BUILDING THE HUMAN ARGONAUTE 2 INTERACTION NETWORK

APPROVED BY SUPERVISORY COMMITTEE

David R. Corey, Ph.D., Advisor

Carole R. Mendelson, Ph.D., Chairman

Qinghua Liu, Ph.D.

Eric N. Olson, Ph.D.

Hongtao Yu, Ph.D.

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BUILDING THE HUMAN ARGONAUTE 2 INTERACTION NETWORK

by

Roya Kalantari

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BUILDING THE HUMAN ARGONAUTE 2 INTERACTION NETWORK

Roya Kalantari, Ph.D.

The University of Texas Southwestern Medical Center at Dallas, 2015

Supervising Professor: David R. Corey, Ph.D.

RNA interference (RNAi) is a system that has been largely studied and defined by its ability to affect gene expression and translation in the cytoplasm. However, Argonaute (AGO) proteins, which are the major catalytic component of the RNA-induced silencing complex (RISC), have been found to be involved in nuclear roles outside of the canonical RNAi pathway. Within non-mammalian systems such as yeast and plants, AGOs have been shown to be involved in functions such as DNA methylation and heterochromatin formation.

My laboratory has utilized systems involving small RNAs to target nuclear events such as transcription and splicing in human cells. In the case of transcription, we have shown that small RNAs are capable of targeting long noncoding RNAs (lncRNAs) along both the promoter and past the 3' end of genes in order to control gene expression. We have also demonstrated that targeting of small RNAs to introns and exons of pre-mRNA can robustly alter the splicing pattern. Within these systems, we have found that AGO proteins are recruited by the small

RNAs to the nuclear target. However, the protein-protein interactions and mechanisms involved remain unclear.

Identification and understanding of the interactions of AGO proteins in the nucleus is essential for comprehension of the mechanisms by which these proteins act. I have studied AGO2 interactions through immunoprecipitation and a novel semi-quantitative mass spectrometry technique known as the Normalized Spectral Index Method (SINQ). Stringent screening of mass spectrometry results identified interactions with the TRNC6 proteins, and AGO3. Most cytoplasmic interacting partners were also partners for AGO2 in the nucleus, however interactions with the loading complex was impaired although it is present in nuclei. These data demonstrate that the core RNAi machinery is largely conserved between cytoplasm and nucleus. This work opens new avenues for the utilization of small RNAs in gene regulation both in the laboratory and in the clinic.

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LIST OF ABBREVIATIONS

AGO	argonaute
ARC	AGO siRNA chaperone
CLRC	Clr4–Rik1–Cul4 Complex
ER	endoplasmic reticulum
HA	hemagglutinin
IP	immunoprecipitation
miRNA	microRNA
mRNA	messenger RNA
P-body	processing body
PCR	polymerase chain reaction
PNA	peptide nucleic acid
PR	progesterone receptor
RACE	rapid amplification of cDNA ends
RDRC	RNA directed RNA polymerase complex
RdRP	RNA-dependent RNA polymerase
RISC	RNA induced silencing complex
RITS	RNA induced transcriptional silencing
RNA	ribonucleic acid
RNAi	RNA interference
RNAseq	RNA sequencing
SINQ	normalized spectral index quantitation
siRNA	small interfering RNA
ss-siRNA	single-stranded silencing RNA

Chapter 1: Historical Background and Significance

1.1 Introduction

RNA interference (RNAi) is widely recognized as a powerful mechanism for using small RNAs to control protein translation in the cytoplasm of mammalian cells (Ipsaro and Joshua-Tor, 2015; Wilson and Doudna, 2013) (**Figure 1.1**). The small RNAs are typically duplex RNAs and consist of a guide strand complementary to the cellular RNA target sequence and a passenger strand. During RNAi the guide strand RNA is loaded into a RNA induced silencing complex (RISC) consisting of protein factors including Argonaute 2 (AGO2) (Liu et al., 2004; Meister et al., 2004; Rand et al., 2004) and TRNC6A (Eulalio et al., 2008; Jakymiw et al., 2005). The guide strand can be supplied within a synthetic RNA duplex (Elbashir et al., 2001), as a chemically stabilized single-strand (Lima et al., 2012), or can be naturally expressed within a cell as microRNA (miRNA) (Ha and Kim, 2014; Hammond, 2015).

The guide strand RNA directs the complex to target sequences through Watson-Crick base-pairing (Ui-Tei et al., 2012). Recognition by Watson-Crick pairing is predictable and many different guide strands can participate in ribonucleoprotein complex formation. These features make RISC programmable - depending on the sequence of the guide strand RNA, many different cellular RNA sequences can be targeted.

The protein domains of RISC serve multiple functions. Single-stranded RNA is labile to digestion by nucleases and its interaction with proteins helps ensure its survival. The guide RNA binds directly to Argonaute 2 protein (Elkayam et al., 2012; Martinez et al., 2002; Schirle and MacRae, 2012). The orientation of binding displays the RNA seed sequence in an ideal position to nucleate binding to target RNA. When the central portion of the guide RNA is fully complementary to its target, AGO2 can cleave the target RNA (Liu et al., 2004). Binding by AGO2 masks the negative charge of the RNA backbone, facilitating recognition of

complementary RNA and accelerating searching and identification of complementary sequences (Elkayam et al., 2012; Schirle and MacRae, 2012).

In mammalian cell cytoplasm, naturally occurring microRNAs recognize sequences with 3'-untranslated regions to control translation (Stark et al., 2005) (**Figure 1.1**). Synthetic duplex RNAs that are fully complementary to targets within mRNA are widely used tools for reducing gene expression in the laboratory (Elbashir et al., 2001). Over a decade of experience with natural and synthetic RNAs has demonstrated the formidable power of RNAi to drive recognition of RNA in the cytoplasm of mammalian cells. Mammalian cell nuclei, however, also contain RNA. What if similar machinery for RNAi was present in mammalian cell nuclei? What RNA species might be recognized? How might such recognition affect gene expression?

1.2 Nuclear RNAi in non-mammalian systems

The potential for RNA to induce sequence-specific changes in the nucleus of non-mammalian organisms has been recognized for over two decades and has been extensively reviewed (Castel and Martienssen, 2013; Creamer and Partridge, 2011; Holoch and Moazed, 2015; Rogers and Chen, 2013).

Nuclear RNAi was first discovered in plants and shown to induce DNA methylation of sequences at gene promoters (Wassenegger et al., 1994). In this study viroid RNA replication was necessary for methylation of integrated viral DNA sequences. Expressed small hairpin RNAs that were targeted against plant promoters also induced DNA methylation (Mette et al., 2000; Wassenegger et al., 1994). Small RNAs are loaded into AGO4 (Zilberman et al., 2003) and AGO6 (McCue et al., 2015) and both AGO variants appear to be important for silencing (Duan et al., 2015; Underwood and Martienssen, 2015). The mechanism of recognition for small RNAs involves recognition of a noncoding transcripts at gene promoters (Haag and Pikaard, 2011; Wierzbicki et al., 2008). Binding of the small RNA-AGO4 or AGO6 complex to the nascent

RNA then triggers cytosine methylation, possibly through the action of SWI/SNF mediated chromatin remodeling (Zhu et al., 2013) (**Figure 1.2A**).

In yeast, RNAi factors modulate gene expression by inducing histone modifications (Creamer and Partridge, 2011; Verdel et al., 2004) (**Figure 1.2B**). These factors, collectively known as the RNA Induced Transcriptional Silencing (RITS) complex, consist of AGO1, Chp1, and Tas3 (Wu et al., 2012). Pol II transcribes RNAs along centromeric repeats that are processed into duplex RNAs by Dicer1, or form priRNAs which work through a Dicer independent mechanism (Halic and Moazed, 2010; Reinhart and Bartel, 2002; Volpe et al., 2002). The small RNAs are then loaded onto Ago1 by the AGO siRNA chaperone (ARC) complex in the nucleus. Loaded Ago1 then binds to the other members of the RITS complex (Holoch and Moazed, 2015). Ago1 binds to nascent transcripts along centromeric repeats where it tethers the RITS complex along with the Clr4–Rik1–Cul4 (CLRC) complex (Hong et al., 2005; Horn et al., 2005; Jia et al., 2005). The CLRC is responsible for H3K9 methylation and subsequent transcriptional silencing. The methylation targets the RNA directed RNA polymerase complex (RDRC) to methylated H3K9, which forms additional siRNAs and promotes further methylation.

C. elegans also employs RNAi factors to direct H3K9 methylation (Holoch and Moazed, 2015) (**Figure 1.2C**). In C. elegans, Double stranded RNAs are processed by Dicer-1 into siRNAs (Grishok et al., 2001; Ketting et al., 2001; Knight and Bass, 2001). These RNAs are loaded into an AGO protein RDE-1 which work with RNA-dependent RNA polymerases (RdRPs) to amplify the number of small RNAs (Gu et al., 2009). These RNAs are known as 22G-RNAs. 22G-RNAs are then loaded into the AGO protein NRDE-3. Loading takes place in the cytoplasm and the NRDE-3/small RNA complex subsequently enters the nucleus (Guang et al., 2008) and binds to nascent transcripts (Guang et al., 2010). NRDE-2, a methylation factor, binds to NRDE-3 at these sites, promotes H3K9 methylation and silences transcription along

with histone methyltransferases (Burkhart et al., 2011; Burton et al., 2011; Gu et al., 2012; Guang et al., 2010).

1.3 Mammalian nuclear RNAi

In spite of the importance of cytoplasmic RNAi in mammalian cells and the role of nuclear RNAi in model organisms, the study of mammalian nuclear RNAi has received little attention. There are several reasons why the study of mammalian nuclear RNAi has lagged behind.

Early work reported that duplex RNAs could not silence expression of introns (Vickers et al. 2003; Cullen et al., 2002). In addition, anecdotal evidence from many laboratories suggested the general silencing of nuclear RNA targets is often difficult to achieve. Microscopy showed predominant localization of AGO2 to cytoplasmic P-bodies and the endoplasmic reticulum, supporting a cytoplasmic role (Ikeda et al., 2006; Stalder et al., 2013). A practical complication is that purifying protein or RNA from cell nuclei in a manner that convincingly eliminates significant amounts of cytoplasmic contaminants is difficult.

In 2004 two reports appeared suggesting that duplex RNAs complementary to gene promoters could repress gene expression in mammalian cells (Kawasaki and Taira, 2004; Morris et al., 2004). These reports implicated DNA methylation and histone modification as causes for silencing. Both reports however, were subject to criticism in a subsequent paper (Ting et al., 2005) and Kawasaki et al. was retracted (Taira, 2006). Taken together, the mix of negative results and questions about published data led to skepticism about fundamental issues such as whether RNAi factors were present or active within mammalian somatic cell nuclei and whether RNAi could influence nuclear gene expression.

1.4 Evidence of RNAi factors in cell nuclei

Several reports have appeared suggesting that RNAi factors are present in mammalian cell nuclei and can be actively processing RNA. Two laboratories reported that small RNAs could silence nuclear localized 7SK RNA (Ohrt et al., 2008; Robb et al., 2005). Both Myc-tagged AGO2 (Robb et al., 2005) and EGFP-tagged AGO2 (Rudel et al., 2008) could be identified in purified cell nuclei (Robb et al., 2005).

Fluorescence correlation and fluorescence cross correlation microscopy suggested that AGO2 is loaded in the cytoplasm and subsequently imported into the nucleus (Ohrt et al., 2008). Knockdown of Importin 8 reduced the pool of nuclear AGO2 (Wei et al., 2014), suggesting a role in import. Nuclear import of AGO2 was implied by the finding that the AGO binding partner TNRC6A actively shuttles between the cytoplasm and the nucleus (Till et al., 2007). Recent work extended this finding by showing that TNRC6A could interact with AGO2 to facilitate the delivery of micro RNAs to cell nuclei.

A significant portion of AGO2 is localized to the endoplasmic reticulum (ER) (Stalder et al., 2013). Since the ER is contiguous with the nuclear membrane and can copurify with nuclei, it was possible that detection of AGO2 might have been due to ER contamination. In addition, nuclear RNAs may be found in the cytoplasm, in which case standard cytoplasmic RNAi might cause cleavage and the subsequent transit of the fragments into the nucleus might result in confounding conclusions. To address these potential concerns, they examined localization by microscopy, gel chromatography, size exclusion chromatography, and activity assays (Gagnon et al., 2014a).

Wide-field immunofluorescence microscopy with high sensitivity 3-D imaging revealed AGO2 in both cell cytoplasm and nuclei. My laboratory developed a stringent protocol for purifying nuclei that removed detectable ER contamination. Using this protocol, they evaluated localization by Western blot of nuclear proteins and observed AGO2, Dicer, TRBP, and

TNRC6A in cell nuclei. They also examined the potential for AGO2-mediated slicer activity in cell nuclei and observed cleavage of RNA substrates in nuclear extracts of RNA duplexes transfected into cells prior to the activity assays. Duplex RNAs could knock down the nuclear localized RNA MALAT1 and eliminate MALAT1 foci. 5'-RACE fragments that were diagnostic of MALAT-1 cleavage at a predicted RNAi target site were found associated with the chromatin fraction.

When RNA substrate and duplex RNA were added directly to cell extract they did not observe cleavage of the RNA substrate. This result is explained by finding that the RNA loading factors Trax and Translin are cytoplasmic proteins that cannot be detected in cell nuclei. Thus, loading takes place in the cytoplasm prior to import into cell nuclei, as previously suggested (Ohrt et al., 2008).

1.5 RNA-mediated transcriptional silencing

As noted above, in 2004 two reports appeared suggesting that duplex RNAs that were complementary to mammalian gene promoters could cause DNA methylation and silence gene expression (Kawasaki and Taira, 2004; Morris et al., 2004). While one paper was subsequently retracted (Taira, 2006), these results focused attention on the potential for duplex RNA to act in cell nuclei. The duplexes used in these studies were standard siRNAs, implying that RNAi factors might be involved.

My laboratory had been studying the ability of peptide nucleic acid oligomers (PNAs) complementary to the progesterone receptor (PR) promoter to inhibit expression of chromosomally encoded PR expression (Janowski et al., 2005b). Because of their experience using PR as a model system they evaluated the effect of transfecting duplex RNAs complementary to sequences at the most upstream transcription start site.

Their initial experiments revealed silencing of PR expression (Janowski et al., 2005a). Silencing was efficient and easily reproducible. PR is a TATA-less promoter with many transcription start sites and they confirmed the identity and that the RNAs were not targeting PR mRNA using 5'-RACE and quantitative PCR. Control experiments using mismatched or scrambled RNAs demonstrated that seed sequence complementarity was necessary for silencing. Nuclear run-on assays showed decreased RNA synthesis and chromatin immunoprecipitation revealed reduced recruitment of RNA polymerase 2, both results consistent with inhibition of gene transcription. They did not observe changes in DNA methylation at the PR promoter.

1.6 RNA mediated transcriptional activation

Some protein transcription factors are known to be associated with gene inhibition in one context and gene activation in another (Gow et al., 2014; Kamachi and Kondoh, 2013; Lee and Chiang, 2009; Mao and Byers, 2011; Schlereth et al., 2013; Shi et al., 1997; Stonestrom et al., 2015; Weth and Renkawitz, 2011; Yoshida et al., 2014). While testing a series of related duplex RNAs targeting adjacent sequences at the PR promoter they repeatedly observed that some RNAs produced a small increase in RNA and protein expression in T47D cells. It was reasoned that this small level of activation might be mediated by RNA and that activation might be more distinct in a cell line with a low basal level of PR expression.

To test this hypothesis, duplex RNAs were transfected into MCF7 breast cancer cells, a cell line with low basal expression of PR. They identified several duplex RNAs capable of activating gene transcription up to level similar to levels observed in T47D cells (Janowski et al., 2007). As had been observed for gene silencing, activation by promoter targeted RNAs was potent, reproducible, and required complementarity to sequences within the PR promoter. Addition of activating RNAs increased recruitment of RNA polymerase 2, pre-mRNA levels, and

mRNA levels, consistent with increased transcription. My laboratory subsequently observed that promoter-targeted duplex RNAs could activate the expression of other genes including LDL receptor (Matsui et al., 2010) and cyclooxygenase 2 (Matsui et al., 2013).

RNA-mediated activation has also been reported by other laboratories. The first study by Dahiya tested the ability of small RNAs to activate three different genes, E-cadherin, p21, and VEGF (Li et al., 2006). They targeted small RNAs to the promoters of each of these genes and saw upregulation of all three in multiple cell lines at both the RNA and protein level. They found that this mechanism was dependent on AGO2 and was associated with loss of H3K9 methylation. Later studies supported this work in multiple human cell line systems (Junxia et al., 2010; Mao et al., 2008; Mao et al., 2010; Yang et al., 2008) Their group went on to find small RNAs that activated p53, PAR4, WT1, and NKX3 (Huang et al., 2010). This study, along with others found that activating small RNAs were not only found in humans, but in other mammals as well (Turunen et al., 2009).

1.7 RNAi factors are involved in transcriptional silencing and activation

The RNAs used to achieve transcriptional silencing or activation are duplex RNAs, identical in structure to those used for standard post-transcriptional RNA interference (Elbashir et al., 2001). The similarity between the RNA triggers for transcriptional silencing, transcriptional activation, and post-transcriptional silencing, coupled with the presence of RNAi factors in cell nuclei, suggests that transcriptional modulation may also involve RNAi factors.

There are four AGO proteins in mammalian cells (AGO1-4) (Meister, 2013). AGO2 is the central RNA factor involved in post-transcriptional RNA silencing and is the only AGO variant capable of catalytic cleavage of RNA substrates (Liu et al., 2004; Meister et al., 2004; Rand et al., 2004). Roles for AGO1, AGO3 and AGO4 are not as well defined but they can bind to RNA

and AGO1 and AGO3 can participate in gene silencing by RNAs targeted to 3'-untranslated regions in the absence of AGO2 (Ruda et al., 2014).

Because of the central role of AGO in post-transcriptional silencing, my laboratory tested involvement of AGO1-4 in transcriptional silencing and activation. They observed that silencing expression of AGO2 reversed transcriptional silencing (**Figure 1.3**) and transcriptional activation (Chu et al., 2010; Grishok et al., 2001; Janowski et al., 2006; Janowski et al., 2007; Matsui et al., 2010). They also observed that silencing expression of TNRC6 proteins also blocked transcriptional activation (Matsui et al., 2013). Other laboratories have observed that AGO1 is critical for transcriptional silencing (Kim et al., 2006). These results implicate RNAi factors in RNA-mediated control of transcription.

TNRC6A is an RNA binding protein and the mammalian homolog of the yeast protein GW182. TNRC6A associates with AGO (Pfaff and Meister, 2013) and with cytoplasmic p-bodies (Liu et al., 2005). Like AGO, TNRC6A has often been assumed to be localized to cell cytoplasm although it possesses a nuclear localization signal and can be visualized in cell nuclei by microscopy (Nishi et al., 2013). TNRC6A has two paralogs in human cells, TNRC6B and TNRC6C. My laboratory has observed that silencing all three paralogs reversed transcriptional activation of COX-2 (Matsui et al., 2013).

1.8 Nascent RNA transcripts are targets for modulatory RNAs

Unlike the duplex RNAs involved in post-transcriptional silencing, the RNAs involved in modulating transcription are not complementary to mRNA. How can duplex RNAs and RNAi factors affect gene expression if they cannot recognize mRNA? One possibility would be that the duplex RNAs bind directly to chromosomal DNA. However, because RNAi factors are involved it was more likely that the mechanism would involve RNA.

Large scale studies of cellular transcription have revealed that much of the genome is transcribed and that transcripts that overlap the 3' or 5' termini of genes are common. These overlapping transcripts provide potential RNA targets for recognition that go beyond mRNA. For PR (Schwartz et al., 2008), COX-2 (Matsui et al., 2013), and LDLR (Matsui et al., 2010), my laboratory identified expressed RNAs that overlap gene promoters and are complementary to duplex RNAs that modulate transcription.

Several lines of evidence support involvement of these RNAs in transcriptional regulation. Upon addition of duplex RNA complementary to gene promoters, RNA immunoprecipitation using anti-AGO2 antibody revealed that AGO2 is recruited to promoter transcripts. Addition of an antisense oligonucleotide designed to induce RNase H mediated cleavage of the promoter transcript causes reversal of RNA-mediated gene activation.

When a duplex RNA is added to cells it forms a complex with AGO2, GW182, and possibly other factors. This RNA-protein complex binds to a nascent transcript in proximity to the promoter. Activation or silencing does not require that the RNA-protein complex bind at a single site. For all model genes my laboratory discovered more than one RNA that was capable of modulating gene expression. This finding suggests that there is no stringent requirement for where binding must occur - multiple sites are adequate.

They also noted that moving the binding site for an RNA just one or two bases would abolish activation or silencing. This sensitivity to slight changes in target site had been previously noted for antisense oligonucleotides that modulate gene splicing. One explanation is that the inactive RNAs are not binding. A second explanation is that they are binding but that they are not in an orientation that affects gene expression. When inactive RNA was added during an initial transfection, followed by an active RNA in a second transfection, it was found that the RNA capable of activating expression was ineffective. Apparently, inactive RNAs can

bind and block activating RNAs. This finding suggests that the exact orientation of binding is critical for RNA-mediate control of transcription.

Upon binding AGO2 has the potential to cleave target transcripts and it is possible that cleavage of a nascent transcript might directly trigger transcriptional change. To test this hypothesis my laboratory compared a fully complementary duplex RNA targeting the COX-2 promoter with a duplex RNA with central mismatches relative to the target site. Central mismatches disrupt the ability of AGO2 to cleave substrate without affecting the ability to bind target sequences. They observed that gene activation by the mismatch-containing duplex RNA was as effective as activation by the fully complementary RNA. This finding suggests that binding to nascent transcription is the trigger for activation, not cleavage of transcript. Consistent with this result, addition of a gapmer antisense oligonucleotide that causes RNase H-mediated cleavage of the nascent transcript does not cause gene activation. Instead the opposite is true, addition of gapmer decreases COX-2 expression. This supports the hypothesis that the transcript is needed for a low level of basal activation by an endogenous miRNA.

1.9 Modulation occurs in *cis* relative to the target gene locus

In the one case where nascent RNA levels have been measured on a per cell basis, one or two copies were detected per cell (Dodd et al., 2013). This low number suggests that the RNA is involved in *cis* relative to the target gene rather than in *trans*. Consistent with an in *cis* effect, overexpression of a promoter transcript from a plasmid has no effect on expression of the parent gene. Taken together, these data suggest that specificity for recognition at a single gene by duplex RNA involves RNAi-mediated recognition of a nascent RNA transcript prior to dissociation from its chromosomal origin.

1.10 Gene looping permits RNA-mediated regulation over long distances

Chromosomal DNA can fold into three-dimensional structures in which chromosomal sites that are distant from one another in one dimension become neighbors and have the potential to be regulated by common factors. Many genes have transcripts that overlap the 3' termini of mRNA. In addition, it has been established that some genes have loops that bring their 3' and 5' regions into close proximity. It is possible therefore, that small RNAs that recognize 3' overlapping transcripts might have the potential to also regulate transcription.

To test that hypothesis my laboratory designed duplex RNAs complementary to a 3' transcript that overlapped the terminus of PR mRNA (Yue et al., 2010). They observed that duplex RNAs complementary to the 3' transcript activated PR expression in MCF7 cells and repressed PR expression in T47D cells. The result from experiments investigating mechanism paralleled results from work involving RNAs complementary to the 5' promoter transcript. Modulation was dependent on expression of AGO2 and addition of duplex RNA controlled recruitment of RNAP2 at the PR gene promoter. RNA immunoprecipitation revealed recruitment of AGO2 to the 3' transcript. Chromosome conformation capture (3C) analysis revealed that the PR gene was looped and the potential for recognition at the 3' terminus of the PR gene to influence activity at the gene promoter.

After observing RNA-mediated activation of COX-2 they noted that the nearest genomic neighbor for COX-2 was PLA2G4A (Matsui et al., 2013). PLA2G4A encodes the enzyme that makes the substrate for COX-2, but in spite of this close functional linkage there was no evidence for a link between the expression of the two genes. The two genes are 149,000 bases distant.

They examined the expression of PLA2G4A after addition of duplex RNAs complementary to the COX-2 promoter and observed an increase in PLA2G4A mRNA expression and RNAP2 recruitment. Expression was dependent on AGO2. 3C analysis revealed a physical linkage

between the COX-2 and PLA2G4A promoters, providing an explanation for how duplex RNAs that target the COX-2 promoter can exert a long distant effect on PLA2G4A that achieves coordinated regulation of the two genes (**Figure 1.4**).

1.11 miRNAs in cell nuclei

In the cytoplasm, miRNAs interact with RNAi factors to recognize sequences within the 3'-untranslated region of mRNA transcripts and control gene translation. miRNAs however, have also been observed in the nuclei of mammalian cells. Recent data have opened the possibility for miRNAs to play a role in splicing and other noncanonical functions in nuclei (Chu et al., 2015).

1.12 Modulation of transcription by miRNAs

There have been a few reports of miRNA-induced transcriptional regulation in mammalian systems. The first study found that miRNA-373 could upregulate E-cadherin and CSDC2, both of which contained complimentary sequences in their promoters (Place et al., 2008). Another study found that a miRNA encoded within the promoter of the gene POLR3D could act in *cis* to recruit AGO1 and other factors to silence POLR3D expression (Kim et al., 2008). More recently, Huang et al. found that depletion of miRNA-774 caused a downregulation of Ccnb1 (Huang et al., 2012).

My laboratory first identified miRNAs that inhibited the expression of PR (Younger and Corey, 2011). Multiple miRNA mimics were found to down regulate expression of PR. The mechanism involved AGO2 and H3K9 methylation. However, downregulation of the miRNAs themselves showed no effect on PR expression. In the study of small RNA regulation of COX-2, they found miR-589, which had two complementary sites on the COX-2 promoter (Matsui et al., 2013). miRNA mimics of miR-589 caused increased expression of COX-2. In this case

downregulation of miR-589 also showed a decrease in COX-2 expression, suggesting that miR-589 is an activating small RNA.

1.13 Activation in one context, repression in another: Lessons from transcription factors

Synthetic RNAs and miRNAs can act as either repressors or activators. The most striking example is RNA-mediated activation of progesterone receptor where closely related duplex RNAs can either repress or activate expression (Janowski and Corey, 2010; Janowski et al., 2005a; Janowski et al., 2007). How can duplex RNAs activate transcription of a gene in one context and repress in another?

The clearest parallel is with protein transcription factors, which often possess the potential to be both activators and repressors (Gow et al., 2014; Kamachi and Kondoh, 2013; Lee and Chiang, 2009; Mao and Byers, 2011; Schlereth et al., 2013; Shi et al., 1997; Stonestrom et al., 2015; Weth and Renkawitz, 2011; Yoshida et al., 2014). This ability to differentiate between activation and repression plays important roles in development, cancer progression, and viral stability.

Mechanisms for transcriptional repression range in how they affect transcription activators (**Figure 1.5**). Proteins can bind to promoter elements at sites which overlap transcriptional activators and displace them (Lee and Chiang, 2009; Shi et al., 1997) (**Figure 1.5A**). They may not only bind at the site of activators, but may directly interfere with the activity of the activators on the promoter (**Figure 1.5B**). Alternatively, they may also bind to co-repressors which in turn interfere with activator activity (**Figure 1.5C**). Within the range of repression there is also blocking of enhancers farther upstream from the promoter (Weth and Renkawitz, 2011). One example of a more unique method of repression is YY1. This protein has been seen in one case

to cause DNA bending, and thus inhibit activator binding to the promoter (Shi et al., 1997). Multiple versions of these activities have been seen to be combined at a single promoter.

The most common mechanism for activation is the recruitment of activating factors (**Figure 1.5**). The activating factors can either guide the transcription factor to the promoter (Kamachi and Kondoh, 2013; Lee and Chiang, 2009; Stonestrom et al., 2015) (**Figure 1.6A**), or binding to the particular promoter recruits the activating factors (Shi et al., 1997) (**Figure 1.6B**). Certain factors can also act as scaffolds along the promoter, on which activators and repressors can compete for binding (Yoshida et al., 2014) (**Figure 1.6C**). Transcription regulators have also been found to bind to transcription initiation factors (Shi et al., 1997). Some have even been found to interact directly with RNA polymerase proteins (Weth and Renkawitz, 2011).

Several transcriptional regulators have been found to either activate or repress depending on the cell type (Mao and Byers, 2011; Shi et al., 1997). Within the transcription factors, there are mapped regions that can be identified as activation or repression domains. In certain cases even some of these domains can act as either an activator or repressor depending on cell type (Shi et al., 1997). This is much like the ability of AGO2 and small RNAs to act as both activators as well as repressors of PR expression.

1.14 RNA-mediated modulation of alternative splicing

Alternative splicing is a classical nuclear process that leads to the production of diverse protein isoforms (Wang et al., 2008). These variants have different functions and regulation of isoform production is necessary for cell function, growth, and development. Splicing is controlled by interactions between pre-mRNA and protein splicing factors. The combination of duplex RNAs and nuclear RNAi factors have the potential to disrupt these interactions and provide another layer of regulation.

1.15 Modulating splicing by affecting histone modification

Splicing can be coupled with transcription, and the kinetics of RNA polymerase elongation has the potential to affect recruitment of splicing factors (Naftelberg et al., 2015). Kornblihtt and colleagues reported that duplex RNAs targeting intronic or exonic sequences near alternative exons can affect splicing of the exon (Allo et al., 2009). RNA-mediated alternative splicing required expression of AGO1 and was associated with increase in histone marks Lys9 dimethylation and Lys27 trimethylation at histone H3. AGO1 was subsequently reported to be associated with transcriptional enhancers and noncoding enhancer RNAs that may also affect splicing (Allo et al., 2014). AGO1 and AGO2 have also been reported to couple chromatin silencing to alternative splicing, although the role of guide RNA in this process, if any, is unclear (Ameyar-Zazoua et al., 2012). Data suggest that antisense transcripts, rather than just mRNA or pre-mRNA, may be major targets for splice-altering duplex RNAs (Batsche and Ameyar-Zazoua, 2015).

1.16 Modulating splicing by blocking sites near exon/intron junctions

Several diseases can be at least partially alleviated by modulating splicing to produce mRNAs that produce protein isoforms that are beneficial to patients. For example Duchenne muscular dystrophy (DMD) is caused by a truncation in dystrophin protein due to a premature stop codon (Arechavala-Gomeza et al., 2007). Antisense oligonucleotides that target sequences near an intron/exon junction cause the exon to be skipped, correcting the reading frame and allowing expression of a longer and partially functional protein (Aartsma-Rus et al., 2003). Oligomers that alter splicing for dystropin and SMN2 protein (the origin of spinal muscular atrophy) are currently being tested in separate clinical trials (van Deutekom et al., 2007; Voit et al., 2014).

Antisense oligonucleotides act by binding pre-mRNA and blocking association of splicing factors (Jarver et al., 2014). It was hypothesized that duplex RNAs in concert with nuclear RNAi

factors would bind to exon-intron junctions and produce similar effects on splicing (Chu et al., 2010) (**Figure 1.7**). My laboratory first analyzed the effect of duplex RNA on a classic model of splicing consisting of an engineered luciferase gene containing a b-globin intron and observed altered splicing and increased expression of active luciferase. They subsequently observed that duplex RNAs could also modulate splicing of dystrophin and SMN2. Single-stranded silencing RNAs (ss-siRNAs) are chemically modified single stranded oligomers that can act through the RNAi pathway and silence gene expression in cells and animals (Lima et al., 2012; Yu et al., 2011). They observed that ss-siRNAs are also able to modulate splicing (Liu et al., 2015). Modulation of splicing by both ss-siRNAs and duplex RNAs is dependent on expression of AGO2 and AGO2 is recruited to splice junctions upon introduction of complementary RNA into cells.

The mechanism for alteration of splicing by RNAs targeting exon/intron junctions is simple, direct, and follows the precedent studies using antisense oligonucleotides to modulate splicing. Given the presence of RNAi factors and miRNAs in human cells, it seems possible that RNAi may play a role in regulating the splicing of endogenous genes. RNA-regulated splicing of endogenous genes has not been reported to date, but RNA sequencing of AGO2 bound species in human cell nuclei has revealed many potential binding sites near exon/intron boundaries (Chu et al., 2015), suggesting that nuclear AGO may have a role in alternative splicing.

1.17 Conclusions

Both miRNAs and RNAi factors exist in mammalian cell nuclei. miRNAs and RNAi factors combine to recognize mRNA sequences in the cytoplasm and control translation. RNA regulation of nuclear processes has been less well-studied and the full impact of RNA on nuclear regulation is not known. However, some progress towards understanding the functions and limitations of nuclear RNAi has been made in the last decade. We now know that RNAi

factors are present and active in cell nuclei. These factors are capable of silencing nuclear RNAs, but are able to be loaded in the cytoplasm. This reveals a regulatory mechanism at the loading step, which has the potential to reveal more about how and why nuclear RNAi is regulated in the way it is. AGO proteins are also capable of regulating nuclear processes including transcription and splicing. This ability opens up new avenues for small RNA targeting, and broadens the possibility of endogenous RNAi's impact on gene expression from translation to transcription and beyond.

1.18 Hypothesis

Both miRNAs and RNAi factors exist in mammalian cell nuclei. While it is known that these factors can function in nuclei when presented with exogenous stimuli, it is still unclear what their endogenous roles are. AGO2 has been identified as a potential key player in nuclear RNAi functions. However, to date there has been no study of the binding partners of AGO2 in mammalian nuclei and how they may differ relative to AGO2 cytoplasmic partners. The focus of this dissertation is to identify the protein partners of nuclear AGO2. This can lead to a better understanding of the functions and limitations of AGO2 and other RNAi factors in the nucleus.

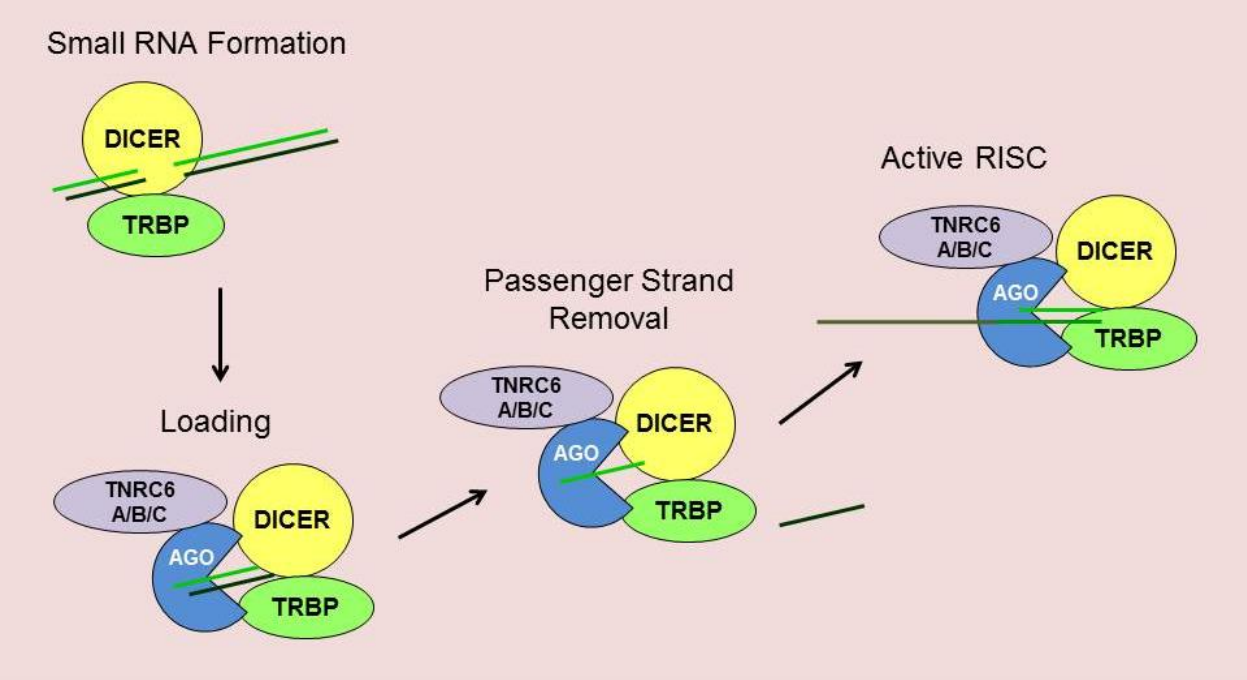


Figure 1.1 RISC loading and activation.

Double-stranded RNAs (such as pre-miRNAs) are cleaved by Dicer to form small double-stranded RNAs (such as siRNAs and miRNAs). Dicer and TRBP load the small RNAs onto AGO proteins, which are bound to TNRC6 proteins. The passenger strand of the small RNA is removed, leaving the guide strand loaded onto the AGO protein and activating the complex. The guide strand then targets the active RISC complex to the mRNA target. Naturally occurring miRNAs guide the complex to the 3'-untranslated region of the mRNA target.

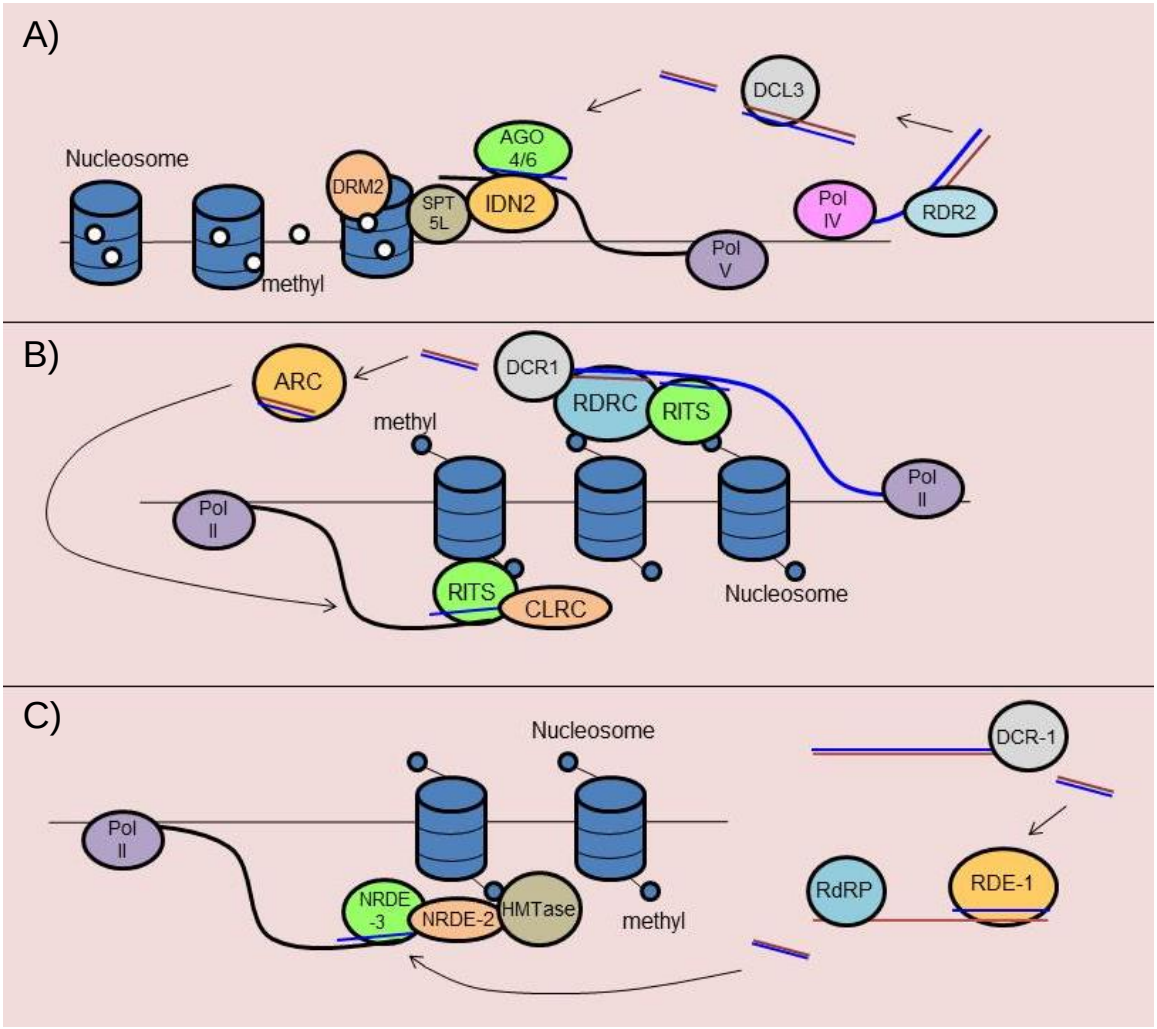


Figure 1.2 RNA interference in non-mammalian nuclei.

A) DNA methylation in plants. Pol IV transcribes long RNA which RDR2 uses as a template to form double stranded RNA. DCL3 processes this to create double-stranded small RNAs that are loaded onto AGO4 or 6. The small RNA targets AGO4/6 to nascent RNA transcribed by Pol V. The methylation factors IDN2, SPT5l, and DRM2 then localize to the site, causing methylation and silencing.

B) Histone methylation in yeast. Pol II transcribes long RNAs that are bound by the RITS complex and RDRC which uses the RNA as a template to form double stranded RNA. DCL1 processes this to create double-stranded small RNAs. The small RNAs are loaded into AGO1 in the RITS complex by the ARC complex. This targets to nascent transcripts along the chromatin The histone methylation complex CLRC then localizes to the site, causing methylation and silencing.

C) Histone methylation in worms. Double stranded RNA is processes by DCR-1 to form double-stranded small RNAs. These are loaded into RDE-1, which cause amplification of the small RNA through RdRPs. The small RNAs are then loaded onto NRDE-3, which targets to nascent transcripts along the chromatin. NRDE-2 and HMTases then localize to the site, causing methylation and silencing.

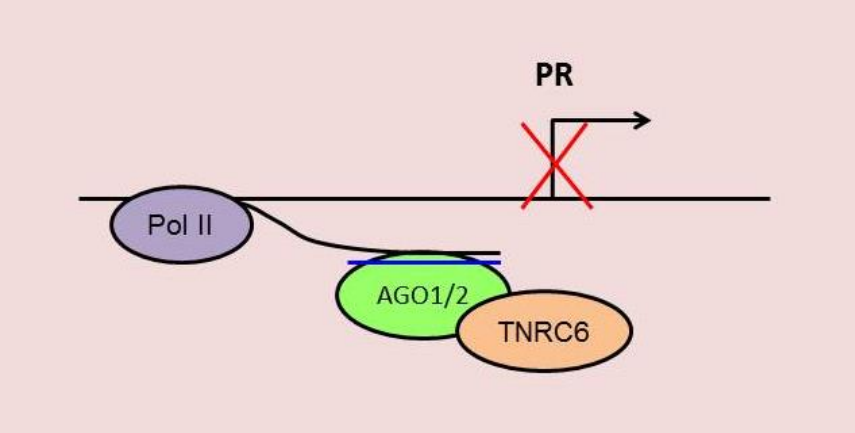


Figure 1.3 Transcriptional silencing by promoter targeted small RNAs.
Small RNAs target either AGO1 or AGO2, along with TNRC6 proteins, to nascent transcripts along the promoter of the Progesterone Receptor gene. This blocks factors required for transcriptional activation from binding, causing a decrease in transcription.

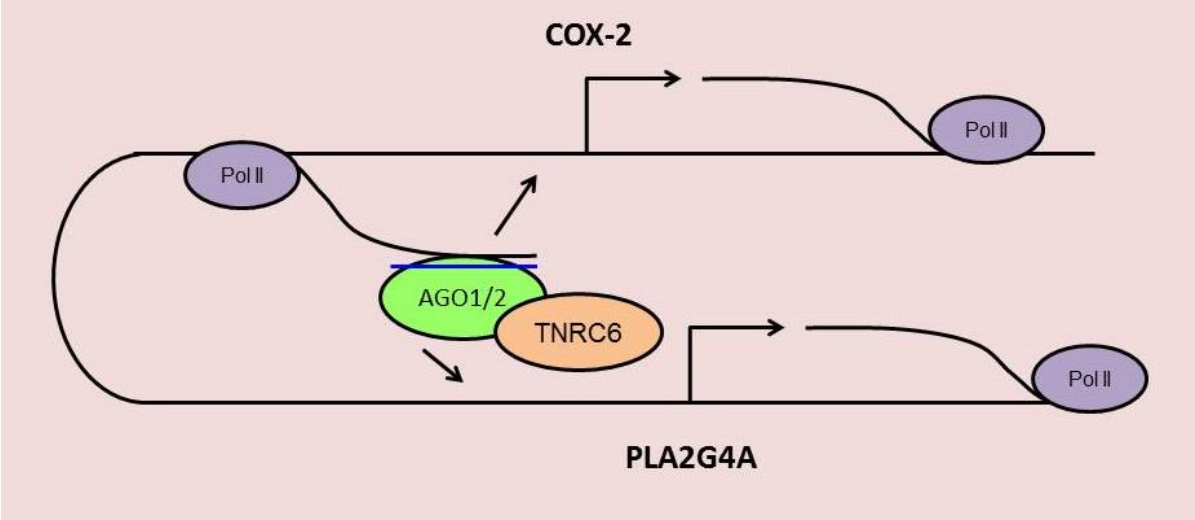


Figure 1.4 Transcriptional activation and gene looping by promoter targeted small RNAs. Small RNAs target either AGO1 or AGO2, along with TNRC6 proteins, to nascent transcripts along the promoter of the COX-2 gene. Gene looping puts the promoter of the PLA2G4A promoter in close proximity of AGO binding. This opens up the promoters to binding by transcription factors and increased transcription of both genes.

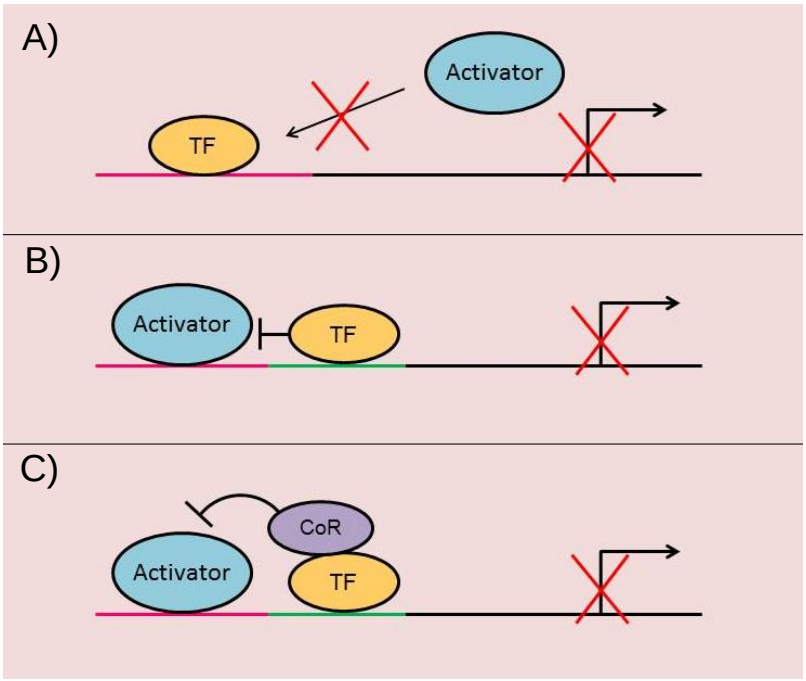


Figure 1.5 Transcription factors acting as repressors.

A) Binding site of a transcription factor (TF) overlaps the binding site of a transcriptional activator, displacing the activator and causing silencing.
B) The transcription factor inhibits the activity of a transcriptional activator, causing silencing.
C) The transcription factor recruits a co-repressor (Co-R), which then inhibits activity of a transcriptional activator, causing silencing.

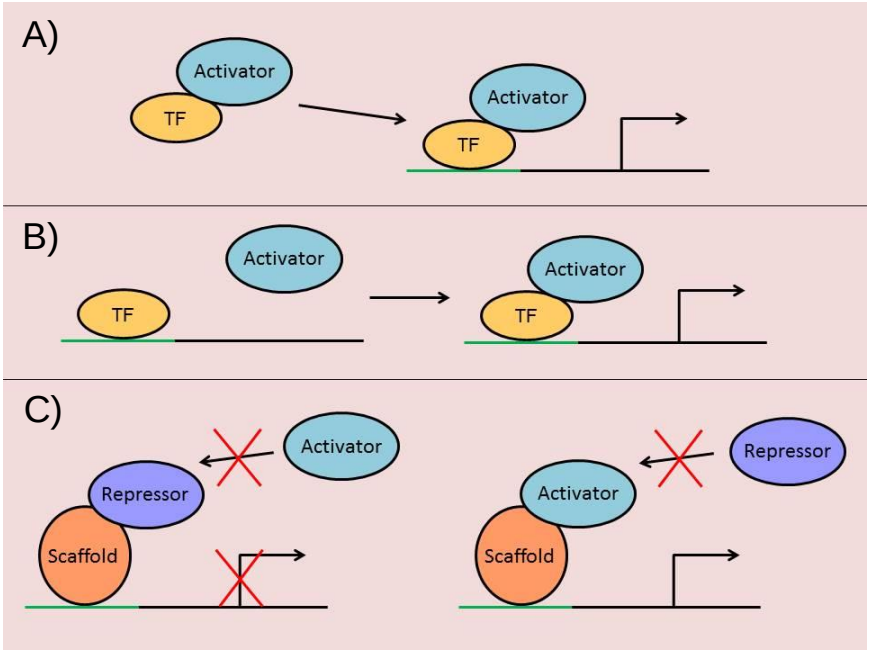


Figure 1.6 Transcriptional factors acting as activators.

