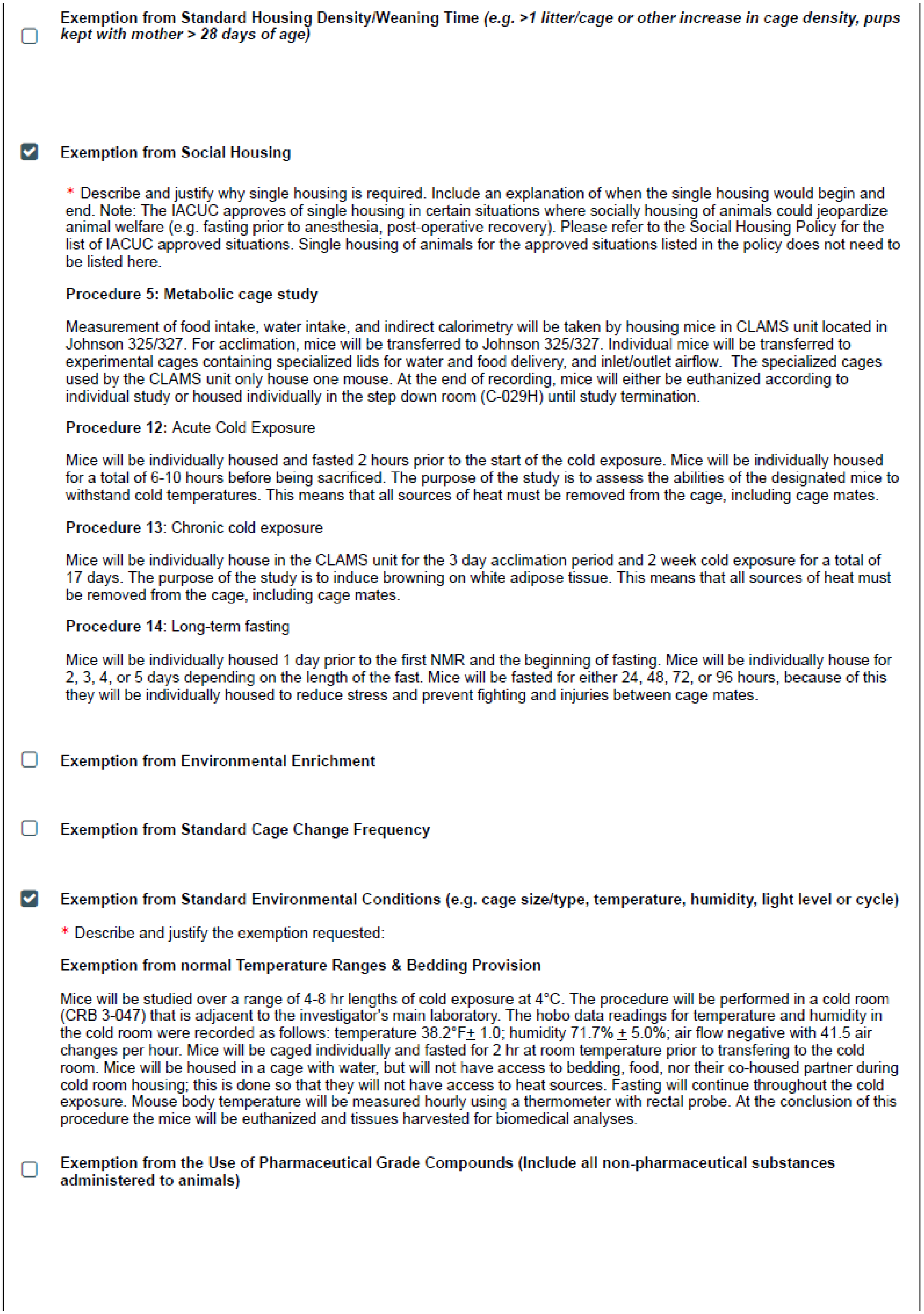
For the mice fasting for 96 hours, we expect the weight loss to be greater than 20%; mice on this study will be sacrificed if an individual has weight loss that is ≥30% of their fed weight.

Blood glucose levels: mice will be sacrificed if blood glucose levels drop below 30mg/dl.

Body Temperature: Long term fasted, acute, and chronic cold exposure mice will be sacrificed if their body temperatures fall below 23°C.

Exemption Request for Mice

This protocol requires the following exemption(s) to IACUC policies and/or the Guide for the Care and Use of Laboratory Animals (check all that apply):



☐ **Exemption from Standard Housing Density/Weaning Time** ***(e.g. >1 litter/cage or other increase in cage density, pups kept with mother > 28 days of age)***

☑ **Exemption from Social Housing**

* Describe and justify why single housing is required. Include an explanation of when the single housing would begin and end. Note: The IACUC approves of single housing in certain situations where socially housing of animals could jeopardize animal welfare (e.g. fasting prior to anesthesia, post-operative recovery). Please refer to the Social Housing Policy for the list of IACUC approved situations. Single housing of animals for the approved situations listed in the policy does not need to be listed here.

Procedure 5: Metabolic cage study

Measurement of food intake, water intake, and indirect calorimetry will be taken by housing mice in CLAMS unit located in Johnson 325/327. For acclimation, mice will be transferred to Johnson 325/327. Individual mice will be transferred to experimental cages containing specialized lids for water and food delivery, and inlet/outlet airflow. The specialized cages used by the CLAMS unit only house one mouse. At the end of recording, mice will either be euthanized according to individual study or housed individually in the step down room (C-029H) until study termination.

Procedure 12: Acute Cold Exposure

Mice will be individually housed and fasted 2 hours prior to the start of the cold exposure. Mice will be individually housed for a total of 6-10 hours before being sacrificed. The purpose of the study is to assess the abilities of the designated mice to withstand cold temperatures. This means that all sources of heat must be removed from the cage, including cage mates.

Procedure 13: Chronic cold exposure

Mice will be individually house in the CLAMS unit for the 3 day acclimation period and 2 week cold exposure for a total of 17 days. The purpose of the study is to induce browning on white adipose tissue. This means that all sources of heat must be removed from the cage, including cage mates.

Procedure 14: Long-term fasting

Mice will be individually housed 1 day prior to the first NMR and the beginning of fasting. Mice will be individually house for 2, 3, 4, or 5 days depending on the length of the fast. Mice will be fasted for either 24, 48, 72, or 96 hours, because of this they will be individually housed to reduce stress and prevent fighting and injuries between cage mates.

☐ **Exemption from Environmental Enrichment**

☐ **Exemption from Standard Cage Change Frequency**

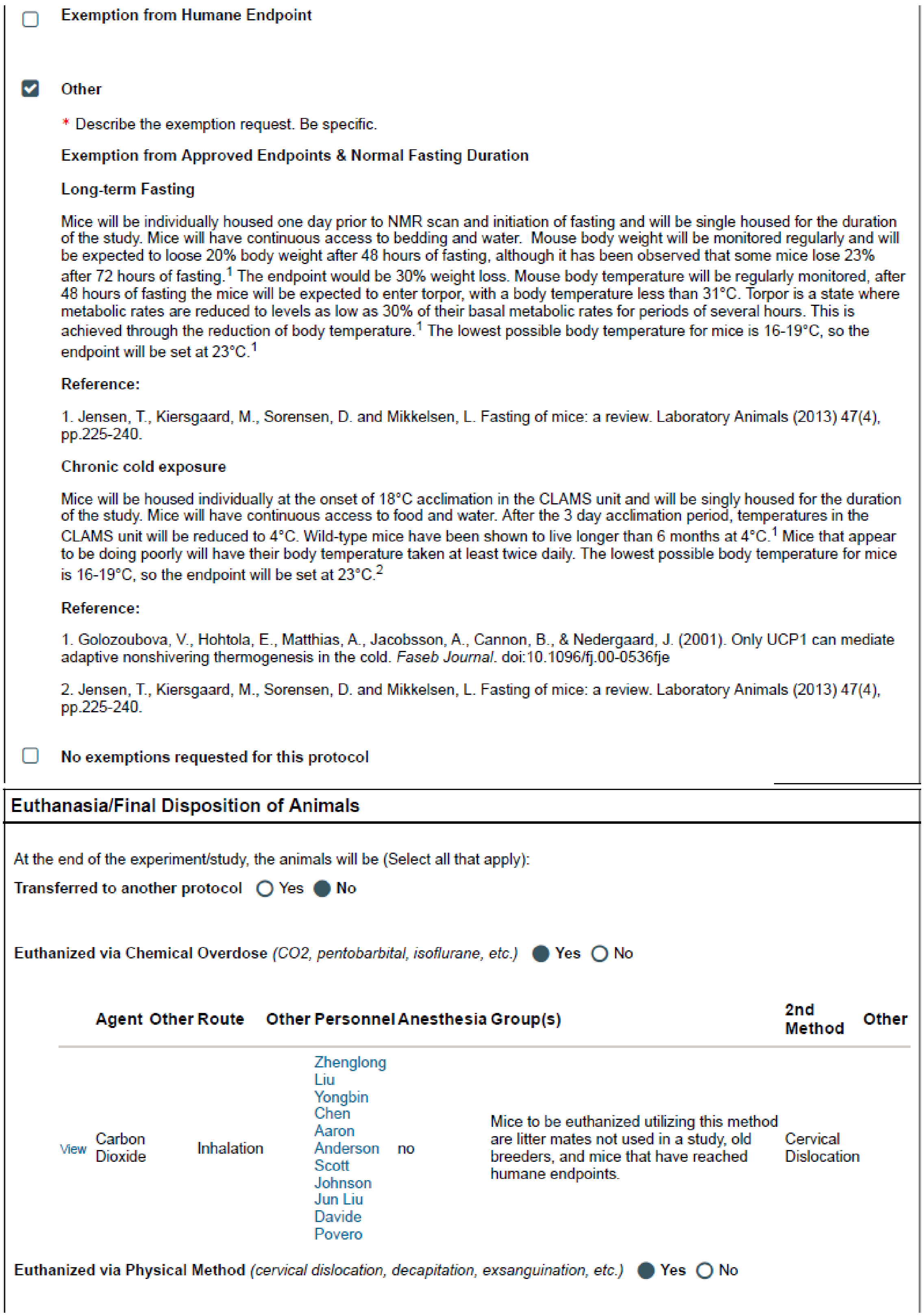
☑ **Exemption from Standard Environmental Conditions (e.g. cage size/type, temperature, humidity, light level or cycle)**

* Describe and justify the exemption requested:

Exemption from normal Temperature Ranges & Bedding Provision

Mice will be studied over a range of 4-8 hr lengths of cold exposure at 4°C. The procedure will be performed in a cold room (CRB 3-047) that is adjacent to the investigator's main laboratory. The hobo data readings for temperature and humidity in the cold room were recorded as follows: temperature 38.2°F± 1.0; humidity 71.7% ± 5.0%; air flow negative with 41.5 air changes per hour. Mice will be caged individually and fasted for 2 hr at room temperature prior to transfering to the cold room. Mice will be housed in a cage with water, but will not have access to bedding, food, nor their co-housed partner during cold room housing; this is done so that they will not have access to heat sources. Fasting will continue throughout the cold exposure. Mouse body temperature will be measured hourly using a thermometer with rectal probe. At the conclusion of this procedure the mice will be euthanized and tissues harvested for biomedical analyses.