A) A transcriptional activator binds to a transcription factor (TF). The transcription factor then brings the activator to a gene promoter, activating transcription.

B) A transcription factor binds to a target promoter, this binding causes the transcription factor to become available for binding by a transcriptional activator, which then activates transcription.

C) Scaffold proteins bind to a gene promoter. Repressors and activators compete for binding. Once an activator is bound it displaces the repressor and activates transcription.

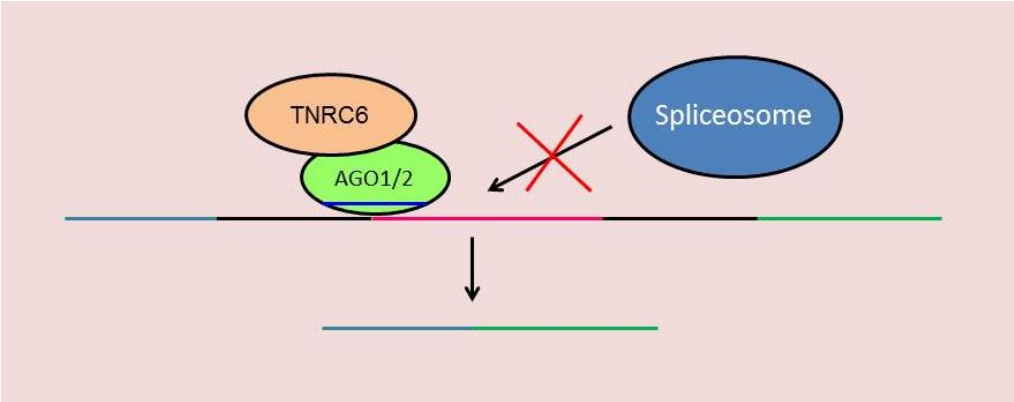


Figure 1.7 Alternative splicing regulation by small RNAs.
Small RNAs target AGO1 or AGO2, along with TNRC6 proteins, to an exon/intron junction. The binding of this complex to the junction inhibits the binding of the splicesosome, causing skipping of the exon.

Chapter 2: The Core RNAi Machinery is Conserved between the Cytoplasm and Nuclei of Human Cells

2.1 Introduction

Argonaute (AGO) proteins are key components of RNA interference (RNAi) (Meister, 2013), which bind directly to miRNAs and siRNAs to form complexes that regulate gene expression. AGO proteins are conserved and are expressed ubiquitously in animals, plants, and yeast. There are four AGO variants in human cells (AGO1-4) (Schurmann et al., 2013). AGO2 is the only AGO protein to retain catalytic activity, and when combined with a siRNA can reconstitute RNAi in defined cell free systems (Liu et al., 2004).

AGO2 is essential for post-translational silencing of mRNA in the cytoplasm of mammalian cells and many studies have focused on this cytoplasmic role. Additional factors known to be involved in cytoplasmic RNAi include TNRC6A (GW182) (Eulalio et al., 2008; Nishi et al., 2013; Pfaff and Meister, 2013), Dicer (Bernstein et al., 2001; Ha and Kim, 2014), and TAR RNA binding protein (TRBP) (Daniels and Gatignol, 2012; Takahashi et al., 2014; Wilson and Doudna, 2013). TNRC6A influences the subcellular localization of AGO2 and is critical for miRNA-guided silencing. Dicer is an endoribonuclease that is responsible for processing pre-miRNAs to form mature, double-stranded miRNAs. Dicer and TRBP bind double-stranded miRNAs and assist loading of the guide strand into AGO.

While most attention has focused on RNAi in the cytoplasm, AGO proteins are also active in the nucleus (Gagnon and Corey, 2012; Gagnon et al., 2014a; Schraivogel and Meister, 2014). AGO2 can regulate transcription (Chu et al., 2010; Matsui et al., 2013) and splicing (Ameyar-Zazoua et al., 2012; Liu et al., 2015) in human cells. While RNAi can be active in cell nuclei, there are also significant differences. Trax, Translin, and Hsp90, factors that assist guide

strand loading onto AGO2, are absent in cell nuclei and loading does not occur in nuclear extracts (Gagnon et al., 2014a).

Understanding the role of RNAi in mechanisms controlling gene expression in cell nuclei will require information about what protein-protein interactions form in nuclei and how these interactions compare with those occurring during cytoplasmic RNAi. Proteomic analysis offers a relatively unbiased strategy for identifying potential protein interacting partners. While no study has specifically examined global nuclear interactions, several studies have investigated potential interactions of AGO2 in whole cell, cytoplasm, and chromatin (Ameyar-Zazoua et al., 2012; Carissimi et al., 2015; Frohn et al., 2012; Hock et al., 2007; Landthaler et al., 2008; Meister et al., 2005; Robb and Rana, 2007; Weinmann et al., 2009).

Tuschl and co-workers examined interactions of FLAG-tagged AGO1 and AGO2 (Meister et al., 2005). They used gel electrophoresis to purify specific bands and observed interactions with TNRC6B and MOV10. In a subsequent study, Meister used cells expressing FLAG-AGO1 or FLAG-AGO2 and immunoprecipitated tagged AGO1 and AGO2 from whole cell extracts (Hock et al., 2007). This study identified a large number of candidate interacting proteins including several involved in RNA metabolism. Robb and Rana took an alternative approach using a biotinylated siRNA to isolate Ago complexes prior to mass spectrometry (Robb and Rana, 2007). Two purified bands were analyzed and the proteins RHA and HSP 90b were identified. Tuschl subsequently examined interactions of FLAG-tagged Ago1-4 in whole cell extract (Landthaler et al., 2008). This study found a wide range of interacting proteins including Dicer, YBX1, RPS6, and RPL7. Meister looked for common interacting factors of all 4 FLAG-tagged AGO proteins and identified Importin 8 (Weinmann et al., 2009). Finally, Meister's group used whole cell extract from mouse embryonic fibroblast cells and found that Ago2 can interact with RNA in the absence of miRNA (Frohn et al., 2012).

One study focused on examining proteins within chromatin. Ameryar-Zazoua focused specifically on interactions between proteins with FLAG-AGO1 and FLAG-AGO2 in chromatin extracts. They identified SRSF splicing factors as candidate interacting partners (Ameyar-Zazoua et al., 2012). Another recent study by Carissimi in whole cell extracts rather than nuclei, reported interactions between endogenous AGO2 and SWI/SNF proteins normally found in the nucleus (Carissimi et al., 2015).

These prior studies have provided important information about candidate interacting proteins, but gaps remain in our understanding of factors that interact with AGO2. One limitation is that most studies rely on detecting over expressed FLAG-tagged AGO2. While use of a tagged protein increases efficiency of many immunoprecipitations, this tag can interfere with interactions with other proteins and overexpression can lead to identification of false positives and increased background (Oeffinger, 2012). None of these previous studies compared interactions of FLAG-tagged AGO with endogenous AGO. Most studies also did not use semi-quantitative or quantitative techniques, further complicating the identification of candidates over background. Finally, none of these studies have characterized the similarities and differences of cytoplasmic and nuclear AGO2 complexes.

To identify nuclear interactions of AGO2, I performed a semi-quantitative proteomic study. I analyzed samples obtained by purifications using anti-FLAG antibody and an antibody that recognized endogenous AGO2. Using two antibodies that recognize different recognition motifs allowed me to crosscheck my results. Analyses that relied on purification of FLAG-tagged AGO2 produced many more candidate interacting proteins than purifications of endogenous AGO2 using anti-AGO2 antibody. By crosschecking candidate lists I effectively prioritized potential interacting factors.

I discovered substantial conservation between key nuclear and cytoplasmic interactions, including interactions with AGO3. The only reliably detected interactions were between AGO2

and other RNAi factors. Other novel binding partners that had been previously described to interact with AGO2 were not identified.

2.2 Prioritizing candidate interacting partners for AGO2

I used mass spectral analysis to investigate interactions of AGO2. Large-scale proteomic analysis of interaction networks often leads to long lists of candidate proteins and it is important to prioritize the candidates for experimental validation. To facilitate identification of high priority candidates, I varied key experimental parameters and compared candidate lists. My comparisons evaluate samples on three levels (**Figure 2.1A**): i) FLAG-tagged AGO2 purified using an anti-FLAG antibody versus endogenous AGO2 immunoprecipitated with an anti-AGO2 antibody; ii) Isolation from purified nuclei or cytoplasm; and iii) Samples isolated either with or without treatment with RNase.

For semi-quantitative proteomic analysis, I used the Normalized Spectral Index (SINQ) method (Griffin et al., 2010). SINQ is a label-free proteomic quantitation method. The spectral counts for each protein are normalized against protein length and peptide ionization. These values can then be used to provide ratios between sample and control for each protein (Griffin et al., 2010; Trudgian et al., 2011a). Protein candidates characterized by both high spectral counts as well as high ratios for sample versus control were identified as top candidates.

2.3 Expression and purification of FLAG-tagged and endogenous AGO2

In this study I used both FLAG-tagged AGO2 and antibodies against endogenous AGO2 in parallel experiments. The advantage of using anti-AGO2 antibody is that that it can detect endogenous AGO2 and its partners at normal levels of AGO2 expression. The disadvantage is that using anti-AGO2 antibody runs the risk of cross-reactivity with AGO1, AGO3, or AGO4 proteins. The use of FLAG-tagged AGO2 is advantageous because the interaction between the

FLAG epitope and the antibody is efficient and maximizes the potential to detect interacting factors. One disadvantage is that introducing a tag may alter the ability of AGO to interact with some proteins. A second potential disadvantage is that tagged AGO2 may not be expressed at the same level as endogenous AGO2. Identifying candidates that are pulled down after both strategies would streamline identification of candidate interaction partners for experimental validation.

I used T47D cells because my laboratory had previously observed the involvement of AGO2 when promoter targeted duplex RNAs were used to modulate gene transcription of progesterone receptor (Janowski et al., 2005a; Janowski et al., 2007). I established T47D cells that stably express FLAG-tagged AGO2 and verified expression by Western blot (Supplementary Figure X). Western analysis using anti-AGO2 antibody suggests that in FLAG-AGO2 cells, AGO2 is expressed approximately 4.7 fold overexpressed in the cytoplasm and 1.9 fold in the nucleus relative to endogenous AGO2 in T47D cells (**Figure 2.1B**). In T47D cells the levels of endogenous AGO2 are approximately 50% in the cytoplasm and 50% in the nucleus (**Figure 2.1C**). FLAG-AGO2 stable line cells have a similar distribution between the cell compartments with 67% cytoplasmic and 33% nuclear.

2.4 Purification of nuclear or cytoplasmic AGO2

The previous studies identifying AGO2 interacting partners focused on preparations from whole cells, ribosomal gradient fractions, or chromatin (Ameyar-Zazoua et al., 2012; Carissimi et al., 2015; Frohn et al., 2012; Hock et al., 2007; Landthaler et al., 2008; Meister et al., 2005; Robb and Rana, 2007; Weinmann et al., 2009). One of my goals was to analyze cytoplasmic and nuclear interactions using purified extracts from either compartment. Analysis of nuclear AGO2 requires rigorous isolation of cell nuclei. AGO2 is found in the endoplasmic reticulum (ER) contiguous with the nuclear envelope (Stalder et al., 2013) and my laboratory previously

developed protocols for separating nuclei from ER (Gagnon et al., 2014b). Coomassie staining was routinely used as a quality control check to confirm the presence of sufficient AGO2 after immunoprecipitation to enable adequate coverage for mass spectrometry (**Figure 2.1D**).

2.5 Cytoplasmic interactions of AGO2

I began my analysis by examining the interactions of FLAG-tagged AGO2 or endogenous AGO2 in isolated cytoplasmic extract from T47D cells (**Figure 2.2; Tables A1 and A2**). For initial experiments, RNase was not added so that RNA-mediated interactions remained intact. Mass spectrometry revealed potential interactions between FLAG-tagged AGO2 and proteins from several different protein families (**Figure 2.2A-C; Figure 2.3**). In contrast to results obtained after use of anti-FLAG purification, the only factors detected after immunoprecipitation of endogenous AGO2 with anti-AGO2 antibody were proteins previously reported to be RNAi factors and the cytoskeletal protein S100A8 (**Figure 2.2D-F**). Data for S100A8 was much less selective for AGO2-immunoprecipitated sample relative to control IPs.

I subsequently extended my analysis to cytoplasmic samples that had been treated with RNase. After purification using FLAG-AGO2, 40 proteins across a range of cellular functions were identified as candidate interacting partners (**Figure 2.4A-C; Table A3**). Many of these proteins possessed selectivity ratios relative to controls above 100:1. Several RNAi factors were identified, including Dicer, TNRC6A, TNRC6B, TRBP, and AGO3. In contrast to thirty candidates identified after immunoprecipitation of FLAG-Ago2, only five candidates were identified after immunoprecipitation of endogenous AGO2 (**Figure 2.4D-F; Table A4**). Of these five candidates, four were RNAi factors. These factors included Dicer, TNRC6B, Ago1, and Ago3. All of these candidates had ratios above 100:1 or were not identified in the control sample.

2.6 Nuclear interactions of AGO2

After completing analysis of cytoplasmic samples, I performed a parallel analysis to identify the interaction network of nuclear AGO2. After mass spectrometry of proteins associated with FLAG-AGO2 I identified twenty-one proteins as candidate interacting partners (**Figure 2.5A-C; Table A5**). The top candidates possessed a wide array of functions, from apoptosis to RNA processing and included the RNAi factors Dicer, TNRC6A, TNRC6B, and TNRC6C. As noted for cytoplasmic samples, use of anti-AGO2 antibody for the immunoprecipitation led to detection of fewer candidate proteins. I identified interactions with the RNAi factors AGO3, AGO1, TNRC6A, TNRC6B, and TNRC6C as well as the signal transduction protein LGALS1 (**Figures 2.5D-F; Table A6**). Identification of LGALS1 was characterized by the fewest spectral counts and the lowest ratio of sample to background.

I then examined the effect of treating nuclear samples with RNase. This treatment dramatically reduced the number of proteins after FLAG-tagged purification, with RNAi factors and the signal transduction protein PEG10 identified (**Figure 2.6A-C; Table A7**). Only RNAi factors were identified after IP with anti-AGO2 antibody (**Figure 2.6D-F; Table A8**). These candidates were all characterized by high ratios relative to control IPs (**Figure 2.6C and 2.6F**).

2.7 Evaluation of predicted binding interactions

My mass spectral analysis allowed me to prioritize candidate interacting partners for validation by co-immunoprecipitation (co-IP). In these experiments samples were immunoprecipated using anti-AGO2 antibody, separated by polyacrylamide gel electrophoresis, and analyzed by Western analysis using an antibody capable of recognizing the candidate protein. These experiments using two different immunoprecipitation strategies confirmed interactions with TNRC6A and AGO3 (**Figure 2.7A**). Consistent with MS results, TRBP was not co-immunoprecipitated with AGO2. This result supports previous findings that small RNA loading onto AGO2 does not occur in the nucleus.

A potential interaction with AGO1 was observed after immunoprecipitation with an anti-AGO2 antibody. This interaction was not observed when FLAG-AGO2 was recovered using an anti-FLAG antibody. This result suggests that the identification of AGO1 as a potential interacting partner may be an artifact from cross-reactivity with AGO variants by the anti-AGO2 antibody (**Figure 2.7B**).

The majority of the factors identified by MS that immunoprecipitated with endogenous AGO2 were RNAi factors; however potentially novel factors were also identified. LGALS1 is a protein that has known extracellular functions (Astorgues-Xerri et al., 2014) but was nonetheless identified in the nuclear MS data as the only non-RNAi candidate. It was not identified in the FLAG-AGO2 MS, and it had the lowest ratio and spectral counts of the endogenous MS data set (**Figure 2.5**). This suggests that if this interaction is biologically relevant it may be very weak. It was not copurified with AGO2 through co-IP (**Figure 2.7A**).

Several factors that did not meet the cutoff standards but were nonetheless immunoprecipitated were also considered because they possessed a plausible biological connection to nuclear RNAi. PTBP1 is a protein involved in splicing (Ghetti et al., 1992) was considered because it was close to the cutoff. However, consistent with MS results, PTBP1 did not co-immunoprecipitate with AGO2. KPNB1 is a karyopherin (Chi et al., 1995) and was considered as a potential factor involved in the nuclear import of AGO2. It was also close to the cutoff and had similar results to PTBP1. I also considered the possibility that AGO2 may be interacting with nuclear bodies involved in RNA processing as it does in the cytoplasm. PSPC1, a paraspeckle protein (Fox et al., 2002), was regularly identified at a 1:1 ratio with control in the MS data. This protein was also not found to co-immunoprecipitate with AGO2.

Several candidates identified in other studies were not identified in my MS experiments or were identified below the cutoff for consideration as a potential candidate. The protein SMARCC1 was identified in whole cell studies as a potential interacting factor of AGO2

(Carissimi et al., 2015). This protein is primarily nuclear and has functions in the SWI/SNF complex. My co-IP analysis in nuclear extract did not identify an interaction between AGO2 and SMARCC1 (**Figure 2.7**), consistent with a lack of detection in the MS data.

2.8 Nuclear RNAi

miRNAs and RNAi factors are present in mammalian somatic cell nuclei (Ohrt et al., 2012; Robb et al., 2005). In the cytoplasm miRNAs and RNAi factors regulate gene translation (Hammond, 2015). The presence of RNAi factors in the nucleus suggests they might also have the ability to regulate uniquely nuclear processes like transcription or splicing. Preliminary RNA sequencing (RNAseq) of nuclear RNAs that interact with AGO2 supports this hypothesis by showing significant read clusters near intron-exon junctions and at gene promoters (Chu et al., 2015). The potential for nuclear regulation by RNAi factors is reinforced by observations that synthetic duplex RNAs in combination with AGO1 or AGO2 can be robust regulators of transcription (Chu et al., 2010; Huang et al., 2010; Janowski et al., 2005a; Li et al., 2006; Matsui et al., 2013; Morris et al., 2004) and splicing (Allo et al., 2014; Allo et al., 2009; Liu et al., 2012; Liu et al., 2015).

Understanding the full potential for RNAi to function in cell nuclei requires a more detailed knowledge of both the RNA-protein and protein-protein interactions made by nuclear RNAi factors. To examine protein associations of RNAi factors I focused on AGO2 because it is i) a central factor for RNAi activity (Hammond et al., 2001; Joshua-Tor and Hannon, 2011; Rand et al., 2004); ii) is present in mammalian cell nuclei (Gagnon et al., 2014a; Ohrt et al., 2012; Robb et al., 2005); and iii) can modulate RNA-mediated control of transcription (Chu et al., 2010; Huang et al., 2010; Janowski et al., 2005a; Li et al., 2006; Matsui et al., 2013) and splicing (Liu et al., 2012; Liu et al., 2015). Defining the interactions of nuclear AGO2 with other proteins and

how they compare to associations in the cytoplasm is essential for understanding the implications of nuclear RNAi for controlling gene expression.

2.9 Focusing candidate identification by crosschecking datasets from different immunoprecipitation strategies

Mass spectrometry is a powerful and relatively unbiased technique for identifying protein-protein interactions. Modern methods are sensitive and can detect evidence for interactions with dozens of candidate proteins. Many of these interactions, however, can be artifactual because of the sensitivity of the mass spectrometry and it may be difficult to prioritize candidates based on raw data. Inadequate prioritization is an important obstacle, because validating protein interactions is time-consuming. A primary challenge confronting the use of mass spectrometry data, therefore, is identifying criteria to prioritize testing interactions for their physiological relevance (Trapp et al., 2014).

I adopted orthogonal approaches that allowed me to cross-check mass spectrometry data to limit the number of candidate proteins for subsequent validation. For each experimental condition, I obtained two sets of data. One dataset was obtained using FLAG-based purification of FLAG-AGO2. The other dataset was based on samples analyzed after purification of endogenous AGO2 using anti-AGO2 antibody.

Crosschecking datasets allowed me to reduce the number of likely candidates. Candidates that are common between the two strategies become be the best candidates for further validation. Candidates found after one isolation method, but not the other, would be considered to be less promising. For most conditions, FLAG purifications yielded many more candidates than did purification with an anti-AGO2 antibody. This may be because the FLAG-AGO2 protein was overexpressed relative to endogenous AGO2 or to the presence of the FLAG tag.

The evaluation of AGO1 as a candidate is an example of the advantage of incorporating crosschecking into mass spectrometry. When purifying endogenous AGO2, I consistently identified AGO1 as an interacting partner. By contrast, AGO1 was not identified as an interacting partner of FLAG-tagged AGO2. AGO2 and AGO1 have similar amino acid sequences, with 78.5% sequence homology, and it is likely that the anti-AGO2 antibody used in these studies can also recognize AGO1 at an efficiency high enough to be detected by mass spectrometry.

2.10 Core RNAi factors are conserved between nuclei and cytoplasm

In most comparisons I observed more candidate interacting factors after purification with using the FLAG-tag than immunoprecipitations with anti-AGO2 antibody (Supplementary Figure 1). The reason for this differential is that use of anti-AGO2 antibody almost exclusively led to recovery of candidates that were RNAi factors. When I compared the candidates identified after FLAG purification with candidates identified after immunoprecipitation with anti-AGO2 antibody, I identified a handful of common factors. In the cytoplasm, only six proteins, TNRC6A, TNRC6B, TNRC6C, Dicer, AGO3, and TARBP2 were found in common without RNase treatment (**Figure 2.8A**). When treated with RNase, three of the same candidates were identified in common (**Figure 2.8B**). Similar to samples that were not treated with RNase, interaction with AGO3, Dicer and TNRC6A were identified.

In the nucleus, when I combine data from the two purification strategies I identity three common interacting factors, TNRC6A, TNRC6B, and TNRC6C under non-RNase treated conditions (**Figure 2.8C**). RNase treatment of nuclear samples identified the same core RNAi factors as non-RNase, along with AGO3 (**Figure 2.8D**). These data suggest that the interactions of AGO2 within the nucleus are limited to a handful of proteins and that most interactions are not affected by treatment with TurboNuclease. The nuclear complex thus appears to be different

from the cytoplasmic complex, where interactions with Dicer and possibly TRBP being much less stable. This supports the findings that AGO loading is a cytoplasmic process (Gagnon et al., 2014a).

I also compared results from nuclear and cytoplasmic samples (**Figure 2.9**). I found that key interactions were conserved between the two compartments regardless the method of purification (anti-FLAG or anti-endogenous AGO2) or whether RNase was added. At least one TNRC6 homolog and usually all three were observed in each case. AGO3 interactions were observed in both compartments in three sets of conditions and Dicer under two conditions.

The most consistently observed interactions detected by mass spectrometry are between AGO2 and members of the TNRC6 family. TNRC6A/GW182 is a well-known partner of AGO2. It is known to stabilize the AGO2-miRNA-mRNA interactions, as well as localizing AGO2 to P-bodies in the cytoplasm (Pfaff et al., 2013; Pfaff and Meister, 2013). The three TNRC6 paralogs (A, B, and C) have some similarities - they each bind AGO2 and localize to P-bodies (Lazzaretti et al., 2009). They all share the same domain organization and have two unstructured GW-repeat regions (Ding and Han, 2007). My laboratory has previously observed that simultaneous knockdown of all three TNRC6 proteins blocked RNA-mediated control, knocking down TNRC6A alone was insufficient (Matsui et al., 2013). Ui-Tei and colleagues have suggested that TNRC6 proteins direct AGO2 shuttling between the nucleus and cytoplasm (Nishi et al., 2013). AGO2 does not possess an obvious nuclear import sequence, and the nuclear localization and export sequences within TNRC6 may be critical for guiding the complex (Nishi et al., 2013).

2.11 Evidence for other interacting factors

TRBP is a component of the loading complex of RISC. After immunoprecipitation and analysis by mass spectrometry, I found TRBP associated with AGO2 in the cytoplasm but did not detect association in nuclei. My laboratory had previously shown that TRBP was present in mammalian

cell nuclei and could be detected in complex with AGO2 (Gagnon et al., 2014). The interaction between TRBP and Ago2 is believed to be more transient than the interaction between Ago2 and Dicer (Wang et al., 2009), and it is possible that it is too transient in the nucleus to be identified by my current purification and mass spectrometry methods. The role of TRBP in RISC loading is to stabilize the Dicer/Ago interaction and aid in guide strand loading (Wang et al., 2009; Wilson et al., 2015). My laboratory has observed that loading is impaired in cell nuclei and loading factors Trax, Translin, and Hsp90 are restricted to the cytoplasm (Gagnon et al., 2014a). Because loading takes place in the cytoplasm, a strong interaction between TRBP and AGO2 may not be necessary in the nucleus.

I also evaluated other interacting candidates suggested from previous studies. Recently identified interacting partners of AGO proteins have been the HSP70/90 family proteins (Pare et al., 2013). The HSP proteins have been implicated in aiding in AGO loading. These proteins, while identified in the mass spectrometry data, consistently appeared around a 1:1 ratio with the controls for both the FLAG-tagged and endogenous IPs and therefore were not identified as stable binding partners for AGO2 in my system.

2.12 Conclusion

Mass spectrometry is a powerful tool for the study of protein interaction. Its successful application, however, is limited by challenges to efficient discrimination between high priority candidate interactions and background. Use of two orthogonal sample purification methods allowed me to cross-check results. Cross-checking reduces the number of promising candidates, cuts down on the number of false leads, and allows a better understanding of biologically relevant interactions. My isolations of AGO2 do not employ crosslinking. The interactions that are detected must be stable enough to survive multiple washings and desalting

using size exclusion chromatography. Further studies will be necessary to fully explore more transitory interactions.

By comparing data from extracts from the cytoplasm and nuclei of cells, I identified similarities and differences between the interactions of AGO2 in these compartments. In both cytoplasm and nuclei, AGO2 forms only a limited number of verified interactions with other protein factors. These limited interactions are largely conserved between cytoplasm and nucleus, supporting the hypothesis that nuclear AGO2, like cytoplasmic AGO2 will have the capacity to facilitate recognition of RNA sequences (**Figure 2.10**). In the future, expanding the proteomic studies to the factors that contact AGO2 such as TNRC6A will open the possibility of gaining further insight into how RNAi factors function in splicing and transcriptional regulation.

2.13 Improving methods for extract preparation

Our laboratory has developed several nuclear extract preparation methods (Gagnon et al., 2014b). For this project I initially used a method of extract preparation where nuclei were sonicated to break up the nuclear membrane and the chromatin. When using this method, I saw large variability among samples. Sonication can cause protein aggregates which can disrupt biologically relevant protein-protein interactions (Stathopulos et al., 2004). I therefore switched to a more mild form of extract preparation in which I used a needle to break nuclear membrane and DNase or TurboNuclease treatment to solubilize chromatin. This method reduced the amount of protein I obtained in each harvest, and removed cytoskeletal proteins such as Lamin A/C with no appreciable difference in chromatin associated factors (**Figure 2.11**).

2.14 Improving methods for large scale immunoprecipitation

Immunoprecipitations were initially performed with 3 mg of starting protein. I used a variety of mass spectral analysis to investigate interactions of AGO2. The first set of samples and

analyses were performed without quantitation. A protein score was provided which gives a small idea as to the abundance of the protein in the sample, but it is not comparable. The samples were highly variable and I was not able to determine whether the amount of protein in my samples was sufficient.

Once I switched to semi-quantitative techniques, I found that the amount of protein I was using per sample was far below the amount needed to obtain reliable data. I increased the amount of protein in each sample to ~15 mg for cytoplasmic samples and ~30 mg for nuclear samples. I used two methods to ensure that I had sufficient protein levels in my samples. I would first take a small portion of my elution and perform a Western blot for AGO2 (**Figure 2.12**). I would also Coomassie stain my samples once I had run them on an SDS-PAGE gel. If the sample did not have a visible AGO2 band I did not submit the sample for mass spectral analysis.

The 5-10-fold increase in sample size created several downstream issues. In order to elute the protein samples off the resin after immunoprecipitation, the elution volume had to be increased from 30 µL to 250 µL. This volume needed to be concentrated in order to run on an SDS-PAGE gel. The most common method of protein digestion for mass spectral analysis is digestion within SDS-PAGE gels. I used centrifugal protein concentrators to reduce the sample volume after elution. Once concentrated, the samples had high salt concentrations that affected the ability of the sample to run on SDS-PAGE gels (**Figure 2.13**). This made it impossible to cut out the samples for mass spectral analysis. An additional step was then included prior to concentration. After elution, the samples were run through desalting columns. This corrected the salt concentration and allowed the samples to be run onto the gels normally.

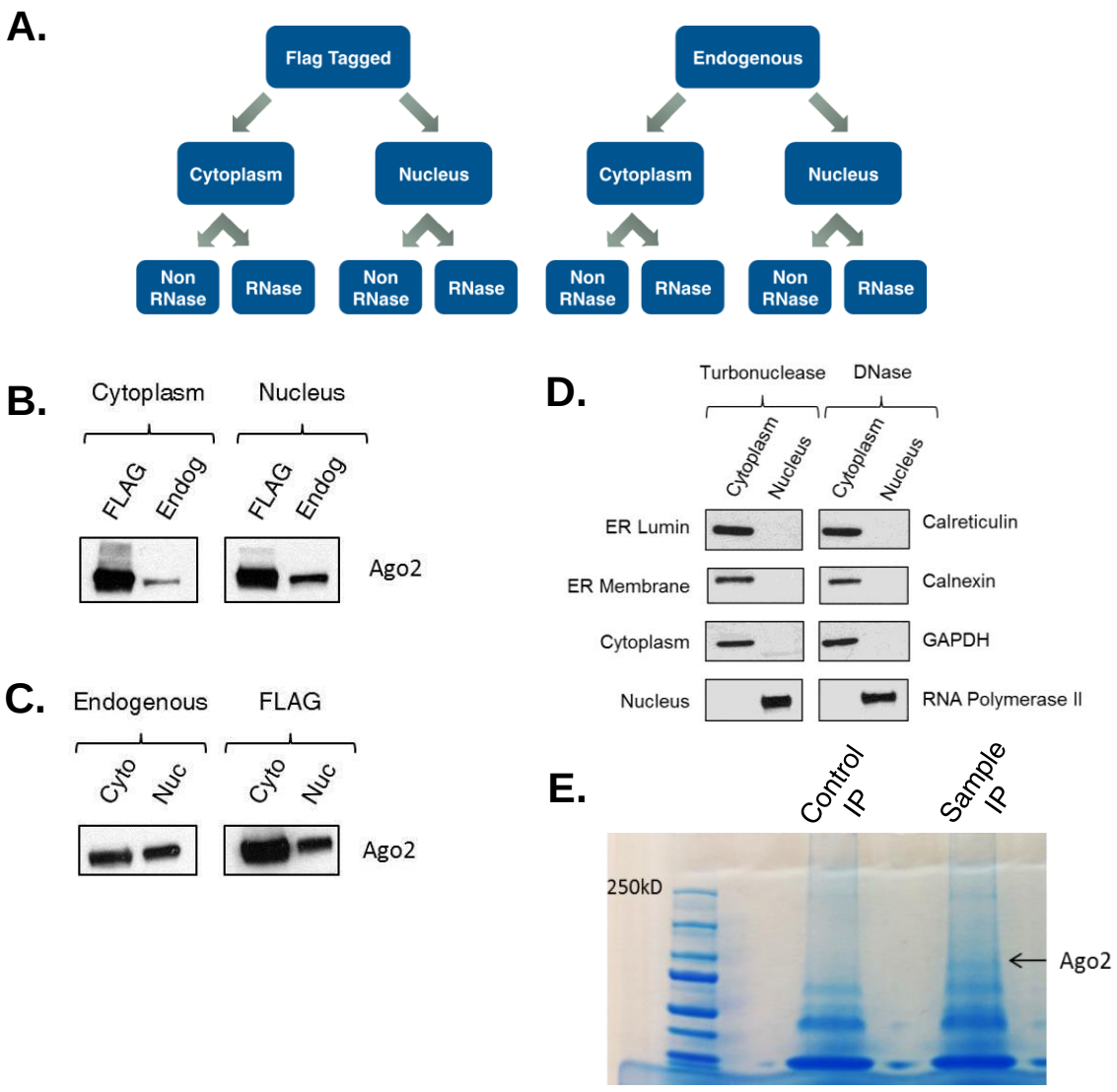


Figure 2.1 Characterization of mass spectrometry samples.

(A) Schematic of experimental comparisons.

(B) Western blot comparing levels of FLAG-AGO2 with endogenous AGO2 in the cytoplasm and with expression in the nucleus. Cytoplasmic and nuclear extracts were separated by SDS-PAGE and blotted with anti-AGO2 antibody. FLAG = AGO2 from FLAG-tagged AGO2 stable line. Endog = endogenous AGO2 from T47D cells.

(C) Western blot comparing expression of FLAG-tagged AGO2 and endogenous AGO2 in the cytoplasm (left) and in the nucleus (right). Cyto = cytoplasm, Nuc = Nucleus.

(D) Western blot analysis of cytoplasmic and nuclear fractions from RNase treated and non-RNase treated extracts of markers for nuclear, cytoplasmic, and ER proteins. Coomassie staining of FLAG immunoprecipitations from cytoplasmic lysate prior to mass spectrometry. The control is using T47D cytoplasmic lysate, the sample is using FLAG-AGO2 stable line cytoplasmic lysate. The band at ~100kDa is identified as AGO2.

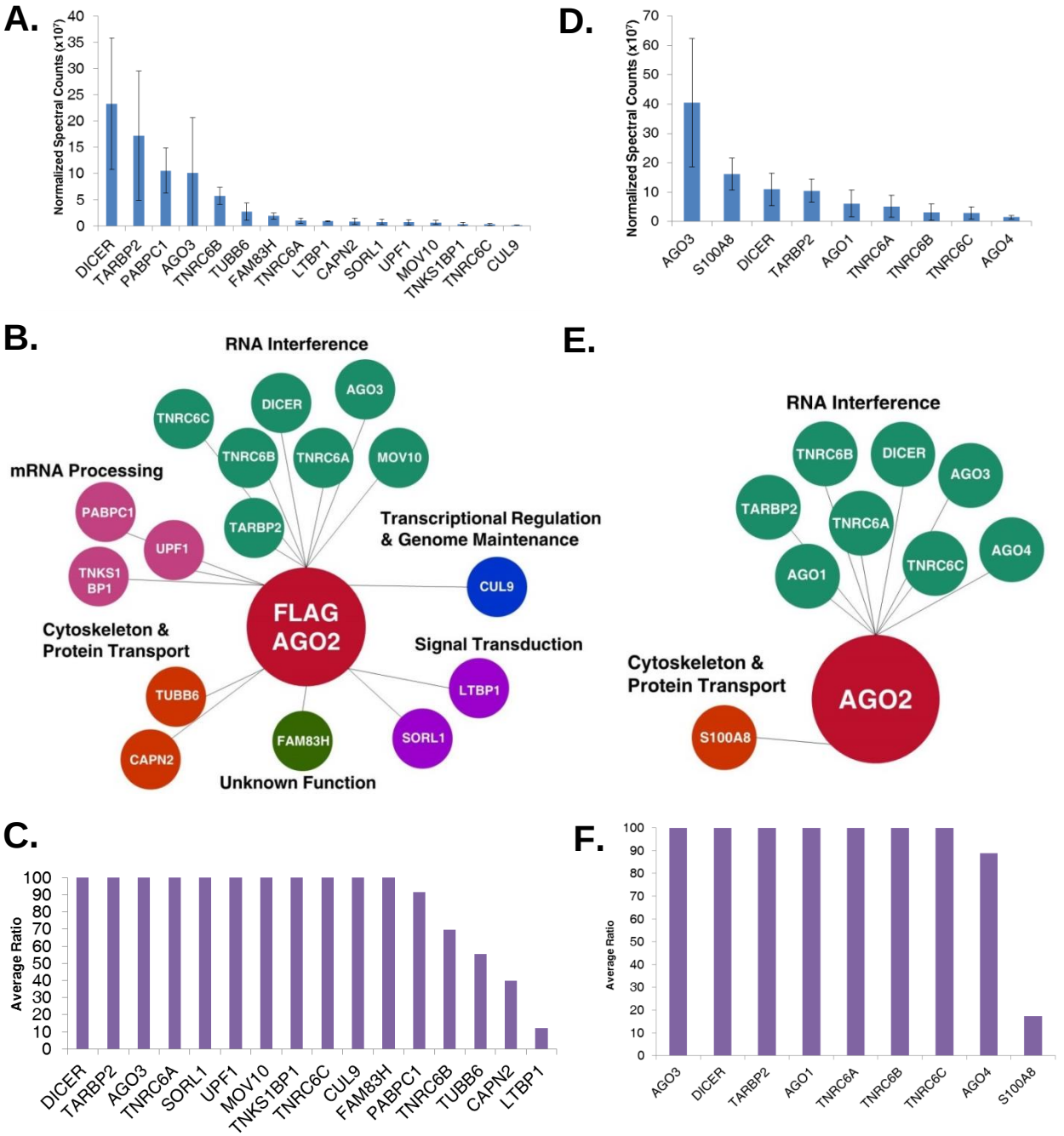

A.
Normalized Spectral Counts (x10⁷)
DICER
TARBP2
PABPC1
AGO3
TNRC6B
TUBB6
FAM83H
TNRC6A
LTBP1
CAPN2
SORL1
UPF1
MOV10
TNKS1BP1
TNRC6C
CUL9
D.
Normalized Spectral Counts (x10⁷)
AGO3
S100A8
DICER
TARBP2
AGO1
TNRC6A
TNRC6B
TNRC6C
AGO4
B.
RNA Interference
AGO3
DICER
TNRC6C
TNRC6B
TNRC6A
MOV10
mRNA Processing
PABPC1
TARBP2
Transcriptional Regulation
& Genome Maintenance
UPF1
TNKS1
BP1
CUL9
FLAG
AGO2
Cytoskeleton &
Protein Transport
Signal Transduction
TUBB6
LTBP1
FAM83H
SORL1
CAPN2
Unknown Function
E.
RNA Interference
TNRC6B
DICER
AGO3
TARBP2
TNRC6A
AGO1
TNRC6C
AGO4
Cytoskeleton &
Protein Transport
AGO2
S100A8
C.
Average Ratio
DICER
TARBP2
AGO3
TNRC6A
SORL1
UPF1
MOV10
TNKS1BP1
TNRC6C
CUL9
FAM83H
PABPC1
TNRC6B
TUBB6
CAPN2
LTBP1
F.
Average Ratio
AGO3
DICER
TARBP2
AGO1
TNRC6A
TNRC6B
TNRC6C
AGO4
S100A8

Figure 2.2 Identification of candidates from cytoplasmic immunoprecipitations (IPs) that had not been treated with RNAse.

(A) Normalized spectral counts of candidates identified from FLAG-AGO2 IPs in the cytoplasm. n=3
(B) Bubble plot of candidates identified from FLAG-AGO2 IPs in the cytoplasm. Candidates are organized by function.
(C) Average ratios of the normalized spectral counts between sample and control for candidates identified from FLAG-Ago2 IPs in the cytoplasm. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. Ratios greater than 100 are represented at the cutoff.
(D) Normalized spectral counts of candidates identified from endogenous AGO2 IPs in the cytoplasm. n=3
(E) Bubble plot of candidates identified from endogenous AGO2 IPs in the cytoplasm. Candidates are organized by function.
(F) Average ratios of the normalized spectral counts between sample and control for candidates identified from endogenous AGO2 IPs in the cytoplasm. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. Ratios greater than 100 are represented at the cutoff.

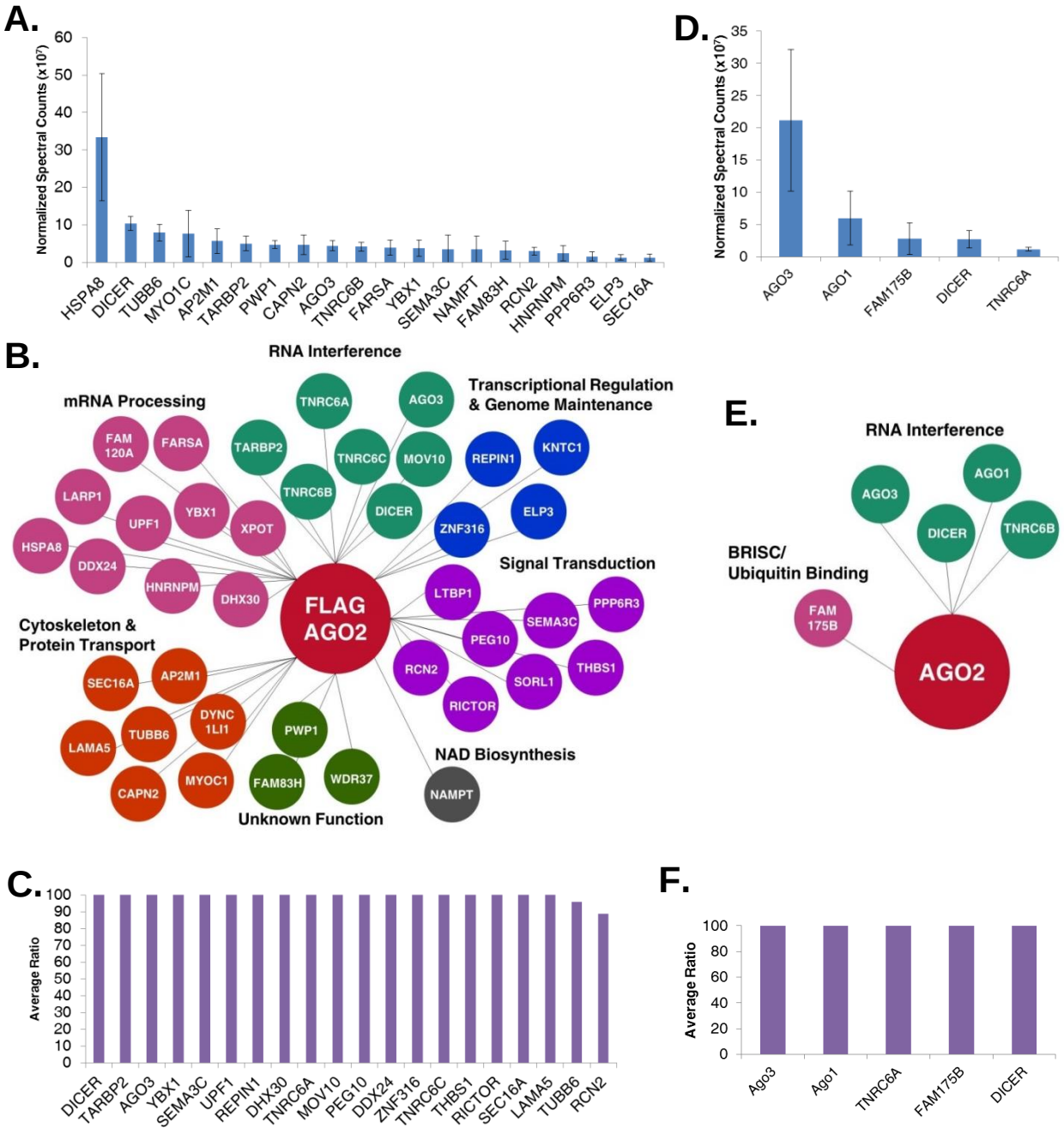

A.
Normalized Spectral Counts (x10⁷)
HSPA8
DICER
TUBB6
MYO1C
AP2M1
TARBP2
PWP1
CAPN2
AGO3
TNRC6B
FARSA
YBX1
SEMA3C
NAMPT
FAM83H
RCN2
HNRNPM
PPP6R3
ELP3
SEC16A
D.
Normalized Spectral Counts (x10⁷)
AGO3
AGO1
FAM175B
DICER
TNRC6A
B.
RNA Interference
mRNA Processing
Transcriptional Regulation & Genome Maintenance
Signal Transduction
Cytoskeleton & Protein Transport
NAD Biosynthesis
Unknown Function
FLAG AGO2
E.
RNA Interference
BRISC/ Ubiquitin Binding
AGO2
C.
Average Ratio
F.
Average Ratio
Ago3
Ago1
TNRC6A
FAM175B
DICER

Figure 2.3 Identification of candidates from cytoplasmic immunoprecipitations (IPs) that had been treated with RNase.

(A) Normalized spectral counts of top 20 candidates (by spectral counts) identified from FLAG-AGO2 IPs in the cytoplasm. n=3

(B) Bubble plot of candidates identified from FLAG-AGO2 IPs in the cytoplasm. Candidates are organized by function.

(C) Average ratios of the normalized spectral counts between sample and control for top 20 candidates (by ratio) identified from FLAG-Ago2 IPs in the cytoplasm. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. A maximum cutoff of 100 was assigned to the graph. Ratios greater than 100 are represented at the cutoff.

(D) Normalized spectral counts of candidates identified from endogenous AGO2 IPs in the cytoplasm. n=3

(E) Bubble plot of candidates identified from endogenous AGO2 IPs in the cytoplasm. Candidates are organized by function.

(F) Average ratios of the normalized spectral counts between sample and control for candidates identified from endogenous AGO2 IPs in the cytoplasm. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. Ratios greater than 100 are represented at the cutoff.

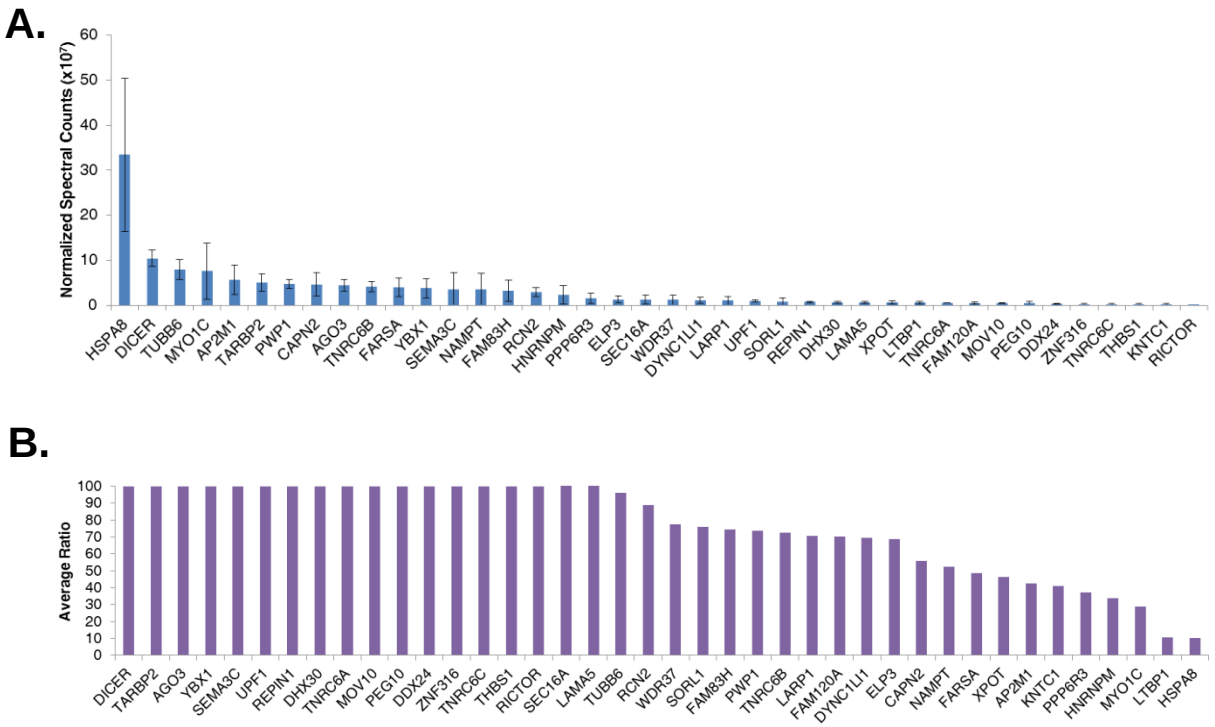


Figure 2.4 FLAG RNase Candidates from the Cytoplasm

(A) Normalized spectral counts of candidates identified from FLAG-AGO2 IPs in the cytoplasm. n=3

(B) Average ratios of the normalized spectral counts between sample and control for candidates identified from FLAG-Ago2 IPs in the cytoplasm. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. Ratios greater than 100 are represented at the cutoff.