☐ **Exemption from the Use of Pharmaceutical Grade Compounds (Include all non-pharmaceutical substances administered to animals)**



☐ **Exemption from Humane Endpoint**

☑ **Other**

* Describe the exemption request. Be specific.

Exemption from Approved Endpoints & Normal Fasting Duration

Long-term Fasting

Mice will be individually housed one day prior to NMR scan and initiation of fasting and will be single housed for the duration of the study. Mice will have continuous access to bedding and water. Mouse body weight will be monitored regularly and will be expected to loose 20% body weight after 48 hours of fasting, although it has been observed that some mice lose 23% after 72 hours of fasting.[1] The endpoint would be 30% weight loss. Mouse body temperature will be regularly monitored, after 48 hours of fasting the mice will be expected to enter torpor, with a body temperature less than 31°C. Torpor is a state where metabolic rates are reduced to levels as low as 30% of their basal metabolic rates for periods of several hours. This is achieved through the reduction of body temperature.[1] The lowest possible body temperature for mice is 16-19°C, so the endpoint will be set at 23°C.[1]

Reference:

1. Jensen, T., Kiersgaard, M., Sorensen, D. and Mikkelsen, L. Fasting of mice: a review. Laboratory Animals (2013) 47(4), pp.225-240.

Chronic cold exposure

Mice will be housed individually at the onset of 18°C acclimation in the CLAMS unit and will be singly housed for the duration of the study. Mice will have continuous access to food and water. After the 3 day acclimation period, temperatures in the CLAMS unit will be reduced to 4°C. Wild-type mice have been shown to live longer than 6 months at 4°C.[1] Mice that appear to be doing poorly will have their body temperature taken at least twice daily. The lowest possible body temperature for mice is 16-19°C, so the endpoint will be set at 23°C.[2]

Reference:

1. Golozoubova, V., Hohtola, E., Matthias, A., Jacobsson, A., Cannon, B., & Nedergaard, J. (2001). Only UCP1 can mediate adaptive nonshivering thermogenesis in the cold. *Faseb Journal*. doi:10.1096/fj.00-0536fje

2. Jensen, T., Kiersgaard, M., Sorensen, D. and Mikkelsen, L. Fasting of mice: a review. Laboratory Animals (2013) 47(4), pp.225-240.

☐ **No exemptions requested for this protocol**

Euthanasia/Final Disposition of Animals

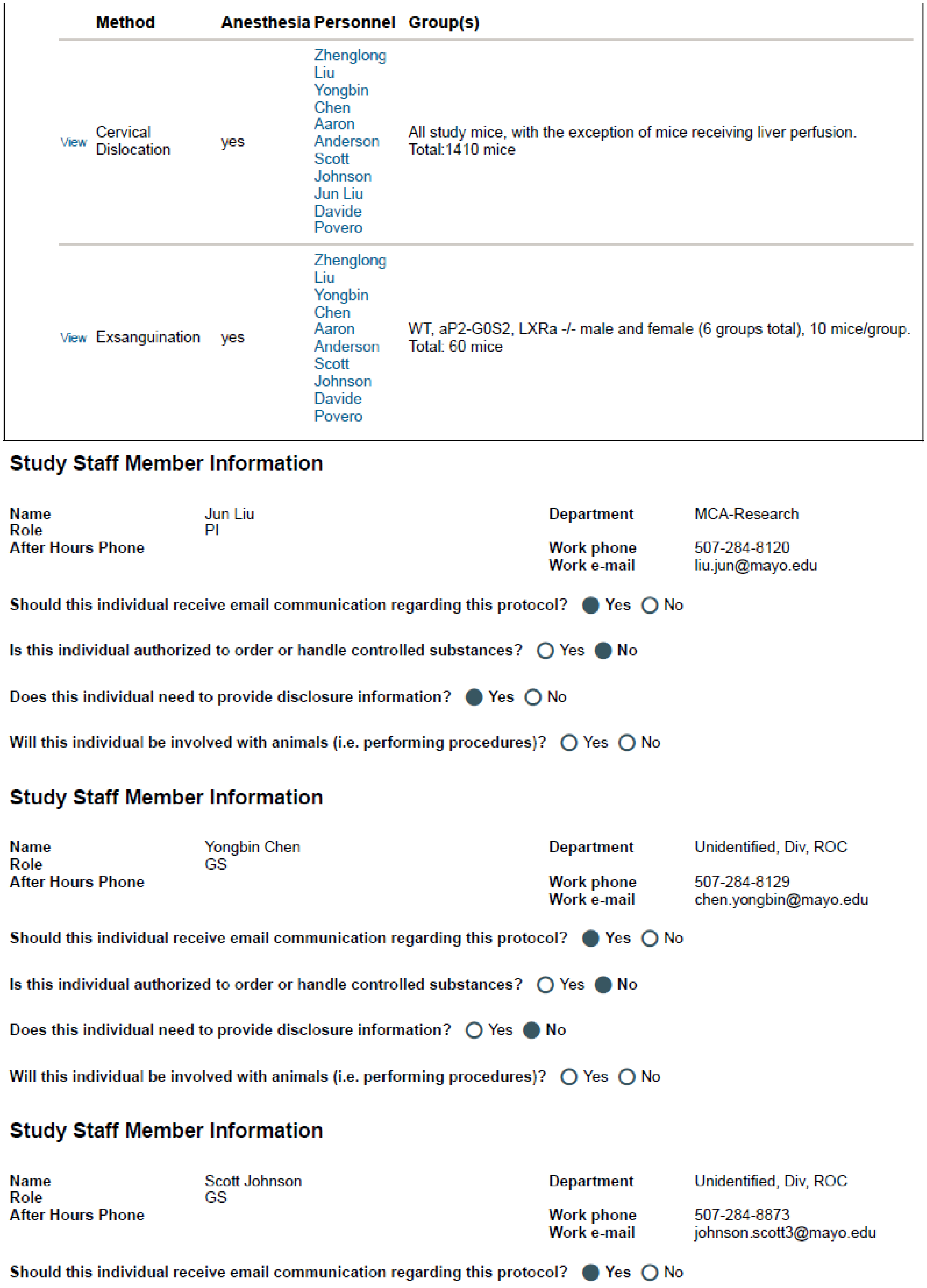
At the end of the experiment/study, the animals will be (Select all that apply):