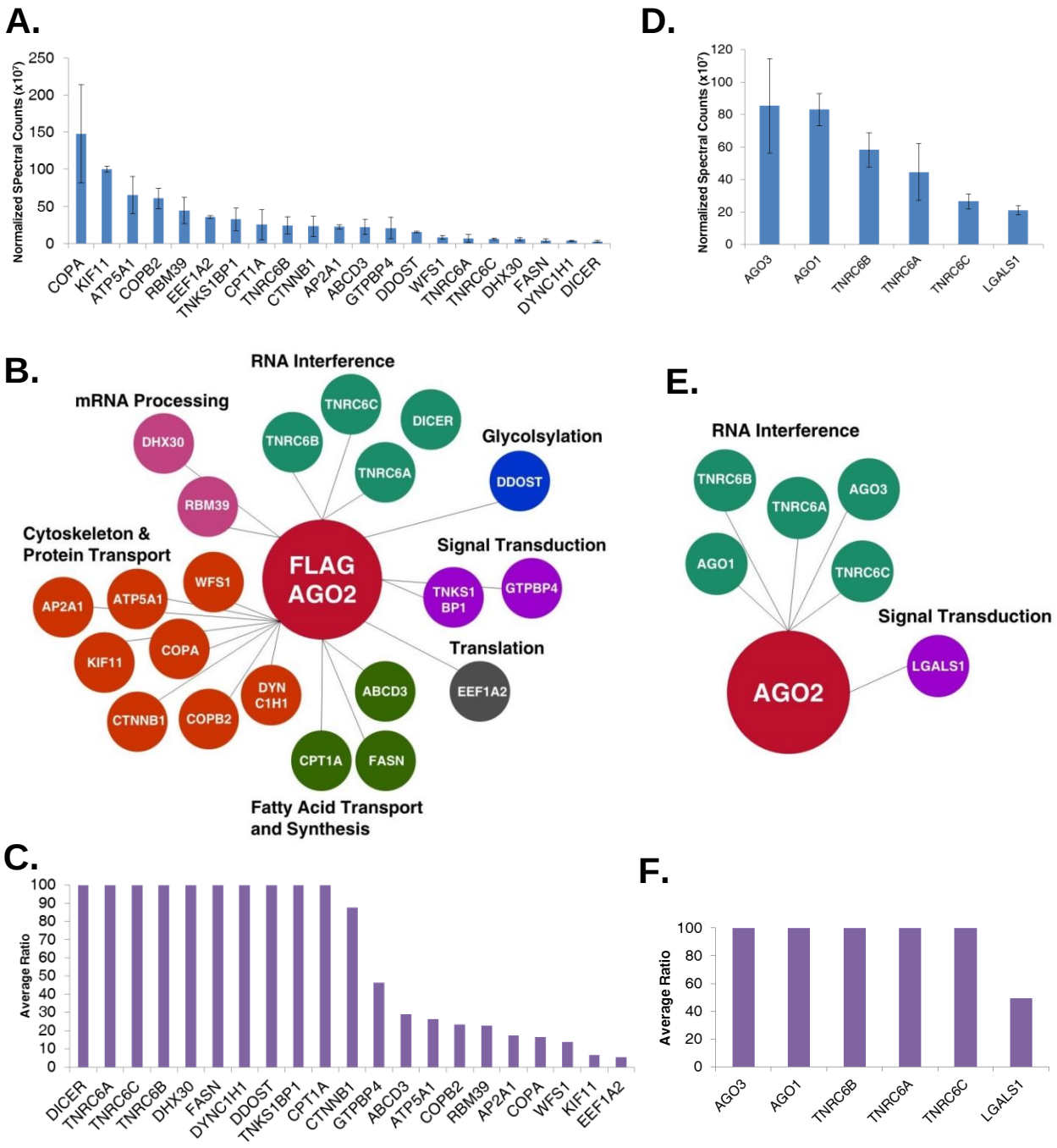

A.
Normalized SPectral Counts (x10⁷)
250
200
150
100
50
0
COPA
KIF11
ATP5A1
COPB2
RBM39
EEF1A2
TNKS1BP1
CPT1A
TNRC6B
CTNNB1
AP2A1
ABCD3
GTPBP4
DDOST
WFS1
TNRC6A
TNRC6C
DHX30
FASN
DYNC1H1
DICER
D.
Normalized Spectral Counts (x10⁷)
120
100
80
60
40
20
0
AGO3
AGO1
TNRC6B
TNRC6A
TNRC6C
LGALS1
B.
RNA Interference
mRNA Processing
Glycolsylation
Cytoskeleton &
Protein Transport
Signal Transduction
Translation
Fatty Acid Transport
and Synthesis
FLAG
AGO2
TNRC6C
DICER
TNRC6B
TNRC6A
DDOST
DHX30
RBM39
WFS1
AP2A1
ATP5A1
KIF11
COPA
CTNNB1
COPB2
DYN
C1H1
TNKS1
BP1
GTPBP4
ABCD3
EEF1A2
CPT1A
FASN
E.
RNA Interference
Signal Transduction
AGO2
TNRC6B
TNRC6A
AGO3
AGO1
TNRC6C
LGALS1
C.
Average Ratio
100
90
80
70
60
50
40
30
20
10
0
DICER
TNRC6A
TNRC6C
TNRC6B
DHX30
FASN
DYNC1H1
DDOST
TNKS1BP1
CPT1A
CTNNB1
GTPBP4
ABCD3
ATP5A1
COPB2
RBM39
AP2A1
COPA
WFS1
KIF11
EEF1A2
F.
Average Ratio
100
80
60
40
20
0
AGO3
AGO1
TNRC6B
TNRC6A
TNRC6C
LGALS1

Figure 2.5 Identification of candidates from nuclear immunoprecipitations (IPs) that had not been treated with RNAse.

(A) Normalized spectral counts of candidates identified from FLAG-AGO2 IPs in the nucleus. n=2
(B) Bubble plot of candidates identified from FLAG-AGO2 IPs in the nucleus. Candidates are organized by function.
(C) Average ratios of the normalized spectral counts between sample and control for candidates identified from FLAG-Ago2 IPs in the nucleus. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. A maximum cutoff of 100 was assigned to the graph. Ratios greater than 100 are represented at the cutoff.
(D) Normalized spectral counts of candidates identified from endogenous AGO2 IPs in the nucleus. n=3
(E) Bubble plot of candidates identified from endogenous AGO2 IPs in the nucleus. Candidates are organized by function.
(F) Average ratios of the normalized spectral counts between sample and control for candidates identified from endogenous Ago2 IPs in the nucleus. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. Ratios greater than 100 are represented at the cutoff.

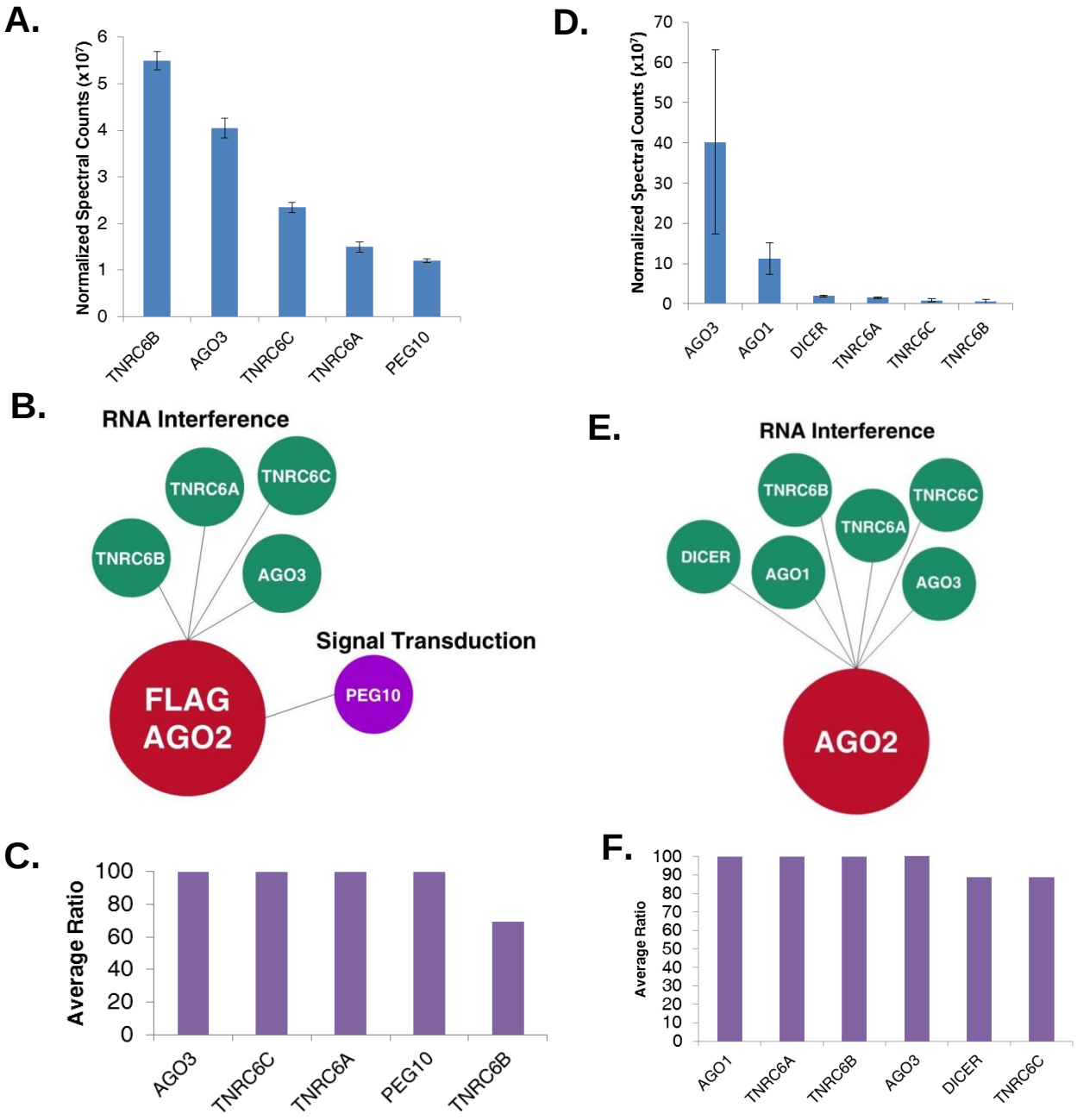

A.
Normalized Spectral Counts (x10^7)
0
1
2
3
4
5
6
TNRC6B
AGO3
TNRC6C
TNRC6A
PEG10
D.
Normalized Spectral Counts (x10^7)
0
10
20
30
40
50
60
70
AGO3
AGO1
DICER
TNRC6A
TNRC6C
TNRC6B
B.
RNA Interference
TNRC6A
TNRC6C
TNRC6B
AGO3
Signal Transduction
FLAG
AGO2
PEG10
E.
RNA Interference
TNRC6B
TNRC6C
TNRC6A
DICER
AGO1
AGO3
AGO2
C.
Average Ratio
0
20
40
60
80
100
AGO3
TNRC6C
TNRC6A
PEG10
TNRC6B
F.
Average Ratio
0
10
20
30
40
50
60
70
80
90
100
AGO1
TNRC6A
TNRC6B
AGO3
DICER
TNRC6C

Figure 2.6 Identification of candidates from nuclear immunoprecipitations (IPs) that that had been treated with RNase.

(A) Normalized spectral counts of candidates identified from FLAG-AGO2 IPs in the nucleus. n=2
(B) Bubble plot of candidates identified from FLAG-AGO2 IPs in the nucleus. Candidates are organized by function.
(C) Average ratios of the normalized spectral counts between sample and control for candidates identified from FLAG-Ago2 IPs in the nucleus. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. A maximum cutoff of 100 was assigned to the graph. Ratios greater than 100 are represented at the cutoff.
(D) Normalized spectral counts of candidates identified from endogenous AGO2 IPs in the nucleus. n=3
(E) Bubble plot of candidates identified from endogenous AGO2 IPs in the nucleus. Candidates are organized by function.
(F) Average ratios of the normalized spectral counts between sample and control for candidates identified from endogenous AGO2 IPs in the nucleus. When no ratio was given (candidate was identified in sample only) a ratio of 100 was assigned. Ratios greater than 100 are represented at the cutoff.

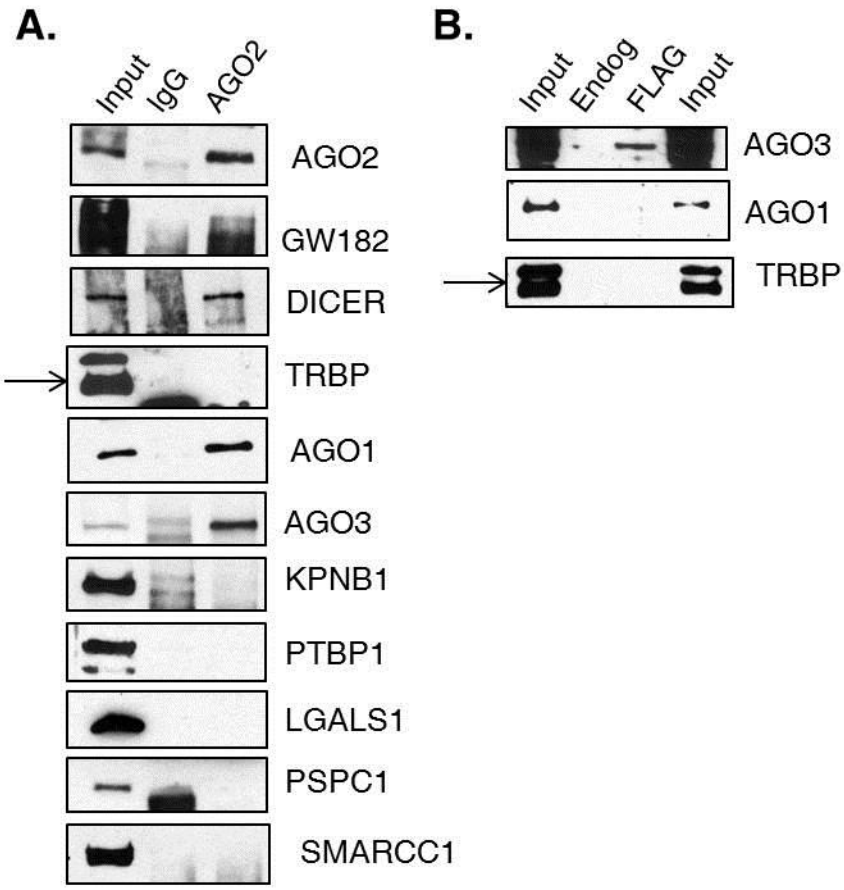


Figure 2.7 Co-immunoprecipitations of candidate interacting factors.

(A) Co-IP of AGO2 with potential interacting factors from the nucleus. AGO2 was immunoprecipitated versus an IgG control and interacting factors were blotted for with antibodies by western blot. The arrows indicate the TRBP band.

(B) Co-IP of FLAG-AGO2 with interacting factors from the nucleus identified by mass spectrometry. FLAG-AGO2 was immunoprecipitated from FLAG-AGO2 stable line cells versus a FLAG IP from endogenous T47D cells. Interacting factors were blotted for with antibodies by western blot.

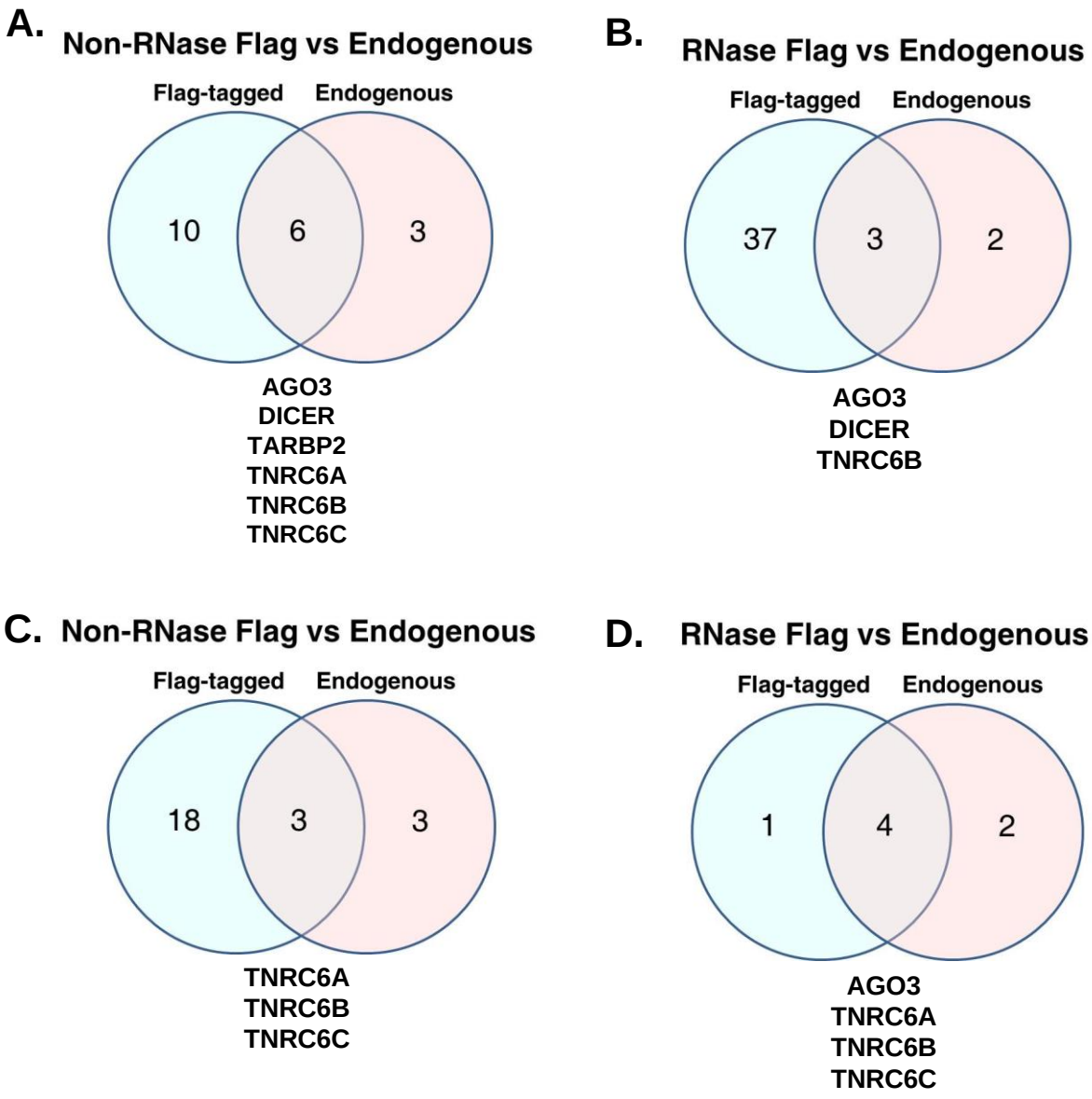


Figure 2.8 Comparison of FLAG and Endogenous candidates.

(A) Comparison of candidates identified from FLAG-AGO2 and endogenous AGO2 IPs in the cytoplasm. Listed proteins are candidates that overlapped in both data sets.

(B) Comparison of candidates identified from FLAG-AGO2 and endogenous AGO2 IPs in the cytoplasm. Listed proteins are candidates that overlapped in both data sets.

(C) Comparison of candidates identified from FLAG-AGO2 and endogenous AGO2 IPs in the nucleus. Listed proteins are candidates that overlapped in both data sets.

(D) Comparison of candidates identified from FLAG-AGO2 and endogenous AGO2 IPs in the nucleus. Listed proteins are candidates that overlapped in both data sets.

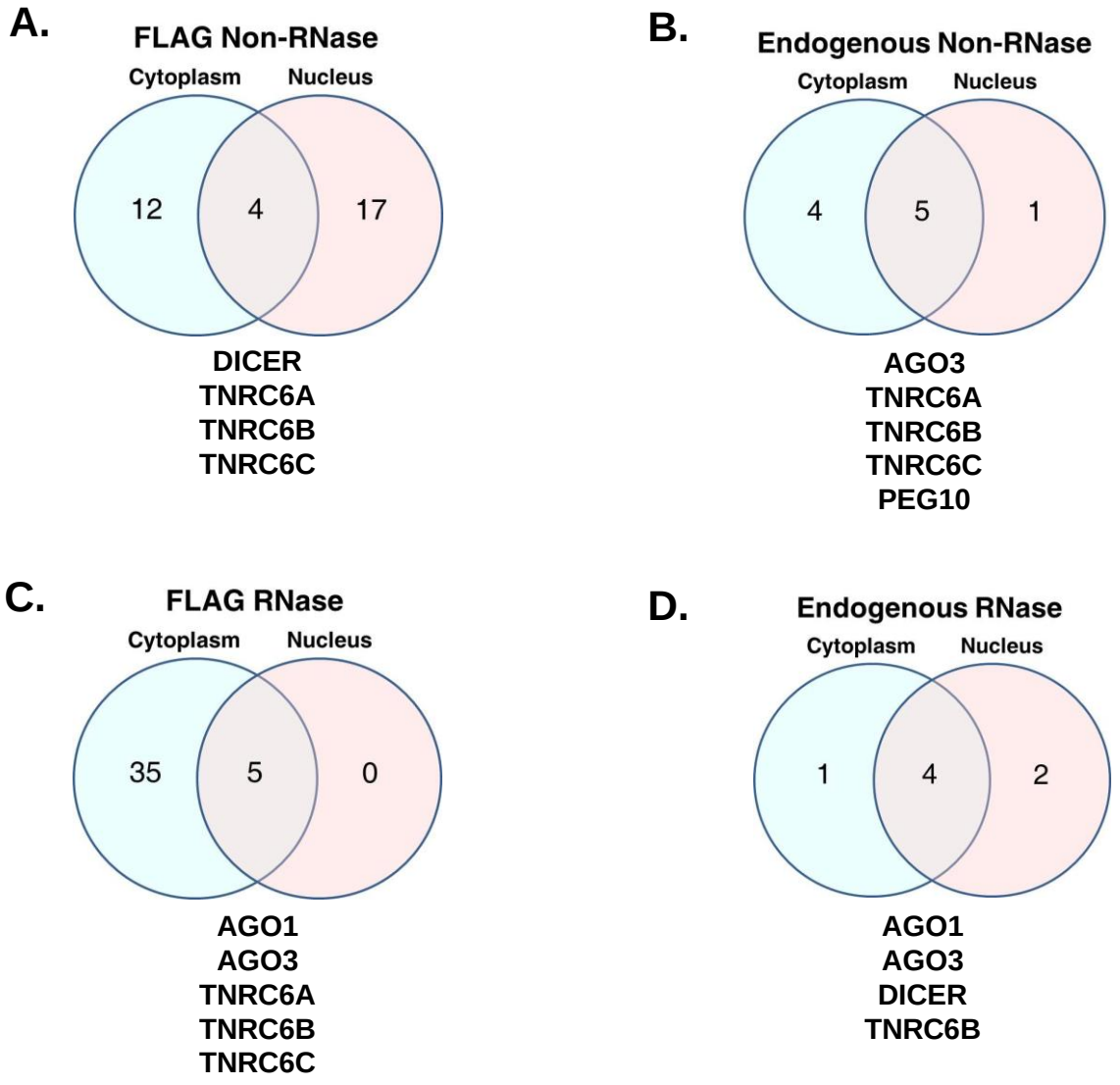


Figure 2.9 Comparison of Cytoplasmic and Nuclear Interactions of AGO2.

(A) Venn diagram of candidate interacting factors identified with FLAG-AGO2 without RNase treatment. Candidates identified in both the cytoplasm and the nucleus are listed.

(B) Venn diagram of candidate interacting factors identified with FLAG-AGO2 with RNase treatment. Candidates identified in both the cytoplasm and the nucleus are listed.

(C) Venn diagram of candidate interacting factors identified with endogenous AGO2 without RNase treatment. Candidates identified in both the cytoplasm and the nucleus are listed.

(D) Venn diagram of candidate interacting factors identified with endogenous AGO2 with RNase treatment. Candidates identified in both the cytoplasm and the nucleus are listed.

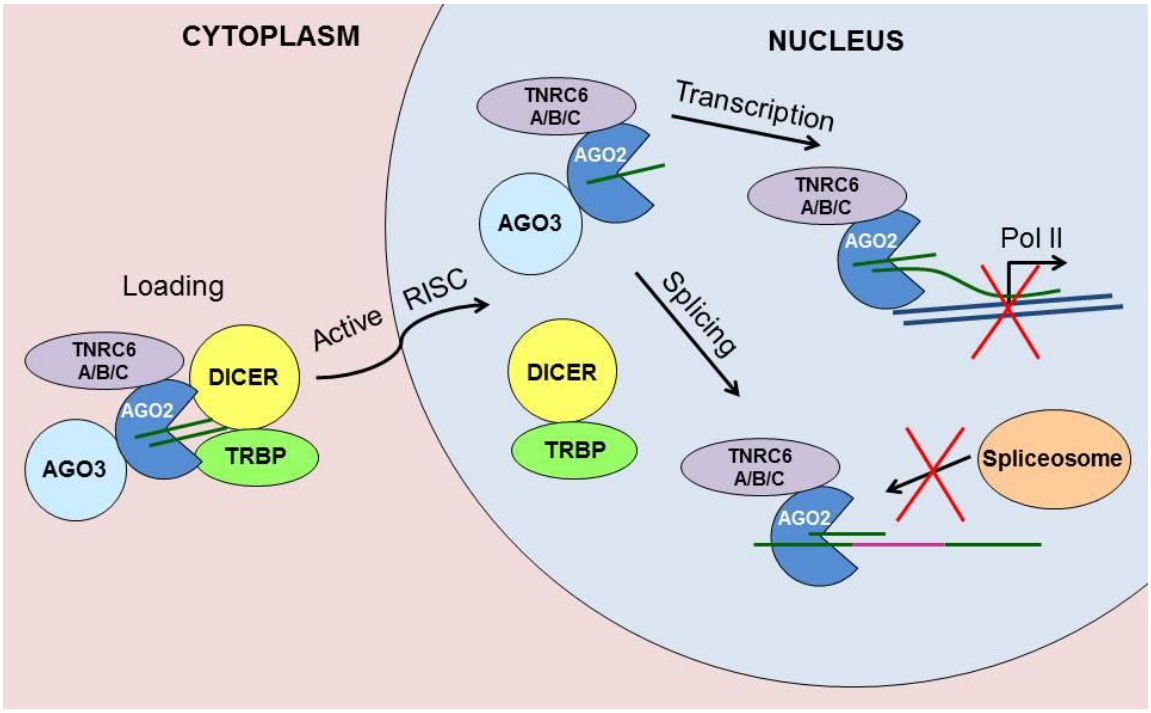


Figure 2.10 Model of nuclear AGO2 activity.

AGO2 is bound by TRNC6 proteins and AGO3 in the cytoplasm. AGO2 is loaded by DICER, TRBP, and other loading factors. Active RISC is then shuttled into the nucleus. Interactions with DICER and TRBP are more transient in the nucleus. Loaded AGO2 and TNRC6 proteins can then alter transcription or splicing within the nucleus, depending on the small RNA bound by AGO2.

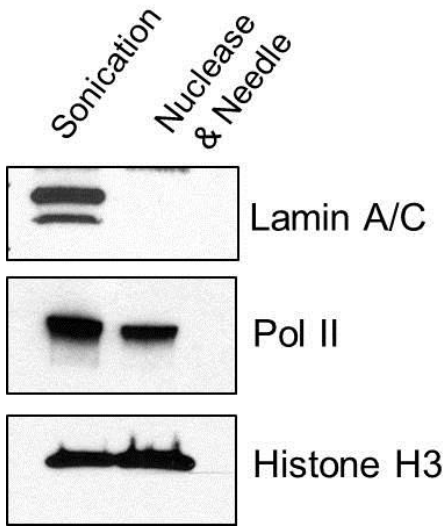


Figure 2.11 Comparison of nuclear extract preparation methods.

Western blots of nuclear marker proteins Lamin A/C, Polymerase II, and Histone H3. 30 μg of each extract were loaded.

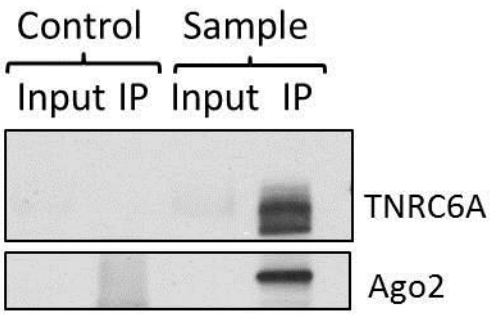


Figure 2.12 Quality control Western blot for mass spectrometry samples.

Western blots of AGO2 and TNRC6A from 17% (5 μL) fraction of mass spectrometry IP samples.

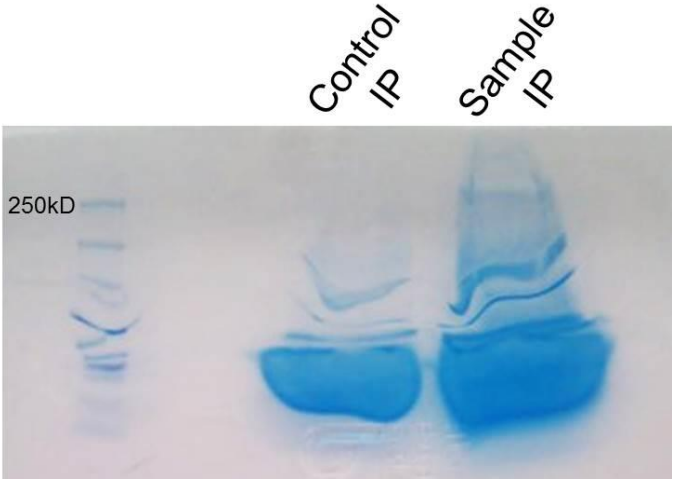


Figure 2.13 Coomassie staining of immunoprecipitations prior to desalting.
Control and sample immunoprecipitations were eluted and concentrated prior to running on the SDS-PAGE gel. Samples were run 15mm into the gel.

Chapter 3: Methods

3.1 Cell Culture

T47D cells (ATCC) were cultured in RPMI medium supplemented with 10% FBS, 0.5% NEAA, 20 µg/mL insulin, 10 mM pH 7.0-7.6 HEPES, and 1 mM sodium pyruvate. T47D cells stably expressing FLAG-HA-tagged AGO2 were cultured identically to T47D cells but media supplemented with 0.2 mg/mL G418. All cells were grown at 37°C in 5% CO2.

The FLAG-HA-tagged AGO2 stable cell line was developed by transfecting T47D cells with the (corrected) pIRESnew-FLAG/HA Ago2 plasmid (Addgene,10822) and Lipofectamine 2000 (Life Technologies, 11668019). Cells were treated with 500 µg/mL G418 for two weeks. Colonies were picked with 5% trypsin and transferred to 24-well dishes. Colonies were tested for expression of FLAG-HA AGO2 by western blot with anti-HA and anti-AGO2 antibodies. Colony labeled 'Colony 1' was used for this study.

3.2 Extract Preparation

Purification of cytoplasmic and nuclear extract from T47D or FLAG-Ago2 cells was performed as described previously (Gagnon et al., 2014) with a few modifications. Rather than using sonication to lyse nuclei, a 27 gauge needle was used. For RNase extracts, TurboNuclease was added at a 1:10000 dilution (Accelagen, N0103M) was added to the extract and incubated for 30min at room temperature. For non-RNase treated nuclear extracts, DNase was added at a 1:40 dilution (Worthington, LS006353) and incubated at 37°C for 30min.

3.3 Extract Analysis

Western blots to determine the purity of nuclear and cytoplasmic fractions from TurboNuclease or DNase treated T47D or FLAG-Ago2 cells were performed as before (Gagnon et al., 2014).

For comparing nuclear and cytoplasmic fractions by Western blot, the same cell equivalents of extract were separated by electrophoresis (1/2 the volume of nuclear extract per 1 volume of cytoplasmic). Blocked Western blot membranes (Hybond-C Extra, GE Healthcare Life Sciences) were incubated with the following primary antibodies for 16 h at 4^{o}C in PBST (PBS + 0.05% TWEEN-20) + 5% milk with rocking: anti-Ago2 at 1:1000 (Abcam, ab57113), anti-Calreticulin at 1:1000 (Cell Signalling, 2891S), anti-Histone H3 at 1:10000 (Abcam, ab1791), anti-Lamin A/C at 1:1500 (Abcam, ab8984), anti-GAPDH at 1:600 (Abcam, ab9484), anti-RNA polymerase II at 1:4000 (Millipore, 05-623).

3.4 Immunoprecipitation

For immunoprecipitations of endogenous Ago2 in T47D extracts, either anti-Ago2 (Abcam, ab57113) or mouse IgG antibody (Millipore, 12-371) were cross-linked to Protein A Plus/ Protein G resin. Antibody was incubated with resin (65 μg/mL resin) in coupling buffer (10mM Sodium Phosphate, pH 7, 75mM NaCl) with rocking at room temperature for 2hrs. Resin was washed 3X with coupling buffer. 0.4mM DSS was added to resin and incubated with rocking for 30min at room temperature. The reaction was quenched with Tris-HCl, pH 8.0 and resin was resuspended in IP-EQ buffer (50mM Tris-HCl, pH 7.4, 2mM $MgCl_2$, 150mM KCl, 0.05% NP-40) for use in experiments.

Immunoprecipitations for mass spectrometry analysis were performed in either T47D or FLAG-Ago2 cytoplasmic or nuclear extracts. Mouse IgG conjugated resin was the control for T47D extracts. FLAG conjugated resin (Sigma, A2220) was incubated with extract from FLAG-Ago2 stable line cells or incubated with extract from T47D cells lacking FLAG-Ago2 as the control. For each extract, a starting protein concentration of 15mg was pre-cleared using mouse IgG conjugated Agarose (Sigma, A0919), rocking at room temperature for 30 minutes. Extracts were transferred to 250 μl of specific-antibody bound resin and incubated over night at 4^{o}C with

rocking. Resin was washed 6X with IP_{300} Buffer (20mM Tris-HCl, pH 7.4, 2mM $MgCl_2$, 300mM NaCl, 0.05% NP-40) and proteins were eluted with 250 µl of 1X SDS loading buffer. To eliminate excess salt, elutions were run through Illustra Nap-5 desalting columns (GE Healthcare, 17-0853-02). To concentrate samples, elutions were run through Amicon Ultra-0.5mL centrifugal protein concentrators (Millipore, UFC901024). Elutions were run 15mm into SDS-PAGE gels, Coomassie stained with GelCode Blue (Thermo, 24592), and each lane was cut into three 5mm slices. The gel slices were submitted to the UT Southwestern Proteomics Core for further analysis.

3.5 Mass Spectrometry

Gel bands were digested overnight with trypsin (Promega) following reduction and alkylation with DTT and iodoacetamide (Sigma–Aldrich). Following solid-phase extraction cleanup with Oasis HLB plates (Waters), the resulting samples were analyzed by LC/MS/MS using an Orbitrap Elite, Q Exactive, or Q Exactive Plus mass spectrometer (Thermo Electron) coupled to an Ultimate 3000 RSLC-Nano liquid chromatography system (Dionex). Samples were injected onto either a 180µm i.d., 15-cm long column packed in-house with a reverse-phase material ReproSil-Pur C18-AQ, 1.9µm resin (Dr. Maisch GmbH, Ammerbuch-Entringen, Germany), or a 75µm i.d., 50-cm long Easy Spray column (Thermo). Peptides were eluted with a gradient from 1-28% buffer B over 40 min (180 µm column) or 60 min (75 µm column). Buffer A contained 2% (v/v) acetonitrile (ACN) and 0.1% formic acid in water, and buffer B contained 80% (v/v) ACN, 10% (v/v) trifluoroethanol, and 0.08% formic acid in water. The mass spectrometer acquired up to 20 MS/MS spectra for each full spectrum acquired.

Raw MS data files were converted to a peak list format and analyzed using the central proteomics facilities pipeline (CPFP), version 2.0.3 (Trudgian and Mirzaei, 2012; Trudgian et al., 2010). Peptide identification was performed using the X!Tandem (Craig and Beavis, 2004) and

open MS search algorithm (OMSSA) (Geer et al., 2004) search engines against the human protein database from Uniprot, with common contaminants and reversed decoy sequences appended (Elias and Gygi, 2007). Fragment and precursor tolerances of 20 ppm and 0.5 Da were specified, and three miscleavages were allowed. Carbamidomethylation of Cys was set as a fixed modification and oxidation of Met was set as a variable modification. Label-free quantitation of proteins across samples was performed using SINQ normalized spectral index Software (Trudgian et al., 2011b).

3.6 Data Analysis

The standard spectral count cutoff for SINQ analysis is a spectral count of 3 or higher. To increase the stringency of my analysis, I used a cutoff of 5 spectral counts for all data sets. The second layer of analysis is through the ratios of sample to control. For this, I set a ratio cutoff of 2:1 respectively. All samples were compared against all controls. The endogenous samples were run in triplicate and needed to meet the cutoff criteria in at least 2 of 3 experiments to be considered. Flag-Ago2 samples were run in duplicate and therefore had to meet the criteria in both data sets to be considered.

3.7 Co-immunoprecipitations

For co-immunoprecipitations, 300 µg of starting protein was used per sample. Extract was precleared with mouse IgG conjugated resin (30 µL of 50% slurry) for 30min at 4C. Samples were then incubated with 3 µg of antibody for 1.5-2hr at 4C. 45 µg of Protein G plus Protein A resin was added and incubated for another hour. For FLAG IPs, 30 µL of a 50% slurry of FLAG conjugated resin was added to the extract after preclear and incubated for 2.5-3hr. Samples were washed 6X with IP_{300} Buffer (20mM Tris-HCl, pH 7.4, 2mM $MgCl_2$, 300mM NaCl, 0.05% NP-40) with 5min incubations and eluted with 95C 1xSDS for 5 minutes with shaking. Samples were loaded onto 4-20% SDS-PAGE gels and Western blots were performed. Antibodies used:

GW182 (Bethyl, A302-329A); DICER (Abcam, ab14601); TRBP (Abcam, ab72110); AGO1 (Cell Signaling, D84G10); AGO3 (Sigma, SAB4200112); KPNB1 (Bethyl, A300-482A); PTBP1 (Abcam, ab5642); LGALS1 (Cell Signaling, 5418S); PSPC1 (Santa Cruz, SC84576); SMARCC1 (Abcam,ab72502).

Chapter 4: Future Directions and Concluding Remarks

4.1 Introduction

The work within this dissertation shows that key RNAi factors are present and interacting in the mammalian cell nucleus. This work also suggests that the nuclear RNAi complex is different from its cytoplasmic counterpart. While this work takes a first step towards understanding the environment of nuclear RNAi factors, further work to understand the endogenous functions and mechanisms of action are needed. Experiments are needed to identify factors outside of the core complex that are involved in nuclear roles such as transcription and splicing.

4.2 Mass spectrometry of identified AGO2 interacting factors

To build upon the nuclear interaction network of AGO2, interaction networks of other RNAi factors need to be produced. My findings have shown that the factors that have the strongest interactions with nuclear AGO2 are the known RNAi factors TNRC6A, B, and C, as well as AGO3. Factors involved in splicing and transcription were not identified. Novel factors may be secondary or tertiary interactions of AGO2 that are bound to other RNAi factors. The other RNAi factors therefore, may bridge interactions that link AGO2 to splicing or transcriptional machinery. With the system used in this dissertation, it would be possible to continue the proteomic studies of these factors to expand the nuclear RNAi interaction network.

The TNRC6 proteins are the most well studied binding partners of AGO2, with the most focus on TNRC6A (Pfaff and Meister, 2013). They may have redundant functions in the context of RNAi, but this is unknown. It is possible that they may hold specific functions, as they only share 19.5% sequence complementarity, however all of their major domains are conserved (**Figure 4.1**). By determining the similarities and differences between the three

TNRC6 paralogs' interaction networks, we can obtain a better understanding of the complexities of nuclear RNAi.

To determine the protein networks of the three TNRC6 paralogs, immunoprecipitation and mass spectrometry of each paralog will be performed and the interacting factors for each will be compared. Antibodies for both TNRC6A and TNRC6B are commercially available. Endogenous IPs could be performed for both of these proteins if the antibodies are suitable. Currently there are no antibodies for TNRC6C, but there are tagged versions of all three paralogs available. By using the cross-checking method employed in this study (endogenous vs tagged) for both TNRC6A and B, insights could be obtained about both proteins and their interacting factors. Mass spectrometry of a tagged construct of TNRC6C can be compared to these studies and additional insights could be gained about this third paralog (**Figure 4.2**). False positives from the tag can be reduced by comparison to the tagged immunoprecipitations of TNRC6A and B. Potential interacting factors of TNRC6C would be factors identified by both endogenous TNRC6A and B, and tagged TNRC6C. Unique interacting factors that are specific to TNRC6C would be identified in the tagged-TNRC6C IP only.

It should be noted that the tagged proteins may also identify novel interacting factors, however priority will be given to those factors identified with the endogenous IPs. Because tagged proteins are commonly over expressed, they can IP interacting factors that are weaker or more transient at higher concentration than the endogenous proteins (Oeffinger, 2012). Tagged IPs can also identify interacting factors that are occluded because the factors may share the antibody binding site in endogenous IPs. While these aspects are taken into account, the endogenous IPs are the data sets most likely to produce biologically relevant candidates.

Co-IPs and activity assays will be used to verify that the candidate interacting proteins are associating with the TNRC6 paralogs. The activity assays will be dependent on the functions of the proteins identified (transcription, translation, splicing, etc.). TNRC6 proteins may

bridge AGO2 interactions to other factors involved in nuclear functions. By identifying their interaction networks it will lead to a better understanding of RNAi in the nucleus.

4.3 Mass spectrometry of Argonautes 1, 3 and 4

A second set of mass spectrometry experiments is the study of the interacting partners of other AGO proteins. AGO1 is known to be involved in both transcription and splicing regulation (Allo et al., 2014; Kim et al., 2006; Ruda et al., 2014). The specific functions of AGO3 and 4 remain largely unknown in mammalian somatic cells. In this study, AGO3 was identified as an interacting partner of AGO2. This leads to further questions about the role of an AGO-AGO interaction in RNAi. Mass spectrometry of each AGO protein will lead to a deeper understanding of the similarities and differences between them and how they may differ in their roles in both the cytoplasm and the nucleus.

Similar to the techniques outlined in section 4.2, comparisons between data sets of Argonautes 1-4 can be made to determine similarities and differences between their interacting partners. While antibodies for all four Argonaute variants exist, variations in expression levels may cause difficulty in immunoprecipitating levels that are sufficient for mass spectrometry. This variation in expression can make data comparisons difficult. Tagged proteins or alternative cell lines may need to be used to obtain sufficient levels of protein for MS analysis. However, even if direct comparisons cannot be made between the four AGO MS data sets, a great deal of information about the networks of each AGO variant can be gained.

4.4 AGO3's role in AGO2 function

AGO2 is the most abundant and well-studied of all four AGO variants in mammals (Wang et al., 2012). AGO3 is less abundant, and whether it holds specific and unique functions within the RNAi pathway is unknown. Identifying an AGO2-AGO3 interaction in this study suggests that

AGO3 may affect or participate in AGO2 activity in some way. Assays can be used to determine how those functions may affect AGO2 activity in canonical RNAi and splicing.

Knockdown of AGO3 can be coupled with AGO2 activity assays to study mRNA cleavage by RNAi. Since AGO2 is the only AGO to retain catalytic activity, this assay is specific to AGO2 function. To study AGO3's effect on AGO2 slicer activity, a biochemical cleavage assay will be used. An siRNA will be introduced into cells which targets an mRNA. Target mRNA levels will be measured by qPCR. If AGO3 affects AGO2 slicer capabilities, knockdown of AGO3 would cause a decrease in target mRNA knockdown.

AGO3's effects on AGO2's role in splicing can be studied in the context of exon skipping. Previously used model systems from my laboratory can be used (Liu et al., 2012). A small RNA targeting an intron-exon junction will be transfected into cells in combination with AGO3 knockdown. If AGO2 is bound to the pre-mRNA, the exon is skipped and a longer, alternate form of the mRNA is produced than if AGO2 is absent. Changes in splicing will be monitored by PCR and PCR products will be run on a gel to separate them by size. If AGO3 affects AGO2 splicing capabilities, knockdown of AGO3 would show an increase in the shorter splice product. To further validate that AGO3 plays a role in splicing, RNA immunoprecipitation can be performed to determine if AGO3 is present on the pre-mRNA after transfection of a small RNA.

The lab has previously attempted knockdown of AGO3 coupled with transcriptional regulation and saw no effect (Chu et al., 2010). This result, in combination with the fact that it is difficult to get efficient knockdown of AGO proteins may make the study of AGO-AGO interactions difficult. Therefore it may be necessary to create an AGO3 knockout line through the CRISPR/Cas9 system to identify more subtle changes in AGO2 activity.

4.5 Concluding Remarks

The experiments described above, along with current studies within the lab to identify AGO1 and AGO2 bound RNAs will provide a detailed picture of RNAi in mammalian cell nuclei. By using relatively unbiased strategies to first build the interaction network of the RNAi factors, the networks can then be broken down into the different aspects of nuclear activity that they are involved in. This data can lead to new advances in RNAi capabilities far beyond what it is currently applied to.

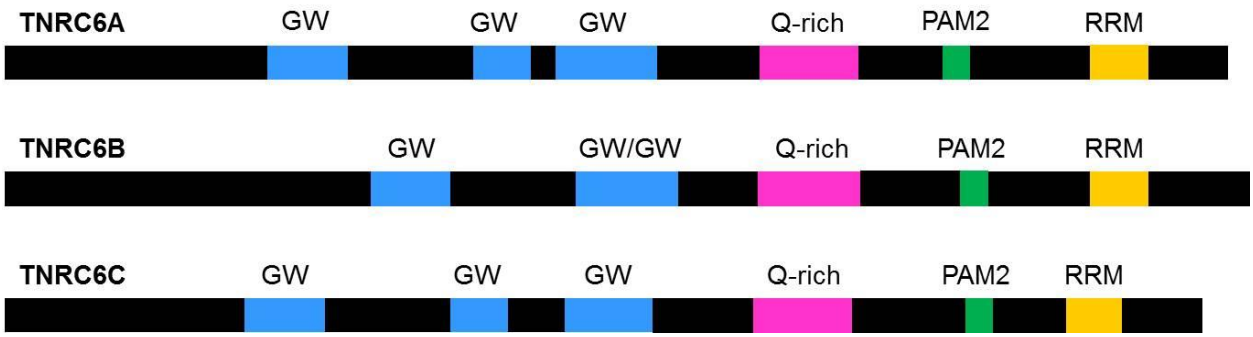


Figure 4.1 Domain organization of TNRC6A, B, and C.
Conserved domains are labeled on the figure. TNRC6A has a nuclear localization sequence between the GW and Q-rich domains. All three paralogs have nuclear export sequences between the GW and Q-rich domains.

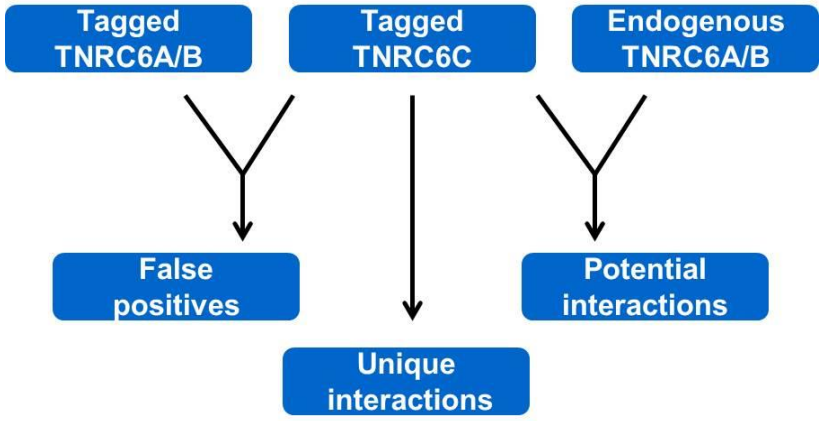


Figure 4.2 Schematic of comparisons for mass spectral analysis of TNRC6A, B, and C.
MS data from immunoprecipiations of tagged TNRC6A and B would be compared to MS data from immunoprecipitations from tagged TNRC6C. Common candidates would be considered false positives. MS data from immunoprecipitations of endogenous TNRC6A and B would be compared to MS data from immunoprecipitations from tagged TNRC6C. Common candidates would be considered as potential interactions. All other interacting factors identified by tagged TNRC6C would be considered unique interacting factors specific to the paralog.

APPENDIX

Key for Tables:

Prot: Protein accession number from UniProtKB

% Cover: Percentage of the protein sequence that was covered by the peptides identified for the protein

SPECTRAL COUNTS: The weighted count of peptide spectrum matches assigned to each protein for the particular sample

SPECTRAL INDEX (MIC SIn): The normalized Spectral Index statistic for the protein for the specified group. Calculated from the intensity of fragment ions in each spectrum assigned to a particular protein.