Transferred to another protocol ○ Yes ● No

Euthanized via Chemical Overdose *(CO2, pentobarbital, isoflurane, etc.)* ● Yes ○ No

	Agent	Other	Route	Other	Personnel	Anesthesia	Group(s)	2nd Method	Other
View	Carbon Dioxide		Inhalation		Zhenglong Liu Yongbin Chen Aaron Anderson Scott Johnson Jun Liu Davide Povero	no	Mice to be euthanized utilizing this method are litter mates not used in a study, old breeders, and mice that have reached humane endpoints.	Cervical Dislocation	

Euthanized via Physical Method *(cervical dislocation, decapitation, exsanguination, etc.)* ● Yes ○ No



	Method	Anesthesia	Personnel	Group(s)
View	Cervical Dislocation	yes	Zhenglong Liu Yongbin Chen Aaron Anderson Scott Johnson Jun Liu Davide Povero	All study mice, with the exception of mice receiving liver perfusion. Total:1410 mice
View	Exsanguination	yes	Zhenglong Liu Yongbin Chen Aaron Anderson Scott Johnson Davide Povero	WT, aP2-G0S2, LXRa -/- male and female (6 groups total), 10 mice/group. Total: 60 mice

Study Staff Member Information

Name	Jun Liu	**Department**	MCA-Research
Role	PI		
After Hours Phone		**Work phone**	507-284-8120
		Work e-mail	liu.jun@mayo.edu

Should this individual receive email communication regarding this protocol? ● Yes ○ No

Is this individual authorized to order or handle controlled substances? ○ Yes ● No

Does this individual need to provide disclosure information? ● Yes ○ No

Will this individual be involved with animals (i.e. performing procedures)? ○ Yes ○ No

Study Staff Member Information

Name	Yongbin Chen	**Department**	Unidentified, Div, ROC
Role	GS		
After Hours Phone		**Work phone**	507-284-8129
		Work e-mail	chen.yongbin@mayo.edu

Should this individual receive email communication regarding this protocol? ● Yes ○ No

Is this individual authorized to order or handle controlled substances? ○ Yes ● No

Does this individual need to provide disclosure information? ○ Yes ● No

Will this individual be involved with animals (i.e. performing procedures)? ○ Yes ○ No

Study Staff Member Information

Name	Scott Johnson	**Department**	Unidentified, Div, ROC
Role	GS		
After Hours Phone		**Work phone**	507-284-8873
		Work e-mail	johnson.scott3@mayo.edu

Should this individual receive email communication regarding this protocol? ● Yes ○ No

Is this individual authorized to order or handle controlled substances? ○ Yes ● **No**

Does this individual need to provide disclosure information? ○ Yes ● **No**

Will this individual be involved with animals (i.e. performing procedures)? ○ Yes ○ No

Study Staff Member Information

Name	Davide Povero	**Department**	Unidentified, Div, ROC
Role	RA		
After Hours Phone		**Work phone**	507-293-9097
		Work e-mail	povero.davide@mayo.edu

Should this individual receive email communication regarding this protocol? ● **Yes** ○ No

Is this individual authorized to order or handle controlled substances? ○ Yes ● **No**

Does this individual need to provide disclosure information? ○ Yes ● **No**

Will this individual be involved with animals (i.e. performing procedures)? ○ Yes ○ No

Study Staff Member Information

Name	Zhenglong Liu	**Department**	Unidentified, Div, ROC
Role	RF		
After Hours Phone		**Work phone**	507-284-8197
		Work e-mail	liu.zhenglong@mayo.edu

Should this individual receive email communication regarding this protocol? ● **Yes** ○ No

Is this individual authorized to order or handle controlled substances? ○ Yes ● **No**

Does this individual need to provide disclosure information? ○ Yes ● **No**

Will this individual be involved with animals (i.e. performing procedures)? ○ Yes ○ No

Study Staff Member Information

Name	Aaron Anderson	**Department**	Unidentified, Div, ROC
Role	RT		
After Hours Phone		**Work phone**	507-284-1945
		Work e-mail	anderson.aaron@mayo.edu

Should this individual receive email communication regarding this protocol? ● **Yes** ○ No

Is this individual authorized to order or handle controlled substances? ○ Yes ● **No**

Does this individual need to provide disclosure information? ○ Yes ● **No**

Will this individual be involved with animals (i.e. performing procedures)? ○ Yes ○ No

PAU Funding

ATTENTION: Listing your PAU in this section does not link it to Animal Ops. To link your PAU and protocol, after the protocol is activated, email Research Finance at resacctlambs@mayo.edu, provide the protocol number and PAU number, and ask that the two items are linked.