Ratio: Quantitative ratio for each protein between groups derived from the MIC Sin value versus Control1 (values versus Control2 and Control3 not shown)

C1/2/3: Control 1/2/3

S1/2/3: Sample 1/2/3

Table A1. FLAG candidates from cytoplasmic immunoprecipitations that had not been treated with RNase.

			SPECTRAL COUNTS						SPECTRAL INDEX (MIC SIn)						RATIOS		
Prot	Description	% Cover	C1	C2	C3	S1	S2	S3	C1	C2	C3	S1	S2	S3	S1/C1	S2/C1	S3/C1
P52732	KIF11_HUMAN Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	76.40	586.00	323.00	238.00	501.00	425.00	133.00	8.66E-05	1.69E-05	3.47E-06	4.17E-05	4.16E-05	1.60E-06	0.48	0.48	0.02
P35579	MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	75.00	293.85	621.30	352.25	254.86	169.33	363.71	3.39E-06	1.49E-05	1.36E-06	2.52E-06	2.27E-06	1.92E-06	0.74	0.67	0.57
Q9UKV8	AGO2_HUMAN Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	84.70		1.00	4.00	439.75	594.67	678.89		4.23E-09	5.69E-09	4.36E-05	1.21E-04	5.09E-05	Sample 1 Only	Sample 2 Only	Sample 3 Only
P04264	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	69.40	201.00	303.00	228.00	212.50	313.00	193.50	1.90E-05	4.57E-05	9.89E-06	2.03E-05	4.99E-05	7.85E-06	1.07	2.62	0.41
O14744	ANM5_HUMAN Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	77.70	218.09	208.76	222.69	225.58	126.96	189.18	6.83E-05	5.28E-05	1.58E-05	5.64E-05	2.04E-05	1.67E-05	0.83	0.30	0.24
P13645	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	70.20	151.84	325.76	144.84	150.84	251.80	142.85	1.22E-05	3.04E-05	8.01E-06	1.58E-05	2.98E-05	4.99E-06	1.30	2.45	0.41
P01614	KV201_HUMAN Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	14.20	215.00	161.00	170.00	207.00	158.00	205.00	6.03E-03	5.27E-03	7.97E-03	5.88E-03	4.45E-03	7.54E-03	0.98	0.74	1.25
P35527	K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	69.50	146.20	232.25	163.87	159.10	197.65	147.97	7.66E-06	1.35E-05	3.79E-06	8.37E-06	1.88E-05	2.60E-06	1.09	2.45	0.34
P35908	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	86.50	119.88	168.70	145.70	125.79	160.76	136.82	6.20E-06	8.65E-06	3.64E-06	7.36E-06	1.01E-05	3.20E-06	1.19	1.63	0.52
P60709	ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	83.20	101.65	147.83	182.30	79.16	165.59	168.66	1.33E-04	1.64E-04	6.25E-05	8.30E-05	2.16E-04	4.74E-05	0.62	1.62	0.36
P05787	K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	91.70	88.34	260.71	127.29	63.62	149.97	86.51	8.43E-06	5.62E-05	5.30E-06	5.33E-06	1.58E-05	2.97E-06	0.63	1.87	0.35
Q9UPY3	DICER_HUMAN Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	61.00				215.38	293.05	231.26				2.19E-06	3.93E-06	8.74E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q15208	STK38_HUMAN Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1	76.30	104.00	134.00	109.00	93.00	98.00	101.00	1.39E-05	1.55E-05	4.70E-06	8.62E-06	8.63E-06	4.56E-06	0.62	0.62	0.33
Q14204	DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	38.70	46.00	91.00	63.00	151.00	81.00	159.00	6.49E-08	1.15E-07	2.46E-08	3.25E-07	1.86E-07	1.14E-07	5.00	2.87	1.76
Q9BQA1	MEP50_HUMAN Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	73.40	111.76	102.67	113.66	97.78	52.84	110.63	5.00E-05	3.33E-05	1.73E-05	3.47E-05	1.27E-05	1.30E-05	0.69	0.25	0.26
P08727	K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	84.50	70.88	154.72	86.91	64.40	104.86	69.94	6.54E-06	4.12E-05	3.33E-06	4.48E-06	1.16E-05	2.11E-06	0.69	1.77	0.32
P19474	RO52_HUMAN E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1	71.60	78.42	99.22	86.31	68.48	65.48	90.27	7.57E-06	7.38E-06	2.48E-06	5.02E-06	3.69E-06	3.04E-06	0.66	0.49	0.40
P49327	FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	44.10	100.00	63.00	65.00	151.00	52.00	44.00	4.90E-07	2.13E-07	5.85E-08	9.95E-07	3.00E-07	4.24E-08	2.03	0.61	0.09
E7EW20	E7EW20_HUMAN Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=2 SV=1	59.70	111.90	154.47	60.41	20.80	56.45	26.75	1.21E-06	1.63E-06	1.01E-07	1.05E-07	5.74E-07	3.78E-08	0.09	0.47	0.03
P05783	K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	72.60	36.98	129.97	66.97	31.99	92.97	41.99	2.80E-06	1.96E-05	2.27E-06	2.18E-06	7.22E-06	1.15E-06	0.78	2.58	0.41
Q9UPQ9	TNR6B_HUMAN Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	38.10	1.99			109.91	101.00	155.46	6.53E-08			3.95E-07	7.95E-07	5.29E-07	6.05	12.18	8.10

P78527	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	26.00	36.97	17.98	42.97	79.95	35.96	117.91	3.78E-08	1.79E-08	1.59E-08	1.19E-07	7.54E-08	8.42E-08	3.13	1.99	2.23
P11142	HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	55.90	24.39	24.35	19.47	57.35	92.32	77.80	4.88E-07	6.88E-07	1.84E-07	1.88E-06	6.80E-06	1.41E-06	3.85	13.94	2.88
Q15149	PLEC_HUMAN Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	33.90	24.98	150.87	48.97	9.99	53.93	12.00	2.35E-08	2.21E-07	1.36E-08	8.53E-09	1.13E-07	3.11E-09	0.36	4.79	0.13
Q9UH99	SUN2_HUMAN SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	60.50	47.51	50.44	33.65	84.14	31.66	55.42	1.81E-06	1.39E-06	3.33E-07	4.61E-06	7.77E-07	8.79E-07	2.54	0.43	0.48
O00159-3	MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	47.70	73.07	5.94	14.81	41.52	79.03	74.12	1.17E-06	2.09E-08	2.03E-08	4.10E-07	1.31E-06	4.37E-07	0.35	1.12	0.37
P23458	JAK1_HUMAN Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2	44.50	60.00	36.00	43.00	60.00	35.00	40.00	6.65E-07	2.82E-07	1.04E-07	5.23E-07	3.90E-07	1.16E-07	0.79	0.59	0.18
P13647	K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	65.90	26.89	68.71	39.78	37.85	65.73	21.89	5.47E-07	3.09E-06	3.63E-07	7.54E-07	2.56E-06	2.40E-07	1.38	4.68	0.44
Q00610	CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	40.30	65.73	26.90	39.86	72.69	8.96	33.84	4.11E-07	9.07E-08	5.24E-08	4.83E-07	4.06E-08	6.36E-08	1.18	0.10	0.15
P15924	DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	31.90	26.00	88.99	25.00	35.49	39.99	18.00	5.23E-08	2.18E-07	1.61E-08	6.86E-08	1.47E-07	1.11E-08	1.31	2.80	0.21
Q7Z406-6	MYH14_HUMAN Isoform 6 of Myosin-14 OS=Homo sapiens GN=MYH14	53.40	10.76	142.58	14.63	16.63	13.66	38.12	2.22E-08	9.13E-07	8.98E-09	3.41E-08	6.57E-08	4.07E-08	1.53	2.96	1.83
P53621	COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	52.80	17.00	26.99	17.99	155.93	5.00	19.99	1.12E-07	1.09E-07	2.31E-08	2.70E-06	2.28E-08	3.10E-08	24.07	0.20	0.28
Q9ULV0	MYO5B_HUMAN Unconventional myosin-Vb OS=Homo sapiens GN=MYO5B PE=1 SV=3	45.20	85.50	40.00	36.00	37.00	2.50		8.17E-07	1.54E-07	4.62E-08	2.27E-07	9.04E-09		0.28	0.01	Control 1 Only
P02786	TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	44.10	70.51	46.65	41.72	51.64	3.97	7.95	1.18E-06	6.59E-07	2.05E-07	6.33E-07	2.48E-08	2.67E-08	0.53	0.02	0.02
P35580	MYH10_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	52.70	28.68	130.56	13.84	3.95	8.89	22.74	8.64E-08	7.36E-07	9.58E-09	6.70E-09	2.01E-08	3.75E-08	0.08	0.23	0.43
P04792	HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	72.20	17.00	52.00	28.00	27.00	37.00	58.00	2.94E-06	9.84E-06	2.39E-06	4.74E-06	4.09E-06	7.11E-06	1.61	1.39	2.42
Q9P219	DAPLE_HUMAN Protein Daple OS=Homo sapiens GN=CCDC88C PE=1 SV=3	28.10	60.00	17.00	33.00	52.99	6.00	23.00	1.87E-07	4.29E-08	2.80E-08	1.50E-07	1.48E-08	2.16E-08	0.80	0.08	0.12
F8VPD4	F8VPD4_HUMAN CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1	28.20	6.00	30.00	19.00	34.00	41.00	60.00	1.79E-08	6.88E-08	1.84E-08	1.73E-07	2.56E-07	1.53E-07	9.63	14.25	8.52
Q13200	PSMD2_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	40.40	37.64	28.71	31.72	55.45	6.95	22.81	4.49E-07	3.57E-07	1.15E-07	8.95E-07	4.22E-08	7.80E-08	1.99	0.09	0.17
P02533	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	73.10	18.00	56.00	24.00	14.50	41.00	16.50	4.47E-07	2.64E-06	1.58E-07	4.54E-07	1.87E-06	1.21E-07	1.01	4.18	0.27
P25705	ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	55.50	31.47	39.27	28.51	35.37	15.67	20.68	2.39E-06	2.01E-06	3.25E-07	1.85E-06	4.97E-07	2.20E-07	0.78	0.21	0.09
Q16875	F263_HUMAN 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1	64.50	53.16	9.86	35.37	25.62	29.51	11.80	5.20E-06	3.25E-07	5.00E-07	1.06E-06	1.59E-06	1.34E-07	0.20	0.31	0.03
P68104	EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	30.70	24.94	24.96	23.94	28.93	39.93	31.93	1.88E-06	1.58E-06	6.42E-07	2.42E-06	2.58E-06	9.57E-07	1.29	1.37	0.51
F5H5D3	F5H5D3_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1	68.40	15.54	31.86	17.40	18.50	37.66	48.66	5.30E-06	8.71E-06	2.14E-06	6.38E-06	1.29E-05	7.14E-06	1.20	2.43	1.35
P46940	IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens	30.70	30.99	47.97	28.97	24.00	16.99	17.97	1.65E-07	2.03E-07	2.70E-08	1.16E-07	7.94E-08	1.86E-08	0.71	0.48	0.11

	GN=IQGAP1 PE=1 SV=1																
P48735	IDHP_HUMAN Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	55.50	24.80	39.65	15.85	56.58	8.93	14.86	1.14E-06	1.44E-06	1.74E-07	4.34E-06	2.24E-07	1.79E-07	3.80	0.20	0.16
Q86YZ3	HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	26.70	13.00	63.00	15.00	14.00	46.00	10.00	3.18E-08	1.32E-07	1.01E-08	3.27E-08	1.49E-07	9.07E-09	1.03	4.68	0.28
E9PLK3	E9PLK3_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1	35.60	34.57	37.57	19.78	63.26			3.14E-07	5.80E-07	3.11E-08	8.38E-07			2.67	Control 1 Only	Control 1 Only
P55060	XPO2_HUMAN Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	31.90	57.42	8.91	14.85	40.59	9.90	21.78	6.60E-07	1.06E-07	6.38E-08	4.44E-07	9.93E-08	8.14E-08	0.67	0.15	0.12
Q13085	ACACA_HUMAN Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	27.80	21.89	25.89	23.88	77.62		1.99	5.06E-08	4.43E-08	1.51E-08	3.28E-07		1.21E-09	6.48	Control 1 Only	0.02
P08238	HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	51.50	13.97	44.92	22.47	37.95	17.98	9.00	2.68E-07	1.54E-06	2.02E-07	1.31E-06	2.71E-07	5.33E-08	4.90	1.01	0.20
P07437	TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	84.00	8.91	31.68	17.82	20.79	34.65	33.66	1.53E-06	3.36E-06	1.30E-06	5.99E-06	6.89E-06	8.07E-06	3.92	4.51	5.28
P62805	H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	53.40	13.00	54.00	6.00	18.00	47.00	6.00	1.80E-06	4.36E-05	3.46E-07	7.28E-06	4.43E-05	4.63E-07	4.03	24.53	0.26
Q01813	K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	35.60	7.43	20.33	14.38	38.17	22.81	25.77	8.94E-08	4.59E-07	6.98E-08	7.87E-07	5.23E-07	1.82E-07	8.80	5.84	2.04
E7EMH5	E7EMH5_HUMAN Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=2 SV=1	44.50	4.98	32.93	20.94	12.93	1.99	61.81	4.81E-08	6.35E-07	2.19E-07	1.83E-07	7.05E-08	1.20E-06	3.80	1.47	24.87
Q8N257	H2B3B_HUMAN Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3	57.90	8.82	42.16	12.77	16.67	37.29	12.76	1.62E-06	2.87E-05	1.17E-06	1.01E-05	2.56E-05	1.51E-06	6.21	15.81	0.93
P11940	PABP1_HUMAN Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	51.40	4.82	6.74	1.94	42.42	36.63	32.85	4.88E-08	1.07E-07	4.33E-09	1.58E-06	1.07E-06	5.16E-07	32.28	21.84	10.57
Q08211	DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	34.40	2.00	7.00	13.00	89.00	2.00	16.00	8.85E-09	2.30E-08	1.66E-08	1.09E-06	8.66E-09	3.82E-08	123.40	0.98	4.31
P06493	CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	56.60	24.86	26.87	9.93	46.78	2.99	12.91	3.62E-06	2.56E-06	4.21E-07	8.04E-06	2.56E-07	4.92E-07	2.22	0.07	0.14
Q16531	DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	28.70	19.70	11.83	17.73	30.52	20.69	25.66	1.37E-07	5.72E-08	3.10E-08	2.22E-07	1.42E-07	8.79E-08	1.62	1.04	0.64
P11021	GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	53.70	13.00	12.00	7.00	20.00	36.00	28.00	2.39E-07	2.13E-07	5.71E-08	4.29E-07	1.08E-06	2.93E-07	1.79	4.50	1.22
P17858	K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	41.80	5.00	21.50	7.50	30.00	22.50	29.50	1.02E-07	4.14E-07	3.75E-08	1.11E-06	5.01E-07	2.23E-07	10.90	4.90	2.18
E7ESA8	E7ESA8_HUMAN U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=2 SV=1	40.00	21.58	15.73	19.65	30.45	11.80	15.72	1.51E-06	7.58E-07	3.76E-07	2.54E-06	3.81E-07	4.78E-07	1.68	0.25	0.32
Q9NQX4	MYO5C_HUMAN Unconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	27.20	45.83	28.86	21.89	11.93		0.99	2.95E-07	9.76E-08	2.74E-08	3.76E-08		1.13E-09	0.13	Control 1 Only	0.00
P07900	HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	44.70	8.98	24.87	12.94	34.91	13.94	11.95	1.28E-07	5.48E-07	6.62E-08	6.32E-07	2.26E-07	6.37E-08	4.94	1.76	0.50
Q9Y2H1	ST38L_HUMAN Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3	46.80	25.83	13.93	24.86	18.89	5.96	14.94	1.34E-06	4.25E-07	2.54E-07	8.06E-07	1.16E-07	1.33E-07	0.60	0.09	0.10
Q9NYL9	TMOD3_HUMAN Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1	45.20	20.93	15.94	11.98	15.94	20.93	16.97	1.46E-06	8.14E-07	3.04E-07	7.07E-07	1.20E-06	3.63E-07	0.48	0.82	0.25

Q14974	IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	21.70	21.89	16.91	10.93	21.87	9.96	17.89	3.90E-07	2.07E-07	3.75E-08	3.06E-07	1.14E-07	8.67E-08	0.78	0.29	0.22
P49411	EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	48.90	4.00	29.00	27.00	5.00	16.00	20.00	8.24E-08	1.16E-06	5.46E-07	9.39E-08	5.90E-07	4.93E-07	1.14	7.17	5.98
P06576	ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	46.30	20.77	23.73	20.78	15.80	5.93	9.92	7.17E-07	7.92E-07	2.12E-07	5.39E-07	8.66E-08	9.17E-08	0.75	0.12	0.13
P52272	HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	45.40	5.93	38.50	8.91	20.73	10.86	10.87	5.12E-07	8.90E-07	3.86E-08	7.29E-07	1.37E-07	5.19E-08	1.42	0.27	0.10
P53618	COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	35.30	10.00	3.00	1.00	24.99	32.97	25.99	9.31E-08	2.83E-08	8.98E-10	2.45E-07	4.46E-07	1.05E-07	2.63	4.79	1.12
P68032	ACTC_HUMAN Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	47.20	16.67	17.65	15.70	14.70	20.59	10.79	6.31E-06	6.11E-06	1.41E-06	3.00E-06	5.62E-06	1.48E-06	0.48	0.89	0.23
F5H335	F5H335_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1	25.70	24.00	19.00	12.00	38.00			1.85E-07	7.97E-08	8.49E-09	2.77E-07			1.50	Control 1 Only	Control 1 Only
P08779	K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	71.70	9.00	39.00	10.00	6.00	18.00	7.00	1.16E-07	1.57E-06	6.59E-08	9.13E-08	6.04E-07	3.58E-08	0.79	5.21	0.31
Q6ZRV2	FA83H_HUMAN Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3	30.70	2.00		1.00	39.00	22.00	30.00	5.46E-09		6.75E-10	2.56E-07	1.99E-07	1.06E-07	46.84	36.50	19.44
Q86VP6	CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	28.10	32.92	4.00	6.99	28.92	1.00	15.97	3.13E-07	2.24E-08	6.81E-09	2.22E-07	4.38E-09	2.96E-08	0.71	0.01	0.09
Q92673	SORL_HUMAN Sortilin-related receptor OS=Homo sapiens GN=SORL1 PE=1 SV=2	21.60				1.99	25.92	63.77				3.12E-09	1.13E-07	1.05E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B7Z6Z4	B7Z6Z4_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	65.50	7.88	40.35	5.90	6.90	19.68	6.89	1.22E-06	1.27E-05	1.47E-07	8.55E-07	3.19E-06	2.18E-07	0.70	2.61	0.18
P07814	SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	20.10	21.00	8.00	19.00	23.00		14.00	1.12E-07	4.11E-08	1.88E-08	1.16E-07		1.64E-08	1.03	Control 1 Only	0.15
P20671	H2A1D_HUMAN Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2	40.80	4.08	19.44	4.56	8.08	14.99	5.07	6.77E-07	1.06E-05	2.28E-07	4.45E-06	9.92E-06	1.82E-07	6.57	14.65	0.27
Q14766	LTBP1_HUMAN Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=1 SV=4	20.20	4.92	1.96	3.94	25.50	12.76	37.33	9.29E-09	1.03E-08	4.56E-09	8.00E-08	1.02E-07	7.71E-08	8.62	10.95	8.30
Q5SWX8	ODR4_HUMAN Protein odr-4 homolog OS=Homo sapiens GN=ODR4 PE=2 SV=1	35.00	10.89	5.94	10.89	24.75	13.86	17.82	4.21E-07	1.94E-07	1.15E-07	1.06E-06	5.16E-07	2.16E-07	2.53	1.23	0.51
E9PDF6	E9PDF6_HUMAN Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=2 SV=1	33.60	15.93	12.94	3.99	25.90	13.95	6.97	7.57E-08	5.64E-08	5.75E-09	1.93E-07	1.05E-07	1.21E-08	2.55	1.39	0.16
O15084	ANR28_HUMAN Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A OS=Homo sapiens GN=ANKRD28 PE=1 SV=5	23.20	20.38	7.95	13.93	23.90	3.98	9.96	1.91E-07	5.96E-08	1.91E-08	1.83E-07	2.67E-08	1.33E-08	0.96	0.14	0.07
P23396	RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	72.00	1.93	3.89	2.90	43.99	12.65	14.60	9.67E-08	1.48E-07	3.02E-08	5.96E-06	5.75E-07	2.51E-07	61.59	5.94	2.60
J3KNL6	J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=2 SV=1	14.90	5.00	6.00	1.00	26.00	19.00	23.00	3.04E-08	1.60E-08	1.39E-09	5.35E-08	1.06E-07	3.93E-08	1.76	3.50	1.29
Q15633	TRBP2_HUMAN RISC-loading complex subunit TARBP2 OS=Homo sapiens GN=TARBP2 PE=1 SV=3	41.70				16.94	33.81	28.85				1.13E-06	3.44E-06	6.01E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
O43242	PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo	47.60	7.99	13.00	11.00	30.94	7.00	9.99	1.50E-07	2.73E-07	7.07E-08	1.11E-06	1.04E-07	7.81E-08	7.40	0.69	0.52

	sapiens GN=PSMD3 PE=1 SV=2																
J3KMW7	J3KMW7_HUMAN E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=2 SV=1	17.00	1.00	2.97	6.98	3.00	2.98	54.90	1.33 E-09	7.86 E-08	1.19 E-08	8.59 E-09	6.05 E-09	8.76 E-08	6.46	4.55	65.86
O94832	MYO1D_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2	30.90	26.73	5.94	11.88	4.95	4.95	17.84	2.88 E-07	5.69 E-08	1.93 E-08	2.90 E-08	4.49 E-08	4.74 E-08	0.10	0.16	0.16
Q92616	GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	15.70	19.00	4.00	1.00	28.00	6.00	15.00	4.48 E-08	8.22 E-09	7.06 E-10	6.35 E-08	8.77 E-09	9.87 E-09	1.42	0.20	0.22
P42704	LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	28.30	44.84	3.00	5.99	7.98		10.97	2.69 E-07	5.85 E-09	7.46 E-09	2.68 E-08		1.57 E-08	0.10	Control 1 Only	0.06
Q9UHB6	LIMA1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	36.10	35.53	12.85	5.92	0.99	16.79		3.51 E-07	1.80 E-07	1.15 E-08	1.34 E-09	2.36 E-07		0.00	0.67	Control 1 Only
Q8NDV7-6	TNR6A_HUMAN Isoform 6 of Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A	16.00				15.80	26.67	29.66				4.67 E-08	1.62 E-07	8.02 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P33993	MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	52.30	3.99	7.96	3.98	40.82	6.96	7.95	4.08 E-08	9.16 E-08	1.18 E-08	1.25 E-06	5.67 E-08	4.12 E-08	30.52	1.39	1.01
P50416	CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	27.60	2.00	8.99	3.00	18.98	16.99	18.98	1.94 E-08	1.05 E-07	9.36 E-09	2.25 E-07	2.22 E-07	1.14 E-07	11.59	11.47	5.88
Q15645	PCH2_HUMAN Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	31.90	7.94	16.93	7.97	9.94	9.93	17.93	3.44 E-07	6.25 E-07	5.85 E-08	4.46 E-07	5.52 E-07	2.05 E-07	1.30	1.61	0.59
P52597	HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	39.80	6.94	6.94	3.98	22.84	14.86	16.90	3.74 E-07	3.02 E-07	1.38 E-07	2.30 E-06	1.09 E-06	6.81 E-07	6.16	2.92	1.82
P58107	EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	33.10	5.00	22.00	1.00	25.00	14.00		1.80 E-08	2.31 E-08	1.97 E-10	5.23 E-08	2.62 E-08		2.91	1.46	Control 1 Only
Q12965	MYO1E_HUMAN Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2	23.60	4.98	23.96	21.94	1.99		16.97	2.34 E-08	1.77 E-07	3.78 E-08	8.71 E-09		2.87 E-08	0.37	Control 1 Only	1.22
Q7Z6Z7	HUWE1_HUMAN E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	10.80	4.99	19.86	7.95	25.89		2.97	3.51 E-09	2.23 E-08	1.80 E-09	4.70 E-08		6.41 E-10	13.38	Control 1 Only	0.18
Q00325	MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	21.10	8.00	14.00	8.00	5.00	18.00	15.00	3.62 E-07	6.83 E-07	9.37 E-08	2.99 E-07	1.06 E-06	2.49 E-07	0.83	2.94	0.69
P41252	SYIC_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	19.30	19.92	12.94	11.93	18.92		0.99	1.54 E-07	4.92 E-08	9.37 E-09	1.34 E-07		4.82 E-10	0.87	Control 1 Only	0.00
P0CG38	POTEI_HUMAN POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1	11.30	9.90	14.85	7.92	5.94	17.81	9.89	9.04 E-08	3.13 E-07	4.80 E-08	3.85 E-08	3.96 E-07	5.69 E-08	0.43	4.38	0.63
K7EIJ6	K7EIJ6_HUMAN Unconventional myosin-Vb (Fragment) OS=Homo sapiens GN=MYO5B PE=4 SV=1	44.70	18.50	6.00	4.00	6.00	0.50		3.25 E-07	3.99 E-08	1.26 E-08	6.70 E-08	6.05 E-09		0.21	0.02	Control 1 Only
Q96P70	IPO9_HUMAN Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	20.30	15.00	3.00	2.00	27.00	3.00	13.00	2.18 E-07	1.75 E-08	1.35 E-09	2.88 E-07	1.61 E-08	4.53 E-08	1.32	0.07	0.21
P52701	MSH6_HUMAN DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2	21.60		2.97	4.95	25.73	3.96	18.81		8.08 E-09	3.24 E-09	1.24 E-07	1.45 E-08	3.00 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q13045	FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	20.00	8.89	16.80	10.88	16.78	0.99	6.92	4.84 E-08	6.39 E-08	1.70 E-08	1.43 E-07	5.26 E-09	1.27 E-08	2.95	0.11	0.26

F8W1S1	F8W1S1_HUMAN Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=2 SV=1	15.30	8.56	6.93	6.02	8.20	6.93	4.41	2.60E-07	2.47E-07	5.47E-08	3.00E-07	2.39E-07	3.61E-08	1.15	0.92	0.14
P05388	RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	38.20	3.84	12.57	0.97	24.04	12.55	8.73	6.48E-08	4.65E-07	4.21E-09	2.60E-06	5.72E-07	5.04E-07	40.08	8.83	7.78
A8MUB1	A8MUB1_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1	64.70	0.97	6.83	7.82	8.79	12.71	23.57	4.11E-08	2.99E-07	3.82E-07	1.51E-06	5.27E-07	1.81E-06	36.62	12.81	43.96
Q92900	RENT1_HUMAN Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	33.70				27.00	1.00	32.99				1.28E-07	4.80E-09	7.03E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P05164	PERM_HUMAN Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	38.50		1.00			58.99			2.53E-09			2.00E-06			Sample 2 Only	
P16615	AT2A2_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	23.00	7.99	4.98	6.98	20.94	5.97	15.92	3.51E-08	4.21E-08	2.13E-08	1.06E-07	5.95E-08	4.16E-08	3.02	1.69	1.18
P01859	IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	44.80	8.00	6.50	6.00	7.00	17.50	6.00	5.33E-06	8.22E-06	1.95E-06	4.96E-06	4.80E-06	1.77E-06	0.93	0.90	0.33
F8WE88	F8WE88_HUMAN Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=2 SV=1	25.00	31.90	18.91	5.98	2.99			7.90E-08	5.00E-08	3.14E-09	3.93E-09			0.05	Control 1 Only	Control 1 Only
P46781	RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	57.20	4.99	3.00	1.00	36.93	4.99	2.00	6.85E-07	3.88E-07	1.13E-07	1.58E-05	5.04E-07	1.85E-08	23.01	0.73	0.03
P62191	PRS4_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	51.40	6.99	11.99	6.00	23.97	3.00	4.00	2.43E-07	3.65E-07	8.12E-08	1.42E-06	6.91E-08	4.14E-08	5.82	0.28	0.17
P01833	PIGR_HUMAN Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4	34.30		7.00			52.00			5.39E-08			3.24E-06			Sample 2 Only	
P00338	LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	31.60	14.72	10.77	7.87	20.67	3.93		7.35E-07	6.70E-07	1.14E-07	1.76E-06	2.37E-07		2.39	0.32	Control 1 Only
P43686	PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	51.00	6.00	4.00	11.00	19.00	3.00	14.00	1.87E-07	1.06E-07	7.70E-08	9.39E-07	8.39E-08	1.27E-07	5.02	0.45	0.68
P02545	LMNA_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	48.80	4.98	35.74	3.96	1.00	3.97	3.96	5.31E-08	8.29E-07	9.70E-09	8.50E-09	2.56E-08	1.04E-08	0.16	0.48	0.20
Q99460	PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	35.10	2.00	3.00	14.99	13.00		17.99	1.32E-08	8.91E-09	2.28E-08	1.09E-07		3.33E-08	8.32	Control 1 Only	2.53
Q9UHL4	DPP2_HUMAN Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3	20.50	7.95	3.96	2.98	14.92	1.98	12.94	1.90E-07	8.43E-08	2.11E-08	4.31E-07	4.00E-08	1.71E-07	2.26	0.21	0.90
P08107	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	31.00	1.97	3.95	1.98	4.93	23.72	7.90	2.02E-08	7.35E-08	8.22E-09	9.73E-08	6.17E-07	6.12E-08	4.80	30.48	3.02
P61247	RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	58.30	0.96			42.78		1.95	2.26E-08			5.41E-06		1.78E-08	239.65	Control 1 Only	0.79
Q5VY93	Q5VY93_HUMAN Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=2 SV=1	31.50		3.00		45.00				1.74E-08		4.35E-07			Sample 1 Only		
Q9UJW0	DCTN4_HUMAN Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1	33.30	8.97	16.93	12.97	8.95	1.00		2.66E-07	1.01E-06	1.04E-07	2.89E-07	1.71E-08		1.09	0.06	Control 1 Only
P40939	ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	36.60	4.00	12.00	3.00	28.00	1.00	1.00	1.02E-07	1.46E-07	1.10E-08	8.31E-07	1.09E-08	4.49E-09	8.12	0.11	0.04
P18124	RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	44.00	1.00	6.00	3.99	15.92	6.99	10.95	4.03E-08	3.15E-07	4.55E-08	2.44E-06	3.38E-07	2.96E-07	60.71	8.40	7.36
O43175	SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens	23.60	9.00	8.98	5.00	8.00	4.98	10.98	3.04E-07	1.93E-07	4.04E-08	2.37E-07	1.26E-07	1.18E-07	0.78	0.41	0.39

	GN=PHGDH PE=1 SV=4																
P01876	IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	30.90		8.50			20.50			2.86 E-07			6.24 E-06			Sample 2 Only	
P26641	EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	28.80	8.00	9.00	5.00	9.00	8.00	7.00	2.24 E-07	2.20 E-07	7.79 E-08	2.54 E-07	2.21 E-07	1.43 E-07	1.13	0.99	0.64
H0YEN5	H0YEN5_HUMAN 40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=2 SV=1	59.00		0.98		37.37	1.96	3.93		3.63 E-08		8.90 E-06	7.64 E-08	5.32 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P35998	PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	38.10	5.00	7.00	10.00	17.00		7.00	9.48 E-08	1.29 E-07	8.52 E-08	4.98 E-07		7.69 E-08	5.25	Control 1 Only	0.81
P54136	SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	37.00	5.94	11.90	2.97	22.86	1.00		1.20 E-07	1.60 E-07	1.42 E-08	4.85 E-07	7.20 E-09		4.03	0.06	Control 1 Only
P02538	K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	63.30	3.49	18.44	3.98	4.98	10.48	1.99	4.42 E-08	1.30 E-06	3.17 E-08	1.45 E-07	6.89 E-07	1.42 E-08	3.28	15.60	0.32
Q9C0C2	TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	18.00				8.00	2.00	34.00				1.88 E-08	6.70 E-09	7.49 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P05109	S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	62.40		7.00	1.00		34.00			4.94 E-07	1.35 E-08		2.28 E-05			Sample 2 Only	
P14923	PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	29.90	1.99	19.98	6.99	0.99	10.98	2.00	1.11 E-08	2.37 E-07	9.82 E-09	3.45 E-09	9.49 E-08	1.71 E-09	0.31	8.56	0.15
B4DWJ2	B4DWJ2_HUMAN Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=2 SV=1	25.40	6.99	8.99	6.99	18.97			5.95 E-08	7.94 E-08	1.91 E-08	3.83 E-07			6.44	Control 1 Only	Control 1 Only
K7ERE3	K7ERE3_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=2 SV=1	42.90	1.96	13.36	5.45	5.93	11.39	1.96	6.59 E-08	6.86 E-07	5.52 E-08	1.23 E-07	4.65 E-07	1.74 E-08	1.87	7.05	0.26
E9PKF6	E9PKF6_HUMAN Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=2 SV=1	13.80	7.92	5.94		14.85	5.94	5.94	4.70 E-08	9.13 E-08		1.40 E-07	3.79 E-08	1.30 E-08	2.98	0.81	0.28
F8WCY5	F8WCY5_HUMAN Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=2 SV=1	34.70	2.00		1.00	3.99	24.98	7.00	1.62 E-07		6.92 E-09	2.57 E-07	8.79 E-07	1.89 E-07	1.59	5.42	1.16
P50502	F10A1_HUMAN Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	25.20	8.92	4.95	6.93	7.93	3.96	8.93	6.97 E-07	1.55 E-07	1.47 E-07	7.11 E-07	1.23 E-07	1.82 E-07	1.02	0.18	0.26
P55884	EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	16.80	7.99	8.00	11.00	13.99	1.00	1.00	8.00 E-08	6.92 E-08	2.31 E-08	1.66 E-07	8.08 E-09	1.07 E-09	2.08	0.10	0.01
Q9H4A4	AMPB_HUMAN Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2	36.00	5.00	12.97	1.00	24.93			5.24 E-08	1.52 E-07	2.10 E-09	8.44 E-07			16.11	Control 1 Only	Control 1 Only
P10412	H14_HUMAN Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	34.20		26.94			15.97			2.03 E-06			1.51 E-06			Sample 2 Only	
P31025	LCN1_HUMAN Lipocalin-1 OS=Homo sapiens GN=LCN1 PE=1 SV=1	28.40		19.00			23.00			2.63 E-06			3.81 E-06			Sample 2 Only	
Q7L576	CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	17.30	5.88	5.89	3.94	25.53			2.16 E-08	2.27 E-08	4.13 E-09	1.68 E-07			7.77	Control 1 Only	Control 1 Only
O95373	IPO7_HUMAN Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	15.30	14.00		4.00	14.00	1.00	7.00	1.41 E-07		4.34 E-09	1.17 E-07	5.04 E-09	1.41 E-08	0.83	0.04	0.10
F8VSC5	F8VSC5_HUMAN SCY1-like protein 2 (Fragment) OS=Homo sapiens GN=SCYL2 PE=2 SV=1	27.00	11.00	9.00	12.00	5.00	1.00	1.00	1.97 E-07	1.30 E-07	1.71 E-07	9.85 E-08	1.06 E-08	2.01 E-09	0.50	0.05	0.01
P36578	RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	25.50	0.99	2.98	2.99	19.88	1.99	10.96	2.09 E-08	6.84 E-08	1.10 E-08	1.01 E-06	4.71 E-08	1.06 E-07	48.49	2.26	5.07
P81605	DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	42.70	1.00	13.00	2.00		20.00	2.00	1.59 E-07	1.90 E-06	4.81 E-08		5.65 E-06	4.09 E-08	Control 1 Only	35.52	0.26

Q9HCE1	MOV10_HUMAN Putative helicase MOV-10 OS=Homo sapiens GN=MOV10 PE=1 SV=2	26.00				14.88	3.97	21.82				1.19E-07	2.23E-08	5.15E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P08237	K6PF_HUMAN 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	25.30	0.99	9.87	0.99	13.83	8.87	4.93	8.74E-09	8.92E-08	1.67E-09	2.73E-07	1.46E-07	4.06E-08	31.27	16.68	4.64
B4DEB1	B4DEB1_HUMAN Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1	29.30	2.00	9.00	4.00	5.00	8.00	6.00	1.06E-06	8.50E-06	2.40E-07	5.07E-06	1.21E-05	6.53E-07	4.78	11.38	0.62
M0R210	M0R210_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=2 SV=1	72.90	1.97	3.95		27.85	4.95		1.81E-07	3.69E-07		1.38E-05	5.21E-07		76.63	2.88	Control 1 Only
P01834	IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	88.70		6.00			32.00			2.50E-07			1.01E-05			Sample 2 Only	
P62195	PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	49.00	3.96	6.90	5.95	10.88	3.98	5.93	1.02E-07	1.30E-07	7.75E-08	3.99E-07	7.22E-08	1.17E-07	3.90	0.71	1.15
Q9NZ32	ARP10_HUMAN Actin-related protein 10 OS=Homo sapiens GN=ACTR10 PE=1 SV=1	31.90	7.99	13.97	8.97	6.98		1.00	3.82E-07	6.92E-07	1.01E-07	3.55E-07		6.40E-09	0.93	Control 1 Only	0.02
B4DL14	B4DL14_HUMAN ATP synthase subunit gamma OS=Homo sapiens GN=ATP5C1 PE=2 SV=1	36.40	7.00	11.00	3.00	11.00	2.00	3.00	5.75E-07	8.59E-07	6.26E-08	8.40E-07	1.06E-07	6.36E-08	1.46	0.18	0.11
P13639	EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	16.70	2.00	9.00	3.00	14.00	6.00	4.00	1.47E-08	1.55E-07	4.48E-09	1.74E-07	6.42E-08	7.24E-09	11.80	4.36	0.49
Q04695	K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	61.30		25.47			8.02			6.36E-07			3.25E-07			Sample 2 Only	
O75340	PDCD6_HUMAN Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	29.80	10.95	5.98	2.98	8.96	4.98	3.98	2.17E-06	1.18E-06	4.02E-08	1.76E-06	4.26E-07	5.44E-08	0.81	0.20	0.03
H3BRG4	H3BRG4_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=2 SV=1	38.80	2.99	3.97	3.97	9.97	3.97	11.94	5.04E-08	8.71E-08	4.74E-08	1.77E-07	1.09E-07	1.01E-07	3.52	2.16	2.00
P01625	KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	27.20	5.00	6.00	5.00	5.00	7.00	5.00	2.99E-06	3.75E-06	7.42E-07	2.23E-06	2.72E-06	2.76E-07	0.75	0.91	0.09
Q8N3C0	ASCC3_HUMAN Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3	14.20	1.00			35.00		1.00	1.50E-08			1.05E-07		9.22E-10	6.97	Control 1 Only	0.06
P38646	GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	28.40	4.99	5.00		6.98	13.97	4.00	8.46E-08	6.54E-08		9.50E-08	2.05E-07	1.57E-08	1.12	2.43	0.19
P68371	TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	83.80	4.00	5.00	4.00	6.00	7.00	10.00	5.51E-07	9.46E-07	3.69E-07	1.98E-06	2.28E-06	2.24E-06	3.60	4.14	4.07
P06702	S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	71.10		7.00			28.00			3.75E-07			1.65E-05			Sample 2 Only	
O00571	DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	24.50	4.99	4.00		15.98	4.99	2.00	7.91E-08	4.19E-08		4.45E-07	7.16E-08	6.81E-09	5.63	0.91	0.09
P14618	KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	38.00		1.20		0.60	19.23			1.25E-08		5.08E-09	4.00E-07		Sample 1 Only	Sample 2 Only	
P14868	SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	33.20	7.99	3.00	6.00	14.99		1.00	1.72E-07	7.47E-08	3.17E-08	4.08E-07		5.00E-09	2.37	Control 1 Only	0.03
G3XAB8	G3XAB8_HUMAN Trinucleotide repeat containing 6C, isoform CRA_a OS=Homo sapiens GN=TNRC6C PE=2 SV=1	14.30				5.00	8.00	21.00				6.35E-09	5.06E-08	2.64E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P04406	G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	53.20	1.00	4.00	2.00	1.00	24.98	1.00	1.68E-08	7.93E-08	6.39E-09	1.29E-08	1.75E-06	2.18E-09	0.77	104.17	0.13

Q9Y285	SYFA_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3	27.40	4.94	2.97		20.71	3.94		1.17E-07	5.91E-08		9.39E-07	7.63E-08		8.05	0.65	Control 1 Only
C9J9K3	C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	36.70	3.00	3.00	2.00	6.99	6.00	9.99	1.08E-07	1.37E-07	3.49E-08	1.37E-06	3.96E-07	3.62E-07	12.70	3.68	3.36
P08729	K2C7_HUMAN Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	49.70		23.66	2.00		5.00	2.00		7.21E-07	1.70E-08		7.72E-08	1.11E-08		Sample 2 Only	Sample 3 Only
P67809	YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	45.40		2.98		12.90	4.96	10.92		7.33E-08		7.06E-07	2.42E-07	2.74E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q92973	TNPO1_HUMAN Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	16.10	9.93	2.97	1.98	6.92		6.96	1.35E-07	2.04E-08	5.16E-09	5.63E-08		2.11E-08	0.42	Control 1 Only	0.16
B4E2W0	B4E2W0_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1	22.80	2.97	1.97	3.95	17.80	0.99	2.97	1.13E-07	8.47E-08	3.23E-08	9.17E-07	3.94E-08	1.40E-08	8.12	0.35	0.12
E9PFW3	E9PFW3_HUMAN AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=2 SV=1	30.50		2.97	0.99	14.91	1.98	4.97		5.27E-08	7.34E-09	1.00E-06	3.53E-08	6.28E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B0FLL2	B0FLL2_HUMAN 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 2 transcript variant 3 OS=Homo sapiens GN=PFKFB2 PE=2 SV=1	39.10	14.88	1.00	3.96	5.94	4.96		3.49E-07	1.35E-08	1.87E-08	1.48E-07	1.61E-07		0.43	0.46	Control 1 Only
P62906	RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	44.70		5.00	1.00	19.00	2.00	3.00		2.02E-07	6.30E-09	1.08E-06	8.97E-08	3.68E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4DZI8	B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	14.80			0.99	23.99	1.00	1.99			8.57E-10	2.00E-07	2.56E-09	2.95E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P21266	GSTM3_HUMAN Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	39.10	13.95	3.98	0.99	6.96	1.99		2.13E-06	2.74E-07	1.30E-08	1.63E-06	1.03E-07		0.77	0.05	Control 1 Only
P62753	RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	35.30	1.00			26.94	1.00		1.94E-08			4.19E-06	4.17E-08		215.65	2.14	Control 1 Only
P63244	GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	26.80		1.94		9.68	5.81	10.63		6.03E-08		3.79E-07	2.08E-07	1.07E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q16822	PCKGM_HUMAN Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3	19.80	4.94	5.90	2.97	12.82		0.99	1.15E-07	8.85E-08	5.47E-09	3.76E-07		9.62E-10	3.26	Control 1 Only	0.01
Q8NHQ1	CEP70_HUMAN Centrosomal protein of 70 kDa OS=Homo sapiens GN=CEP70 PE=1 SV=2	15.20	4.95	1.98	1.98	9.90	2.97	1.98	1.05E-07	1.70E-08	1.22E-08	2.66E-07	3.75E-08	1.05E-08	2.53	0.36	0.10
Q96CU9	FXRD1_HUMAN FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=1 SV=2	15.90	11.88	3.96	2.97	6.93		2.97	4.47E-07	9.26E-08	2.48E-08	1.89E-07		1.88E-08	0.42	Control 1 Only	0.04
C9J2Y9	C9J2Y9_HUMAN DNA-directed RNA polymerase OS=Homo sapiens GN=POLR2B PE=2 SV=2	20.90		2.00	1.00	12.00		12.99		1.09E-08	8.21E-10	3.63E-08		1.91E-08	Sample 1 Only		Sample 3 Only
P39023	RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	16.60		0.99	1.97	15.85	1.98	6.93		3.09E-08	7.57E-09	8.78E-07	6.06E-08	8.69E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P01024	CO3_HUMAN Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	18.60	1.00	2.00			26.00		1.14E-08	7.13E-09			1.50E-07		Control 1 Only	13.14	Control 1 Only
P62917	RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	28.00	0.99	3.94	0.99	9.89	3.95	7.89	3.78E-08	3.17E-07	8.85E-09	1.67E-06	3.05E-07	1.16E-07	44.32	8.06	3.07
B3KXW5	B3KXW5_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=2 SV=1	15.70	3.96	5.94	1.98	7.91	4.95	0.99	2.73E-08	5.42E-08	1.74E-09	1.23E-07	3.97E-08	8.01E-10	4.51	1.45	0.03
Q9P2R3	ANFY1_HUMAN Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo	17.50	1.98	4.99	10.99	7.97			4.51E-09	1.71E-08	1.14E-08	4.20E-08			9.32	Control 1 Only	Control 1 Only

	sapiens GN=ANKFY1 PE=1 SV=2																
P16401	H15_HUMAN Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	36.30		17.00			9.00	1.00		1.40E-06			7.97E-07	7.66E-09		Sample 2 Only	Sample 3 Only
B7Z817	B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1	9.10	3.98	1.00	2.00	6.97	3.99	4.98	1.12E-07	1.64E-08	6.24E-09	3.13E-07	1.82E-07	2.46E-08	2.79	1.63	0.22
E7EX17	E7EX17_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=2 SV=1	12.60	9.87	0.99	0.98	11.84	0.99	0.98	2.26E-07	5.04E-09	2.72E-09	3.28E-07	5.17E-09	7.87E-09	1.45	0.02	0.03
M0QZC5	M0QZC5_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=2 SV=1	67.80	1.00	2.00	1.00	15.00	5.00	3.00	1.48E-07	3.63E-07	2.32E-08	9.95E-06	5.54E-07	1.76E-07	67.44	3.76	1.20
B0YJC4	B0YJC4_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=2 SV=1	48.70					26.86						7.98E-07			Sample 2 Only	
Q9Y6Q5	AP1M2_HUMAN AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2 PE=1 SV=4	36.40	0.98	2.97	1.98	13.82	2.97	3.94	1.11E-08	6.57E-08	2.36E-08	5.29E-07	1.06E-07	2.78E-08	47.91	9.60	2.51
P17655	CAN2_HUMAN Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6	13.20	1.00	1.00		10.00	7.00	3.00	7.57E-09	1.06E-08		1.52E-07	9.50E-08	7.17E-09	20.10	12.56	0.95
P33992	MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	21.50		4.99	2.99	16.96	0.99			4.76E-08	8.66E-09	3.42E-07	6.22E-09		Sample 1 Only	Sample 2 Only	
J3QRS3	J3QRS3_HUMAN Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=2 SV=1	66.70	5.00	7.00	3.00	4.00	2.00	5.00	5.58E-07	2.33E-06	1.57E-07	3.41E-07	3.68E-07	3.19E-07	0.61	0.66	0.57
P62277	RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	48.30	1.00	2.00	1.00	15.96	3.00	1.00	1.17E-07	1.47E-07	7.63E-09	8.20E-06	2.92E-07	1.83E-08	70.09	2.50	0.16
P62701	RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	38.80	1.00	3.00		14.93	4.00	2.98	2.53E-08	1.52E-07		1.21E-06	1.59E-07	2.41E-08	47.70	6.28	0.95
Q9BUF5	TBB6_HUMAN Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	68.60	0.99		0.99	3.98	10.98	8.95	1.31E-08		5.99E-09	8.72E-08	2.43E-07	4.87E-07	6.67	18.59	37.23
Q9Y678	COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	15.20	4.99	1.00	1.00	14.98	2.00		8.02E-08	4.35E-09	1.89E-09	2.81E-07	3.26E-08		3.50	0.41	Control 1 Only
P62241	RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	48.40				24.00						2.16E-06			Sample 1 Only		
P42025	ACTY_HUMAN Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1	27.10	1.50	4.50	2.50	2.00	1.50	0.50	5.10E-08	2.02E-07	3.13E-08	7.84E-08	4.20E-08	6.79E-09	1.54	0.82	0.13
Q8TDL5	BPIB1_HUMAN BPI fold-containing family B member 1 OS=Homo sapiens GN=BPIFB1 PE=2 SV=1	38.40		1.00			23.00			6.17E-09			7.69E-07			Sample 2 Only	
Q9Y265	RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	40.80		5.94	1.00		4.95	11.91		8.08E-08	5.39E-09		7.95E-08	1.95E-07		Sample 2 Only	Sample 3 Only
P06733	ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	42.40		1.98			21.93			2.11E-08			8.62E-07			Sample 2 Only	
J3KN39	J3KN39_HUMAN NACHT, LRR and PYD domains-containing protein 2 OS=Homo sapiens GN=NLRP2 PE=2 SV=1	8.80	3.97	2.97	2.97	13.88			1.00E-08	1.19E-08	3.43E-09	8.02E-08			8.00	Control 1 Only	Control 1 Only
P00738	HPT_HUMAN Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	37.90		3.94			18.72			3.51E-08			8.15E-07			Sample 2 Only	
P04083	ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	50.60		1.00			22.92			1.01E-08			2.34E-06			Sample 2 Only	
Q8TEX9	IPO4_HUMAN Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2	10.70	8.88	0.99		9.86		1.96	4.66E-08	4.58E-09		8.04E-08		1.98E-09	1.73	Control 1 Only	0.04
P30050	RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	52.70		3.00	1.00	5.00	4.00	5.00		2.40E-07	9.00E-10	9.89E-07	4.19E-07	1.21E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
H0Y4R1	H0Y4R1_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo	31.90	1.99	15.98	4.99				8.51E-08	4.93E-07	5.03E-08				Control 1 Only	Control 1 Only	Control 1 Only

	sapiens GN=IMPDH2 PE=3 SV=1																
O00743	PPP6_HUMAN Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1	20.80	5.00	1.00		9.00	2.00	4.00	2.14 E-07	3.57 E-08		4.70 E-07	7.59 E-08	2.37 E-08	2.20	0.36	0.11
P62269	RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	46.10		1.00		16.00	4.00	1.00		1.18 E-07		8.29 E-06	3.27 E-07	4.69 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9H9G7	AGO3_HUMAN Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	14.00				3.00	15.00	5.00				4.04 E-07	2.49 E-06	1.49 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P12273	PIP_HUMAN Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	42.50		10.00			12.00			5.80 E-07			2.08 E-06			Sample 2 Only	
Q9BRS2	RIOK1_HUMAN Serine/threonine-protein kinase RIO1 OS=Homo sapiens GN=RIOK1 PE=1 SV=2	13.90	6.00	1.00	3.00	9.00		2.00	1.54 E-07	5.54 E-09	2.84 E-08	3.18 E-07		1.17 E-08	2.06	Control 1 Only	0.08
B4E022	B4E022_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=2 SV=1	34.50		1.00			19.99			6.75 E-10			3.57 E-07			Sample 2 Only	
P17987	TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	23.40	2.97	1.00	1.00	13.88	1.00	0.99	3.06 E-08	1.26 E-08	2.04 E-09	2.33 E-07	1.40 E-08	1.75 E-09	7.63	0.46	0.06
O95163	ELP1_HUMAN Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	14.30	1.00	1.00		13.00	2.00	4.00	3.30 E-09	2.49 E-09		6.53 E-08	7.34 E-09	5.92 E-09	19.75	2.22	1.79
O95347	SMC2_HUMAN Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	17.40				19.00						7.71 E-08			Sample 1 Only		
P04259	K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	63.30		12.00	2.00		5.00	3.00		3.66 E-07	3.43 E-09		1.15 E-07	8.76 E-09		Sample 2 Only	Sample 3 Only
Q16401	PSMD5_HUMAN 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3	20.60	5.00	5.00	4.00	5.00		1.00	1.27 E-07	5.99 E-08	2.42 E-08	1.84 E-07		3.84 E-09	1.45	Control 1 Only	0.03
Q9H4Y5	GSTO2_HUMAN Glutathione S-transferase omega-2 OS=Homo sapiens GN=GSTO2 PE=1 SV=1	34.90	0.98	4.92	3.94	1.97	4.92	4.92	4.61 E-08	3.64 E-07	7.22 E-08	7.63 E-08	3.21 E-07	1.64 E-07	1.65	6.96	3.55
Q9Y6D6	BIG1_HUMAN Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2	9.30	3.97		1.98	6.94		7.93	5.79 E-09		7.36 E-10	1.76 E-08		7.82 E-09	3.04	Control 1 Only	1.35
Q5T749	KPRP_HUMAN Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	8.80		5.00	7.00		4.00	4.00		3.85 E-08	3.50 E-08		3.15 E-08	1.62 E-08		Sample 2 Only	Sample 3 Only
P43490	NAMPT_HUMAN Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	17.10	1.00	3.00	2.00	2.99		9.98	1.56 E-08	3.89 E-08	9.01 E-09	4.62 E-08		7.59 E-08	2.97	Control 1 Only	4.88
P19013	K2C4_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	34.10		4.96	2.99	6.94	4.97			4.37 E-08	1.13 E-08	4.57 E-08	6.77 E-08		Sample 1 Only	Sample 2 Only	
Q6DD88	ATLA3_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1	18.10	0.99	3.96	5.94	4.95		4.96	8.09 E-09	9.02 E-08	2.68 E-08	9.52 E-08		3.52 E-08	11.77	Control 1 Only	4.36
Q93008	USP9X_HUMAN Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	3.80	3.98	1.00	4.98	7.98		2.00	5.68 E-09	2.14 E-09	2.67 E-09	1.29 E-08		2.93 E-09	2.26	Control 1 Only	0.52
B4DWW4	B4DWW4_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=2 SV=1	14.00	7.99			8.99			3.05 E-08			5.83 E-08			1.91	Control 1 Only	Control 1 Only
P13796	PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6	30.50					19.95						3.79 E-07			Sample 2 Only	
H0Y368	H0Y368_HUMAN Dolichol-phosphate mannosyltransferase (Fragment) OS=Homo sapiens GN=DPM1 PE=4 SV=1	30.40		5.95	0.99	0.99	6.94	3.96		3.84 E-07	4.85 E-09	3.02 E-08	4.57 E-07	5.73 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only

H7BXW3	H7BXW3_HUMAN Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=2 SV=1	25.30		5.00	1.00	10.00	2.00	2.00		7.99 E-08	8.51 E-09	1.98 E-07	2.74 E-08	1.65 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O75083	WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	23.90		1.98		13.94	2.98			3.40 E-08		4.53 E-07	5.38 E-08		Sample 1 Only	Sample 2 Only	
P51659	DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	14.30	4.96	0.99	5.92	1.98		5.94	4.30 E-08	9.03 E-09	2.91 E-08	3.83 E-08		3.18 E-08	0.89	Control 1 Only	0.74
P02647	APOA1_HUMAN Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	50.20		1.00			18.00			9.60 E-09			1.16 E-06			Sample 2 Only	
Q562R1	ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	27.10	3.00	2.00	2.00	4.00	1.00	3.00	1.08 E-07	8.77 E-08	1.93 E-06	1.56 E-06	3.22 E-08	7.25 E-08	14.49	0.30	0.67
Q08J23	NSUN2_HUMAN tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2	16.70				17.00	2.00					2.74 E-07	8.05 E-08		Sample 1 Only	Sample 2 Only	
Q5T4S7	UBR4_HUMAN E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	3.50		3.50	2.50	3.00	0.50	2.99		1.56 E-09	4.20 E-10	1.36 E-09	2.60 E-10	9.07 E-10	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9NZB2	F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	18.00	1.98			16.91			6.40 E-09			9.02 E-08			14.09	Control 1 Only	Control 1 Only
Q9P2M7	CING_HUMAN Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	11.50	6.99	7.98		1.99	0.99	1.00	2.41 E-08	2.43 E-08		4.05 E-09	1.67 E-09	1.30 E-09	0.17	0.07	0.05
Q9Y230	RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	32.20			0.99			18.86			8.56 E-09			3.39 E-07			Sample 3 Only
B4DER1	B4DER1_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1	13.50		12.00	6.00					3.51 E-08	6.14 E-09						
B9EGP5	B9EGP5_HUMAN MON2 protein OS=Homo sapiens GN=MON2 PE=2 SV=1	6.60	3.00	1.00		8.99	2.00	3.00	6.63 E-09	2.14 E-09		2.25 E-08	5.64 E-09	2.86 E-09	3.39	0.85	0.43
E5KLJ5	E5KLJ5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1	10.60	3.00	6.00	2.00	7.00			1.31 E-08	1.88 E-08	3.62 E-09	4.35 E-08			3.31	Control 1 Only	Control 1 Only
E9PEZ1	E9PEZ1_HUMAN Cullin-9 OS=Homo sapiens GN=CUL9 PE=2 SV=1	5.30				1.00	7.00	11.00				1.28 E-09	2.42 E-08	6.18 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P40429	RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	27.60		2.00	1.00	5.98	2.99	3.98		1.32 E-07	4.59 E-09	5.47 E-07	1.72 E-07	7.52 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P05141	ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	35.20	4.00	2.00		4.00	4.00	5.00	2.04 E-07	1.11 E-07		2.12 E-07	2.40 E-07	1.32 E-07	1.04	1.18	0.65
Q02413	DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	14.30		9.00	7.00		3.00			4.47 E-08	1.09 E-08		2.06 E-08			Sample 2 Only	
Q02878	RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	25.70		2.98		7.96	1.00	3.98		7.61 E-08		3.49 E-07	1.74 E-08	4.83 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7EPB3	E7EPB3_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=2 SV=1	28.20		2.00	2.00	4.00	2.00	6.00		3.40 E-07	6.29 E-08	2.23 E-06	1.50 E-07	3.61 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P01857	IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	52.40		3.00			10.50			5.99 E-08			1.60 E-06			Sample 2 Only	
P07737	PROF1_HUMAN Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	73.60					16.99						2.35 E-06			Sample 2 Only	
P0CG05	LAC2_HUMAN Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	55.70		3.00			11.92			1.44 E-07			2.98 E-06			Sample 2 Only	
B9ZVX0	B9ZVX0_HUMAN Diaphanous homolog 1 (Drosophila), isoform CRA_a OS=Homo sapiens GN=DIAPH1 PE=2 SV=1	8.20	1.00	1.00		16.00			3.15 E-09	3.57 E-09		7.07 E-08			22.47	Control 1 Only	Control 1 Only
O15269	SPTC1_HUMAN Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1	24.50		1.00	4.00	3.00	1.00	8.00		1.84 E-08	2.58 E-08	4.79 E-08	1.40 E-08	5.94 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only

P56192	SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	13.60	0.99	2.98	0.99	4.97	1.00	6.93	4.14 E-09	3.04 E-08	4.83 E-10	2.66 E-08	6.10 E-09	1.39 E-08	6.43	1.47	3.36
Q07960	RHG01_HUMAN Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1	31.00		8.97	1.99	5.97				1.16 E-07	9.34 E-09	1.11 E-07			Sample 1 Only		
P59665	DEF1_HUMAN Neutrophil defensin 1 OS=Homo sapiens GN=DEFA1 PE=1 SV=1	20.20		4.00	1.00		11.00			4.47 E-07	1.14 E-08		3.69 E-05			Sample 2 Only	
Q92538	GBF1_HUMAN Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2	6.40	3.00	1.00	1.00	5.00		6.00	3.37 E-09	9.94 E-10	6.77 E-10	7.99 E-09		5.79 E-09	2.37	Control 1 Only	1.72
P12429	ANXA3_HUMAN Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3	47.70					16.88						8.53 E-07			Sample 2 Only	
P17980	PRS6A_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	31.40	2.97	4.91		6.89		0.98	1.51 E-07	8.92 E-08		3.01 E-07		6.81 E-09	2.00	Control 1 Only	0.05
D3DQ30	D3DQ30_HUMAN HCG40295, isoform CRA_d OS=Homo sapiens GN=TTC39A PE=2 SV=1	24.70		2.97		3.96	4.95	4.94		3.25 E-08		9.99 E-08	7.26 E-08	5.57 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P24752	THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	30.70		3.00	2.00	11.96				4.87 E-08	1.11 E-08	2.78 E-07			Sample 1 Only		
Q96DA0	ZG16B_HUMAN Zymogen granule protein 16 homolog B OS=Homo sapiens GN=ZG16B PE=1 SV=3	49.00		2.00			15.00			5.20 E-08			2.76 E-06			Sample 2 Only	
E9PG35	E9PG35_HUMAN Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=MCCC1 PE=2 SV=1	13.40	0.99	4.96	0.99	2.98		3.97	1.63 E-08	1.32 E-07	7.26 E-09	4.46 E-08		2.43 E-08	2.74	Control 1 Only	1.50
P46777	RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	19.20			1.00	8.00	2.00	4.00			6.85 E-09	3.53 E-07	4.95 E-08	5.85 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O43592	XPOT_HUMAN Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	11.50	3.00	3.00		1.00	3.00	6.00	1.81 E-08	1.89 E-08		4.23 E-09	1.70 E-08	1.04 E-08	0.23	0.94	0.57
P61353	RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	27.90		4.00	1.00	4.00	4.00	3.00		4.91 E-07	2.24 E-08	8.99 E-07	4.79 E-07	8.24 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q14247	SRC8_HUMAN Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	22.20	3.00			13.00			3.47 E-08			2.09 E-07			6.03	Control 1 Only	Control 1 Only
Q9Y6D5	BIG2_HUMAN Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3	6.90	1.00	1.00		8.00	1.00	4.50	5.09 E-09	1.87 E-09		2.43 E-08	3.69 E-09	3.73 E-09	4.77	0.73	0.73
K7EQG1	K7EQG1_HUMAN Glutaminyl-peptide cyclotransferase-like protein (Fragment) OS=Homo sapiens GN=QPCTL PE=2 SV=1	18.20	2.00	2.00	2.00	4.00	2.00	3.00	1.28 E-07	6.95 E-08	3.02 E-08	3.16 E-07	9.92 E-08	4.89 E-08	2.47	0.77	0.38
G8JLH9	G8JLH9_HUMAN Signal transducer and activator of transcription OS=Homo sapiens GN=STAT3 PE=2 SV=1	14.70	2.00	4.00		2.00		2.00	2.00 E-08	3.37 E-08		4.78 E-08		8.68 E-09	2.40	Control 1 Only	0.44
P12004	PCNA_HUMAN Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	26.80		1.00	2.00		3.00	6.00		4.22 E-08	1.50 E-08		1.06 E-07	1.10 E-07		Sample 2 Only	Sample 3 Only
Q5D862	FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	1.40		5.00	4.00	1.00	1.00	3.00		1.13 E-08	1.22 E-08	1.87 E-09	5.36 E-09	2.11 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9NP55	BPIA1_HUMAN BPI fold-containing family A member 1 OS=Homo sapiens GN=BPIFA1 PE=1 SV=1	19.50		5.00			10.00			8.93 E-08			3.25 E-07			Sample 2 Only	
B4E0X2	B4E0X2_HUMAN RAF proto-oncogene serine/threonine-protein kinase OS=Homo sapiens GN=RAF1 PE=2 SV=1	32.80				3.50	3.00	4.50				4.82 E-08	4.27 E-08	2.92 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only

E9PMI6	E9PMI6_HUMAN Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=2 SV=1	44.30	7.99	1.00	2.00	3.00		1.00	1.87 E-06	3.33 E-07	8.84 E-08	9.58 E-07		6.53 E-08	0.51	Control 1 Only	0.03
F5H2F4	F5H2F4_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1	9.50	1.00	5.00	4.00	1.00	2.00	1.00	4.26 E-09	4.26 E-08	3.84 E-09	1.78 E-09	7.15 E-09	1.23 E-09	0.42	1.68	0.29
O75367	H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	22.50		13.90			1.00			4.37 E-07			1.93 E-08			Sample 2 Only	
P02675	FIBB_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	26.30					15.00						4.44 E-07			Sample 2 Only	
P61313	RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	26.00	0.99	0.99		7.90	0.99	1.99	2.61 E-08	2.37 E-08		1.08 E-06	4.61 E-08	2.88 E-08	41.19	1.77	1.10
Q5T4S7-5	UBR4_HUMAN Isoform 5 of E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4	4.60		1.50	1.50	3.00	0.50	1.00		1.48 E-09	5.84 E-10	2.88 E-09	5.48 E-10	7.60 E-10	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y3Z3	SAMH1_HUMAN Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2	15.90		0.99		3.96	2.97	5.94		1.25 E-08		5.23 E-08	5.58 E-08	3.75 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JNW5	C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1	29.80		1.00		8.00	1.00	2.00		7.51 E-08		1.85 E-06	7.30 E-08	2.66 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JC84	C9JC84_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=2 SV=1	28.80					14.00						4.73 E-07			Sample 2 Only	
F8W7C6	F8W7C6_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=2 SV=1	38.00		1.99		7.95	1.99	1.99		1.17 E-07		1.48 E-06	1.64 E-07	4.19 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
M0R117	M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=2 SV=1	39.70		2.00		6.00	1.00	2.00		2.25 E-07		8.62 E-07	1.15 E-07	8.76 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O14980	XPO1_HUMAN Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	9.00	6.00			6.00		1.00	2.52 E-08			2.65 E-08		3.12 E-09	1.05	Control 1 Only	0.12
P49748	ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	14.50	2.00	5.96	3.96	0.99			1.09 E-08	6.65 E-08	1.32 E-08	1.15 E-08			1.06	Control 1 Only	Control 1 Only
Q13263	TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	12.90		1.00	1.00	5.00		5.00		5.58 E-09	2.04 E-07	5.66 E-08		1.75 E-08	Sample 1 Only		Sample 3 Only
Q9UBV2	SE1L1_HUMAN Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3	9.30	1.00	2.00		6.00	2.00	1.00	5.06 E-09	1.54 E-08		7.34 E-08	2.18 E-08	1.07 E-09	14.52	4.32	0.21
B4DVY1	B4DVY1_HUMAN Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=2 SV=1	12.60		1.00	1.00	8.98				5.43 E-09	1.40 E-09	2.37 E-07			Sample 1 Only		
E5RI99	E5RI99_HUMAN 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=2 SV=1	58.80		2.00		3.00	2.00	5.00		1.86 E-07		5.81 E-07	3.18 E-07	2.07 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P24928	RPB1_HUMAN DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2	6.10				9.00		3.00				2.76 E-08		9.80 E-10	Sample 1 Only		Sample 3 Only
E9PD53	E9PD53_HUMAN Structural maintenance of chromosomes protein OS=Homo sapiens GN=SMC4 PE=2 SV=1	10.50		2.00	1.00	6.97		2.00		2.66 E-09	8.74 E-10	3.30 E-08		1.39 E-09	Sample 1 Only		Sample 3 Only
P35749	MYH11_HUMAN Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	15.70		4.00	0.50	1.00	0.50	1.00		1.72 E-08	5.07 E-10	4.77 E-09	1.72 E-09	1.10 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
J3KR97	J3KR97_HUMAN Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=2 SV=1	9.50	4.94	2.96		3.95			1.73 E-08	1.66 E-08		1.92 E-08			1.11	Control 1 Only	Control 1 Only
H7BXY3	H7BXY3_HUMAN Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=2 SV=1	11.40				12.00						4.58 E-08			Sample 1 Only		
Q9BXJ9	NAA15_HUMAN N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens	8.90	1.00	1.00		10.00			4.77 E-09	7.62 E-09		1.03 E-07			21.64	Control 1 Only	Control 1 Only

	GN=NAA15 PE=1 SV=1																
Q9UGM3	DMBT1_HUMAN Deleted in malignant brain tumors 1 protein OS=Homo sapiens GN=DMBT1 PE=1 SV=2	17.20		2.00			11.00			6.50E-09			1.40E-07			Sample 2 Only	
P14780	MMP9_HUMAN Matrix metalloproteinase-9 OS=Homo sapiens GN=MMP9 PE=1 SV=3	14.90					12.00						2.50E-07			Sample 2 Only	
Q05086	UBE3A_HUMAN Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A PE=1 SV=4	11.70	2.00			9.00			1.19E-08			5.97E-08			5.01	Control 1 Only	Control 1 Only
P11388	TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	6.90		1.00	2.00	8.99				2.01E-09	1.32E-09	1.89E-08			Sample 1 Only		
B4DUR8	B4DUR8_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=2 SV=1	14.40	3.00	1.00		4.00	1.00	1.00	4.50E-08	9.45E-09		9.48E-08	2.11E-08	4.49E-09	2.11	0.47	0.10
B4DZH6	B4DZH6_HUMAN Histone deacetylase 6 OS=Homo sapiens GN=HDAC6 PE=2 SV=1	5.30	0.99		0.99	0.99	6.93	0.99	7.05E-09		6.27E-10	1.43E-09	4.56E-08	6.38E-10	0.20	6.46	0.09
E5RJ68	E5RJ68_HUMAN AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=2 SV=1	9.90		2.00		8.96	1.00			9.16E-09		3.93E-08	3.34E-09		Sample 1 Only	Sample 2 Only	
F8VUA6	F8VUA6_HUMAN 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=2 SV=1	36.20		1.00		4.00	2.00	2.00		1.17E-08		8.71E-07	6.46E-08	1.02E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8N1N4	K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	20.00		4.99	1.00		2.99	2.00		5.02E-08	1.09E-09		4.44E-08	3.27E-09		Sample 2 Only	Sample 3 Only
P60866	RS20_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	36.10	0.99	0.99		3.96	1.98	1.98	1.09E-07	1.35E-07		6.40E-07	3.38E-07	3.12E-08	5.88	3.10	0.29
Q14139	UBE4A_HUMAN Ubiquitin conjugation factor E4 A OS=Homo sapiens GN=UBE4A PE=1 SV=2	7.80	2.00		3.00	5.00		2.00	1.30E-08		2.29E-09	2.17E-08		3.57E-09	1.66	Control 1 Only	0.27
Q7L775	EPMIP_HUMAN EPM2A-interacting protein 1 OS=Homo sapiens GN=EPM2AIP1 PE=1 SV=1	15.00	2.00			9.75			3.29E-08			1.79E-07			5.45	Control 1 Only	Control 1 Only
P32119	PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	19.70	3.00	0.50	1.50		1.50	0.50	4.54E-07	2.06E-08	1.38E-08		1.05E-07	3.16E-09	Control 1 Only	0.23	0.01
P24158	PRTN3_HUMAN Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3	24.70					8.00						1.27E-06			Sample 2 Only	
Q14692	BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	6.90				11.00						5.10E-08			Sample 1 Only		
P10398	ARAF_HUMAN Serine/threonine-protein kinase A-Raf OS=Homo sapiens GN=ARAF PE=1 SV=2	18.50				3.50	3.00	2.50				3.85E-08	3.96E-08	1.67E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P23258	TBG1_HUMAN Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	8.40	0.99	0.99		3.97		3.97	1.19E-08	8.32E-09		8.37E-08		3.16E-08	7.01	Control 1 Only	2.64
P26373	RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	24.60		1.98		3.99	2.99	1.99		1.07E-07		5.44E-07	1.14E-07	2.17E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q08378	GOGA3_HUMAN Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2	5.50	1.00			4.00	1.00	4.00	1.48E-09			1.05E-08	1.37E-09	2.43E-09	7.09	0.93	1.64
Q6YN16	HSDL2_HUMAN Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	23.80	3.00	1.00	4.00	1.00	2.00		6.06E-08	1.54E-08	2.10E-08	2.58E-08	2.34E-08		0.43	0.39	Control 1 Only
Q8IZ83	A16A1_HUMAN Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=1 SV=2	12.80	0.99			9.90			1.04E-08			1.65E-07			15.85	Control 1 Only	Control 1 Only
Q13509	TBB3_HUMAN Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	44.40		2.00	1.00		4.00	4.00		1.81E-07	5.40E-09		3.87E-07	8.12E-08		Sample 2 Only	Sample 3 Only

Q9UBM7	DHCR7_HUMAN 7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	4.40			2.00	2.00	2.00	3.00			1.07 E-08	7.88 E-08	5.33 E-08	2.26 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7ETK0	E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1	41.50				9.00						2.09 E-06			Sample 1 Only		
O75165	DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5	6.10		1.00		9.00				9.74 E-10		1.56 E-08			Sample 1 Only		
Q99523	SORT_HUMAN Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3	7.80				2.00	1.00	5.00				1.30 E-08	4.31 E-09	1.69 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P11216	PYGB_HUMAN Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	7.50	0.51	2.00		4.53	0.51		2.37 E-09	9.96 E-09		5.16 E-08	4.94 E-09		21.80	2.09	Control 1 Only
P26038	MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	12.70					10.00						1.58 E-07			Sample 2 Only	
M0R2B7	M0R2B7_HUMAN DNA polymerase OS=Homo sapiens GN=POLD1 PE=2 SV=1	10.90	0.99			7.92			7.73 E-10			3.33 E-08			43.03	Control 1 Only	Control 1 Only
O00231	PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	20.90		1.00	1.99			6.99		1.21 E-08	5.28 E-09			6.33 E-08			Sample 3 Only
P43246	MSH2_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	9.40		1.00	4.00	1.00		3.00		3.41 E-09	2.98 E-09	4.34 E-09		5.79 E-09	Sample 1 Only		Sample 3 Only
O75643	U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	5.80		1.00		8.00				8.22 E-10		2.14 E-08			Sample 1 Only		
P62266	RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	29.40				8.98	1.00					3.01 E-06	5.29 E-08		Sample 1 Only	Sample 2 Only	
Q01469	FABP5_HUMAN Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	39.30		1.00			8.00			1.10 E-07			1.07 E-06			Sample 2 Only	
Q8WVX9	FACR1_HUMAN Fatty acyl-CoA reductase 1 OS=Homo sapiens GN=FAR1 PE=1 SV=1	11.30	2.00	2.00	2.00		1.00	3.00	1.56 E-08	2.30 E-08	1.74 E-08		6.93 E-09	2.64 E-08	Control 1 Only	0.45	1.70
Q9BVA1	TBB2B_HUMAN Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	70.60	0.50		0.50	1.50	1.50	2.50	7.54 E-09		6.94 E-09	2.85 E-08	2.67 E-08	5.17 E-08	3.78	3.55	6.86
Q9Y6G9	DC1L1_HUMAN Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3	13.60	1.00			2.00	3.00	3.00	7.31 E-09			3.30 E-08	4.56 E-08	1.72 E-08	4.51	6.24	2.35
E7EMM2	E7EMM2_HUMAN AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=2 SV=1	10.50	1.00			8.00			2.30 E-09			4.05 E-08			17.62	Control 1 Only	Control 1 Only
H0Y8E6	H0Y8E6_HUMAN DNA replication licensing factor MCM2 (Fragment) OS=Homo sapiens GN=MCM2 PE=3 SV=1	10.40				8.00						5.26 E-08			Sample 1 Only		
P49257	LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	5.70			3.00			4.00			3.24 E-08			3.57 E-08			Sample 3 Only
Q9H2M9	RBGPR_HUMAN Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1	4.20	1.00	1.00	3.00	2.00		2.00	1.64 E-09	2.39 E-09	1.68 E-09	4.52 E-09		1.98 E-09	2.77	Control 1 Only	1.21
B7ZA04	B7ZA04_HUMAN Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1	8.80				2.99	2.00	3.99				3.29 E-08	2.10 E-08	3.83 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JPM4	C9JPM4_HUMAN ADP-ribosylation factor 4 (Fragment) OS=Homo sapiens GN=ARF4 PE=2 SV=1	32.30	0.99	1.98	0.99	0.99	2.97	0.99	5.46 E-08	2.87 E-07	1.92 E-08	1.04 E-07	2.42 E-07	3.16 E-08	1.90	4.42	0.58

P31146	COR1A_HUMAN Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4	18.90					8.96						1.91 E-07			Sample 2 Only	
P33991	MCM4_HUMAN DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5	10.80		1.00	1.00	6.00				8.17 E-09	1.89 E-09	5.83 E-08			Sample 1 Only		
F5H8J2	F5H8J2_HUMAN Uncharacterized protein OS=Homo sapiens GN=P4HB PE=3 SV=1	18.20		0.99			7.93			5.16 E-09			1.43 E-07			Sample 2 Only	
H9KV75	H9KV75_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=2 SV=1	20.70					8.90						7.08 E-08			Sample 2 Only	
P41218	MNDA_HUMAN Myeloid cell nuclear differentiation antigen OS=Homo sapiens GN=MNDA PE=1 SV=1	24.80					7.00						1.40 E-07			Sample 2 Only	
P61978	HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	10.30	2.00	2.00		2.00	2.00	1.00	8.41 E-08	2.14 E-08		4.93 E-08	3.96 E-08	6.59 E-09	0.59	0.47	0.08
P62333	PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	12.60	1.00	1.98	0.99	2.98	0.99		1.90 E-08	1.73 E-08	7.00 E-09	1.91 E-07	1.06 E-08		10.06	0.56	Control 1 Only
P12236	ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	31.90		2.00	1.00	1.00	3.00	2.00		6.61 E-08	1.54 E-08	4.88 E-08	1.60 E-07	6.40 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6DT37	MRCKG_HUMAN Serine/threonine-protein kinase MRCK gamma OS=Homo sapiens GN=CDC42BPG PE=1 SV=2	5.00	1.00			7.00		1.00	1.59 E-09			2.96 E-08		1.14 E-09	18.63	Control 1 Only	0.71
Q99714	HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	21.80	1.00	1.98	0.99	1.99	2.99		4.98 E-08	6.96 E-08	5.15 E-09	9.86 E-08	1.22 E-07		1.98	2.45	Control 1 Only
Q9BUP0	EFHD1_HUMAN EF-hand domain-containing protein D1 OS=Homo sapiens GN=EFHD1 PE=1 SV=1	31.00		8.98						7.54 E-07							
Q9H9T3	ELP3_HUMAN Elongator complex protein 3 OS=Homo sapiens GN=ELP3 PE=1 SV=2	16.70		0.99		2.97	1.98	2.97		3.40 E-09		3.81 E-08	3.04 E-08	1.24 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P20930	FILA_HUMAN Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	1.00		3.00			3.00	1.00		4.80 E-09			8.10 E-09	6.65 E-10		Sample 2 Only	Sample 3 Only
P01860	IGHG3_HUMAN Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	32.10	1.00	2.00	2.00	1.00	1.00	1.00	4.48 E-08	3.95 E-08	1.28 E-08	2.08 E-08	3.60 E-08	5.42 E-09	0.46	0.80	0.12
M0QZN2	M0QZN2_HUMAN 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=2 SV=1	25.40			1.00	3.00	1.00	2.00			1.08 E-08	4.80 E-07	8.31 E-08	3.22 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B5MCP9	B5MCP9_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=2 SV=1	12.80		1.00	1.00	2.00	1.00	1.00		1.83 E-07	9.49 E-09	3.74 E-07	6.75 E-08	2.73 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P31930	QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	14.80				7.00						1.74 E-07			Sample 1 Only		
Q15075	EEA1_HUMAN Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	6.00	4.00		1.00			2.00	1.20 E-08		5.20 E-10			2.25 E-09	Control 1 Only	Control 1 Only	0.19
A1L0T0	ILVBL_HUMAN Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2	8.70		1.00	1.00	1.00	1.00	4.00		1.48 E-08	5.86 E-09	2.58 E-08	2.22 E-08	3.21 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JA05	C9JA05_HUMAN Immunoglobulin J chain (Fragment) OS=Homo sapiens GN=IGJ PE=2 SV=1	38.60		2.00			6.00			1.49 E-07			4.58 E-06			Sample 2 Only	
P21333	FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	2.40	1.98	0.99			5.00		3.80 E-09	8.58 E-10			1.20 E-08		Control 1 Only	3.15	Control 1 Only
P29508	SPB3_HUMAN Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	13.60		1.00			6.94			7.54 E-09			2.30 E-07			Sample 2 Only	
P30740	ILEU_HUMAN Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1	24.80					7.99						2.67 E-07			Sample 2 Only	

	SV=1																
J3KRX5	J3KRX5_HUMAN 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=2 SV=1	26.10				5.00		2.00				6.99 E-07		4.49 E-08	Sample 1 Only		Sample 3 Only
M0QXB4	M0QXB4_HUMAN Coatomer protein complex, subunit epsilon, isoform CRA_g OS=Homo sapiens GN=COPE PE=2 SV=1	23.40				5.95						4.31 E-07			Sample 1 Only		
M0QXL5	M0QXL5_HUMAN rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=2 SV=1	23.20				1.98		4.95				6.70 E-08		4.68 E-08	Sample 1 Only		Sample 3 Only
P61163	ACTZ_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	37.20		3.96	1.98	0.99		0.99		2.00 E-07	1.67 E-08	1.49 E-07		2.89 E-09	Sample 1 Only		Sample 3 Only
O15270	SPTC2_HUMAN Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1	15.30	1.00	2.00		2.00		3.00	1.05 E-08	1.39 E-08		2.89 E-08		1.52 E-08	2.75	Control 1 Only	1.45
O60884	DNJA2_HUMAN DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	13.10				1.00	3.00	4.00				4.70 E-08	1.15 E-07	5.81 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P01605	KV113_HUMAN Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1	25.00		4.00	2.00			1.00		3.46 E-07	3.18 E-08			2.02 E-08			Sample 3 Only
Q6KB66	K2C80_HUMAN Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	14.90	1.00	2.00	1.00	1.00	2.00	1.00	8.87 E-09	2.78 E-08	5.41 E-09	1.49 E-08	3.23 E-08	5.23 E-09	1.68	3.64	0.59
P62854	RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	20.90		1.00		6.00		1.00		1.40 E-07		7.96 E-06		4.06 E-08	Sample 1 Only		Sample 3 Only
P62913	RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	17.50		1.00		4.00	2.00	1.00		2.04 E-07		6.75 E-07	2.43 E-07	2.86 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
J3KPD9	J3KPD9_HUMAN Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=2 SV=1	25.90	0.99			1.99	3.96		1.56 E-07			2.77 E-07	2.84 E-07		1.78	1.83	Control 1 Only
C9IZE4	C9IZE4_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=2 SV=1	11.60			1.98			3.96			6.92 E-09			2.10 E-08			Sample 3 Only
P62851	RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	12.80		1.00		3.00	1.00			7.28 E-08		1.22 E-06	4.98 E-08		Sample 1 Only	Sample 2 Only	
H9KV70	H9KV70_HUMAN Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=2 SV=1	26.80					7.00						3.56 E-07			Sample 2 Only	
P01861	IGHG4_HUMAN Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	37.00	1.00		2.00	1.00	1.00	2.00	2.70 E-08		1.92 E-08	1.78 E-08	4.14 E-08	1.40 E-08	0.66	1.53	0.52
P08246	ELNE_HUMAN Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	9.70					7.00						2.05 E-06			Sample 2 Only	
P31949	S10AB_HUMAN Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	39.00					7.00						1.04 E-06			Sample 2 Only	
Q7Z3Y8	K1C27_HUMAN Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	17.90			4.96			1.99			1.41 E-08			6.42 E-09			Sample 3 Only
B4E1G6	B4E1G6_HUMAN Galactokinase OS=Homo sapiens GN=GALK1 PE=2 SV=1	11.50		1.00	1.00	2.00	2.00	1.00		2.56 E-08	1.65 E-09	3.13 E-08	5.27 E-08	3.19 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4E2V5	B4E2V5_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=2 SV=1	24.50					6.00						3.15 E-07			Sample 2 Only	
D6RAN4	D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1	17.00					0.99	1.98					8.54 E-08	4.57 E-08		Sample 2 Only	Sample 3 Only
F5H2S7	F5H2S7_HUMAN Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=2 SV=1	12.00	3.96			0.99		1.98	7.39 E-08			2.20 E-08		9.87 E-09	0.30	Control 1 Only	0.13

G5EA52	G5EA52_HUMAN Protein disulfide isomerase family A, member 3, isoform CRA_b OS=Homo sapiens GN=PDIA3 PE=2 SV=1	7.20	1.00	2.00	2.00	1.00	1.00		1.49 E-08	3.07 E-08	8.98 E-09	1.38 E-08	9.17 E-09		0.93	0.62	Control 1 Only
H0YKD8	H0YKD8_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=2 SV=1	34.30		1.00		3.00	1.00	1.00		1.36 E-07		1.76 E-06	1.43 E-07	1.12 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P20700	LMNB1_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	10.60		5.98			1.00			9.43 E-08			1.19 E-08			Sample 2 Only	
Q7Z794	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	19.40			6.00						1.90 E-08						
P62424	RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	16.20		1.00		2.00		3.00		2.38 E-08		7.66 E-08		2.58 E-08	Sample 1 Only		Sample 3 Only
Q5QPL9	Q5QPL9_HUMAN RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1	19.80		4.98		1.00	0.99			2.49 E-07		1.68 E-08	2.63 E-08		Sample 1 Only	Sample 2 Only	
Q9BV44	THUM3_HUMAN THUMP domain-containing protein 3 OS=Homo sapiens GN=THUMPD3 PE=1 SV=1	13.20						6.99						6.00 E-08			Sample 3 Only
Q9HAV4	XPO5_HUMAN Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1	9.40	3.00			4.00			1.06 E-08			2.17 E-08			2.05	Control 1 Only	Control 1 Only
Q9ULX6	AKP8L_HUMAN A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L PE=1 SV=3	7.90				1.00	2.99	3.00				4.92 E-09	5.42 E-08	1.22 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6PKG0	LARP1_HUMAN La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	4.50				5.95		0.99				3.14 E-08		1.47 E-09	Sample 1 Only		Sample 3 Only
Q9UPN7	PP6R1_HUMAN Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5	3.30	1.00			2.00		2.00	1.45 E-09			1.07 E-08		3.26 E-09	7.39	Control 1 Only	2.26
E7ESC6	E7ESC6_HUMAN Exportin-7 OS=Homo sapiens GN=XPO7 PE=2 SV=1	4.40	1.00			2.00		3.00	2.70 E-09			4.13 E-09		4.18 E-09	1.53	Control 1 Only	1.55
K7EJT5	K7EJT5_HUMAN 60S ribosomal protein L22 (Fragment) OS=Homo sapiens GN=RPL22 PE=2 SV=1	51.10		1.00	1.00	1.00	2.00	1.00		5.12 E-07	1.38 E-07	1.55 E-06	7.47 E-07	1.57 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7EMS6	E7EMS6_HUMAN Catechol O-methyltransferase (Fragment) OS=Homo sapiens GN=COMT PE=2 SV=1	17.60	0.99	0.99	0.99	1.98			5.16 E-08	7.17 E-08	1.39 E-08	3.72 E-07			7.21	Control 1 Only	Control 1 Only
Q96HS1	PGAM5_HUMAN Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	13.70				1.00	2.99	1.00				1.78 E-08	1.36 E-07	8.14 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
B7Z4C8	B7Z4C8_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=2 SV=1	20.30	1.00	1.00		3.00	1.00		8.15 E-08	1.28 E-07		8.19 E-07	1.01 E-07		10.05	1.24	Control 1 Only
P04080	CYTB_HUMAN Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	24.50		2.00			3.00			2.84 E-07			5.10 E-07			Sample 2 Only	
Q08554	DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	5.40		2.00	2.00			1.00		3.14 E-08	8.64 E-09			1.49 E-09			Sample 3 Only
P11215	ITAM_HUMAN Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2	6.60					6.00						4.56 E-08			Sample 2 Only	
P20061	TCO1_HUMAN Transcobalamin-1 OS=Homo sapiens GN=TCN1 PE=1 SV=2	12.50					6.00						1.18 E-07			Sample 2 Only	
P31944	CASPE_HUMAN Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	21.10					5.00						2.00 E-07			Sample 2 Only	
B9A064	IGLL5_HUMAN Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	32.70		1.00			5.00			1.60 E-08			3.13 E-07			Sample 2 Only	
P10809	CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	7.30	2.00	2.00		1.00		1.00	2.58 E-08	2.37 E-08		1.46 E-08		2.22 E-09	0.57	Control 1 Only	0.09

B4DEM7	B4DEM7_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1	11.00	0.99	0.99		0.99	1.98		1.11 E-08	7.80 E-09		1.51 E-08	4.03 E-08		1.36	3.64	Control 1 Only
B4DQJ8	B4DQJ8_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1	16.50					5.94						1.60 E-07			Sample 2 Only	
B4DXW1	B4DXW1_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=2 SV=1	13.50		2.00		1.00	1.99			4.94 E-08		2.59 E-08	3.42 E-08		Sample 1 Only	Sample 2 Only	
P17213	BPI_HUMAN Bactericidal permeability-increasing protein OS=Homo sapiens GN=BPI PE=1 SV=4	9.00					6.00						1.43 E-07			Sample 2 Only	
E9PK25	E9PK25_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=2 SV=1	45.60					5.96						6.96 E-07			Sample 2 Only	
F5GYR8	F5GYR8_HUMAN General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=2 SV=1	6.20	1.00	1.00	3.00	1.00			4.48 E-09	2.30 E-09	1.94 E-09	3.53 E-09			0.79	Control 1 Only	Control 1 Only
G3V3G9	G3V3G9_HUMAN DDB1- and CUL4-associated factor 8 OS=Homo sapiens GN=DCAF8 PE=2 SV=1	6.50		1.99		1.99		2.00		2.31 E-08		1.33 E-08		9.02 E-09	Sample 1 Only		Sample 3 Only
H0Y6C3	H0Y6C3_HUMAN Pyrroline-5-carboxylate reductase 3 (Fragment) OS=Homo sapiens GN=PYCRL PE=2 SV=1	20.70	1.00			1.00		4.00	4.31 E-08			1.09 E-07		6.42 E-08	2.52	Control 1 Only	1.49
H3BN98	H3BN98_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2	38.00				4.00	1.00					6.16 E-07	1.52 E-08		Sample 1 Only	Sample 2 Only	
P37837	TALDO_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2	16.30					5.00						1.34 E-07			Sample 2 Only	
O15397	IPO8_HUMAN Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2	4.50	1.00			2.99		2.00	1.08 E-08			2.44 E-08		1.79 E-09	2.27	Control 1 Only	0.17
P01620	KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	45.90		0.99			4.96			2.15 E-08			1.09 E-06			Sample 2 Only	
P01871	IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	12.80					4.96						1.43 E-07			Sample 2 Only	
P04843	RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	11.20	2.00		1.00	2.00			2.63 E-08		3.55 E-09	3.11 E-08			1.18	Control 1 Only	Control 1 Only
Q5RKV6	EXOS6_HUMAN Exosome complex component MTR3 OS=Homo sapiens GN=EXOSC6 PE=1 SV=1	9.90	2.00		3.00	1.00			1.60 E-07		3.60 E-08	7.00 E-08			0.44	Control 1 Only	Control 1 Only
B3KNT8	B3KNT8_HUMAN Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	8.90	0.99		0.99	1.99		0.99	3.17 E-08		1.27 E-08	9.46 E-08		1.52 E-08	2.99	Control 1 Only	0.48
Q4ZG55	GREB1_HUMAN Protein GREB1 OS=Homo sapiens GN=GREB1 PE=2 SV=1	2.50				2.00	1.00	2.00				5.78 E-09	2.01 E-09	1.74 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P18077	RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	28.20				1.99	0.99					4.07 E-07	6.46 E-08		Sample 1 Only	Sample 2 Only	
P25311	ZA2G_HUMAN Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	8.70		1.00	1.00		3.00			3.99 E-08	3.24 E-09		1.31 E-07			Sample 2 Only	
B4DH70	B4DH70_HUMAN F-box/WD repeat-containing protein 11 OS=Homo sapiens GN=FBXW11 PE=2 SV=1	4.30	1.00	1.00	1.00	2.00			8.97 E-09	8.71 E-09	3.90 E-09	2.02 E-08			2.25	Control 1 Only	Control 1 Only
F8W9B4	F8W9B4_HUMAN Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=2 SV=1	9.80		1.99		2.98				6.48 E-08		1.58 E-07			Sample 1 Only		
O00232	PSD12_HUMAN 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	8.00			2.00			2.99			1.16 E-08			2.06 E-08			Sample 3 Only

P09382	LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	23.70		1.00			4.00			5.14 E-08			7.71 E-07			Sample 2 Only	
P50336	PPOX_HUMAN Protoporphyrinogen oxidase OS=Homo sapiens GN=PPOX PE=1 SV=1	4.00			0.99	0.99					5.58 E-09	4.47 E-08			Sample 1 Only		
P30041	PRDX6_HUMAN Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	20.50	1.00	1.00			2.00		7.86 E-08	1.93 E-08			8.56 E-08		Control 1 Only	1.09	Control 1 Only
Q3SYB4	Q3SYB4_HUMAN SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1	9.90		2.00			1.00			1.55 E-08			9.25 E-09			Sample 2 Only	
Q8TEQ6	GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	4.40				5.00						1.76 E-08			Sample 1 Only		
A8MYB8	A8MYB8_HUMAN Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=2 SV=1	15.40					4.94						1.20 E-07			Sample 2 Only	
G5E9V5	G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1	13.50		1.00		4.00				6.17 E-09		7.44 E-08			Sample 1 Only		
H7BXD5	H7BXD5_HUMAN Grancalcin OS=Homo sapiens GN=GCA PE=2 SV=1	39.00					4.99						2.25 E-07			Sample 2 Only	
J3KPZ3	J3KPZ3_HUMAN Probable E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens GN=MYCBP2 PE=2 SV=1	1.90				5.00						5.46 E-09			Sample 1 Only		
P41240	CSK_HUMAN Tyrosine-protein kinase CSK OS=Homo sapiens GN=CSK PE=1 SV=1	5.30		1.99	1.00	0.99				5.09 E-08	7.14 E-09	3.03 E-08			Sample 1 Only		
P00966	ASSY_HUMAN Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	10.00		3.00	1.00					4.37 E-08	3.83 E-09						
P60174	TPIS_HUMAN Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	31.70					3.99						2.03 E-07			Sample 2 Only	
Q9Y2T7	YBOX2_HUMAN Y-box-binding protein 2 OS=Homo sapiens GN=YBX2 PE=1 SV=2	20.30				4.00		1.00				8.97 E-08		9.83 E-09	Sample 1 Only		Sample 3 Only
Q32MZ4	LRRF1_HUMAN Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2	6.80	3.00		1.00			1.00	1.28 E-08		9.90 E-10			7.51 E-10	Control 1 Only	Control 1 Only	0.06
Q93100-3	KPBB_HUMAN Isoform 3 of Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB	4.60	0.99			3.96			2.44 E-09			1.99 E-08			8.13	Control 1 Only	Control 1 Only
Q9BT22	ALG1_HUMAN Chitobiosyldiphosphodolichol beta-mannosyltransferase OS=Homo sapiens GN=ALG1 PE=1 SV=2	9.30				1.98	0.99	0.99				4.13 E-08	1.83 E-08	1.08 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y2I8	WDR37_HUMAN WD repeat-containing protein 37 OS=Homo sapiens GN=WDR37 PE=1 SV=2	7.50				2.98		1.00				7.62 E-08		3.37 E-09	Sample 1 Only		Sample 3 Only
O75306	NDUS2_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=1 SV=2	7.40		1.00			1.00	3.00		1.31 E-08			1.34 E-08	1.72 E-08		Sample 2 Only	Sample 3 Only
Q96NB2	SFXN2_HUMAN Sideroflexin-2 OS=Homo sapiens GN=SFXN2 PE=1 SV=2	6.80					2.00	2.00					7.35 E-08	2.28 E-08		Sample 2 Only	Sample 3 Only
Q8TE77	SSH3_HUMAN Protein phosphatase Slingshot homolog 3 OS=Homo sapiens GN=SSH3 PE=1 SV=2	6.40		2.98		1.98				2.04 E-08		1.90 E-08			Sample 1 Only		
P12830	CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	2.90			0.99	0.99		1.99			7.27 E-10	3.17 E-09		4.33 E-09	Sample 1 Only		Sample 3 Only
E5RHU3	E5RHU3_HUMAN Syndecan-2 (Fragment) OS=Homo sapiens GN=SDC2 PE=2 SV=2	16.80		3.00	1.00					1.39 E-07	1.05 E-08						
Q9UBX3	DIC_HUMAN Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10	10.10		0.99			1.99	0.99		2.37 E-08			8.70 E-08	1.59 E-08		Sample 2 Only	Sample 3 Only