Please list all funding sources (PAU and activity numbers) that will be used to pay for animals used on this protocol. Funding source(s) must be appropriate for this IACUC protocol. A congruency check between the submitted IACUC protocol and associated funding must be performed.

PAU Number: 93694

Activity Number:93694999

Nonionizing Source

Source:
Other (ex. NMR) EchoMRI

Locations of intended use:

Building	Room
Guggenheim Building	RO-GU-07-02

Is this new equipment? ○ Yes ● No

List of Operators *(The following name(s) are generated from the Personnel Information page. Select all names that apply)*:

	Member
☑	**Aaron Anderson**
☑	**Yongbin Chen**
☑	**Scott Johnson**
☑	**Zhenglong Liu**
☐	Jun Liu
☐	Davide Povero

☐ **Check to indicate if any personnel are new operators.**

NOTE: New individuals must complete appropriate training. Click on help icon below for more information.

List other personnel that may be in the room during the operation of the device:
NOTE: These individuals must complete appropriate safety training. Click on help icon below for more information.

Number of animals to be used: 140

Will anesthesia be used? ○ Yes ● No

Will paralytics be used? ○ Yes ● No

Briefly describe the imaging procedure (include a description of animal positioning and restraint):

Following calibration, conscious rodents are individually restrained in a clear cylindrical plastic tube (sized by animal weight) and are placed in the scanner. The tubes have holes for breathing and are maintained in a horizontal plane during the procedure. One scan will be conducted for each animal (2 minutes/scan, entire procedure will be 2 minutes). Mice will be returned to their cages following the scan.

Specimen Sample

Type of sample collected:
Blood

Method of sample collection:

Retroorbital Sinus

Anatomical site of sample collection: retroorbital venous plexus	**Volume (include units):** 15-100ul

Frequency of Collection:
Lipolysis - 0, 30, 60 and 120 min post injection; TG Secretion - 0, 30, 60, and 120 min post injection

Total Number of Samples Collected Per Animal:
4

What is the purpose of sample collection?
Procedure 7: In vivo lipolysis assay - Plasma will be harvested from the blood samples and used to quantify glycerol and free fatty acids by enzymatic assays.

Procedure 11: Triglyceride Secretion - Plasma will be harvested from the blood samples and used to quantify TG mass by enzymatic assays

Describe sample collection procedure:

Mice will be anesthetized with isoflurane prior to blood collection from the retroorbital venous plexus with a microhematocrit tube. Blood collections will be alternated between the right and left retroorbital venous plexus for no more than 4 bleeds.

Will an anesthetic need to be used to collect sample? ● Yes ○ No

If yes, list anesthetic agent(s) that will be administered:

Agent	Dose (mg/kg or mg/kg/hr)	Route
Isoflurane-vaporizer	1.5-2.5%	Inhalation

If yes, personnel performing anesthesia *(The following name(s) are generated from the Personnel Information page. Select all names that apply)*:

	Member
☑	**Yongbin Chen**
☑	**Scott Johnson**
☑	**Zhenglong Liu**
☑	**Jun Liu**
☐	Davide Povero

Specimen Sample

Type of sample collected:
Blood

Method of sample collection:
Intravenous

Anatomical site of sample collection: Tail vein/Saphenous vein	**Volume (include units):** 15ul

Frequency of Collection:
24, 48, 60, 72, 76, 84, and 96 hours after fasting, and mice will be anesthetized for the terminal blood collection (100ul) at time of sacrifice.

Total Number of Samples Collected Per Animal:
7

What is the purpose of sample collection?

Procedure 14: Glucose measurements. Blood samples will only be collected if the mouse appears to be doing poorly to reduce the stress the mice experience over the extended fasting periods. Mice will be euthanized when they reach one of the predetermined end points.

Describe sample collection procedure:

Mice will be properly restrained prior to blood collection from the tail vein, a needle will be used to puncture the skin on the tail, and the blood (~15ul) will be collected with a glucometer. Gauze and physical pressure will be used to stop bleeding. Clots are removed for multiple blood collections.

Will an anesthetic need to be used to collect sample? ○ Yes ● No

If yes, list anesthetic agent(s) that will be administered:

Agent	Dose (mg/kg or mg/kg/hr)	Route
There are no items to display		

If yes, personnel performing anesthesia *(The following name(s) are generated from the Personnel Information page. Select all names that apply)*:

	Member
☐	Yongbin Chen
☐	Scott Johnson
☐	Zhenglong Liu
☐	Jun Liu
☐	Davide Povero

Specimen Sample

Type of sample collected:
Blood

Method of sample collection:
Intravenous

Anatomical site of sample collection:
Tail vein/Saphenous vein

Volume (include units):
~15 ul

Frequency of Collection:
IPGTT - baseline, 15 30, 60, 90, and 120 min; IPITT - baseline, 15, 30, 60, 90, and 120 min/Total of 6 times

Total Number of Samples Collected Per Animal:
6

What is the purpose of sample collection?

Procedure 6: Blood glucose measurements post D-glucose injection (IPGTT) and post insulin (IPITT) injections.

Describe sample collection procedure:

Mice will be properly restrained prior to blood collection from the tail vein, a needle will be used to puncture the skin on the tail, and the blood (~15ul) will be collected with a glucometer. Gauze and physical pressure will be used to stop bleeding. Clots are removed for multiple blood collections.