	PE=1 SV=2																
F5GWF6	F5GWF6_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=2 SV=2	5.80	1.00	1.00		1.00	1.00		7.65 E-09	1.41 E-08		9.55 E-09	1.50 E-08		1.25	1.95	Control 1 Only
H0Y764	H0Y764_HUMAN Neurobeachin-like protein 2 (Fragment) OS=Homo sapiens GN=NBEAL2 PE=4 SV=1	1.50	1.00		1.00	1.00		1.00	2.30 E-09		2.38 E-10	3.24 E-09		8.66 E-10	1.41	Control 1 Only	0.38
J3KNB4	J3KNB4_HUMAN Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=2 SV=1	14.70					3.00						7.63 E-07			Sample 2 Only	
K7EL20	K7EL20_HUMAN Eukaryotic translation initiation factor 3 subunit G (Fragment) OS=Homo sapiens GN=EIF3G PE=2 SV=1	11.00		1.00	1.00	1.00				3.97 E-08	6.12 E-09	3.05 E-08			Sample 1 Only		
P01009	A1AT_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	10.60					3.00						8.87 E-08			Sample 2 Only	
P60228	EIF3E_HUMAN Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	3.40			0.99	1.98					4.90 E-09	9.08 E-08			Sample 1 Only		
P02671	FIBA_HUMAN Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	9.50					4.00						7.41 E-08			Sample 2 Only	
P25815	S100P_HUMAN Protein S100-P OS=Homo sapiens GN=S100P PE=1 SV=2	31.60					3.00						6.67 E-07			Sample 2 Only	
P06744	G6PI_HUMAN Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	9.00					3.97						6.28 E-08			Sample 2 Only	
F5H897	F5H897_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=2 SV=1	8.30			1.00	1.00		1.00			4.33 E-09	7.34 E-09		4.08 E-09	Sample 1 Only		Sample 3 Only
Q14566	MCM6_HUMAN DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	5.10				4.00						2.25 E-08			Sample 1 Only		
Q9NYU2	UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	3.80		1.00	1.00	2.00				1.68 E-09	3.70 E-10	6.27 E-09			Sample 1 Only		
Q9Y657	SPIN1_HUMAN Spindlin-1 OS=Homo sapiens GN=SPIN1 PE=1 SV=3	15.30	2.00	1.00	1.00				9.12 E-08	4.80 E-08	1.00 E-08				Control 1 Only	Control 1 Only	Control 1 Only
B4DEK7	B4DEK7_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=2 SV=1	23.90		2.97			0.99			1.51 E-07			3.87 E-08			Sample 2 Only	
B4DYD8	B4DYD8_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	9.40	1.00			3.00			2.84 E-08			1.39 E-07			4.90	Control 1 Only	Control 1 Only
B7Z1N3	B7Z1N3_HUMAN GPI transamidase component PIG-T OS=Homo sapiens GN=PIGT PE=2 SV=1	11.40				4.00						1.35 E-07			Sample 1 Only		
E7ERK9	E7ERK9_HUMAN Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=2 SV=1	9.00				1.00	1.00	2.00				1.08 E-08	1.62 E-08	1.51 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E9PEM5	E9PEM5_HUMAN Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=2 SV=1	2.70		1.99	0.99	1.00				4.37 E-09	6.14 E-11	7.51 E-10			Sample 1 Only		
F5GXC8	F5GXC8_HUMAN Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=2 SV=1	9.40				1.00		3.00				9.94 E-09		2.59 E-08	Sample 1 Only		Sample 3 Only
F5GZS6	F5GZS6_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2	6.60	0.99			1.98		0.99	6.18 E-09			2.61 E-08		2.96 E-09	4.21	Control 1 Only	0.48

	PE=2 SV=1																
H0YBB3	H0YBB3_HUMAN Epithelial-splicing regulatory protein 1 (Fragment) OS=Homo sapiens GN=ESRP1 PE=2 SV=1	5.40				1.00	1.00	1.00				1.04 E-08	1.48 E-08	9.04 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
I3L2C7	I3L2C7_HUMAN Gem-associated protein 4 OS=Homo sapiens GN=GEMIN4 PE=2 SV=1	5.20						3.00						3.11 E-09			Sample 3 Only
P01766	HV305_HUMAN Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	25.00		0.99			2.97			1.83 E-08			7.67 E-07			Sample 2 Only	
Q13501	SQSTM_HUMAN Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1	11.50						3.99						5.07 E-08			Sample 3 Only
Q14764	MVP_HUMAN Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	5.70				3.00		1.00				1.16 E-08		1.91 E-09	Sample 1 Only		Sample 3 Only
B4DPJ8	B4DPJ8_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=2 SV=1	5.10	1.00			1.00	2.00		1.47 E-08			1.87 E-08	2.78 E-08		1.27	1.89	Control 1 Only
B7Z2F4	B7Z2F4_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1	11.60			1.00		1.00	2.00			5.05 E-09		2.55 E-08	9.53 E-09		Sample 2 Only	Sample 3 Only
P31689	DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	10.00					2.00	2.00					5.63 E-08	2.91 E-08		Sample 2 Only	Sample 3 Only
Q15477	SKIV2_HUMAN Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=1 SV=3	5.50				2.99		0.99				1.03 E-08		1.02 E-09	Sample 1 Only		Sample 3 Only
B3KVR1	B3KVR1_HUMAN Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPN PE=2 SV=1	8.90		2.97		0.99				8.90 E-08		6.39 E-08			Sample 1 Only		
P05089	ARGI1_HUMAN Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	9.30			1.00		3.00				5.30 E-09		6.77 E-08			Sample 2 Only	
Q00839	HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	2.90	1.00			2.00	1.00		2.80 E-09			1.94 E-08	1.45 E-08		6.92	5.18	Control 1 Only
Q96N67	DOCK7_HUMAN Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4	1.50	2.98						5.25 E-09						Control 1 Only	Control 1 Only	Control 1 Only
B3KSH1	B3KSH1_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1	26.00		1.00	1.00	2.00				2.16 E-08	8.35 E-09	5.23 E-08			Sample 1 Only		
Q8NF37	PCAT1_HUMAN Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2	4.70				2.00						3.50 E-08			Sample 1 Only		
F5GWX5	F5GWX5_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=2 SV=1	1.80				2.98						6.84 E-09			Sample 1 Only		
H3BR94	H3BR94_HUMAN Dynactin subunit 5 OS=Homo sapiens GN=DCTN5 PE=2 SV=1	20.40	0.99	1.99					5.83 E-08	8.60 E-08					Control 1 Only	Control 1 Only	Control 1 Only
P01877	IGHA2_HUMAN Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3	25.90		1.00			2.00			1.09 E-08			2.02 E-07			Sample 2 Only	
B9A067	B9A067_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=2 SV=2	4.50		2.96						2.53 E-08							
O95969	SG1D2_HUMAN Secretoglobin family 1D member 2 OS=Homo sapiens GN=SCGB1D2 PE=2 SV=1	22.20					3.00						6.08 E-07			Sample 2 Only	
P07996	TSP1_HUMAN Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	2.60						3.00						4.36 E-09			Sample 3 Only

P01700	LV102_HUMAN Ig lambda chain V-I region HA OS=Homo sapiens PE=1 SV=1	18.80		0.99			1.98			3.38 E-08			1.96 E-07			Sample 2 Only	
E9PKH2	E9PKH2_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=2 SV=1	11.40						2.99						3.64 E-08			Sample 3 Only
E9PBJ0	E9PBJ0_HUMAN Mucin-5B OS=Homo sapiens GN=MUC5B PE=2 SV=1	0.80					3.00						4.20 E-09			Sample 2 Only	
F5H1Z7	F5H1Z7_HUMAN Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=2 SV=1	2.90				1.00	2.00					7.93 E-09	2.40 E-08		Sample 1 Only	Sample 2 Only	
P20160	CAP7_HUMAN Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3	12.40					3.00						1.24 E-07			Sample 2 Only	
G3V1B3	G3V1B3_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=4 SV=1	29.90		1.00		2.00				1.84 E-07		6.50 E-07			Sample 1 Only		
Q96HJ9-2	CG055_HUMAN Isoform 2 of UPF0562 protein C7orf55 OS=Homo sapiens GN=C7orf55	5.90				3.00						3.13 E-08			Sample 1 Only		
P14174	MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	17.40		1.00			1.00			1.16 E-07			4.66 E-08			Sample 2 Only	
Q9H993	CF211_HUMAN UPF0364 protein C6orf211 OS=Homo sapiens GN=C6orf211 PE=1 SV=1	3.20		0.99		1.99				1.49 E-08		5.96 E-08			Sample 1 Only		
O15020	SPTN2_HUMAN Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	1.60		3.00						3.42 E-09							
Q9NUQ8	ABCF3_HUMAN ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2	2.70		1.00		1.00		1.00		8.60 E-09		4.91 E-09		1.15 E-09	Sample 1 Only		Sample 3 Only
B4DR61	B4DR61_HUMAN Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=2 SV=1	4.60					1.98	0.99					3.76 E-08	2.05 E-09		Sample 2 Only	Sample 3 Only
P39019	RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	6.90				3.00						2.43 E-07			Sample 1 Only		
P07305	H10_HUMAN Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	17.50		2.00			1.00			8.23 E-08			6.27 E-08			Sample 2 Only	
Q13464	ROCK1_HUMAN Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	2.00	1.00		1.00	1.00			2.98 E-09		7.92 E-10	2.73 E-09			0.92	Control 1 Only	Control 1 Only
Q9P1Y5	CAMP3_HUMAN Calmodulin-regulated spectrin-associated protein 3 OS=Homo sapiens GN=CAMSAP3 PE=1 SV=2	2.70	1.00			2.00			2.30 E-09			7.86 E-09			3.42	Control 1 Only	Control 1 Only
P14625	ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	4.10		2.00						2.15 E-08							
B4DRT2	B4DRT2_HUMAN 28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=2 SV=1	11.70				1.99						5.25 E-08			Sample 1 Only		
J3QRD1	J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=2 SV=1	8.70		0.99	1.00					5.05 E-09	4.93 E-09						
A0FGR8-2	ESYT2_HUMAN Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2	4.30					1.00	2.00					3.82 E-09	6.23 E-09		Sample 2 Only	Sample 3 Only
P13010	XRCC5_HUMAN X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	4.10		3.00						3.27 E-08							
B4E102	B4E102_HUMAN Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=2 SV=1	35.30						3.00						7.93 E-08			Sample 3 Only

C9JC03	C9JC03_HUMAN EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=2 SV=1	15.00				2.98						4.93 E-08			Sample 1 Only		
E7EM57	E7EM57_HUMAN Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens GN=G6PD PE=2 SV=1	10.60					2.98						4.93 E-08			Sample 2 Only	
P31431	SDC4_HUMAN Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2	24.20		3.00						5.78 E-08							
P34897	GLYM_HUMAN Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3	12.40		0.99	0.99	0.99				5.64 E-09	2.03 E-09	1.09 E-08			Sample 1 Only		
F5GXS0	F5GXS0_HUMAN Complement C4-B OS=Homo sapiens GN=C4B_2 PE=2 SV=1	5.50					3.00						1.52 E-08			Sample 2 Only	
H0YGX7	H0YGX7_HUMAN Rho GDP-dissociation inhibitor 2 (Fragment) OS=Homo sapiens GN=ARHGDIB PE=4 SV=1	20.00					2.00						1.59 E-07			Sample 2 Only	
O43707	ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	11.10					2.98						2.79 E-08			Sample 2 Only	
P24844	MYL9_HUMAN Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4	54.70		3.00						2.69 E-07							
B4DLW8	B4DLW8_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=2 SV=1	5.80	0.99			1.99			9.46 E-09			3.18 E-08			3.36	Control 1 Only	Control 1 Only
G3V2X6	G3V2X6_HUMAN Protein arginine N-methyltransferase 5 (Fragment) OS=Homo sapiens GN=PRMT5 PE=2 SV=1	91.90															
P04899	GNAI2_HUMAN Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	10.70					2.97						6.10 E-08			Sample 2 Only	
Q15758	AAAT_HUMAN Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2	7.90		1.00			2.00			8.84 E-09			2.16 E-08			Sample 2 Only	
Q99575	POP1_HUMAN Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2	6.40				3.00						2.51 E-08			Sample 1 Only		
Q9BZE1	RM37_HUMAN 39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2	9.20					3.00						4.67 E-08			Sample 2 Only	
F5H6T1	F5H6T1_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=2 SV=1	8.50						2.00						1.66 E-08			Sample 3 Only
G3V3A0	G3V3A0_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=2 SV=1	14.10		1.00			2.00			1.72 E-08			1.09 E-07			Sample 2 Only	
O95394	AGM1_HUMAN Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1	3.90		0.99		1.98				4.64 E-09		3.34 E-08			Sample 1 Only		
P62263	RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	15.90				3.00						5.93 E-07			Sample 1 Only		
Q96I59	SYNM_HUMAN Probable asparagine--tRNA ligase, mitochondrial OS=Homo sapiens GN=NARS2 PE=1 SV=3	5.50				2.97						6.86 E-08			Sample 1 Only		
P33176	KINH_HUMAN Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	2.40			1.99			0.99			2.14 E-09			1.65 E-09			Sample 3 Only
Q7Z4H8	KDEL2_HUMAN KDEL motif-containing protein 2 OS=Homo sapiens GN=KDELC2 PE=1 SV=2	12.60	3.00						1.07 E-07						Control 1 Only	Control 1 Only	Control 1 Only

Q14697	GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	3.50		1.00		2.00				2.85 E-09		1.87 E-08			Sample 1 Only		
O15230	LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	0.90				1.00	1.00	1.00				1.06 E-09	7.25 E-10	5.21 E-10	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JV77	C9JV77_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=2 SV=1	4.60					2.00						9.91 E-08			Sample 2 Only	
F5H2X0	F5H2X0_HUMAN Tight junction protein ZO-3 OS=Homo sapiens GN=TJP3 PE=2 SV=1	3.90				2.00						7.19 E-09			Sample 1 Only		
B4E189	B4E189_HUMAN Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=2 SV=1	3.50				1.98						3.21 E-08			Sample 1 Only		
E7EWT1	E7EWT1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=2 SV=1	5.30				0.99		1.00				2.96 E-08		2.91 E-09	Sample 1 Only		Sample 3 Only
P02790	HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	4.80					2.00						7.46 E-08			Sample 2 Only	
H7C086	H7C086_HUMAN ATP synthase subunit O, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5O PE=4 SV=1	33.80		2.00						3.13 E-07							
F8W845	F8W845_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=2 SV=1	3.10						1.98						3.12 E-09			Sample 3 Only
O00299	CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	12.40					2.00						4.96 E-08			Sample 2 Only	
B4DFA2	B4DFA2_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1	3.40		1.00		0.99				6.63 E-09		6.40 E-09			Sample 1 Only		
B0YIW6	B0YIW6_HUMAN Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=2 SV=1	4.70				1.00		1.00				1.14 E-08		5.88 E-09	Sample 1 Only		Sample 3 Only
F6SBX2	F6SBX2_HUMAN Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=2 SV=1	3.50						2.00						3.39 E-09			Sample 3 Only
F5H5N0	F5H5N0_HUMAN Serine/threonine-protein kinase MRCK alpha OS=Homo sapiens GN=CDC42BPA PE=2 SV=1	1.70				2.00						3.67 E-09			Sample 1 Only		
M0R009	M0R009_HUMAN Alpha-1B-glycoprotein (Fragment) OS=Homo sapiens GN=A1BG PE=2 SV=1	7.80					2.00						2.82 E-08			Sample 2 Only	
H7C3Q8	H7C3Q8_HUMAN Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 (Fragment) OS=Homo sapiens GN=ACAP2 PE=4 SV=1	7.00		1.00				1.00		7.72 E-09				2.08 E-08			Sample 3 Only
Q14258	TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	8.60		2.00						3.40 E-08							
F8WCF6	F8WCF6_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=2 SV=1	19.50					2.00						1.35 E-07			Sample 2 Only	
P01764	HV303_HUMAN Ig heavy chain V-III region VH26 OS=Homo sapiens PE=1 SV=1	25.60					2.00						2.20 E-07			Sample 2 Only	
E9PE17	E9PE17_HUMAN 28S ribosomal protein S17, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS17 PE=2 SV=1	14.00		2.00						1.05 E-07							
D6RGE5	D6RGE5_HUMAN Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=2 SV=2	21.80					1.99						4.17 E-07			Sample 2 Only	

B4DN45	B4DN45_HUMAN S-adenosylmethionine synthase OS=Homo sapiens GN=MAT2A PE=2 SV=1	10.00			1.00	1.00					2.45 E-08	6.56 E-08			Sample 1 Only		
P22894	MMP8_HUMAN Neutrophil collagenase OS=Homo sapiens GN=MMP8 PE=1 SV=1	4.70					2.00						5.99 E-08			Sample 2 Only	
H0Y3Y9	H0Y3Y9_HUMAN 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens GN=PSMD4 PE=4 SV=1	8.80			1.00	0.99					7.02 E-09	6.36 E-08			Sample 1 Only		
B4E3P0	B4E3P0_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=2 SV=1	4.00				2.00						1.42 E-08			Sample 1 Only		
C9JZR2	C9JZR2_HUMAN Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=2 SV=2	2.00				1.98						1.84 E-08			Sample 1 Only		
Q8NB46	ANR52_HUMAN Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C OS=Homo sapiens GN=ANKRD52 PE=1 SV=3	2.70				2.00						1.02 E-08			Sample 1 Only		
Q01518	CAP1_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5	9.90		0.99			0.99			1.26 E-08			7.57 E-09			Sample 2 Only	
P49406	RM19_HUMAN 39S ribosomal protein L19, mitochondrial OS=Homo sapiens GN=MRPL19 PE=1 SV=2	11.90					2.00						5.83 E-08			Sample 2 Only	
B3KQF6	B3KQF6_HUMAN Vacuolar protein sorting 33B (Yeast), isoform CRA_b OS=Homo sapiens GN=VPS33B PE=2 SV=1	3.40				2.00						1.63 E-08			Sample 1 Only		
O00567	NOP56_HUMAN Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4	7.10				2.00						2.07 E-08			Sample 1 Only		
Q6UX06	OLFM4_HUMAN Olfactomedin-4 OS=Homo sapiens GN=OLFM4 PE=1 SV=1	5.10					2.00						3.26 E-08			Sample 2 Only	
E9PK47	E9PK47_HUMAN Phosphorylase OS=Homo sapiens GN=PYGL PE=2 SV=1	6.40					2.00						1.02 E-08			Sample 2 Only	
B4DET3	B4DET3_HUMAN Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=2 SV=1	1.40			2.00						4.29 E-09						
P0C0S5	H2AZ_HUMAN Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2	23.40					0.99						5.10 E-08			Sample 2 Only	
P31946	1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	39.20					2.00						8.58 E-08			Sample 2 Only	
P40121	CAPG_HUMAN Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2	10.20					2.00						4.25 E-08			Sample 2 Only	
C9JZR7	C9JZR7_HUMAN Actin, cytoplasmic 1 (Fragment) OS=Homo sapiens GN=ACTB PE=2 SV=1	83.50					2.00						9.21 E-07			Sample 2 Only	
P80748	LV302_HUMAN Ig lambda chain V-III region LOI OS=Homo sapiens PE=1 SV=1	21.60					2.00						4.14 E-07			Sample 2 Only	
Q13127	REST_HUMAN RE1-silencing transcription factor OS=Homo sapiens GN=REST PE=1 SV=3	2.80						2.00						3.52 E-09			Sample 3 Only
Q53G59	KLH12_HUMAN Kelch-like protein 12 OS=Homo sapiens GN=KLHL12 PE=1 SV=2	6.20		1.98						2.42 E-08							
Q7Z2W9	RM21_HUMAN 39S ribosomal protein L21, mitochondrial OS=Homo sapiens GN=MRPL21 PE=1 SV=2	24.20					1.99						1.07 E-07			Sample 2 Only	
Q13885	TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	60.90				1.00	1.00					4.74 E-08	3.45 E-08		Sample 1 Only	Sample 2 Only	
P04350	TBB4A_HUMAN Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	76.80					2.00						5.85 E-08			Sample 2 Only	

E7ENJ6	E7ENJ6_HUMAN AP-1 complex subunit mu-1 OS=Homo sapiens GN=AP1M1 PE=2 SV=1	13.50		0.99		0.99				1.29 E-08		5.03 E-08			Sample 1 Only		
E1P5S2	E1P5S2_HUMAN RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=2 SV=1	8.00				2.00						3.84 E-08			Sample 1 Only		
A8MXP9	A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	10.90				2.00						1.93 E-08			Sample 1 Only		
H0Y512	H0Y512_HUMAN Adipocyte plasma membrane-associated protein (Fragment) OS=Homo sapiens GN=APMAP PE=4 SV=1	8.00					2.00						2.98 E-08			Sample 2 Only	
B4DXI8	B4DXI8_HUMAN 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=2 SV=1	10.10						2.00						2.58 E-08			Sample 3 Only
P00352	AL1A1_HUMAN Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	3.60					2.00						3.09 E-08			Sample 2 Only	
Q9Y5V3	MAGD1_HUMAN Melanoma-associated antigen D1 OS=Homo sapiens GN=MAGED1 PE=1 SV=3	3.50					2.00						1.56 E-08			Sample 2 Only	
O75594	PGRP1_HUMAN Peptidoglycan recognition protein 1 OS=Homo sapiens GN=PGLYRP1 PE=1 SV=1	12.20					1.00						2.90 E-08			Sample 2 Only	
P23083	HV103_HUMAN Ig heavy chain V-I region V35 OS=Homo sapiens PE=1 SV=1	20.50					1.00						1.11 E-07			Sample 2 Only	
A6NG51	A6NG51_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=2 SV=2	2.30		1.00						1.02 E-09							
P01023	A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	1.50					1.00						6.59 E-09			Sample 2 Only	
B4DZ61	B4DZ61_HUMAN Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=2 SV=1	9.10				1.00						5.47 E-09			Sample 1 Only		
B7Z1R5	B7Z1R5_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=2 SV=1	4.60		1.00						7.04 E-09							
O94761	RECQ4_HUMAN ATP-dependent DNA helicase Q4 OS=Homo sapiens GN=RECQL4 PE=1 SV=1	2.20				1.00						1.09 E-08			Sample 1 Only		
P06858	LIPL_HUMAN Lipoprotein lipase OS=Homo sapiens GN=LPL PE=1 SV=1	7.60		1.00						1.55 E-08							
Q9P2E3	ZNFX1_HUMAN NFX1-type zinc finger-containing protein 1 OS=Homo sapiens GN=ZNFX1 PE=1 SV=2	1.40				1.00						1.58 E-09			Sample 1 Only		
Q9C075	K1C23_HUMAN Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2	5.70		0.99						1.39 E-08							
Q9H223	EHD4_HUMAN EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1	4.10				1.00						1.82 E-08			Sample 1 Only		
P14618-2	KPYM_HUMAN Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM	32.40					0.98						1.63 E-08			Sample 2 Only	
E5RGE1	E5RGE1_HUMAN 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1	55.80					1.00						4.72 E-07			Sample 2 Only	
P31947	1433S_HUMAN 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	13.40					1.00						1.18 E-08			Sample 2 Only	
P62258	1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	10.20					0.99						3.12 E-08			Sample 2 Only	
Q14CN4	K2C72_HUMAN Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2	14.90			0.99						5.42 E-09						

P16989	YBOX3_HUMAN Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4	19.80				1.00						2.97 E-08			Sample 1 Only		

Table A2. Endogenous candidates from cytoplasmic immunoprecipitations that had not been treated with RNase

			SPECTRAL COUNTS						SPECTRAL INDEX (MIC SIn)						RATIOS		
Prot	Description	% Cover	C1	C2	C3	S1	S2	S3	C1	C2	C3	S1	S2	S3	S1/C1	S2/C1	S3/C1
Q9UKV8	AGO2_HUMAN Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	81.60				316.44	527.40	559.90				2.08E-05	7.11E-05	9.35E-05	Sample 1 Only	Sample 2 Only	Sample 3 Only
P01625	KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	27.20	18.00	19.00	23.00		1.00		1.50E-05	4.96E-05	5.69E-05		1.89E-07		Control 1 Only	0.01	Control 1 Only
P01605	KV113_HUMAN Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1	25.00	20.00	21.00	22.00		1.00	1.00	1.39E-05	4.78E-05	4.72E-05		2.43E-07	2.05E-07	Control 1 Only	0.02	0.01
P01614	KV201_HUMAN Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	20.40	14.00	11.00	12.00	6.00	5.00	5.00	3.57E-05	1.23E-04	1.08E-04	9.26E-07	4.12E-06	3.54E-06	0.03	0.12	0.10
P01764	HV303_HUMAN Ig heavy chain V-III region VH26 OS=Homo sapiens PE=1 SV=1	24.80	8.14	16.42	17.42				1.74E-06	1.27E-05	1.10E-05				Control 1 Only	Control 1 Only	Control 1 Only
Q9H9G7	AGO3_HUMAN Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	65.70				44.50	107.00	116.50				1.17E-06	4.56E-06	6.44E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P13646	K1C13_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	72.70	5.89	3.96	1.97	19.73	23.74	134.25	1.72E-06	4.59E-08	1.76E-07	1.95E-06	1.11E-06	3.24E-05	1.14	0.65	18.82
P12035	K2C3_HUMAN Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3	67.00				3.00	2.00	64.00				3.77E-08	2.12E-08	5.11E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P19013	K2C4_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	67.20				11.99	11.98	79.92				2.32E-07	3.28E-07	4.21E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9UPY3	DICER_HUMAN Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	39.10				55.91	129.74	136.69				3.39E-07	1.29E-06	1.67E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q15633	TRBP2_HUMAN RISC-loading complex subunit TARBP2 OS=Homo sapiens GN=TARBP2 PE=1 SV=3	18.80				11.88	6.93	9.90				5.48E-07	1.08E-06	1.51E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P01781	HV320_HUMAN Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1	15.50	3.00	5.00	5.00				1.90E-07	9.47E-07	7.94E-07				Control 1 Only	Control 1 Only	Control 1 Only
P01763	HV302_HUMAN Ig heavy chain V-III region WEA OS=Homo sapiens PE=1 SV=1	15.80	1.00	5.00	3.00				1.09E-07	8.56E-07	6.44E-07				Control 1 Only	Control 1 Only	Control 1 Only
Q9UL18	AGO1_HUMAN Protein argonaute-1 OS=Homo sapiens GN=AGO1 PE=1 SV=3	57.90				4.00	33.00	39.00				4.21E-08	6.71E-07	1.14E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8NDV7	TNR6A_HUMAN Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	20.80				13.50	34.50	59.50				1.18E-07	4.24E-07	1.02E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P35321	SPR1A_HUMAN Cornifin-A OS=Homo sapiens GN=SPRR1A PE=1 SV=2	61.80					1.00	6.97					6.19E-08	1.49E-06		Sample 2 Only	Sample 3 Only
P01765	HV304_HUMAN Ig heavy chain V-III region TIL OS=Homo sapiens PE=1 SV=1	19.10	1.00	1.00	1.00				2.42E-07	4.43E-07	2.92E-07				Control 1 Only	Control 1 Only	Control 1 Only
P01620	KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	22.90	3.97	3.97	4.97		0.99	0.99	6.44E-07	1.77E-06	2.35E-06		1.33E-07	1.24E-07	Control 1 Only	0.21	0.19
Q9UPQ9	TNR6B_HUMAN Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	24.80				8.90	46.43	91.89				2.95E-08	2.26E-07	6.89E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
G3XAB8	G3XAB8_HUMAN Trinucleotide repeat containing 6C, isoform CRA_a OS=Homo sapiens GN=TNRC6C PE=2 SV=1	18.50				12.00	32.00	57.99				6.63E-08	2.22E-07	5.70E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q01469	FABP5_HUMAN Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	38.50					3.00	6.00					3.68E-07	4.82E-07		Sample 2 Only	Sample 3 Only
J3KQS6	J3KQS6_HUMAN BRISC and BRCA1-A complex member 1 OS=Homo sapiens	55.60				1.98	1.98	3.96				7.01E-08	2.43E-07	3.33E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only

	GN=BABAM1 PE=2 SV=1																
H7C269	H7C269_HUMAN Trinucleotide repeat-containing gene 6A protein (Fragment) OS=Homo sapiens GN=TNRC6A PE=2 SV=1	19.50				4.50	6.50	13.50				5.54 E-08	1.65 E-07	3.56 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
H9KVA9	H9KVA9_HUMAN Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=2 SV=1	22.70				0.99	1.98	4.95				3.67 E-08	1.13 E-07	4.26 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P47929	LEG7_HUMAN Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	39.00				2.00	2.00	5.00				2.91 E-08	1.22 E-07	4.14 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
F8W733	F8W733_HUMAN BRCA1-A complex subunit BRE (Fragment) OS=Homo sapiens GN=BRE PE=2 SV=1	9.90				3.00	1.00	3.00				1.03 E-07	6.48 E-08	3.22 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q13257	MD2L1_HUMAN Mitotic spindle assembly checkpoint protein MAD2A OS=Homo sapiens GN=MAD2L1 PE=1 SV=1	8.80				0.99	1.00	1.00				3.88 E-08	1.32 E-07	1.56 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9HCK5	AGO4_HUMAN Protein argonaute-4 OS=Homo sapiens GN=AGO4 PE=1 SV=2	28.80					7.00	10.00					9.29 E-08	2.00 E-07		Sample 2 Only	Sample 3 Only
P31947	1433S_HUMAN 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	34.30					1.00	8.00					4.04 E-08	2.38 E-07		Sample 2 Only	Sample 3 Only
P30041	PRDX6_HUMAN Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	19.60				1.00	1.00	4.00				4.57 E-08	2.51 E-08	2.07 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q5JXJ0	Q5JXJ0_HUMAN Mitochondrial ribosome-associated GTPase 2 (Fragment) OS=Homo sapiens GN=MTG2 PE=2 SV=1	6.90				1.00	1.00	1.00				5.37 E-08	7.85 E-08	1.43 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P08123	CO1A2_HUMAN Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	3.90		7.00	1.00					1.59 E-07	6.58 E-08						
O96007	MOC2B_HUMAN Molybdopterin synthase catalytic subunit OS=Homo sapiens GN=MOCS2 PE=1 SV=1	18.60	2.00		1.00				1.12 E-07		8.02 E-08				Control 1 Only	Control 1 Only	Control 1 Only
Q15018	F175B_HUMAN BRISC complex subunit Abro1 OS=Homo sapiens GN=FAM175B PE=1 SV=2	11.80					4.00	2.00					1.60 E-07	6.89 E-08		Sample 2 Only	Sample 3 Only
Q08188	TGM3_HUMAN Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	17.30			1.00		2.00	14.00			2.86 E-09		2.27 E-08	2.12 E-07		Sample 2 Only	Sample 3 Only
P05109	S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	57.00	1.00	1.00	4.00		5.00	9.00	3.32 E-08	7.68 E-08	2.08 E-07		1.07 E-06	2.17 E-06	Control 1 Only	32.20	65.30
P61026	RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	17.00				2.00	1.00					6.68 E-08	6.92 E-08		Sample 1 Only	Sample 2 Only	
P11413	G6PD_HUMAN Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4	7.00	2.00	1.00	1.00				3.55 E-08	3.79 E-08	3.81 E-08				Control 1 Only	Control 1 Only	Control 1 Only
Q9H7D7	WDR26_HUMAN WD repeat-containing protein 26 OS=Homo sapiens GN=WDR26 PE=1 SV=3	7.10	0.99	3.96	2.97				6.63 E-09	5.22 E-08	4.48 E-08				Control 1 Only	Control 1 Only	Control 1 Only
P40938	RFC3_HUMAN Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2	9.20	2.00		1.00				3.03 E-08		5.02 E-08				Control 1 Only	Control 1 Only	Control 1 Only
Q13835	PKP1_HUMAN Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	9.90			1.00		6.00	4.00			4.54 E-09		8.66 E-08	4.71 E-08		Sample 2 Only	Sample 3 Only
E7ERK9	E7ERK9_HUMAN Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=2 SV=1	5.00				1.00		1.00				1.27 E-08		4.72 E-08	Sample 1 Only		Sample 3 Only
Q16204	CCDC6_HUMAN Coiled-coil domain-containing protein 6 OS=Homo sapiens GN=CCDC6 PE=1 SV=2	8.40	2.00	2.00	1.00	1.00			3.10 E-08	1.26 E-07	8.10 E-08	1.75 E-08			0.57	Control 1 Only	Control 1 Only
Q7L775	EPMIP_HUMAN EPM2A-interacting protein 1 OS=Homo sapiens GN=EPM2AIP1 PE=1 SV=1	3.50				1.00		1.00				1.28 E-08		2.89 E-08	Sample 1 Only		Sample 3 Only

P00367	DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2	9.00	0.99	1.98	4.97		0.99		1.89 E-08	7.05 E-08	2.31 E-07		3.29 E-08		Control 1 Only	1.74	Control 1 Only
P01859	IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	12.60	1.00	2.00	1.00	2.00	5.00	5.00	3.22 E-08	1.94 E-07	5.85 E-08	8.33 E-08	9.10 E-07	8.97 E-07	2.58	28.24	27.83
B4DRF4	B4DRF4_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=2 SV=1	12.10	3.00	1.00		2.00			1.48 E-07	1.85 E-07		3.99 E-08			0.27	Control 1 Only	Control 1 Only
Q96AG4	LRC59_HUMAN Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	7.20	2.00	1.00	1.00	1.00			7.76 E-08	7.64 E-08	8.29 E-08	2.59 E-08			0.33	Control 1 Only	Control 1 Only
P54652	HSP72_HUMAN Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	20.00	1.00		1.00				1.30 E-08		9.29 E-09				Control 1 Only	Control 1 Only	Control 1 Only
Q9H307	PININ_HUMAN Pinin OS=Homo sapiens GN=PNN PE=1 SV=4	5.10				1.00	1.00	0.99				4.62 E-09	5.96 E-09	1.59 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P04350	TBB4A_HUMAN Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	73.00		2.00	1.00	2.00	2.00	1.00		3.08 E-08	8.11 E-08	3.16 E-07	3.38 E-07	1.20 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B3KQ25	B3KQ25_HUMAN Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=2 SV=1	14.50	1.00	1.00	1.00	1.00			6.78 E-08	1.39 E-07	1.38 E-07	5.03 E-08			0.74	Control 1 Only	Control 1 Only
Q96I99	SUCB2_HUMAN Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2	8.10	1.00			2.00	1.00	1.00	7.69 E-09			2.67 E-08	3.07 E-08	3.33 E-08	3.47	3.99	4.33
P60891	PRPS1_HUMAN Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	19.50			0.99		2.98	3.96			8.28 E-08		2.63 E-07	2.86 E-07		Sample 2 Only	Sample 3 Only
B4DY35	B4DY35_HUMAN Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 PE=2 SV=1	12.40	1.00	2.00		1.00			5.59 E-08	2.87 E-07		5.53 E-08			0.99	Control 1 Only	Control 1 Only
Q6S8J3	POTEE_HUMAN POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	11.10		0.99		4.95		0.99		8.62 E-09		6.86 E-08		2.14 E-08	Sample 1 Only		Sample 3 Only
Q6ZVX7	FBX50_HUMAN F-box only protein 50 OS=Homo sapiens GN=NCCRP1 PE=1 SV=1	8.40			1.00	1.00	2.00	3.00			1.55 E-08	1.05 E-08	7.19 E-08	5.33 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P53597	SUCA_HUMAN Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4	10.40	3.00	1.00	1.00	2.00			5.06 E-08	8.17 E-08	6.10 E-08	3.16 E-08			0.63	Control 1 Only	Control 1 Only
K7EKI8	K7EKI8_HUMAN Periplakin OS=Homo sapiens GN=PPL PE=2 SV=1	7.90	2.00		1.00		1.00	10.99	2.34 E-09		8.14 E-10		1.16 E-09	3.47 E-08	Control 1 Only	0.50	14.85
G8JLG2	G8JLG2_HUMAN Corneodesmosin OS=Homo sapiens GN=CDSN PE=2 SV=1	13.00		1.00	1.00	1.00	5.00	1.00		4.72 E-09	7.54 E-09	5.35 E-09	8.63 E-08	6.47 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
B7ZL00	B7ZL00_HUMAN Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=2 SV=1	3.10	0.99	1.98	1.98	0.99			1.12 E-09	8.08 E-09	7.50 E-09	1.08 E-09			0.97	Control 1 Only	Control 1 Only
Q9UBV8	PEF1_HUMAN Peflin OS=Homo sapiens GN=PEF1 PE=1 SV=1	8.50	1.00	1.00	1.00	1.00			2.48 E-08	2.98 E-08	3.04 E-08	1.23 E-08			0.50	Control 1 Only	Control 1 Only
Q9NQX4	MYO5C_HUMAN Unconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	9.50	1.99	1.00	1.00	12.93		4.95	3.85 E-09	1.48 E-09	9.79 E-10	3.56 E-08		1.76 E-08	9.23	Control 1 Only	4.57
P04080	CYTB_HUMAN Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	79.60	2.00			2.00		7.00	3.14 E-07			2.42 E-07		1.15 E-06	0.77	Control 1 Only	3.66
F6RFD5	F6RFD5_HUMAN Destrin OS=Homo sapiens GN=DSTN PE=2 SV=1	22.20	2.98		0.99	1.98			5.95 E-07		4.36 E-07	2.49 E-07			0.42	Control 1 Only	Control 1 Only

C9JW96	C9JW96_HUMAN Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=2 SV=2	21.40	2.00	1.00	2.00	3.00	1.00		6.46 E-08	1.94 E-08	2.44 E-07	5.23 E-08	1.55 E-08		0.81	0.24	Control 1 Only
C9IZE4	C9IZE4_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=2 SV=1	10.30	0.99		1.98	0.99			1.29 E-08		6.95 E-08	1.34 E-08			1.04	Control 1 Only	Control 1 Only
Q3SYB4	Q3SYB4_HUMAN SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1	15.30	1.00	2.00	2.00		7.00	1.00	4.58 E-09	1.81 E-08	1.90 E-08		2.14 E-07	6.82 E-09	Control 1 Only	46.61	1.49
A6NES3	A6NES3_HUMAN Etoposide-induced protein 2.4 homolog OS=Homo sapiens GN=EI24 PE=2 SV=1	25.30	0.99		2.00	1.99	1.99	2.99	7.37 E-08		1.26 E-08	1.10 E-07	1.38 E-07	1.65 E-07	1.50	1.88	2.25
Q6UWP8	SBSN_HUMAN Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2	15.30				1.00		1.00				3.44 E-09		5.43 E-09	Sample 1 Only		Sample 3 Only
P22059	OSBP1_HUMAN Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1	6.20		2.00	3.00		1.00			1.29 E-08	1.96 E-08		4.54 E-09			Sample 2 Only	
Q9NYL9	TMOD3_HUMAN Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1	29.80	4.98		1.99	20.97		1.99	9.70 E-08		1.02 E-07	7.44 E-07		8.64 E-08	7.67	Control 1 Only	0.89
Q9BY49	PECR_HUMAN Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2	19.50		3.00	2.00	1.00	1.00	1.00		4.30 E-07	2.39 E-07	2.50 E-08	5.52 E-08	8.86 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q92890	UFD1_HUMAN Ubiquitin fusion degradation protein 1 homolog OS=Homo sapiens GN=UFD1L PE=1 SV=3	17.30		0.99	0.99		2.97	2.97		1.58 E-08	1.79 E-08		9.04 E-08	8.40 E-08		Sample 2 Only	Sample 3 Only
F5H012	F5H012_HUMAN E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=2 SV=1	11.20	2.00	1.00		2.00	5.00	5.00	5.32 E-08	6.09 E-08		6.31 E-08	1.99 E-07	2.39 E-07	1.19	3.74	4.49
E7EW20	E7EW20_HUMAN Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=2 SV=1	35.40	23.76	10.89	4.95	97.03		12.88	9.93 E-08	8.82 E-08	1.73 E-08	7.35 E-07		8.33 E-08	7.40	Control 1 Only	0.84
Q9NZ08	ERAP1_HUMAN Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3	5.00		3.00	1.00		1.00	1.00		4.30 E-08	1.22 E-08		9.17 E-09	1.04 E-09		Sample 2 Only	Sample 3 Only
O43852	CALU_HUMAN Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	11.40	0.99	2.97	3.96	0.99	1.98	0.99	2.45 E-08	3.15 E-07	4.31 E-07	4.09 E-08	1.04 E-07	6.59 E-08	1.67	4.23	2.70
O00231	PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	15.60	3.00	2.00	4.00	3.00		2.00	7.68 E-08	2.02 E-07	3.20 E-07	5.09 E-08		1.12 E-07	0.66	Control 1 Only	1.46
Q13247	SRSF6_HUMAN Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2	13.70	2.99			1.99	3.99	4.98	6.81 E-08			3.88 E-08	1.47 E-07	1.08 E-07	0.57	2.17	1.59
Q7Z794	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	28.00	4.00	8.00	21.50	5.00	4.50	3.50	4.52 E-08	1.33 E-07	5.04 E-07	4.55 E-08	8.32 E-08	6.30 E-08	1.01	1.84	1.39
P23528	COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	26.50	1.98			1.98	4.93	0.98	1.79 E-07			1.37 E-07	5.05 E-07	3.20 E-08	0.77	2.82	0.18
B7Z3I9	B7Z3I9_HUMAN Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=2 SV=1	14.70	4.97	3.97	5.96	3.98	0.99	1.98	1.93 E-07	6.33 E-07	6.85 E-07	1.52 E-07	8.45 E-08	2.34 E-07	0.79	0.44	1.21
Q9UPN9	TRI33_HUMAN E3 ubiquitin-protein ligase TRIM33 OS=Homo sapiens GN=TRIM33 PE=1 SV=3	6.80		3.99	4.97		1.99	2.99		4.56 E-08	5.52 E-08		7.36 E-09	1.66 E-08		Sample 2 Only	Sample 3 Only
P78318	IGBP1_HUMAN Immunoglobulin-binding protein 1 OS=Homo sapiens GN=IGBP1 PE=1 SV=1	7.40	1.00			1.00	1.00	1.00	1.57 E-08			1.17 E-08	3.08 E-08	3.23 E-08	0.75	1.97	2.06
Q8N335	GPD1L_HUMAN Glycerol-3-phosphate dehydrogenase 1-like protein OS=Homo sapiens GN=GPD1L PE=1 SV=1	5.40	1.00	1.99	1.00			0.99	1.89 E-08	1.40 E-07	4.87 E-08			5.59 E-08	Control 1 Only	Control 1 Only	2.97

J3QKW2	J3QKW2_HUMAN 28S ribosomal protein S7, mitochondrial OS=Homo sapiens GN=MRPS7 PE=2 SV=1	15.10	2.00	1.00	1.00	1.00	3.00	3.00	6.63 E-08	6.69 E-08	7.53 E-08	2.25 E-08	3.21 E-07	3.57 E-07	0.34	4.84	5.38
P22314	UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	6.30		6.00	4.00		1.00	1.00		3.55 E-08	2.98 E-08		8.50 E-09	7.18 E-09		Sample 2 Only	Sample 3 Only
F6S0T5	F6S0T5_HUMAN Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=2 SV=1	5.90		2.00	4.00		1.00			2.44 E-08	3.54 E-08		1.39 E-08			Sample 2 Only	
B4DJV2	B4DJV2_HUMAN Citrate synthase OS=Homo sapiens GN=CS PE=2 SV=1	8.60	2.97	0.99	0.99	0.99	0.99		8.98 E-08	8.64 E-08	6.35 E-08	3.70 E-08	3.06 E-08		0.41	0.34	Control 1 Only
P49642	PRI1_HUMAN DNA primase small subunit OS=Homo sapiens GN=PRIM1 PE=1 SV=1	21.40	3.00	4.98	8.97	2.00	3.98	1.99	4.13 E-08	2.38 E-07	3.29 E-07	2.81 E-08	1.18 E-07	4.39 E-08	0.68	2.86	1.06
F8W9S7	F8W9S7_HUMAN GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=2 SV=1	4.90	0.99	2.00	3.99	1.99		1.00	7.00 E-09	2.28 E-08	4.54 E-08	1.25 E-08		6.25 E-09	1.79	Control 1 Only	0.89
Q92499	DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	30.80	8.00	15.00	29.00	4.00	8.00	9.00	1.63 E-07	3.26 E-07	6.91 E-07	6.46 E-08	1.21 E-07	2.17 E-07	0.40	0.74	1.33
O14965	AURKA_HUMAN Aurora kinase A OS=Homo sapiens GN=AURKA PE=1 SV=2	28.30	2.99	6.95	9.91	2.99	2.98	5.95	1.19 E-07	6.72 E-07	1.22 E-06	7.41 E-08	2.03 E-07	4.40 E-07	0.62	1.70	3.69
K7EIG7	K7EIG7_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=2 SV=1	11.90		0.99	2.97	3.97	1.98	3.96		4.21 E-09	3.10 E-08	5.73 E-08	1.60 E-08	5.94 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JEH3	C9JEH3_HUMAN Angio-associated migratory cell protein OS=Homo sapiens GN=AAMP PE=2 SV=1	5.80	0.99	2.97	0.99		0.99	0.99	3.63 E-08	2.30 E-07	6.59 E-08		5.37 E-08	4.79 E-08	Control 1 Only	1.48	1.32
Q9H3U1	UN45A_HUMAN Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1	3.10	1.00	3.00	3.00	1.00		1.00	6.16 E-09	2.22 E-08	2.50 E-08	5.59 E-09		7.72 E-09	0.91	Control 1 Only	1.25
A8MU44	A8MU44_HUMAN Protein Hook homolog 1 OS=Homo sapiens GN=HOOK1 PE=2 SV=2	15.20		3.00	4.00			2.00		2.98 E-08	3.11 E-08			1.55 E-08			Sample 3 Only
F5GYR8	F5GYR8_HUMAN General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=2 SV=1	6.90	1.00	4.00	5.00		3.00	1.00	4.46 E-09	3.62 E-08	4.95 E-08		1.72 E-08	8.17 E-09	Control 1 Only	3.86	1.83
A6NGW1	A6NGW1_HUMAN Protein YIF1A OS=Homo sapiens GN=YIF1A PE=2 SV=1	11.20	0.99				0.99	0.99	4.22 E-08				8.51 E-08	5.99 E-08	Control 1 Only	2.02	1.42
E7EP00	E7EP00_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=2 SV=2	10.90	2.00	8.00	9.00		3.00	4.00	8.06 E-09	1.15 E-07	1.24 E-07		3.40 E-08	4.57 E-08	Control 1 Only	4.22	5.67
P27694	RFA1_HUMAN Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2	52.60	40.97	43.98	63.96	35.98	24.99	34.98	1.66 E-06	3.65 E-06	3.44 E-06	1.08 E-06	1.08 E-06	1.56 E-06	0.65	0.65	0.94
M0R2B7	M0R2B7_HUMAN DNA polymerase OS=Homo sapiens GN=POLD1 PE=2 SV=1	9.50	0.99	6.93	2.97		0.99	1.98	6.78 E-09	4.25 E-08	1.66 E-08		6.66 E-09	1.19 E-08	Control 1 Only	0.98	1.76
C9JSQ1	C9JSQ1_HUMAN Creatine kinase U-type, mitochondrial (Fragment) OS=Homo sapiens GN=CKMT1B PE=2 SV=1	11.30	1.00		1.00		1.00	1.00	7.90 E-09		3.51 E-08		7.27 E-08	6.96 E-08	Control 1 Only	9.20	8.80
P52732	KIF11_HUMAN Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	5.80		2.00	5.00		1.00	2.00		1.15 E-08	4.22 E-08		5.79 E-09	9.22 E-09		Sample 2 Only	Sample 3 Only
P50336	PPOX_HUMAN Protoporphyrinogen oxidase OS=Homo sapiens GN=PPOX PE=1 SV=1	12.40		1.00	1.00		3.99	2.98		8.12 E-08	7.29 E-08		2.91 E-07	1.42 E-07		Sample 2 Only	Sample 3 Only
O95347	SMC2_HUMAN Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	12.80		8.00	6.00		3.00	4.00		6.05 E-08	5.04 E-08		1.09 E-08	2.51 E-08		Sample 2 Only	Sample 3 Only
Q9UBX3	DIC_HUMAN Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10	16.70	1.00	1.00	2.00	1.99	2.99	3.99	1.70 E-08	4.22 E-08	1.23 E-07	3.72 E-08	1.97 E-07	2.59 E-07	2.19	11.58	15.23

	PE=1 SV=2																
O60884	DNJA2_HUMAN DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	10.20		3.00	2.00	1.00	1.00	3.00		2.95 E-07	2.64 E-07	1.08 E-08	2.08 E-08	1.81 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B3KQC5	B3KQC5_HUMAN Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase OS=Homo sapiens GN=MAN1B1 PE=2 SV=1	16.40		3.97	4.96		1.98	2.98		1.08 E-07	1.21 E-07		3.15 E-08	4.99 E-08		Sample 2 Only	Sample 3 Only
Q99832	TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	19.80	9.90	4.95	8.91	6.93	2.97	2.97	2.46 E-07	3.07 E-07	5.53 E-07	1.48 E-07	1.40 E-07	1.59 E-07	0.60	0.57	0.65
E3W978	E3W978_HUMAN Hyaluronan mediated motility receptor OS=Homo sapiens GN=HMMR PE=2 SV=2	19.70	2.00	1.00	6.00	1.00	1.00	6.00	2.51 E-08	6.76 E-08	1.45 E-07	7.90 E-09	5.09 E-09	7.37 E-08	0.31	0.20	2.94
E9PPM8	E9PPM8_HUMAN Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=2 SV=1	26.20	0.99	4.95	5.94	0.99	2.97	2.97	3.17 E-08	5.70 E-07	7.21 E-07	2.71 E-08	1.83 E-07	3.36 E-07	0.85	5.77	10.60
Q9Y2S7	PDIP2_HUMAN Polymerase delta-interacting protein 2 OS=Homo sapiens GN=POLDIP2 PE=1 SV=1	9.00	1.00	1.00			1.00	2.00	1.24 E-08	3.09 E-08			3.16 E-08	9.46 E-08	Control 1 Only	2.55	7.66
P78371	TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	43.60	19.83	13.88	17.87	15.86	6.93	11.90	6.00 E-07	9.44 E-07	1.21 E-06	4.98 E-07	2.14 E-07	4.94 E-07	0.83	0.36	0.82
P30043	BLVRB_HUMAN Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3	38.30	7.93	7.95	6.97	7.94	3.97	3.98	9.34 E-07	1.83 E-06	1.66 E-06	6.82 E-07	5.27 E-07	7.84 E-07	0.73	0.56	0.84
J3KN16	J3KN16_HUMAN Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=KIAA0368 PE=2 SV=1	2.50	2.00	2.00	3.00		1.00	1.00	5.02 E-09	4.34 E-09	9.90 E-09		1.97 E-09	3.50 E-09	Control 1 Only	0.39	0.70
Q53H96	P5CR3_HUMAN Pyrroline-5-carboxylate reductase 3 OS=Homo sapiens GN=PYCRL PE=1 SV=2	40.50	0.99			0.99		0.99	6.79 E-08			5.58 E-08		1.33 E-07	0.82	Control 1 Only	1.96
Q08379	GOGA2_HUMAN Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3	7.30		2.00	2.00		1.00	1.00		1.27 E-08	1.15 E-08		2.11 E-09	5.15 E-09		Sample 2 Only	Sample 3 Only
H7BYY1	H7BYY1_HUMAN Tropomyosin 1 (Alpha), isoform CRA_m OS=Homo sapiens GN=TPM1 PE=2 SV=1	79.80	2.94	1.96	1.96	11.76	1.96	1.96	3.77 E-07	2.51 E-07	2.99 E-07	1.65 E-06	2.50 E-07	2.40 E-07	4.38	0.66	0.64
Q8WXX5	DNJC9_HUMAN DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1	42.70	7.00			16.00		1.00	3.37 E-07			8.20 E-07		5.59 E-09	2.43	Control 1 Only	0.02
P07954	FUMH_HUMAN Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3	19.90	6.00	2.00	4.00	4.00	1.00	2.00	1.26 E-07	6.66 E-08	1.77 E-07	6.48 E-08	2.39 E-08	5.62 E-08	0.51	0.19	0.44
P62249	RS16_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	61.00	13.80			10.83	0.98	0.98	3.45 E-06			1.38 E-06	8.08 E-08	1.04 E-07	0.40	0.02	0.03
Q06210	GFPT1_HUMAN Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3	31.60	10.00	17.00	23.00	5.00	12.00	15.00	1.92 E-07	4.29 E-07	6.13 E-07	7.26 E-08	2.16 E-07	2.38 E-07	0.38	1.13	1.24
Q9H9T3	ELP3_HUMAN Elongator complex protein 3 OS=Homo sapiens GN=ELP3 PE=1 SV=2	6.20	0.99			1.98	0.99		1.94 E-08			2.80 E-08	3.07 E-08		1.44	1.58	Control 1 Only
P07355	ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	28.60	3.89	2.92	4.86	3.89	10.73	6.84	6.90 E-08	1.19 E-07	1.51 E-07	6.55 E-08	5.15 E-07	2.37 E-07	0.95	7.46	3.44
Q8N1N4	K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	36.90	4.98	5.98	7.98	5.99	17.98	11.99	6.41 E-08	7.96 E-08	8.52 E-08	5.66 E-08	3.41 E-07	1.68 E-07	0.88	5.32	2.62
P24844	MYL9_HUMAN Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4	66.30	8.00			15.00		1.00	9.56 E-07			1.98 E-06		1.81 E-07	2.07	Control 1 Only	0.19

F5H698	F5H698_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1	26.50	2.97	31.68	23.76	1.98	17.82	6.93	1.80E-07	3.40E-07	2.62E-07	1.11E-08	1.59E-07	8.53E-08	0.62	8.82	4.73
P33176	KINH_HUMAN Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	22.90		14.98	15.97	2.00	6.00	7.00		1.68E-07	1.55E-07	1.00E-08	5.70E-08	6.07E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
K7ENL3	K7ENL3_HUMAN Signal transducer and activator of transcription OS=Homo sapiens GN=STAT3 PE=2 SV=1	34.10	13.00	20.00	23.00	15.00	11.00	13.00	2.51E-07	7.38E-07	5.89E-07	2.14E-07	2.40E-07	2.38E-07	0.85	0.95	0.95
P11172	UMPS_HUMAN Uridine 5'-monophosphate synthase OS=Homo sapiens GN=UMPS PE=1 SV=1	12.10	0.99		1.98	0.99		0.99	2.69E-08		7.06E-08	1.49E-08		2.03E-08	0.55	Control 1 Only	0.75
K7EJC1	K7EJC1_HUMAN 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=2 SV=1	9.30	1.00	1.00		1.00			8.29E-08	5.75E-08		5.21E-08			0.63	Control 1 Only	Control 1 Only
E9PMD7	E9PMD7_HUMAN Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CA PE=2 SV=1	14.20		1.00	1.99	0.99		1.00		9.47E-08	1.80E-07	2.72E-08		8.09E-08	Sample 1 Only		Sample 3 Only
O14980	XPO1_HUMAN Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	5.10	3.00	1.00	2.00	1.00		1.00	1.65E-08	3.36E-08	5.25E-08	6.39E-09		3.12E-08	0.39	Control 1 Only	1.89
A6NED2	RCCD1_HUMAN RCC1 domain-containing protein 1 OS=Homo sapiens GN=RCCD1 PE=1 SV=1	9.60	1.00	2.00	2.00	1.00		2.00	2.28E-08	1.62E-07	1.55E-07	2.47E-08		1.12E-07	1.08	Control 1 Only	4.92
Q14258	TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	14.80	10.00	6.00	6.00	6.00	1.00	4.00	1.94E-07	1.51E-07	1.19E-07	9.04E-08	2.90E-08	7.38E-08	0.46	0.15	0.38
P30460	1B08_HUMAN HLA class I histocompatibility antigen, B-8 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1	18.00	2.91	1.94	3.91	1.94	0.98	2.93	9.30E-08	2.36E-07	4.54E-07	4.83E-08	1.15E-07	1.74E-07	0.52	1.23	1.88
Q9NRF8	PYRG2_HUMAN CTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1	3.60	1.00	2.00	2.00	1.00		1.00	1.54E-08	6.27E-08	1.94E-08	1.04E-08		2.59E-08	0.68	Control 1 Only	1.68
P01621	KV303_HUMAN Ig kappa chain V-III region NG9 (Fragment) OS=Homo sapiens PE=1 SV=1	25.00	1.00	3.00	1.00	1.00	2.00	1.00	9.93E-08	1.05E-06	2.88E-07	4.63E-08	4.32E-07	1.71E-07	0.47	4.35	1.72
Q99460	PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	32.60	3.00	20.98	16.99	4.00	10.99	8.98	4.51E-08	3.17E-07	2.69E-07	4.58E-08	1.38E-07	8.78E-08	1.02	3.06	1.95
B7Z8V7	B7Z8V7_HUMAN NAD kinase 2, mitochondrial OS=Homo sapiens GN=NADK2 PE=2 SV=1	10.00	1.00	2.00	1.00		1.00	1.00	1.63E-08	1.45E-07	8.41E-08		4.22E-08	5.69E-08	Control 1 Only	2.60	3.50
Q00653	NFKB2_HUMAN Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens GN=NFKB2 PE=1 SV=4	2.70		1.00	1.00		1.00			1.11E-08	7.94E-09		5.87E-09			Sample 2 Only	
Q5SSJ5	HP1B3_HUMAN Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1	20.30	11.80	0.99		5.90			3.20E-07	5.65E-09		1.35E-07			0.42	Control 1 Only	Control 1 Only
C9J9W2	C9J9W2_HUMAN LIM and SH3 domain protein 1 (Fragment) OS=Homo sapiens GN=LASP1 PE=2 SV=1	38.60	3.00	1.00	1.99	5.00	4.99	2.99	1.79E-07	1.27E-07	1.69E-07	2.09E-07	5.56E-07	2.96E-07	1.17	3.10	1.65
P12270	TPR_HUMAN Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3	1.00	2.00		1.00				1.83E-09		9.79E-10				Control 1 Only	Control 1 Only	Control 1 Only
P06702	S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	44.70	4.00	1.00	7.00	7.00	8.00	8.00	1.17E-07	2.89E-08	7.27E-07	4.12E-07	5.99E-07	8.59E-07	3.52	5.12	7.34
P16401	H15_HUMAN Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	48.70	45.00			55.00		5.00	1.04E-05			1.96E-05		1.70E-07	1.87	Control 1 Only	0.02
Q8NCW5	NNRE_HUMAN NAD(P)H-hydrate epimerase OS=Homo sapiens GN=APOA1BP PE=1 SV=2	14.60	1.00	1.00	1.00			1.00	9.09E-09	3.73E-08	4.03E-08			3.29E-08	Control 1 Only	Control 1 Only	3.62

O60678	ANM3_HUMAN Protein arginine N-methyltransferase 3 OS=Homo sapiens GN=PRMT3 PE=1 SV=3	5.30	1.00	1.00	2.00	1.00	1.00		2.24E-08	7.13E-08	7.79E-08	1.47E-08	5.49E-08		0.66	2.45	Control 1 Only
Q04837	SSBP_HUMAN Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1	50.00	10.00	2.00	1.00	6.00	1.00	2.00	1.82E-06	2.60E-07	2.53E-07	5.96E-07	2.25E-07	2.95E-07	0.33	0.12	0.16
K7EMW4	K7EMW4_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=2 SV=1	12.50		1.00	2.99		2.00	1.00		7.24E-08	1.54E-07		7.66E-08	1.78E-08		Sample 2 Only	Sample 3 Only
Q9H223	EHD4_HUMAN EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1	4.60			1.00		1.00	1.00			2.78E-08		3.58E-08	3.70E-08		Sample 2 Only	Sample 3 Only
P21964	COMT_HUMAN Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2	46.60	12.92	2.97	2.97	9.94	0.99	2.97	1.67E-06	6.48E-07	6.32E-07	9.21E-07	8.71E-08	4.48E-07	0.55	0.05	0.27
P18669	PGAM1_HUMAN Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	28.00	8.96	3.97	6.97	5.97	3.97	6.98	5.51E-07	4.06E-07	1.07E-06	3.23E-07	2.88E-07	3.72E-07	0.59	0.52	0.68
Q9UJ70	NAGK_HUMAN N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4	23.00	2.97	4.94	4.94	3.95	1.00	3.95	1.33E-07	5.34E-07	5.63E-07	1.22E-07	6.83E-08	3.91E-07	0.92	0.51	2.93
O14950	ML12B_HUMAN Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	83.70	24.00	5.00	4.00	45.00	5.00	9.00	1.14E-05	2.10E-06	2.03E-06	2.38E-05	1.40E-06	3.05E-06	2.09	0.12	0.27
P35749	MYH11_HUMAN Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	16.90	8.00	4.00	4.00	18.00	3.00	8.00	2.10E-08	1.52E-08	8.13E-09	6.50E-08	1.19E-08	3.08E-08	3.10	0.57	1.47
G5E9Q2	G5E9Q2_HUMAN Cold shock domain containing E1, RNA-binding, isoform CRA_d OS=Homo sapiens GN=CSDE1 PE=2 SV=1	37.50	10.98	42.93	39.94	7.98	24.96	28.95	1.59E-07	1.03E-06	1.14E-06	8.53E-08	4.16E-07	6.43E-07	0.54	2.62	4.04
J3KP15	J3KP15_HUMAN Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens GN=SRSF2 PE=2 SV=1	34.30	2.97			1.98	3.99	5.98	4.99E-07			3.39E-07	2.90E-07	4.26E-07	0.68	0.58	0.85
F8VZ44	F8VZ44_HUMAN Aladin OS=Homo sapiens GN=AAAS PE=2 SV=1	9.50			1.99		1.99	1.99			1.16E-07		1.54E-07	1.12E-07		Sample 2 Only	Sample 3 Only
Q9UHD2	TBK1_HUMAN Serine/threonine-protein kinase TBK1 OS=Homo sapiens GN=TBK1 PE=1 SV=1	15.90	1.00	5.00	10.00	1.00	3.00	4.00	1.16E-08	5.73E-08	1.23E-07	1.06E-08	2.96E-08	4.24E-08	0.92	2.55	3.65
P61962	DCAF7_HUMAN DDB1- and CUL4-associated factor 7 OS=Homo sapiens GN=DCAF7 PE=1 SV=1	22.80	3.99	1.00	1.00	3.00	3.00	3.00	1.13E-07	5.47E-08	6.65E-08	7.15E-08	2.02E-07	2.38E-07	0.63	1.79	2.10
Q7Z406-6	MYH14_HUMAN Isoform 6 of Myosin-14 OS=Homo sapiens GN=MYH14	59.90	125.96	95.74	65.47	195.33	65.47	132.87	5.84E-07	5.81E-07	2.83E-07	1.56E-06	3.81E-07	9.41E-07	2.66	0.65	1.61
Q6DD88	ATLA3_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1	34.90	9.90	6.94	12.87	5.93	6.94	8.92	1.97E-07	5.11E-07	9.21E-07	1.16E-07	3.10E-07	3.69E-07	0.59	1.57	1.88
Q15181	IPYR_HUMAN Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	10.70	1.00	2.00	1.00	2.00	1.00		3.08E-08	2.07E-07	1.07E-07	7.74E-08	7.73E-08		2.51	2.51	Control 1 Only
E9PJF0	E9PJF0_HUMAN Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3 PE=2 SV=1	13.00		1.00	2.00		1.00	1.00		1.84E-07	2.95E-07		8.94E-08	1.30E-07		Sample 2 Only	Sample 3 Only
P34896	GLYC_HUMAN Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1	29.10	2.88	11.73	16.66	1.92	10.75	9.76	6.94E-08	1.43E-06	1.42E-06	4.09E-08	6.77E-07	7.56E-07	0.59	9.77	10.90
P35579	MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	82.00	968.10	964.10	670.38	1363.47	674.35	1060.97	2.77E-05	3.00E-05	1.41E-05	6.31E-05	2.04E-05	3.74E-05	2.28	0.73	1.35
P62701	RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	58.60	19.94		0.99	23.93	4.98	5.99	1.27E-06		1.49E-07	1.40E-06	6.05E-07	7.87E-07	1.10	0.48	0.62
P10412	H14_HUMAN Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	55.30	12.00			18.00		3.00	2.87E-06			5.26E-06		2.05E-07	1.83	Control 1 Only	0.07

Q9P2M7	CING_HUMAN Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	5.00		1.99	3.99	1.00	1.00			8.71E-09	1.40E-08	2.55E-09	6.03E-09		Sample 1 Only	Sample 2 Only	
C9J1Z8	C9J1Z8_HUMAN ADP-ribosylation factor 5 (Fragment) OS=Homo sapiens GN=ARF5 PE=2 SV=1	41.30	1.00			1.00	1.00	1.00	7.59E-08			4.20E-08	3.32E-08	9.69E-08	0.55	0.44	1.28
P22735	TGM1_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=1 SV=4	5.10			1.00		1.99	1.00			4.71E-09		9.27E-09	4.51E-09		Sample 2 Only	Sample 3 Only
P04259	K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	70.90	1.00	4.50	6.00	3.00	7.00	8.50	5.18E-08	1.10E-07	3.40E-07	5.04E-08	4.79E-07	4.93E-07	0.97	9.24	9.52
P12273	PIP_HUMAN Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	19.20	5.00	1.00		2.00	1.00		4.14E-07	6.83E-08		1.76E-07	5.04E-08		0.43	0.12	Control 1 Only
O43837	IDH3B_HUMAN Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2	13.50	1.99	3.98	2.99	2.98	3.99	3.00	8.74E-08	5.77E-07	5.30E-07	1.03E-07	2.71E-07	2.16E-07	1.17	3.10	2.47
K7EQ48	K7EQ48_HUMAN Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=2 SV=2	6.80	1.00	2.00	2.00		1.00	1.00	3.14E-08	1.40E-07	9.56E-08		6.34E-08	5.82E-08	Control 1 Only	2.02	1.85
J3KQD0	J3KQD0_HUMAN Prostamide/prostaglandin F synthase OS=Homo sapiens GN=FAM213B PE=2 SV=1	38.90	10.94	3.97	1.99	7.95	1.99	1.99	1.09E-06	8.44E-07	4.52E-07	5.81E-07	3.16E-07	3.25E-07	0.54	0.29	0.30
P30086	PEBP1_HUMAN Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	30.50	2.00			4.00	2.00		1.05E-07			1.51E-07	8.01E-08		1.44	0.76	Control 1 Only
P35249	RFC4_HUMAN Replication factor C subunit 4 OS=Homo sapiens GN=RFC4 PE=1 SV=2	24.80	5.93	1.00	2.00	5.93			1.41E-07	4.20E-08	7.49E-08	1.18E-07			0.83	Control 1 Only	Control 1 Only
Q9Y305	ACOT9_HUMAN Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2	44.30	13.92	26.83	21.85	12.93	15.89	20.86	4.44E-07	3.32E-06	2.93E-06	3.06E-07	1.48E-06	1.83E-06	0.69	3.33	4.12
P29508	SPB3_HUMAN Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	19.20			3.00		1.00	3.99			2.67E-07		4.07E-08	8.28E-08		Sample 2 Only	Sample 3 Only
B4E022	B4E022_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=2 SV=1	25.30	9.98	8.99	13.98	5.99	10.98	9.99	1.81E-07	5.24E-07	3.87E-07	8.33E-08	2.44E-07	2.18E-07	0.46	1.35	1.20
Q6P1M0	S27A4_HUMAN Long-chain fatty acid transport protein 4 OS=Homo sapiens GN=SLC27A4 PE=1 SV=1	4.50	1.00	2.00	3.00		1.00	2.00	1.10E-08	4.47E-08	6.67E-08		2.53E-08	2.87E-08	Control 1 Only	2.30	2.60
P14923	PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	45.20	38.39	12.96	26.92	45.40	49.34	35.91	6.82E-07	1.48E-07	2.51E-07	7.33E-07	9.18E-07	4.36E-07	1.08	1.35	0.64
P63208	SKP1_HUMAN S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	61.30	18.85	10.89	7.92	19.84	6.93	4.96	2.77E-06	1.78E-06	1.39E-06	1.78E-06	7.37E-07	7.04E-07	0.64	0.27	0.25
P24752	THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	46.60	4.99	22.95	17.98	2.00	13.98	13.97	1.24E-07	3.18E-06	2.51E-06	6.59E-08	1.54E-06	1.55E-06	0.53	12.38	12.44
B2R5P6	B2R5P6_HUMAN Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=2 SV=1	13.10	1.98	3.96	1.98	2.97	1.98		4.67E-08	2.00E-07	8.62E-08	6.34E-08	9.38E-08		1.36	2.01	Control 1 Only
P51153	RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1	18.20		2.00	1.00	1.00	1.00			9.45E-08	4.91E-08	1.87E-08	4.61E-08		Sample 1 Only	Sample 2 Only	
P49257	LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	16.70	5.00	6.00	5.00	5.00	2.00	4.00	1.76E-07	5.58E-07	4.80E-07	1.76E-07	1.59E-07	2.85E-07	1.00	0.90	1.62
P46777	RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	36.40	12.00		1.00	22.00		4.00	5.71E-07		3.87E-08	9.16E-07		2.71E-07	1.60	Control 1 Only	0.48
P33991	MCM4_HUMAN DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5	32.10	4.00	20.98	20.97	2.00	13.98	16.97	3.92E-08	3.99E-07	3.60E-07	1.70E-08	1.81E-07	2.03E-07	0.43	4.62	5.18

F5H039	F5H039_HUMAN Molybdopterin molybdenumtransferase OS=Homo sapiens GN=GPHN PE=2 SV=1	8.20		2.00	2.00		1.00	1.00		2.98 E-08	2.68 E-08		1.52 E-08	9.24 E-09		Sample 2 Only	Sample 3 Only
P04843	RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	20.80	6.00	4.00	7.00	2.00	3.00	6.00	1.24 E-07	1.52 E-07	1.63 E-07	4.16 E-08	3.97 E-08	1.33 E-07	0.34	0.32	1.08
F5GXC8	F5GXC8_HUMAN Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=2 SV=1	4.90		1.00			1.00	1.00		7.35 E-08			7.04 E-08	8.84 E-08		Sample 2 Only	Sample 3 Only
Q14558	KPRA_HUMAN Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 SV=2	18.30	0.99		0.99			3.51	2.56 E-08		9.18 E-08			2.45 E-07	Control 1 Only	Control 1 Only	9.55
Q96CN7	ISOC1_HUMAN Isochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3	25.80	3.00	1.00	2.00	4.00	4.00	4.00	9.46 E-08	1.08 E-07	1.72 E-07	1.28 E-07	2.90 E-07	3.19 E-07	1.35	3.07	3.37
Q8WUK0	PTPM1_HUMAN Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Homo sapiens GN=PTPMT1 PE=1 SV=1	28.90	4.99	0.99	0.99	2.99	0.99	0.99	4.39 E-07	1.60 E-07	2.75 E-07	2.57 E-07	4.84 E-08	1.40 E-07	0.58	0.11	0.32
Q9Y3I0	RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	29.30	8.00	9.00	10.00	7.00	6.00	5.00	1.92 E-07	6.30 E-07	7.07 E-07	1.29 E-07	3.01 E-07	3.70 E-07	0.67	1.57	1.92
P62333	PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	23.40	7.94	7.94	8.93	5.95	4.97	3.97	1.96 E-07	7.72 E-07	7.27 E-07	1.21 E-07	4.57 E-07	3.18 E-07	0.62	2.33	1.62
P22234	PUR6_HUMAN Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	31.10	9.90	8.91	13.87	9.90	4.95	7.92	2.50 E-07	9.06 E-07	1.19 E-06	2.20 E-07	3.42 E-07	6.97 E-07	0.88	1.37	2.79
Q96CS3	FAF2_HUMAN FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2	10.80	2.00	2.00		1.00	1.00	4.00	4.32 E-08	4.68 E-08		8.69 E-09	4.35 E-08	1.36 E-07	0.20	1.01	3.15
P11216	PYGB_HUMAN Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	10.80		7.99	7.99		6.00	5.99		9.77 E-08	1.09 E-07		4.59 E-08	5.33 E-08		Sample 2 Only	Sample 3 Only
C9JQ42	C9JQ42_HUMAN Glycogenin-1 (Fragment) OS=Homo sapiens GN=GYG1 PE=2 SV=1	18.70	1.00	1.99	1.00	2.99	2.00	3.00	1.15 E-08	4.98 E-08	1.26 E-08	4.83 E-08	4.57 E-08	6.04 E-08	4.19	3.97	5.24
E5KLJ5	E5KLJ5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1	32.20	4.00	30.97	31.97	1.00	21.00	19.99	2.57 E-08	3.76 E-07	4.01 E-07	1.17 E-09	1.97 E-07	2.16 E-07	0.05	7.68	8.41
B4DNJ6	B4DNJ6_HUMAN Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=2 SV=1	34.60	3.98	7.98	9.96	4.97	4.98	8.96	1.20 E-07	9.20 E-07	1.19 E-06	1.14 E-07	4.22 E-07	6.71 E-07	0.95	3.53	5.61
Q8NF37	PCAT1_HUMAN Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2	7.10	1.00	2.00	1.00	2.00	3.00	2.00	6.16 E-09	8.31 E-08	1.32 E-08	1.85 E-08	1.32 E-07	5.93 E-08	3.01	21.40	9.63
Q15427	SF3B4_HUMAN Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	10.80	1.00	3.00	3.00	1.00	1.00	3.00	2.72 E-08	2.95 E-07	3.32 E-07	2.52 E-08	6.36 E-08	2.47 E-07	0.93	2.34	9.10
O75382	TRIM3_HUMAN Tripartite motif-containing protein 3 OS=Homo sapiens GN=TRIM3 PE=1 SV=2	13.60	3.99	1.99	2.99	3.99		1.00	5.39 E-08	5.01 E-08	4.52 E-08	5.51 E-08		1.59 E-08	1.02	Control 1 Only	0.30
K7ELX4	K7ELX4_HUMAN Ferrochelatase, mitochondrial (Fragment) OS=Homo sapiens GN=FECH PE=2 SV=1	19.90	3.00	3.99	4.99	3.00	1.99	5.00	7.49 E-08	4.32 E-07	6.97 E-07	4.62 E-08	1.03 E-07	4.89 E-07	0.62	1.38	6.53
P04406	G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	80.50	39.99	35.96	35.97	41.99	33.99	28.98	1.82 E-06	5.04 E-06	5.76 E-06	1.57 E-06	2.97 E-06	2.83 E-06	0.86	1.63	1.56

Q147X3	NAA30_HUMAN N-alpha-acetyltransferase 30 OS=Homo sapiens GN=NAA30 PE=1 SV=1	12.30		1.99	2.99		0.99	0.99		1.06E-07	2.32E-07		7.54E-08	9.36E-08		Sample 2 Only	Sample 3 Only
O00159-3	MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	28.70	3.94	16.77	14.82	34.56	6.89	15.79	4.26E-08	1.35E-07	1.45E-07	3.99E-07	5.88E-08	1.62E-07	9.38	1.38	3.79
Q9Y6D5	BIG2_HUMAN Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3	2.30	2.00			1.00		1.00	1.86E-09			1.31E-09		4.50E-09	0.71	Control 1 Only	2.43
P28482	MK01_HUMAN Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3	32.20	9.08	11.61	12.61	8.62	9.08	10.08	5.50E-07	2.46E-06	2.49E-06	4.46E-07	1.13E-06	1.54E-06	0.81	2.06	2.80
B3KXW5	B3KXW5_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=2 SV=1	17.50	2.00	9.99	10.98	1.00	5.00	7.00	8.87E-09	1.24E-07	1.80E-07	1.55E-09	6.77E-08	8.75E-08	0.17	7.63	9.86
P30153	2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	38.90	18.79	16.81	21.75	14.83	11.86	19.78	5.53E-07	1.20E-06	1.32E-06	3.63E-07	5.12E-07	8.35E-07	0.66	0.93	1.51
Q86VP6	CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	19.00	14.97	16.98	17.99	13.98	10.00	11.00	1.89E-07	2.06E-07	2.35E-07	1.33E-07	8.31E-08	1.14E-07	0.70	0.44	0.60
P49006	MRP_HUMAN MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2	14.40	3.00	2.00	3.00	2.00	2.00	2.00	6.01E-08	2.38E-07	2.35E-07	4.22E-08	1.28E-07	1.07E-07	0.70	2.14	1.77
P0CG05	LAC2_HUMAN Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	23.60			1.00	1.00	2.00	1.00			1.72E-07	3.87E-08	2.08E-07	9.00E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P21333	FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	2.50	1.99	2.97	0.99		0.99	0.99	2.17E-09	5.84E-09	3.43E-09		1.94E-09	2.60E-09	Control 1 Only	0.89	1.20
Q13618	CUL3_HUMAN Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2	25.10	2.00	6.97	13.96	1.00	7.98	6.97	1.93E-08	6.92E-08	2.17E-07	5.69E-09	6.89E-08	8.08E-08	0.29	3.57	4.19
C9J050	C9J050_HUMAN Choline-phosphate cytidylyltransferase A (Fragment) OS=Homo sapiens GN=PCYT1A PE=2 SV=1	29.90	2.97	2.97	4.96	2.97	0.99	1.99	1.12E-07	7.31E-07	6.45E-07	7.26E-08	3.50E-07	3.91E-07	0.65	3.13	3.50
P53396	ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	34.70	15.96	44.94	43.95	10.97	25.96	30.94	1.91E-07	8.06E-07	8.00E-07	1.06E-07	3.84E-07	5.05E-07	0.56	2.01	2.64
E9PCG9	E9PCG9_HUMAN D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=2 SV=1	14.10	0.99		1.99	0.99	0.99		2.75E-08		1.78E-07	2.36E-08	7.98E-08		0.86	2.90	Control 1 Only
Q9Y6I8	PXMP4_HUMAN Peroxisomal membrane protein 4 OS=Homo sapiens GN=PXMP4 PE=1 SV=3	25.90	5.00	1.00	1.00	2.00	4.00	3.00	4.98E-07	2.71E-07	1.47E-07	1.13E-07	1.02E-06	5.12E-07	0.23	2.04	1.03
Q8IXQ6	PARP9_HUMAN Poly [ADP-ribose] polymerase 9 OS=Homo sapiens GN=PARP9 PE=1 SV=2	6.30		2.00	4.00		1.00	3.00		2.00E-08	4.95E-08		7.16E-09	2.62E-08		Sample 2 Only	Sample 3 Only
P62081	RS7_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	43.80	7.00			12.00	1.00	3.00	1.20E-06			1.40E-06	2.74E-07	4.40E-07	1.16	0.23	0.37
Q9BZK7	TBL1R_HUMAN F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens GN=TBL1XR1 PE=1 SV=1	26.50		6.96	5.97		4.97	3.98		3.81E-07	2.89E-07		2.06E-07	1.55E-07		Sample 2 Only	Sample 3 Only
C9IZQ1	C9IZQ1_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=2 SV=1	8.90	2.00			1.00		1.00	7.50E-08			3.25E-08		1.16E-07	0.43	Control 1 Only	1.54
P35580	MYH10_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	65.20	163.23	126.62	75.15	245.36	65.25	175.07	7.39E-07	7.88E-07	2.74E-07	1.50E-06	4.49E-07	1.15E-06	2.03	0.61	1.56
Q15370	ELOB_HUMAN Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1	66.90	26.81	16.85	16.85	28.79	12.88	15.86	1.18E-05	6.16E-06	5.56E-06	6.02E-06	4.28E-06	4.30E-06	0.51	0.36	0.36

P50748	KNTC1_HUMAN Kinetochore-associated protein 1 OS=Homo sapiens GN=KNTC1 PE=1 SV=1	6.90	9.00	1.00	2.00	4.00	1.00		1.29E-08	3.03E-09	2.62E-09	6.52E-09	1.64E-09		0.50	0.13	Control 1 Only
B7Z2G1	B7Z2G1_HUMAN Kelch-like protein 22 OS=Homo sapiens GN=KLHL22 PE=2 SV=1	9.80	1.00		1.00		1.98	0.99	8.85E-09		8.21E-09		2.23E-08	1.37E-08	Control 1 Only	2.52	1.55
Q9NUQ8	ABCF3_HUMAN ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2	17.40	7.00	9.00	15.00	4.00	7.00	8.00	1.41E-07	2.39E-07	2.90E-07	7.28E-08	1.70E-07	1.22E-07	0.52	1.21	0.87
H7C314	H7C314_HUMAN Src substrate cortactin (Fragment) OS=Homo sapiens GN=CTTN PE=4 SV=1	14.30		2.00	3.00		1.00	3.00		1.33E-07	1.80E-07		3.28E-08	1.32E-07		Sample 2 Only	Sample 3 Only
P16402	H13_HUMAN Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2	51.60	9.00			14.00		1.00	1.18E-06			2.05E-06		2.09E-09	1.74	Control 1 Only	0.00
P15927	RFA2_HUMAN Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1	61.90	20.00	22.00	21.00	25.00	19.00	19.00	2.06E-06	5.08E-06	4.50E-06	1.77E-06	2.49E-06	2.82E-06	0.86	1.21	1.37
P01857	IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	28.50	2.00	4.00	8.00	6.00	13.00	7.00	4.86E-08	2.86E-07	5.14E-07	9.88E-08	9.85E-07	4.09E-07	2.03	20.27	8.40
Q5T749	KPRP_HUMAN Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	9.80	2.00	5.00	5.00	2.00	10.00	6.00	1.16E-08	5.92E-08	5.98E-08	1.97E-08	1.75E-07	5.26E-08	1.70	15.03	4.52
P04844	RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	23.30	3.99	5.98	7.97	3.99	3.99	3.98	1.20E-07	4.53E-07	4.04E-07	9.64E-08	3.27E-07	1.21E-07	0.81	2.73	1.01
Q5T440	CAF17_HUMAN Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1	66.90	34.00	30.00	30.00	30.00	21.00	26.00	4.14E-06	1.01E-05	8.63E-06	3.08E-06	5.06E-06	6.15E-06	0.75	1.22	1.49
Q6BDS2	URFB1_HUMAN UHRF1-binding protein 1 OS=Homo sapiens GN=UHRF1BP1 PE=1 SV=1	15.10	6.00	13.00	14.00	9.00	10.00	9.00	4.99E-08	1.93E-07	1.87E-07	6.06E-08	9.27E-08	7.89E-08	1.22	1.86	1.58
Q9BVA1	TBB2B_HUMAN Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	78.00	1.99	0.99	1.99	1.98	4.99	2.99	4.13E-08	7.76E-08	1.12E-07	4.46E-08	2.41E-07	1.38E-07	1.08	5.84	3.33
P00505	AATM_HUMAN Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3	9.50	3.00	2.00	1.00	1.00	1.00	1.00	6.91E-08	1.49E-07	1.02E-07	3.04E-08	6.66E-08	7.45E-08	0.44	0.96	1.08
Q96HY7	DHTK1_HUMAN Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial OS=Homo sapiens GN=DHTKD1 PE=1 SV=2	7.50		4.99	3.99		3.00	3.00		8.17E-08	5.53E-08		3.40E-08	3.66E-08		Sample 2 Only	Sample 3 Only
B7Z4C8	B7Z4C8_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=2 SV=1	42.60	7.00			6.00		1.00	2.13E-06			1.04E-06		1.95E-07	0.49	Control 1 Only	0.09
H7BY58	H7BY58_HUMAN Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=2 SV=1	69.20	56.88	56.89	56.89	56.87	40.90	47.88	1.18E-05	2.81E-05	2.81E-05	9.41E-06	1.73E-05	1.76E-05	0.80	1.47	1.50
P55884	EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	10.40	1.00	7.98	6.99	1.00	6.00	6.00	3.90E-09	1.30E-07	1.18E-07	4.23E-09	4.37E-08	8.70E-08	1.08	11.20	22.33
P15924	DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	58.70	282.99	52.00	74.00	276.97	137.00	134.00	1.16E-06	1.35E-07	2.21E-07	1.18E-06	8.43E-07	5.32E-07	1.01	0.73	0.46
Q9BUF5	TBB6_HUMAN Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	46.40	8.00	8.00	6.00	6.00	5.00	5.00	1.59E-07	5.66E-07	2.77E-07	1.19E-07	2.24E-07	2.26E-07	0.75	1.41	1.42
Q16531	DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	62.50	210.91	293.83	259.27	174.42	239.57	213.95	7.87E-06	1.98E-05	1.75E-05	5.25E-06	1.20E-05	1.20E-05	0.67	1.53	1.52
Q9NRD5	PICK1_HUMAN PRKCA-binding protein OS=Homo sapiens GN=PICK1 PE=1 SV=2	14.00	4.00		2.00	3.00	1.00	2.00	1.61E-07		1.50E-07	4.16E-08	2.92E-08	9.81E-08	0.26	0.18	0.61

F5H365	F5H365_HUMAN Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=2 SV=1	25.30	0.99	4.95	7.92	0.99	4.95	4.95	4.14 E-09	5.06 E-08	2.13 E-07	3.65 E-09	6.02 E-08	8.05 E-08	0.88	14.54	19.44
P26373	RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	38.40	9.96		2.00	10.94	1.00	1.00	1.24 E-06		1.90 E-07	8.08 E-07	1.09 E-08	1.10 E-08	0.65	0.01	0.01
P14618	KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	67.40	54.96	54.02	73.67	46.12	58.85	65.77	2.69 E-06	5.92 E-06	6.27 E-06	1.85 E-06	3.57 E-06	3.96 E-06	0.69	1.33	1.47
P43246	MSH2_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	20.30	1.98	8.94	15.88	1.98	9.93	7.95	3.29 E-08	8.96 E-08	2.12 E-07	1.43 E-08	7.83 E-08	9.15 E-08	0.44	2.38	2.78
Q13263	TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	58.30	60.65	169.83	144.04	62.63	141.12	123.22	1.57 E-06	1.10 E-05	7.74 E-06	1.32 E-06	6.16 E-06	5.47 E-06	0.84	3.92	3.48
P20930	FILA_HUMAN Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	0.40		2.00	1.00	1.00	2.00	3.00		1.50 E-09	1.12 E-09	3.18 E-10	3.89 E-09	2.12 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
J3QRD1	J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=2 SV=1	12.50	2.00	2.00	1.00	2.00	3.00	3.00	8.87 E-08	8.91 E-08	9.50 E-08	6.97 E-08	1.91 E-07	2.21 E-07	0.79	2.16	2.49
J3KNQ3	J3KNQ3_HUMAN 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=2 SV=1	4.90	1.00		1.00	2.00			9.38 E-09		5.18 E-08	3.11 E-08			3.32	Control 1 Only	Control 1 Only
P46778	RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	25.60	4.95			8.92	0.99		8.49 E-07			1.31 E-06	1.21 E-07		1.54	0.14	Control 1 Only
Q14566	MCM6_HUMAN DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	21.70	3.00	13.00	16.00		9.00	11.00	3.50 E-08	2.03 E-07	2.36 E-07		1.24 E-07	1.44 E-07	Control 1 Only	3.55	4.10
O15260	SURF4_HUMAN Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3	40.90	4.00		1.00	5.00	1.00		1.92 E-07		8.98 E-08	2.65 E-07	2.27 E-07		1.38	1.18	Control 1 Only
P49748	ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	18.80	5.99	4.00	6.00	1.00	2.98	4.00	1.10 E-07	1.78 E-07	9.08 E-08	1.96 E-08	1.25 E-07	6.81 E-08	0.18	1.14	0.62
P50991	TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	20.20	8.93	5.96	9.94	6.95	6.95	6.95	2.83 E-07	3.65 E-07	5.74 E-07	1.97 E-07	2.52 E-07	2.69 E-07	0.70	0.89	0.95
P19387	RPB3_HUMAN DNA-directed RNA polymerase II subunit RPB3 OS=Homo sapiens GN=POLR2C PE=1 SV=2	23.60	2.00	4.00	2.00	2.00	3.00	1.00	1.02 E-07	4.46 E-07	1.77 E-07	6.15 E-08	2.77 E-07	7.95 E-08	0.60	2.71	0.78
P11586	C1TC_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3	55.10	12.00	29.00	27.50	11.00	23.50	20.00	2.69 E-07	1.34 E-06	1.26 E-06	2.03 E-07	7.33 E-07	8.07 E-07	0.75	2.72	3.00
P25205	MCM3_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	41.70	21.79	67.35	59.44	16.84	45.57	48.53	3.77 E-07	1.77 E-06	1.59 E-06	2.17 E-07	9.53 E-07	1.13 E-06	0.58	2.53	2.99
F5H2F4	F5H2F4_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1	50.50	12.00	29.00	27.50	11.00	23.50	20.00	2.47 E-07	1.23 E-06	1.15 E-06	1.86 E-07	6.72 E-07	7.40 E-07	0.75	2.72	3.00
Q14139	UBE4A_HUMAN Ubiquitin conjugation factor E4 A OS=Homo sapiens GN=UBE4A PE=1 SV=2	6.00	1.00	3.00	4.00	1.00	4.00	2.00	1.20 E-08	3.11 E-08	4.45 E-08	7.49 E-09	2.47 E-08	1.45 E-08	0.62	2.06	1.21
B3KNT8	B3KNT8_HUMAN Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	23.70	2.00	1.00	1.00	1.00	1.00	1.00	1.13 E-07	8.33 E-08	8.49 E-08	3.72 E-08	5.92 E-08	6.11 E-08	0.33	0.53	0.54
P31946	1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	23.40	2.00	2.00	2.00	3.00	5.00	3.00	1.08 E-07	1.68 E-07	1.90 E-07	1.40 E-07	3.32 E-07	3.20 E-07	1.29	3.07	2.96
G3V295	G3V295_HUMAN Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2	21.50	0.99		0.99	1.98	1.98	0.99	5.88 E-08		1.47 E-07	1.05 E-07	1.39 E-07	1.15 E-07	1.79	2.36	1.95

	SV=1																
P62714	PP2AB_HUMAN Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1	26.50	6.93	4.95	9.89	7.92	3.96	7.91	4.02 E-07	6.93 E-07	1.44 E-06	3.20 E-07	4.62 E-07	7.71 E-07	0.80	1.15	1.92
Q13347	EIF3I_HUMAN Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	14.80	1.00	3.00	2.00	2.00	2.00	1.00	2.98 E-08	2.63 E-07	1.92 E-07	3.89 E-08	1.71 E-07	7.04 E-08	1.30	5.72	2.36
P62829	RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	51.40	17.84	2.97	1.98	11.90	0.99	1.98	2.58 E-06	3.82 E-07	3.41 E-07	1.48 E-06	1.99 E-07	3.65 E-07	0.57	0.08	0.14
P00491	PNPH_HUMAN Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2	19.70	1.00		1.00	3.00			3.12 E-08		5.72 E-08	4.73 E-08			1.52	Control 1 Only	Control 1 Only
E9PAL9	E9PAL9_HUMAN 5'-nucleotidase domain-containing protein 2 OS=Homo sapiens GN=NT5DC2 PE=2 SV=1	25.90	3.97	2.98	1.00	4.96	2.98	4.98	5.30 E-08	1.18 E-07	6.60 E-08	7.32 E-08	1.13 E-07	2.23 E-07	1.38	2.13	4.21
P62280	RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	55.10	10.93			13.93	1.99	2.99	1.44 E-06			1.28 E-06	4.20 E-07	6.38 E-07	0.89	0.29	0.44
Q9UHD8	SEPT9_HUMAN Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	12.00		1.98	6.93	0.99	0.99	4.95		9.92 E-08	1.71 E-07	5.96 E-10	3.35 E-08	1.19 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P17655	CAN2_HUMAN Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6	11.40			7.00		4.00	7.00			8.69 E-08		3.84 E-08	1.18 E-07		Sample 2 Only	Sample 3 Only
P10809	CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	42.40	12.96	16.96	18.97	10.99	13.00	19.00	3.13 E-07	9.12 E-07	1.12 E-06	2.33 E-07	4.92 E-07	7.14 E-07	0.75	1.57	2.28
F8VTV8	F8VTV8_HUMAN Cyclin-dependent kinase 4 OS=Homo sapiens GN=CDK4 PE=2 SV=1	17.10	0.99		0.99	0.99	0.99	0.99	1.10 E-07		2.30 E-07	6.91 E-08	2.40 E-07	2.69 E-07	0.63	2.18	2.44
P15531	NDKA_HUMAN Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	46.70	22.42	8.73	10.67	18.50	7.76	4.85	7.14 E-06	4.26 E-06	4.60 E-06	5.00 E-06	2.96 E-06	2.48 E-06	0.70	0.41	0.35
A1A528	A1A528_HUMAN Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=2 SV=1	11.60	2.00	3.00	2.00	1.00		1.00	4.78 E-08	2.54 E-08	2.09 E-08	4.58 E-08		5.20 E-09	0.96	Control 1 Only	0.11
Q15393	SF3B3_HUMAN Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	9.80	10.00			5.00		1.00	1.08 E-07			5.39 E-08		5.49 E-09	0.50	Control 1 Only	0.05
O75323	NIPS2_HUMAN Protein NipSnap homolog 2 OS=Homo sapiens GN=GBAS PE=1 SV=1	24.10	5.96	4.95	5.95	6.95	1.99	2.98	4.05 E-07	1.19 E-06	1.15 E-06	3.49 E-07	5.61 E-07	7.91 E-07	0.86	1.38	1.95
Q8N163	CCAR2_HUMAN Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2	19.30	1.98	10.89	9.89	0.99	6.93	3.96	1.74 E-08	7.79 E-08	9.32 E-08	6.95 E-09	5.30 E-08	4.63 E-08	0.40	3.05	2.66
F5GY05	F5GY05_HUMAN Constitutive coactivator of peroxisome proliferator-activated receptor gamma OS=Homo sapiens GN=FAM120B PE=2 SV=1	42.40	46.51	74.21	84.11	41.54	55.41	73.23	1.31 E-06	3.06 E-06	3.44 E-06	9.01 E-07	1.73 E-06	2.38 E-06	0.69	1.32	1.82
Q96LD4	TRI47_HUMAN Tripartite motif-containing protein 47 OS=Homo sapiens GN=TRIM47 PE=1 SV=2	9.60	2.99			1.00	1.00		4.26 E-08			9.75 E-09	1.30 E-08		0.23	0.31	Control 1 Only
Q9BW61	DDA1_HUMAN DET1- and DDB1-associated protein 1 OS=Homo sapiens GN=DDA1 PE=1 SV=1	62.70	9.00	2.00	3.00	10.00	1.00	1.00	1.47 E-06	3.60 E-07	6.14 E-07	1.24 E-06	2.61 E-07	2.23 E-08	0.84	0.18	0.02
M0R0F0	M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=2 SV=1	50.50	6.94			9.94		0.99	4.56 E-07			6.45 E-07		1.10 E-07	1.41	Control 1 Only	0.24
P28799	GRN_HUMAN Granulins OS=Homo sapiens GN=GRN PE=1 SV=2	25.60	10.83	52.20	50.22	10.84	41.38	44.32	5.02 E-07	6.63 E-06	5.06 E-06	4.42 E-07	3.43 E-06	4.12 E-06	0.88	6.83	8.20
J3KR97	J3KR97_HUMAN Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=2 SV=1	9.10	2.95	6.89	5.91	1.96	3.92	4.94	1.64 E-08	8.01 E-08	6.64 E-08	8.70 E-09	3.06 E-08	5.31 E-08	0.53	1.87	3.24

Q96J66	ABCCB_HUMAN ATP-binding cassette sub-family C member 11 OS=Homo sapiens GN=ABCC11 PE=1 SV=1	1.90		1.00	1.00		1.00			3.10E-09	5.11E-09		3.65E-09			Sample 2 Only	
B5MC07	B5MC07_HUMAN Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=2 SV=1	22.30	5.95		0.99	6.95	5.97	1.00	3.87E-07		1.76E-07	4.49E-07	3.51E-07	1.22E-07	1.16	0.91	0.31
P62805	H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	59.20	134.00	10.00	11.00	143.00	29.00	28.00	6.71E-04	2.45E-06	2.68E-06	4.67E-04	9.93E-06	1.41E-05	0.70	0.01	0.02
P54136	SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	41.80	21.80	34.68	43.62	14.86	34.68	35.65	5.63E-07	2.03E-06	1.73E-06	3.43E-07	1.28E-06	1.14E-06	0.61	2.26	2.02
P40939	ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	39.40	13.00	42.00	40.00	9.00	26.00	28.00	2.30E-07	7.75E-07	8.47E-07	1.22E-07	4.68E-07	5.63E-07	0.53	2.04	2.45
Q3SY84	K2C71_HUMAN Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=3	23.90			2.00	1.00		2.00			1.61E-08	4.27E-09		2.64E-08	Sample 1 Only		Sample 3 Only
P14868	SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	57.50	15.85	25.81	32.74	14.88	20.82	25.78	6.49E-07	2.86E-06	3.66E-06	4.87E-07	1.88E-06	2.31E-06	0.75	2.89	3.56
P18583	SON_HUMAN Protein SON OS=Homo sapiens GN=SON PE=1 SV=4	9.80	44.63	1.96	0.98	28.77		1.97	1.69E-07	1.14E-08	5.86E-09	1.02E-07		5.43E-09	0.60	Control 1 Only	0.03
P16152	CBR1_HUMAN Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	33.20	4.98	3.00	5.00	2.00	2.00	4.00	2.08E-07	2.96E-07	5.06E-07	6.02E-08	2.31E-07	3.30E-07	0.29	1.11	1.59
Q86X76	NIT1_HUMAN Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 PE=1 SV=2	37.50	2.00	2.00	2.00	2.00	1.50	2.00	1.23E-07	3.30E-07	3.17E-07	8.80E-08	1.83E-07	1.99E-07	0.72	1.49	1.63
O00487	PSDE_HUMAN 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	7.40	1.00	1.00	1.00	1.00	1.00		5.03E-08	1.06E-07	1.28E-07	5.84E-08	1.09E-07		1.16	2.17	Control 1 Only
P78347	GTF2I_HUMAN General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	18.50		10.00	20.98		8.00	13.99		1.27E-07	3.43E-07		7.02E-08	2.12E-07		Sample 2 Only	Sample 3 Only
Q09666	AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	5.10	3.00	3.00	3.00	3.00	5.00	8.00	1.95E-09	2.94E-09	3.22E-09	1.16E-09	4.88E-09	9.23E-09	0.59	2.50	4.73
Q86X76-3	NIT1_HUMAN Isoform 4 of Nitrilase homolog 1 OS=Homo sapiens GN=NIT1	29.70	2.00	2.00	2.00	2.00	1.50	2.00	1.09E-07	2.94E-07	2.82E-07	7.84E-08	1.63E-07	1.78E-07	0.72	1.49	1.63
B4DW73	B4DW73_HUMAN Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=2 SV=1	15.40	0.99	4.91	7.86	1.98	10.80	6.88	3.79E-09	2.09E-07	2.01E-07	2.56E-08	4.01E-07	2.44E-07	6.74	105.75	64.34
P49419-2	AL7A1_HUMAN Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1	37.00	12.85	18.79	18.77	12.85	14.83	14.82	3.60E-07	1.47E-06	1.44E-06	2.88E-07	9.37E-07	8.84E-07	0.80	2.60	2.46
P08238	HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	56.50	19.96	53.91	41.91	12.97	48.91	32.91	5.93E-07	3.11E-06	2.50E-06	3.59E-07	2.37E-06	1.35E-06	0.61	3.99	2.27
O95881	TXD12_HUMAN Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	71.50	24.00	18.00	16.00	29.00	16.00	14.00	6.66E-06	6.55E-06	6.01E-06	4.80E-06	4.52E-06	3.73E-06	0.72	0.68	0.56
P23921	RIR1_HUMAN Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1	21.50	2.00	17.86	14.90	2.00	10.93	10.92	2.73E-08	2.63E-07	2.40E-07	2.00E-08	1.48E-07	1.56E-07	0.73	5.42	5.70
P49189	AL9A1_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3	33.00	17.98	16.98	18.98	17.97	13.98	14.98	9.83E-07	2.67E-06	2.93E-06	9.17E-07	1.58E-06	1.85E-06	0.93	1.61	1.88
P07900	HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1	44.70	13.99	39.91	40.92	11.99	33.93	27.94	3.25E-07	1.46E-06	1.62E-06	2.64E-07	9.14E-07	1.03E-06	0.81	2.81	3.18