Will an anesthetic need to be used to collect sample? ○ Yes ● No

If yes, list anesthetic agent(s) that will be administered:

Agent	Dose (mg/kg or mg/kg/hr)	Route
There are no items to display		

If yes, personnel performing anesthesia *(The following name(s) are generated from the Personnel Information page. Select all names that apply)*:

	Member
☐	Yongbin Chen
☐	Scott Johnson

	Member
☐	Zhenglong Liu
☐	Jun Liu
☐	Davide Povero

Surgery - Terminal Non-Survival

Procedure Name (e.g. Perfusion, Cardiectomy, etc.):
Liver perfusion for isolation of primary hepatocytes

Which group will have this surgery?*(e.g. Group 1, Experiment 3, the High Fat Diet group, etc.)*

C57BL/6J Wild type, C57BL/6J ATGL null, and C57BL/6J G0S2 null

Fasting for Procedure:

● **Not Applicable (Rats, Mice, etc)**
○ No food the day of surgery. Animals receive their normal ration the day before the surgery. Fluid will not be removed.
○ Other (specify)

Induction agent(s) to be administered:

Agent	Dose (mg/kg or mg/kg/hr)	Route
Isoflurane-vaporizer	1.5-2.5%	Inhalation

Maintenance agent(s) to be administered:

Agent	Dose (mg/kg or mg/kg/hr)	Route	Frequency	Time
Isoflurane-vaporizer	1.5-2.5%	Inhalation	Continuous	15 minutes

Will paralytics be administered for this procedure? ○ Yes ● No

Analgesic(s) to be administered for this procedure:

Agent	Dose (mg/kg or mg/kg/hr)	Route	Frequency	Duration
There are no items to display				

Provide a detailed description of the surgical procedure including:

- **anatomical approach**
- **tissue manipulation**
- **timepoint in which animals will be euthanized**

Procedure description:

Surgery: Liver perfusion for isolation of primary hempatocytes

1. Anesthetize the mouse with isoflurane.

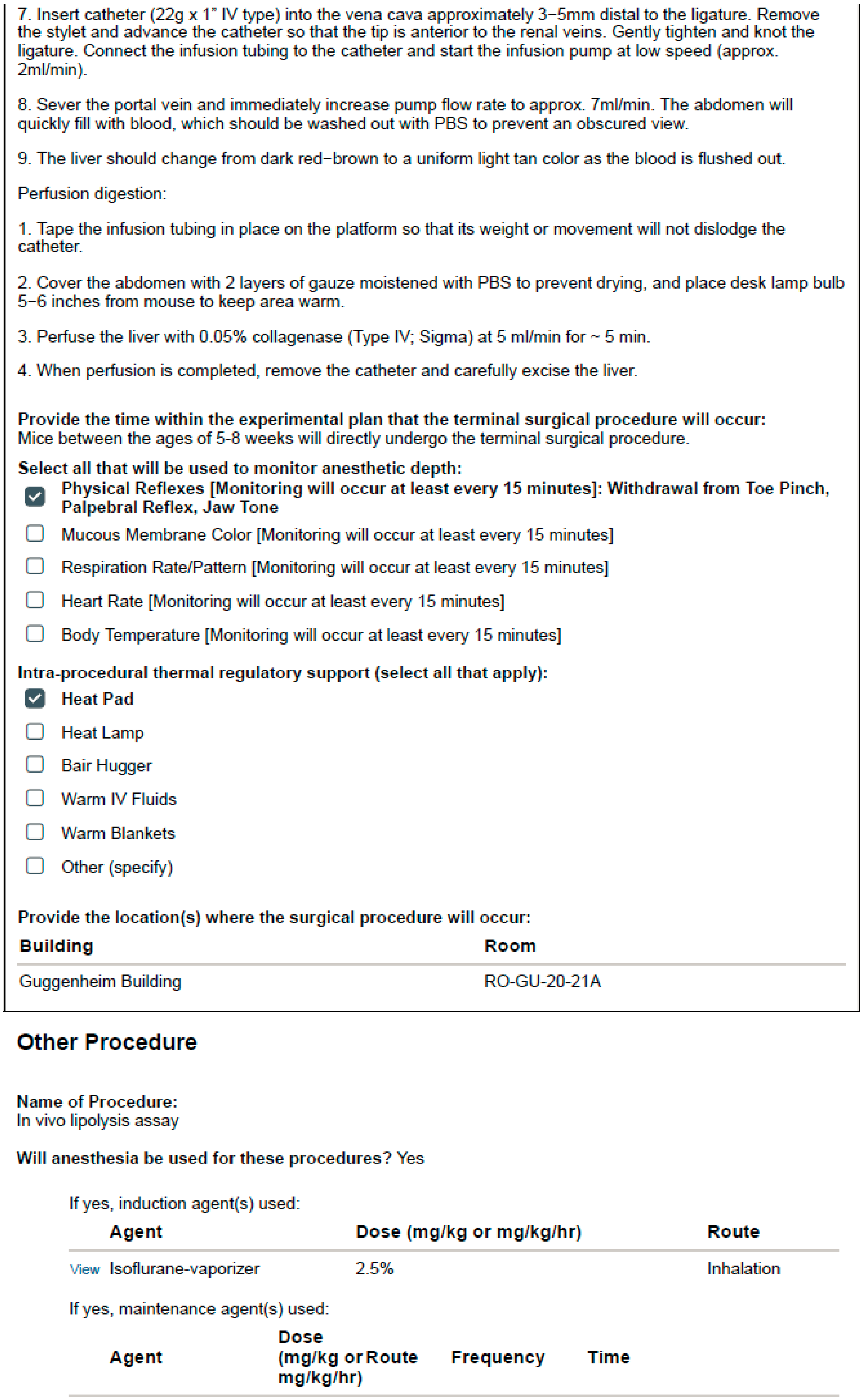
2.Place mouse in dorsal recumbency on surgical platform. Use tape to hold feet and tail in position. Swab the abdomen with ethanol.

3. Make an incision through the skin along the ventral midline, and dissect the skin away to reveal the muscle layer. Wash away and hair or debris with PBS.

4. Cut through the ventral midline carefully and dissect away the abdominal muscle layer to expose the viscera.

5. Displace the viscera to expose the inferior vena cava and the portal vein.

6. Using curved forceps, place a ligature (2–0 silk works well) around the vena cava just posterior to the renal veins. Tie it loosely (one throw), but do not knot it at this point.



7. Insert catheter (22g x 1" IV type) into the vena cava approximately 3–5mm distal to the ligature. Remove the stylet and advance the catheter so that the tip is anterior to the renal veins. Gently tighten and knot the ligature. Connect the infusion tubing to the catheter and start the infusion pump at low speed (approx. 2ml/min).

8. Sever the portal vein and immediately increase pump flow rate to approx. 7ml/min. The abdomen will quickly fill with blood, which should be washed out with PBS to prevent an obscured view.

9. The liver should change from dark red–brown to a uniform light tan color as the blood is flushed out.

Perfusion digestion:

1. Tape the infusion tubing in place on the platform so that its weight or movement will not dislodge the catheter.

2. Cover the abdomen with 2 layers of gauze moistened with PBS to prevent drying, and place desk lamp bulb 5–6 inches from mouse to keep area warm.

3. Perfuse the liver with 0.05% collagenase (Type IV; Sigma) at 5 ml/min for ~ 5 min.

4. When perfusion is completed, remove the catheter and carefully excise the liver.

Provide the time within the experimental plan that the terminal surgical procedure will occur:
Mice between the ages of 5-8 weeks will directly undergo the terminal surgical procedure.

Select all that will be used to monitor anesthetic depth:

☑ **Physical Reflexes [Monitoring will occur at least every 15 minutes]: Withdrawal from Toe Pinch, Palpebral Reflex, Jaw Tone**

☐ Mucous Membrane Color [Monitoring will occur at least every 15 minutes]

☐ Respiration Rate/Pattern [Monitoring will occur at least every 15 minutes]

☐ Heart Rate [Monitoring will occur at least every 15 minutes]

☐ Body Temperature [Monitoring will occur at least every 15 minutes]

Intra-procedural thermal regulatory support (select all that apply):

☑ **Heat Pad**

☐ Heat Lamp

☐ Bair Hugger

☐ Warm IV Fluids

☐ Warm Blankets

☐ Other (specify)

Provide the location(s) where the surgical procedure will occur:

Building	Room
Guggenheim Building	RO-GU-20-21A

Other Procedure

Name of Procedure:
In vivo lipolysis assay

Will anesthesia be used for these procedures? Yes

If yes, induction agent(s) used:

	Agent	Dose (mg/kg or mg/kg/hr)	Route
View	Isoflurane-vaporizer	2.5%	Inhalation

If yes, maintenance agent(s) used:

Agent	Dose (mg/kg or mg/kg/hr)	Route	Frequency	Time

	Agent		Dose (mg/kg or mg/kg/hr)	Route	Frequency	Time
View	Other (specify)	No maintenance dose	0	Inhalation	Mice will be anesthetized every 30 min (total 4 times) for blood collection	Once the mice reach the surgical plane, the anesthesia is removed so that blood can be collected from the retro-orbital venous plexus.

If yes, personnel performing anesthesia *(The following name(s) are generated from the Personnel Information page. Select all names that apply)*:

Member
Yongbin Chen
Scott Johnson
Zhenglong Liu
Jun Liu

Will paralytics be used for these procedures? No

If yes, paralytic agent(s) used:

Agent	Dose (mg/kg)	Route	Frequency
There are no items to display			

If yes, explain how it will be determined that the paralyzed animal is adequately anesthetized:

If yes, provide rationale for the use of a paralytic:

Analgesic agent(s) used:

Agent	Dose (mg/kg or mg/kg/hr)	Route	Frequency	Duration
There are no items to display				

Describe Procedure:

After a 4 hour fast, mice will be weighed and anesthetized with isoflurane. 50 ul of baseline blood samples will be collected from the right retro-orbital venous plexus. Mice will then be injected intraperitoneally with CL 316,243 (0.1 mg/kg body weight). CL 316,243 is a beta-3-andrenoceptor agonist, which stimulates adipose lipolysis. At 30, 60, and 120 minutes post injection, blood samples will be collected from the alternating retro-orbital venous plexus following isoflurane-induced anesthesia. Plasma will be harvested from the blood samples and used to quantify glycerol and free fatty acids by enzymatic assays. This procedure will be performed in a rodent procedure room on the 20th floor of Guggenheim building.

Induction Information

Induction:
Isoflurane-vaporizer

Dose (mg/kg or mg/kg/hr):
2.5%

Route:
Inhalation

Maintenance Information

Maintenance:
Other (specify)

Other:
No maintenance dose

Dose (mg/kg or mg/kg/hr):
0

Route:
Inhalation

Frequency of Administration:
Mice will be anesthetized every 30 min (total 4 times) for blood collection

Length of time anesthesia session is anticipated to last:

Once the mice reach the surgical plane, the anesthesia is removed so that blood can be collected from the retro-orbital venous plexus.

Other Procedure

Name of Procedure:
Triglyceride secretion

Will anesthesia be used for these procedures? Yes

If yes, induction agent(s) used:

	Agent	Dose (mg/kg or mg/kg/hr)	Route
View	Isoflurane-vaporizer	2.5%	Inhalation

If yes, maintenance agent(s) used:

	Agent		Dose (mg/kg or mg/kg/hr)	Route	Frequency	Time
View	Other (specify)	No maintenance dose	0	Inhalation	Mice will be anesthetized every 30 min (total 4 times) for blood collection	Once the mice reach the surgical plane, the anesthesia is removed so that blood can be collected from the retro-orbital venous plexus.

If yes, personnel performing anesthesia *(The following name(s) are generated from the Personnel Information page. Select all names that apply)*:

Member
Yongbin Chen
Scott Johnson
Zhenglong Liu
Jun Liu

Will paralytics be used for these procedures? No

If yes, paralytic agent(s) used:

Agent	Dose (mg/kg)	Route	Frequency
There are no items to display			

If yes, explain how it will be determined that the paralyzed animal is adequately anesthetized:

If yes, provide rationale for the use of a paralytic:

Analgesic agent(s) used:

Agent	Dose (mg/kg or mg/kg/hr)	Route	Frequency	Duration
There are no items to display				

Describe Procedure:

Mice will be switched to a fat-free/62% sucrose diet (Harlan TD.03314) to eliminate triglyceride ingestion for 5-6 hours. Mice will be weighed and 50ul of baseline blood will be collected from the left retro-orbital venous plexus. Then 25% Tyloxapol (Fitzgerald 51R-U704003, 100ul/30g body weight) will be injected in the tail vein to provide mice with a final concentration of 500mg/kg body weight. 50ul of blood samples will be collected at 30, 60, and 120 minutes post-injection. Plasma will be harvested from the blood samples and used to quantify TG mass by enzymatic assays. At the conclusion of the procedure, mice will be euthanized and various tissue samples will be collected for biochemical and histological analyses. This procedure will be performed in a rodent procedure room on the 20th floor of Guggenheim building.

Induction Information

Induction:
Isoflurane-vaporizer

Dose (mg/kg or mg/kg/hr):
2.5%

Route:
Inhalation

Maintenance Information

Maintenance: Other (specify)	Other: No maintenance dose

Dose (mg/kg or mg/kg/hr):
0

Route:
Inhalation

Frequency of Administration:
Mice will be anesthetized every 30 min (total 4 times) for blood collection

Length of time anesthesia session is anticipated to last:
Once the mice reach the surgical plane, the anesthesia is removed so that blood can be collected from the retro-orbital venous plexus.

Biosafety

Agent/Organism: Other (specify) Recombinant adenovirus

Biosafety Level:BSL2

Select all administration routes to be used:
Retroorbital Sinus

Are cells first transduced by or exposed to this biological material *in vitro* and then implanted, engrafted, or otherwise introduced into an animal subject?

Provide cell name, type, and/or description of cells used with this biological material" *NOTE: no new cell lines should be in this section if they haven't been listed in the previous tumor section.*

What dose will be administered?
1 X 10^9 to 1X10^10 plaque-forming units (pfu)

What volume will be administered?
200ul

What vehicle will be used for administration?
PBS

What is the frequency of administration?
Once 6-7 days post injection for long term cold exposure, other experiments will receive only one dose.

What is the duration of administration?
<30 seconds

Location where animals are exposed/injected with agents:

RO-GU-20-08B

Location where animals are housed after exposure:

RO-GU-20-08E Migrated: Post adenoviral administration, animals will be housed in a designated BSL-2 areas.

NOTE:

1. Animals classified as BSL 2 or higher must be housed in Guggenheim 2008 (Rochester), Griffin Building Biohazard Room (Florida), or SJC Building Biohazard Room (Arizona)
2. Animals classified as BSL2, BSL2+, or BSL3 will remain classified as such until death or exception by IBC

Is this agent infectious to other animals? ○ Yes ● No

Communication with the Department of Comparative Medicine is required to establish guidelines for animal housing.

Is this Biosafety protocol already approved by Biosafety? ● Yes ○ No

If so, provide the Biosafety or HazID Registration Number(s):

Euthanasia - Chemical Method

Agent:
Carbon Dioxide

Route:
Inhalation

Will animal be anesthetized? ○ Yes ● **No**

Group(s)/Animals euthanized by this method:
Mice to be euthanized utilizing this method are litter mates not used in a study, old breeders, and mice that have reached humane endpoints.

Secondary method to confirm euthanasia:
Cervical Dislocation

Euthanasia - Physical Method

Method:
Cervical Dislocation

Will animal be anesthetized? ● **Yes** ○ No

* Anesthesia animal will be under for euthanasia method:

Agent	Dose (mg/kg or mg/kg/hr)	Route
Isoflurane-vaporizer	1.5-2.5%	Inhalation

* **Group(s)/Animals euthanized by this method:**
All study mice, with the exception of mice receiving liver perfusion. Total:1410 mice

Euthanasia - Physical Method

Method:
Exsanguination

Will animal be anesthetized? ● **Yes** ○ No

* Anesthesia animal will be under for euthanasia method:

Agent	Dose (mg/kg or mg/kg/hr)	Route
Isoflurane-vaporizer	1.5-2.5%	Inhalation

* **Group(s)/Animals euthanized by this method:**
WT, aP2-G0S2, LXRa -/- male and female (6 groups total), 10 mice/group. Total: 60 mice