	PE=1 SV=5																
P06733	ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	58.80	31.85	27.85	30.87	22.92	36.88	23.93	1.48E-06	3.09E-06	3.49E-06	9.77E-07	2.36E-06	2.02E-06	0.66	1.59	1.37
Q9UN37	VPS4A_HUMAN Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1	15.60	4.98	1.00	1.00	2.98	0.99	1.99	1.32E-07	2.99E-09	6.02E-08	4.46E-08	3.73E-08	3.35E-08	0.34	0.28	0.25
P05198	IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	36.80	6.97	3.98	4.97	6.95	2.00	10.92	2.49E-07	3.40E-07	4.14E-07	2.03E-07	1.49E-07	1.22E-06	0.82	0.60	4.91
O75369	FLNB_HUMAN Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	6.90	2.97	6.92	1.98	1.98	1.98	4.95	2.85E-09	1.35E-08	6.37E-09	1.60E-09	3.25E-09	7.51E-09	0.56	1.14	2.63
P14174	MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	23.50	9.00	1.00	1.00	8.00	2.00	1.00	4.25E-06	3.80E-07	3.47E-07	2.62E-06	4.14E-07	2.37E-07	0.62	0.10	0.06
O43707	ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	17.10	0.97	9.81	10.82	1.96	3.91	5.91	1.88E-08	1.13E-07	1.49E-07	3.71E-08	5.46E-08	7.70E-08	1.97	2.90	4.09
Q8TD19	NEK9_HUMAN Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=1 SV=2	9.00	3.00	6.00	6.00	2.00	4.00	4.00	2.03E-08	6.14E-08	4.27E-08	1.01E-08	3.18E-08	3.07E-08	0.50	1.57	1.52
Q9Y5M8	SRPRB_HUMAN Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3	25.50	5.00	3.00	5.00	5.00	2.00	5.00	3.14E-07	5.24E-07	6.81E-07	2.52E-07	2.63E-07	4.51E-07	0.80	0.84	1.44
Q96NB2	SFXN2_HUMAN Sideroflexin-2 OS=Homo sapiens GN=SFXN2 PE=1 SV=2	28.30	2.98	2.99	3.98	2.99	3.98	7.97	7.73E-08	2.34E-07	3.29E-07	5.83E-08	1.88E-07	7.66E-07	0.75	2.43	9.90
E9PLK3	E9PLK3_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1	36.00	6.93	51.32	30.60	4.95	36.55	25.67	6.28E-08	9.60E-07	5.72E-07	4.60E-08	5.41E-07	4.33E-07	0.73	8.61	6.88
B4DRT2	B4DRT2_HUMAN 28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=2 SV=1	19.60	3.99	0.99	2.00	2.99	2.00	3.99	8.37E-08	2.43E-08	1.14E-07	7.39E-08	1.02E-07	1.86E-07	0.88	1.22	2.23
Q8WUY1	THEM6_HUMAN Protein THEM6 OS=Homo sapiens GN=THEM6 PE=1 SV=2	27.40	4.00	2.00	1.00	4.00	3.00	4.00	1.55E-07	2.31E-07	1.45E-07	1.37E-07	2.94E-07	4.10E-07	0.88	1.90	2.65
Q9Y4C2	F115A_HUMAN Protein FAM115A OS=Homo sapiens GN=FAM115A PE=1 SV=3	15.10	1.00	10.00	11.00	3.00	8.00	5.00	5.02E-09	1.11E-07	1.21E-07	1.95E-08	7.10E-08	5.23E-08	3.89	14.14	10.42
Q9BPX3	CND3_HUMAN Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1	2.40		1.00	1.00	1.00				6.82E-09	4.53E-09	5.68E-09			Sample 1 Only		
Q08380	LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	10.10	0.99	3.98	3.98	0.99	2.99	1.99	5.30E-09	3.74E-08	4.07E-08	4.02E-09	3.06E-08	1.40E-08	0.76	5.76	2.63
F5H897	F5H897_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=2 SV=1	16.40	2.99	3.99	3.99	3.99	2.99	4.98	5.45E-08	1.40E-07	9.89E-08	5.68E-08	3.51E-08	8.71E-08	1.04	0.64	1.60
P53618	COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	24.80	12.00	18.00	27.00	9.00	18.00	16.00	1.89E-07	3.72E-07	4.16E-07	8.28E-08	2.87E-07	2.50E-07	0.44	1.52	1.32
Q5T4S7	UBR4_HUMAN E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	0.90	1.00	1.00	1.00	1.00			4.92E-10	1.06E-09	9.07E-10	6.45E-10			1.31	Control 1 Only	Control 1 Only
P50454	SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	47.40	17.74	20.72	25.66	22.65	17.73	22.67	5.71E-07	2.55E-06	2.97E-06	5.87E-07	1.33E-06	2.16E-06	1.03	2.33	3.79
Q96RQ1	ERGI2_HUMAN Endoplasmic reticulum-Golgi intermediate compartment protein 2 OS=Homo sapiens GN=ERGIC2 PE=1 SV=2	9.50	1.98	1.98	2.97	1.98	1.98	1.98	4.52E-08	1.72E-07	9.92E-08	3.40E-08	7.29E-08	8.71E-08	0.75	1.61	1.93
Q13045	FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	6.60	2.00	7.00	3.00		2.00	4.00	4.28E-09	4.63E-08	1.92E-08		1.28E-08	2.76E-08	Control 1 Only	2.98	6.45

Q9H900	ZWILC_HUMAN Protein zwilch homolog OS=Homo sapiens GN=ZWILCH PE=1 SV=2	4.10	1.00		1.00	1.00			2.06 E-08		5.07 E-09	1.40 E-08			0.68	Control 1 Only	Control 1 Only
P23246	SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	19.20	4.00	9.00	14.97	5.00	7.00	8.98	8.64 E-08	2.24 E-07	4.65 E-07	8.68 E-08	1.71 E-07	2.34 E-07	1.00	1.98	2.71
F5H5D3	F5H5D3_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1	71.30	6.00	6.50	6.50	6.50	5.00	6.00	1.68 E-07	9.49 E-07	6.25 E-07	1.26 E-07	4.92 E-07	5.15 E-07	0.75	2.93	3.07
Q15067	ACOX1_HUMAN Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3	21.70	7.98	6.97	6.99	4.98	4.98	4.99	1.23 E-07	3.14 E-07	2.01 E-07	9.00 E-08	1.59 E-07	1.55 E-07	0.73	1.30	1.26
P62906	RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	50.20	13.00	1.00	4.00	20.00	4.00	3.00	1.44 E-06	3.36 E-08	1.62 E-07	1.68 E-06	4.14 E-07	3.76 E-07	1.17	0.29	0.26
D6RFM5	D6RFM5_HUMAN Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=2 SV=1	7.90	3.00	3.00	4.00	1.00	4.00	4.00	1.10 E-07	2.40 E-07	3.22 E-07	2.00 E-08	2.35 E-07	1.72 E-07	0.18	2.13	1.57
Q13162	PRDX4_HUMAN Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	57.60	21.89	17.94	16.94	22.91	15.95	18.92	2.26 E-06	6.45 E-06	5.93 E-06	1.87 E-06	3.99 E-06	4.28 E-06	0.82	1.76	1.89
Q9Y6N5	SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	21.10		4.96	6.96	0.99	2.97	5.95		3.10 E-07	5.96 E-07	7.52 E-09	1.24 E-07	4.53 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B9EGP5	B9EGP5_HUMAN MON2 protein OS=Homo sapiens GN=MON2 PE=2 SV=1	5.60	3.00	3.00	5.99	1.99	3.00	2.99	1.95 E-08	1.74 E-08	4.55 E-08	4.35 E-09	2.03 E-08	2.45 E-08	0.22	1.04	1.26
Q0PNE2	ELP6_HUMAN Elongator complex protein 6 OS=Homo sapiens GN=ELP6 PE=1 SV=1	25.90	1.99	1.98	1.00	2.98	1.99	2.97	6.79 E-08	1.73 E-07	9.29 E-08	8.19 E-08	1.63 E-07	2.78 E-07	1.21	2.40	4.09
P47897	SYQ_HUMAN Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	48.90	4.94	56.43	45.54	3.94	41.60	38.66	8.46 E-08	1.86 E-06	1.53 E-06	1.02 E-07	1.24 E-06	9.91 E-07	1.20	14.63	11.71
P61313	RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	33.80	4.96	0.99	0.99	9.90	1.98	1.98	6.17 E-07	3.36 E-08	2.07 E-07	6.70 E-07	3.28 E-07	3.07 E-07	1.09	0.53	0.50
P06753	TPM3_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2	54.00	21.86	15.20	15.17	59.98	14.21	14.21	2.49 E-06	3.29 E-06	2.97 E-06	8.50 E-06	1.78 E-06	2.24 E-06	3.41	0.71	0.90
P55060	XPO2_HUMAN Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	22.90	31.68	17.82	23.76	35.64	13.86	15.84	7.49 E-07	1.01 E-06	1.20 E-06	7.34 E-07	5.48 E-07	7.15 E-07	0.98	0.73	0.95
Q07960	RHG01_HUMAN Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1	32.80	1.99	14.96	10.97		11.97	8.98	3.93 E-08	1.42 E-06	1.08 E-06		9.82 E-07	7.25 E-07	Control 1 Only	24.97	18.43
B4DVB8	B4DVB8_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=2 SV=1	11.70	2.00			3.00	1.00		8.40 E-08			9.27 E-08	4.34 E-08		1.10	0.52	Control 1 Only
P02538	K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	70.90	5.98	11.95	17.94	10.95	14.94	15.94	1.79 E-07	7.86 E-07	2.20 E-06	4.11 E-07	2.42 E-06	1.78 E-06	2.30	13.51	9.96
Q9HCC0	MCCB_HUMAN Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	29.10	15.00	2.00	4.00	9.00	3.00	3.00	3.85 E-07	8.17 E-08	1.78 E-07	1.90 E-07	1.06 E-07	1.22 E-07	0.49	0.27	0.32
Q02413	DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	28.50	15.00	19.00	22.00	14.00	30.00	11.00	5.98 E-08	1.22 E-07	1.50 E-07	7.84 E-08	3.55 E-07	7.96 E-08	1.31	5.94	1.33
Q9C0C2	TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	3.90	1.00	4.00	2.00	1.00	4.00	4.00	3.27 E-09	1.58 E-08	1.09 E-08	5.44 E-09	2.07 E-08	2.38 E-08	1.67	6.34	7.27
P17987	TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	36.90	12.82	17.78	19.74	10.86	11.86	17.75	3.41 E-07	1.14 E-06	8.45 E-07	2.67 E-07	6.22 E-07	6.77 E-07	0.78	1.82	1.99
G3V4J7	G3V4J7_HUMAN DDB1- and CUL4-associated factor 5 OS=Homo sapiens GN=DCAF5 PE=2 SV=1	31.60	66.69	66.66	76.61	50.77	58.67	71.61	3.69 E-06	7.51 E-06	7.67 E-06	2.50 E-06	5.16 E-06	5.74 E-06	0.68	1.40	1.56
Q86UY0	Q86UY0_HUMAN Protein BLOC1S5-TXNDC5 OS=Homo sapiens GN=TXNDC5 PE=2 SV=1	25.60	4.00	6.00	4.00	3.00	5.00	4.00	1.16 E-07	4.44 E-07	3.77 E-07	5.93 E-08	2.71 E-07	2.89 E-07	0.51	2.34	2.50

Q92820	GGH_HUMAN Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2	22.60	1.00	3.00	4.00	2.00	4.00	3.00	2.74E-08	4.26E-07	7.13E-07	3.16E-08	4.27E-07	3.18E-07	1.15	15.59	11.61
Q9HA64	KT3K_HUMAN Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2	41.40	19.79	23.77	27.73	18.84	20.83	21.83	8.79E-07	3.87E-06	3.93E-06	7.90E-07	2.64E-06	2.66E-06	0.90	3.00	3.03
C9JMU5	C9JMU5_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=2 SV=1	13.80	3.00		0.50	2.00			8.03E-08		8.43E-09	5.44E-08			0.68	Control 1 Only	Control 1 Only
Q3LXA3	DHAK_HUMAN Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2	19.00	4.97	3.98	0.99	6.97	1.99	1.00	9.62E-08	1.28E-07	4.04E-08	1.04E-07	4.87E-08	1.67E-08	1.08	0.51	0.17
Q6YN16	HSDL2_HUMAN Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	33.00	6.96	9.95	11.95	7.96	5.96	8.95	2.31E-07	6.56E-07	8.16E-07	2.70E-07	3.41E-07	5.40E-07	1.17	1.48	2.33
H0Y2P8	H0Y2P8_HUMAN SLIT-ROBO Rho GTPase-activating protein 2 (Fragment) OS=Homo sapiens GN=SRGAP2 PE=4 SV=1	2.20		0.99	0.99		0.99			8.83E-09	1.04E-08		1.09E-08			Sample 2 Only	
P49368	TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	29.70	11.85	9.88	10.88	9.88	7.89	10.88	4.87E-07	7.43E-07	7.13E-07	2.96E-07	4.22E-07	6.02E-07	0.61	0.87	1.24
Q86YZ3	HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	28.10	73.00	72.00	90.00	94.00	102.00	62.00	1.07E-07	1.73E-07	2.75E-07	1.69E-07	5.04E-07	1.59E-07	1.59	4.72	1.49
P33992	MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	66.80	36.91	103.71	107.74	29.93	85.77	81.81	1.39E-06	5.20E-06	5.56E-06	8.52E-07	3.62E-06	4.17E-06	0.61	2.61	3.01
C9JZR2	C9JZR2_HUMAN Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=2 SV=2	3.50	0.99	0.99	1.98	0.99		0.99	1.03E-08	8.14E-09	1.67E-08	1.10E-08		1.00E-08	1.06	Control 1 Only	0.97
P00390	GSHR_HUMAN Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2	33.60	8.95	10.93	10.93	7.96	9.93	9.94	2.75E-07	9.51E-07	1.21E-06	1.99E-07	6.17E-07	8.61E-07	0.73	2.25	3.14
F8WA86	F8WA86_HUMAN Calponin-3 OS=Homo sapiens GN=CNN3 PE=2 SV=1	8.50		0.99	1.98	0.99	0.99	0.99		1.40E-07	2.56E-07	8.49E-09	1.21E-07	1.31E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
A3KFL4	A3KFL4_HUMAN Exosome complex component RRP4 OS=Homo sapiens GN=EXOSC2 PE=2 SV=1	14.40		2.00	2.00	1.00	2.00	2.00		3.79E-07	3.67E-07	1.39E-08	2.41E-07	2.46E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P22102	PUR2_HUMAN Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	29.00	5.98	35.88	21.93	4.97	17.92	17.89	9.79E-08	5.65E-07	4.06E-07	7.38E-08	3.18E-07	3.33E-07	0.75	3.25	3.40
F6SBX2	F6SBX2_HUMAN Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=2 SV=1	20.10		11.00	11.00		11.00	6.00		1.59E-07	1.60E-07		1.24E-07	8.56E-08		Sample 2 Only	Sample 3 Only
P51659	DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	30.60	13.85	14.84	24.77	11.88	11.87	13.85	3.03E-07	3.29E-07	6.63E-07	2.54E-07	2.59E-07	3.72E-07	0.84	0.85	1.23
Q8WUM4	PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	4.10		2.00	2.00		2.00	1.00		1.32E-08	1.85E-08		1.28E-08	6.58E-09		Sample 2 Only	Sample 3 Only
Q93034	CUL5_HUMAN Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4	62.20	98.00	164.00	158.00	79.00	130.00	148.00	5.25E-06	1.21E-05	1.39E-05	3.47E-06	8.06E-06	1.15E-05	0.66	1.54	2.19
O14920	IKKB_HUMAN Inhibitor of nuclear factor kappa-B kinase subunit beta OS=Homo sapiens GN=IKBKB PE=1 SV=1	3.20		1.98	1.98		0.99	0.99		1.69E-08	1.95E-08		1.06E-08	1.18E-08		Sample 2 Only	Sample 3 Only
B4DLC0	B4DLC0_HUMAN Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1	36.70	0.99	0.99	1.98	1.98	0.99	1.98	5.60E-08	1.27E-07	1.82E-07	5.18E-08	6.84E-08	1.22E-07	0.92	1.22	2.17
E9PB18	E9PB18_HUMAN UPF0577 protein KIAA1324 (Fragment) OS=Homo sapiens GN=KIAA1324	4.60		2.00	2.00		2.00	1.00		2.18E-08	1.98E-08		1.11E-08	1.47E-08		Sample 2 Only	Sample 3 Only

	PE=2 SV=1																
F5H6X6	F5H6X6_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=2 SV=1	12.00	1.00	8.98	4.99	1.00	2.99	3.98	1.39 E-08	7.91 E-08	5.57 E-08	1.27 E-08	2.55 E-08	5.82 E-08	0.92	1.84	4.18
F5H335	F5H335_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1	2.00		1.00	2.00		2.00	2.00		3.36 E-09	4.32 E-09		5.68 E-09	7.25 E-09		Sample 2 Only	Sample 3 Only
Q9NYU2	UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	33.10	47.97	63.97	45.99	36.98	41.97	32.98	2.42 E-07	4.96 E-07	2.84 E-07	1.35 E-07	3.44 E-07	2.21 E-07	0.56	1.42	0.91
C9JNW5	C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1	55.40	9.00	2.00		11.00	4.00	5.00	1.21 E-06	3.65 E-07		1.08 E-06	4.60 E-07	7.09 E-07	0.89	0.38	0.58
E5RJ68	E5RJ68_HUMAN AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=2 SV=1	4.90	3.00	5.00	5.00	2.00	4.00	3.00	3.40 E-08	1.14 E-07	7.76 E-08	1.31 E-08	7.90 E-08	5.63 E-08	0.38	2.32	1.66
B4DPJ8	B4DPJ8_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=2 SV=1	30.00	8.94	7.96	7.97	10.94	5.97	6.98	2.42 E-07	7.84 E-07	6.48 E-07	2.52 E-07	4.27 E-07	4.84 E-07	1.04	1.77	2.00
O95486	SC24A_HUMAN Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2	6.60		3.00	4.00		2.00	2.00		1.74 E-08	3.22 E-08		1.38 E-08	1.75 E-08		Sample 2 Only	Sample 3 Only
H0YFA4	H0YFA4_HUMAN Cysteine-rich protein 2 (Fragment) OS=Homo sapiens GN=CRIP2 PE=4 SV=1	34.90	6.00	2.00	4.00	4.00	3.00	2.00	6.12 E-07	2.45 E-07	8.02 E-07	3.95 E-07	5.65 E-07	1.97 E-07	0.65	0.92	0.32
B9A064	IGLL5_HUMAN Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	10.70	5.00	11.00	9.00	5.00	12.00	7.00	1.30 E-06	8.84 E-06	6.63 E-06	7.21 E-07	6.70 E-06	4.90 E-06	0.55	5.15	3.77
J3KR12	J3KR12_HUMAN Uncharacterized protein OS=Homo sapiens PE=4 SV=1	16.20	0.98	1.96	1.96	1.98	1.98	3.92	2.71 E-08	1.91 E-07	2.53 E-07	7.65 E-08	2.08 E-07	4.04 E-07	2.82	7.68	14.91
Q86YV9	HPS6_HUMAN Hermansky-Pudlak syndrome 6 protein OS=Homo sapiens GN=HPS6 PE=1 SV=1	2.80		1.00	1.00		2.00	2.00		3.70 E-08	4.11 E-08		5.86 E-08	6.12 E-08		Sample 2 Only	Sample 3 Only
P23526	SAHH_HUMAN Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	31.50	11.99	12.99	14.99	9.99	13.99	11.99	4.39 E-07	1.68 E-06	1.63 E-06	3.38 E-07	1.13 E-06	1.20 E-06	0.77	2.58	2.74
B1ANR0	B1ANR0_HUMAN Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e OS=Homo sapiens GN=PABPC4 PE=2 SV=1	21.50	13.57	4.83	5.77	11.62	9.70	13.55	4.65 E-07	2.81 E-07	2.14 E-07	3.77 E-07	4.59 E-07	5.40 E-07	0.81	0.99	1.16
P62195	PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	46.80	2.97	10.85	7.90	5.94	8.92	8.90	6.29 E-08	8.48 E-07	6.00 E-07	1.14 E-07	4.35 E-07	5.06 E-07	1.82	6.92	8.05
J3KS22	J3KS22_HUMAN L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=2 SV=1	18.80	6.98	1.99	2.99	3.98	2.99	1.99	5.75 E-07	3.43 E-07	6.30 E-07	2.59 E-07	5.09 E-07	3.15 E-07	0.45	0.89	0.55
P46781	RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	53.10	15.96	2.00	5.00	19.95	6.99	4.99	1.82 E-06	2.47 E-07	2.74 E-07	1.79 E-06	6.00 E-07	8.91 E-07	0.98	0.33	0.49
Q9Y2A7	NCKP1_HUMAN Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	8.20	1.00	5.00	6.00		4.00	5.00	7.18 E-10	3.99 E-08	6.44 E-08		2.71 E-08	4.11 E-08	Control 1 Only	37.72	57.23
E9PEM5	E9PEM5_HUMAN Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=2 SV=1	3.50		8.00	8.00		6.00	8.00		3.34 E-08	3.02 E-08		1.70 E-08	2.39 E-08		Sample 2 Only	Sample 3 Only
B4DR63	B4DR63_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=2 SV=1	48.00	9.00	13.00	14.00	7.00	16.00	16.00	5.03 E-07	1.75 E-06	2.12 E-06	3.04 E-07	1.36 E-06	1.48 E-06	0.61	2.71	2.94
Q9NZL9	MAT2B_HUMAN Methionine adenosyltransferase 2 subunit beta OS=Homo	9.70	1.98		1.98	1.98	1.98	1.98	7.46 E-08		2.35 E-07	4.87 E-08	1.96 E-07	2.09 E-07	0.65	2.63	2.80

	sapiens GN=MAT2B PE=1 SV=1																
F5H223	F5H223_HUMAN Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=2 SV=1	16.90	0.99		0.99	4.94			1.41 E-08		4.54 E-08	9.08 E-08			6.46	Control 1 Only	Control 1 Only
P30084	ECHM_HUMAN Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4	11.70	1.00	2.00	3.00		2.00	2.00	2.86 E-08	2.84 E-07	4.36 E-07		2.63 E-07	2.54 E-07	Control 1 Only	9.19	8.90
H0YJ97	H0YJ97_HUMAN Thyroid receptor-interacting protein 11 (Fragment) OS=Homo sapiens GN=TRIP11 PE=4 SV=1	1.50	3.00	1.00		1.00		1.00	5.39 E-09	2.79 E-09		2.52 E-09		2.33 E-09	0.47	Control 1 Only	0.43
Q8TAA9	VANG1_HUMAN Vang-like protein 1 OS=Homo sapiens GN=VANGL1 PE=1 SV=1	20.70		5.00	4.00		3.00	10.00		2.89 E-07	2.46 E-07		1.98 E-07	5.73 E-07		Sample 2 Only	Sample 3 Only
J3QRV5	J3QRV5_HUMAN Lethal(2) giant larvae protein homolog 2 OS=Homo sapiens GN=LLGL2 PE=2 SV=1	9.30		7.98	6.98	1.00	5.00	5.00		1.20 E-07	1.02 E-07	1.87 E-08	6.01 E-08	7.03 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y295	DRG1_HUMAN Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1	56.40	20.00	25.00	29.00	21.00	26.00	27.00	8.86 E-07	6.25 E-06	6.55 E-06	7.61 E-07	4.50 E-06	4.85 E-06	0.86	5.08	5.48
Q13011	ECH1_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	40.90	17.94	8.97	13.94	16.94	8.97	13.95	1.20 E-06	1.59 E-06	2.27 E-06	9.22 E-07	1.08 E-06	1.66 E-06	0.77	0.90	1.39
F5H4B6	F5H4B6_HUMAN Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=2 SV=1	10.50		1.00	1.00		2.00	3.00		1.18 E-08	1.75 E-08		1.90 E-08	2.66 E-08		Sample 2 Only	Sample 3 Only
P60709	ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	88.80	147.16	100.64	82.84	226.25	96.73	117.46	1.04 E-04	1.48 E-04	1.22 E-04	2.15 E-04	9.66 E-05	1.62 E-04	2.07	0.93	1.55
P16403	H12_HUMAN Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	52.10	10.00			15.00	1.00	1.00	2.67 E-06			3.57 E-06	1.02 E-07	2.64 E-08	1.34	0.04	0.01
P42704	LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	21.20	16.91	25.89	30.85	17.90	14.94	21.89	1.39 E-07	3.40 E-07	4.05 E-07	1.33 E-07	1.92 E-07	2.92 E-07	0.96	1.38	2.10
P13647	K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	68.50	74.67	113.47	144.38	81.65	159.29	131.41	1.85 E-06	6.06 E-06	8.41 E-06	2.06 E-06	1.29 E-05	6.83 E-06	1.11	6.96	3.69
B4E1G1	B4E1G1_HUMAN Derlin-1 OS=Homo sapiens GN=DERL1 PE=2 SV=1	16.60	1.99		0.99	1.98	0.99	0.99	1.12 E-07		1.31 E-07	1.06 E-07	1.43 E-07	1.06 E-07	0.95	1.28	0.95
Q9Y5Y6	ST14_HUMAN Suppressor of tumorigenicity 14 protein OS=Homo sapiens GN=ST14 PE=1 SV=2	4.90	2.00	1.00	2.00	2.00	1.00	1.00	2.99 E-08	7.36 E-08	6.72 E-08	2.75 E-08	4.30 E-08	4.41 E-08	0.92	1.44	1.48
P37108	SRP14_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2	41.20	6.00	1.00	2.00	4.00	1.00	1.00	5.61 E-07	1.79 E-07	2.84 E-07	3.53 E-07	1.41 E-07	2.26 E-07	0.63	0.25	0.40
P01876	IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	24.40	8.00	5.00	9.00	9.00	3.00	6.00	3.69 E-07	5.20 E-07	5.32 E-07	3.46 E-07	2.39 E-07	4.24 E-07	0.94	0.65	1.15
B4DZI8	B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	10.50	1.00	3.99	4.99	1.00	1.00	5.99	2.44 E-09	5.14 E-08	7.01 E-08	4.48 E-09	3.68 E-09	7.47 E-08	1.84	1.51	30.59
Q02878	RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	45.50	14.45	0.99	0.99	13.95	2.97	4.95	1.31 E-06	2.07 E-08	3.92 E-08	1.42 E-06	2.17 E-07	2.76 E-07	1.09	0.17	0.21
Q6PI48	SYDM_HUMAN Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1	2.60	1.00		1.00	1.00			9.03 E-09		8.52 E-09	1.07 E-08			1.18	Control 1 Only	Control 1 Only
B0FLL2	B0FLL2_HUMAN 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 2 transcript variant 3 OS=Homo sapiens GN=PFKFB2 PE=2 SV=1	18.70	0.99		1.98			0.99	1.23 E-08		6.88 E-08			5.33 E-08	Control 1 Only	Control 1 Only	4.34

P23396	RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	81.90	27.33	2.91	4.86	31.22	6.82	9.72	2.30E-06	3.87E-07	4.65E-07	2.15E-06	8.52E-07	1.31E-06	0.94	0.37	0.57
Q08257	QOR_HUMAN Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	35.00	4.95	3.95	4.94	4.95	1.97	5.93	1.58E-07	2.32E-07	4.17E-07	1.10E-07	1.10E-07	3.48E-07	0.70	0.70	2.21
P35998	PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	41.80	9.00	11.00	13.00	8.00	17.00	18.00	2.29E-07	8.84E-07	1.07E-06	2.42E-07	1.44E-06	1.32E-06	1.06	6.30	5.77
P48735	IDHP_HUMAN Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	53.30	38.68	40.70	35.71	31.73	34.73	36.73	1.78E-06	5.45E-06	5.04E-06	1.32E-06	3.67E-06	4.18E-06	0.74	2.07	2.36
J3KR24	J3KR24_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=2 SV=1	31.90	28.97	56.92	52.90	23.99	40.95	32.95	2.02E-07	7.86E-07	6.22E-07	1.63E-07	5.18E-07	4.74E-07	0.81	2.56	2.34
P00338	LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	67.20	18.53	43.90	46.72	16.62	44.81	39.98	1.44E-06	2.12E-05	2.01E-05	1.14E-06	1.58E-05	1.58E-05	0.79	10.93	10.92
P54803	GALC_HUMAN Galactocerebrosidase OS=Homo sapiens GN=GALC PE=1 SV=2	35.80	34.37	52.01	46.14	32.39	46.11	48.08	1.33E-06	6.91E-06	5.82E-06	1.00E-06	4.82E-06	4.74E-06	0.75	3.62	3.56
P35527	K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	87.80	381.26	394.26	432.91	382.28	479.59	351.46	3.33E-05	5.99E-05	7.88E-05	3.39E-05	1.40E-04	4.41E-05	1.02	4.22	1.33
P60866	RS20_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	30.30	8.91		0.99	5.94	0.99		1.17E-06		3.30E-07	8.67E-07	2.10E-07		0.74	0.18	Control 1 Only
P50416	CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	42.60	24.93	53.82	52.82	17.94	40.89	43.85	5.30E-07	1.39E-06	1.59E-06	3.89E-07	9.88E-07	1.19E-06	0.73	1.87	2.25
F5H2U1	F5H2U1_HUMAN Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=2 SV=1	7.60		0.99			1.99	1.00		9.81E-08			1.22E-07	2.26E-08		Sample 2 Only	Sample 3 Only
P52292	IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	17.20	6.00	4.00	2.00	6.00	3.00	2.00	2.83E-07	2.83E-07	1.63E-07	2.19E-07	1.53E-07	1.44E-07	0.77	0.54	0.51
E9PC74	E9PC74_HUMAN Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=2 SV=1	3.10			1.00		1.00	0.99			2.36E-08		1.32E-08	2.19E-09		Sample 2 Only	Sample 3 Only
P14649	MYL6B_HUMAN Myosin light chain 6B OS=Homo sapiens GN=MYL6B PE=1 SV=1	23.60	10.67	2.91	2.91	12.67	3.88	3.88	6.59E-06	1.14E-06	8.82E-07	9.43E-06	9.63E-07	1.04E-06	1.43	0.15	0.16
B4E2S7	B4E2S7_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1	5.00	1.00	3.00	3.00	1.00	1.00	3.00	2.69E-08	1.44E-07	1.06E-07	2.21E-08	5.31E-08	1.17E-07	0.82	1.97	4.35
Q6KB66	K2C80_HUMAN Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	32.20	4.00		1.00	4.00	5.00		1.08E-07		9.06E-09	8.71E-08	8.32E-08		0.81	0.77	Control 1 Only
F6TQG2	F6TQG2_HUMAN Probable global transcription activator SNF2L1 (Fragment) OS=Homo sapiens GN=SMARCA1 PE=2 SV=1	4.50	5.00			4.50	0.50	0.50	4.37E-08			2.53E-08	1.13E-09	2.91E-09	0.58	0.03	0.07
P45880	VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	43.10	19.78		1.98	16.82	0.98	0.99	1.52E-06		2.02E-07	1.16E-06	4.19E-08	4.65E-08	0.77	0.03	0.03
P36542	ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	52.00	15.00	23.00	19.00	20.00	18.00	19.00	1.40E-06	5.72E-06	5.18E-06	1.28E-06	4.25E-06	3.75E-06	0.91	3.03	2.67
P43686	PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	40.00	7.00	9.00	13.00	6.00	7.00	11.00	3.85E-07	1.18E-06	1.46E-06	2.69E-07	9.23E-07	1.03E-06	0.70	2.39	2.67
P55072	TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	13.40		9.99	8.00	2.00	6.00	6.00		1.25E-07	1.06E-07	1.42E-08	5.90E-08	8.75E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O60547	GMDS_HUMAN GDP-mannose 4,6 dehydratase OS=Homo sapiens GN=GMDS	30.40	4.00	6.00	4.00	2.00	4.00	6.00	1.48E-07	4.82E-07	2.93E-07	4.71E-08	2.42E-07	3.74E-07	0.32	1.64	2.53

	PE=1 SV=1																
P08779	K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	70.40	19.00	30.00	87.00	44.00	86.00	47.00	3.97 E-07	1.57 E-06	5.49 E-06	1.08 E-06	6.58 E-06	2.20 E-06	2.72	16.57	5.54
Q9H479	FN3K_HUMAN Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1	23.30	1.00	3.00	6.00	3.00	2.00	4.00	2.98 E-08	3.49 E-07	4.99 E-07	1.01 E-07	2.02 E-07	3.28 E-07	3.39	6.77	11.02
P32119	PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	46.00	16.46	17.97	18.47	13.50	20.46	17.98	3.05 E-06	9.59 E-06	9.20 E-06	1.63 E-06	8.02 E-06	7.09 E-06	0.53	2.63	2.32
O60264	SMCA5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1	10.60	9.00			7.50	0.50	0.50	1.16 E-07			7.61 E-08	1.08 E-09	2.78 E-09	0.66	0.01	0.02
Q9NZT2	OGFR_HUMAN Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3	51.80	47.99	59.98	62.97	48.99	58.98	65.96	2.01 E-06	5.19 E-06	5.48 E-06	1.69 E-06	3.72 E-06	4.22 E-06	0.84	1.85	2.10
P62854	RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	27.00	5.00			5.00	1.00		1.90 E-06			1.36 E-06	3.07 E-08		0.72	0.02	Control 1 Only
H3BMW1	H3BMW1_HUMAN Cytosolic Fe-S cluster assembly factor NUBP2 (Fragment) OS=Homo sapiens GN=NUBP2 PE=2 SV=1	45.70	1.00		2.00	2.00	1.00	1.00	8.21 E-08		4.67 E-07	1.43 E-07	1.51 E-07	9.78 E-08	1.74	1.83	1.19
O94952	FBX21_HUMAN F-box only protein 21 OS=Homo sapiens GN=FBXO21 PE=2 SV=2	16.60	5.98	14.96	17.94	4.97	14.95	19.91	1.62 E-07	8.55 E-07	7.51 E-07	9.66 E-08	5.16 E-07	6.81 E-07	0.60	3.18	4.20
Q9Y265	RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	47.10	24.75	16.85	19.82	18.85	13.87	18.83	1.23 E-06	1.75 E-06	2.04 E-06	6.61 E-07	1.35 E-06	1.74 E-06	0.54	1.10	1.41
P16615	AT2A2_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	27.60	16.83	40.60	40.59	14.86	39.63	36.63	1.99 E-07	7.92 E-07	8.34 E-07	1.45 E-07	5.78 E-07	6.14 E-07	0.73	2.90	3.09
P48047	ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	44.60	4.00	3.00	5.00	7.99	7.99	6.99	2.84 E-07	6.73 E-07	7.81 E-07	4.58 E-07	1.07 E-06	8.26 E-07	1.61	3.77	2.91
Q08554	DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	6.70	1.00	3.00	3.00	3.00	9.00	1.00	6.02 E-09	4.09 E-08	4.23 E-08	1.76 E-08	1.02 E-07	9.36 E-09	2.92	17.01	1.56
Q53FA7	QORX_HUMAN Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2	31.30	10.95	11.94	8.96	15.92	7.96	10.95	4.87 E-07	1.85 E-06	1.81 E-06	5.62 E-07	1.06 E-06	1.47 E-06	1.15	2.17	3.02
B5MCQ5	B5MCQ5_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=2 SV=1	16.50	3.00	3.00	5.00	2.00	2.00	4.00	1.47 E-07	2.98 E-07	3.75 E-07	8.59 E-08	2.08 E-07	2.98 E-07	0.59	1.42	2.03
Q9HB71	CYBP_HUMAN Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	17.80	2.00			1.00		1.00	5.93 E-08			1.45 E-08		7.19 E-08	0.24	Control 1 Only	1.21
P39023	RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	34.20	11.86	1.98	3.96	17.78	3.96	4.95	5.49 E-07	2.25 E-08	1.21 E-07	7.08 E-07	8.97 E-08	1.51 E-07	1.29	0.16	0.27
P14625	ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	21.00	5.00	12.00	9.00	5.00	10.00	7.00	1.14 E-07	3.19 E-07	2.29 E-07	1.18 E-07	1.86 E-07	1.75 E-07	1.03	1.63	1.53
E7ESK6	E7ESK6_HUMAN Syndecan OS=Homo sapiens GN=SDC2 PE=2 SV=1	19.40	12.00	1.00	1.00	13.00	1.00	4.00	5.99 E-07	2.44 E-08	3.30 E-08	6.39 E-07	6.02 E-08	1.99 E-07	1.07	0.10	0.33
E7EMH5	E7EMH5_HUMAN Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=2 SV=1	12.10	3.00	2.00	3.00	1.00	5.00	3.99	4.23 E-08	6.98 E-08	1.11 E-07	1.03 E-08	1.87 E-07	1.15 E-07	0.24	4.43	2.72
Q15075	EEA1_HUMAN Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	7.50	2.00	2.00	5.00		3.00	2.00	3.83 E-09	6.57 E-09	1.42 E-08		1.34 E-08	2.77 E-09	Control 1 Only	3.51	0.72
P07814	SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	36.70	42.00	93.00	68.00	19.00	73.00	66.00	2.39 E-07	9.20 E-07	7.25 E-07	9.77 E-08	7.00 E-07	5.99 E-07	0.41	2.93	2.50
P50502	F10A1_HUMAN Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	24.10	18.86	7.95	15.91	18.87	9.93	9.95	1.48 E-06	2.17 E-06	2.96 E-06	1.60 E-06	1.50 E-06	1.92 E-06	1.08	1.01	1.30
Q99523	SORT_HUMAN Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3	7.30		5.00	5.00		5.00	3.00		1.24 E-07	9.64 E-08		8.41 E-08	7.19 E-08		Sample 2 Only	Sample 3 Only

Q53GQ0	DHB12_HUMAN Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2	46.50	18.98	3.99	4.99	14.98	2.99	6.98	1.03E-06	3.97E-07	5.91E-07	6.92E-07	2.68E-07	5.43E-07	0.67	0.26	0.53
R4GNH3	R4GNH3_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=3 SV=1	50.60	10.80	18.63	16.66	9.80	17.64	18.59	5.08E-07	1.97E-06	1.73E-06	3.01E-07	1.48E-06	1.40E-06	0.59	2.90	2.76
E9PJN0	E9PJN0_HUMAN Acyl-coenzyme A thioesterase 8 OS=Homo sapiens GN=ACOT8 PE=2 SV=1	30.10	2.00	2.00	5.00	4.00	7.00	5.00	1.23E-07	3.35E-07	8.59E-07	1.92E-07	8.58E-07	7.17E-07	1.56	6.95	5.81
Q15233	NONO_HUMAN Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	28.80	3.95	1.97	5.92	3.96	0.98	3.95	7.48E-08	1.10E-07	4.43E-07	1.33E-07	5.72E-08	2.68E-07	1.77	0.76	3.58
C9J1V9	C9J1V9_HUMAN HCG2043275 OS=Homo sapiens GN=hCG_2043275 PE=4 SV=2	22.30	4.97	2.99	2.99	4.97	1.99	2.98	4.95E-07	4.16E-07	4.19E-07	3.37E-07	2.10E-07	4.39E-07	0.68	0.42	0.89
P08107	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	53.20	35.64	57.42	79.25	29.68	67.35	78.25	1.74E-06	5.21E-06	6.06E-06	1.21E-06	3.71E-06	5.15E-06	0.70	2.13	2.96
Q12933	TRAF2_HUMAN TNF receptor-associated factor 2 OS=Homo sapiens GN=TRAF2 PE=1 SV=2	13.70	2.00	5.00	5.00	3.00	4.00	6.00	2.43E-08	3.02E-07	2.74E-07	4.16E-08	1.71E-07	2.27E-07	1.71	7.01	9.31
O43175	SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	27.80	15.99	17.98	14.99	12.99	13.99	15.98	6.49E-07	1.71E-06	1.60E-06	3.84E-07	1.28E-06	1.35E-06	0.59	1.97	2.08
Q9Y224	CN166_HUMAN UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	29.50	5.98	1.00	2.98	6.96	1.00	2.98	2.81E-07	1.68E-07	4.10E-07	2.19E-07	9.22E-08	3.24E-07	0.78	0.33	1.15
Q8TEQ6	GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	3.80	2.00	1.00	4.00	1.00	1.00	3.00	4.27E-09	4.22E-09	2.40E-08	1.03E-09	5.51E-09	1.58E-08	0.24	1.29	3.69
O76071	CIAO1_HUMAN Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens GN=CIAO1 PE=1 SV=1	7.10	1.00	2.00	2.00		3.00	3.00	1.69E-08	1.42E-07	1.33E-07		2.08E-07	1.91E-07	Control 1 Only	12.29	11.25
B4E2W0	B4E2W0_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1	15.70	2.96	4.94	5.93	3.95	3.95	5.93	1.73E-07	1.01E-06	1.06E-06	1.83E-07	6.36E-07	8.75E-07	1.06	3.67	5.06
P13645	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	68.70	359.80	402.77	472.68	343.79	409.71	405.74	3.90E-05	1.06E-04	1.30E-04	3.09E-05	1.06E-04	8.74E-05	0.79	2.71	2.24
P02533	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	78.40	55.50	68.50	84.00	50.50	89.50	66.50	1.67E-06	3.79E-06	5.82E-06	1.56E-06	9.38E-06	3.47E-06	0.94	5.63	2.08
Q9H773	DCTP1_HUMAN dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1	62.40	16.00	8.99	11.99	20.99	12.99	8.99	2.80E-06	3.33E-06	4.52E-06	2.44E-06	3.73E-06	2.11E-06	0.87	1.33	0.75
O14880	MGST3_HUMAN Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1	18.40	3.00			4.00	1.00		3.64E-07			2.18E-07	4.79E-08		0.60	0.13	Control 1 Only
F8W7C6	F8W7C6_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=2 SV=1	42.90	11.89			15.87	0.98	1.97	1.58E-06			1.93E-06	6.64E-09	1.46E-07	1.22	0.00	0.09
O95197	RTN3_HUMAN Reticulon-3 OS=Homo sapiens GN=RTN3 PE=1 SV=2	8.10	1.00	2.00	2.00	2.00	3.00	3.00	1.92E-08	7.87E-08	7.27E-08	2.02E-08	1.09E-07	1.05E-07	1.05	5.69	5.50
P18124	RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	45.60	23.95	1.00	4.00	21.93	4.99	5.99	2.46E-06	1.42E-07	4.03E-07	2.52E-06	6.36E-07	7.47E-07	1.02	0.26	0.30
P11142	HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	76.60	126.56	221.96	250.19	107.06	231.59	248.30	1.63E-05	4.44E-05	4.60E-05	9.92E-06	3.44E-05	4.21E-05	0.61	2.11	2.59
Q15024	EXOS7_HUMAN Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3	13.10	1.00	1.00	2.00	1.00	2.00	3.00	1.98E-08	1.12E-07	1.54E-07	1.41E-08	1.36E-07	2.36E-07	0.71	6.87	11.89
Q9BPW8	NIPS1_HUMAN Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1	48.20	9.92	19.85	16.87	11.91	15.88	12.90	5.62E-07	4.27E-06	3.42E-06	6.40E-07	3.16E-06	2.64E-06	1.14	5.61	4.70

P31689	DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	6.00		0.99	0.99	1.00	0.99	0.99		9.43 E-08	1.50 E-07	2.18 E-08	6.89 E-08	8.84 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4E0X2	B4E0X2_HUMAN RAF proto-oncogene serine/threonine-protein kinase OS=Homo sapiens GN=RAF1 PE=2 SV=1	9.90	1.00		1.00	1.00			6.99 E-09		1.01 E-08	1.14 E-08			1.63	Control 1 Only	Control 1 Only
P52907	CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	58.40	15.00	15.00	14.50	14.50	14.00	15.50	8.77 E-07	2.55 E-06	2.76 E-06	7.48 E-07	1.93 E-06	2.14 E-06	0.85	2.20	2.44
Q6ZRV2	FA83H_HUMAN Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3	21.30	27.00		1.00	19.00	3.00	1.00	2.78 E-07		6.55 E-09	1.81 E-07	1.67 E-08	1.21 E-08	0.65	0.06	0.04
P68104	EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	55.20	112.50	91.61	86.62	102.55	89.63	91.62	1.61 E-05	3.79 E-05	3.75 E-05	1.26 E-05	2.81 E-05	3.37 E-05	0.78	1.74	2.09
F8W845	F8W845_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=2 SV=1	11.50	2.96	5.93	6.92	2.96	1.97	6.92	4.18 E-08	6.61 E-08	9.58 E-08	4.07 E-08	2.82 E-08	8.06 E-08	0.97	0.67	1.93
Q6PJ69	TRI65_HUMAN Tripartite motif-containing protein 65 OS=Homo sapiens GN=TRIM65 PE=1 SV=3	18.00	1.99	1.99	4.98	2.98	2.99	2.99	5.38 E-08	1.49 E-07	2.59 E-07	7.58 E-08	1.27 E-07	1.42 E-07	1.41	2.37	2.63
Q9UBN7	HDAC6_HUMAN Histone deacetylase 6 OS=Homo sapiens GN=HDAC6 PE=1 SV=2	14.40	3.94	14.81	20.71	2.95	19.73	21.72	3.19 E-08	1.95 E-07	3.73 E-07	3.36 E-08	3.32 E-07	4.27 E-07	1.05	10.40	13.37
I3L1P8	I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens GN=SLC25A11 PE=2 SV=1	35.10	8.00	6.00	11.00	7.00	8.00	9.00	3.31 E-07	7.42 E-07	1.21 E-06	2.28 E-07	7.06 E-07	8.23 E-07	0.69	2.13	2.48
P46977	STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	5.20	2.00	2.00	3.00	1.00	2.00	2.00	3.10 E-08	4.69 E-08	1.29 E-07	1.27 E-08	7.39 E-08	6.57 E-08	0.41	2.39	2.12
Q00610	CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	53.00	147.33	169.31	159.34	123.47	96.56	142.42	1.30 E-06	1.86 E-06	1.62 E-06	1.10 E-06	1.04 E-06	1.59 E-06	0.85	0.80	1.22
H0YNW5	H0YNW5_HUMAN Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=2 SV=1	51.20	15.90	8.95	9.95	15.89	12.92	9.95	2.92 E-06	3.67 E-06	3.91 E-06	2.16 E-06	3.51 E-06	2.63 E-06	0.74	1.20	0.90
P41240	CSK_HUMAN Tyrosine-protein kinase CSK OS=Homo sapiens GN=CSK PE=1 SV=1	8.70		2.00	2.00		4.00	2.00		1.22 E-07	1.10 E-07		2.04 E-07	1.07 E-07		Sample 2 Only	Sample 3 Only
C9J9K3	C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	50.80	24.92	9.97	12.95	22.91	14.95	16.95	2.43 E-06	3.23 E-06	2.79 E-06	2.27 E-06	4.10 E-06	4.27 E-06	0.93	1.69	1.76
Q9H4M9	EHD1_HUMAN EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2	19.90		4.93	4.95	2.97	3.96	1.98		2.26 E-07	2.53 E-07	4.22 E-08	1.98 E-07	1.20 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
E5RHG8	E5RHG8_HUMAN Transcription elongation factor B polypeptide 1 (Fragment) OS=Homo sapiens GN=TCEB1 PE=2 SV=1	83.10	20.79	2.97	3.96	17.82	3.96	5.94	6.86 E-06	1.44 E-06	1.63 E-06	3.71 E-06	1.85 E-06	2.31 E-06	0.54	0.27	0.34
Q14974	IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	29.00	28.85	41.78	41.77	30.83	34.80	36.79	9.57 E-07	1.58 E-06	1.54 E-06	8.30 E-07	1.19 E-06	1.17 E-06	0.87	1.24	1.22
P46779	RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	64.20	19.83		0.99	20.83		1.98	2.96 E-06		1.30 E-07	2.26 E-06		1.47 E-07	0.76	Control 1 Only	0.05
B4DWW1	B4DWW1_HUMAN ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=2 SV=1	44.50	12.87	0.99	4.95	13.86	2.97	2.97	1.60 E-06	1.39 E-07	9.50 E-07	1.00 E-06	5.15 E-07	5.75 E-07	0.63	0.32	0.36
B4DKY1	B4DKY1_HUMAN Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS PE=2 SV=1	13.20		4.95	8.91		5.94	6.93		7.27 E-08	1.70 E-07		8.77 E-08	9.37 E-08		Sample 2 Only	Sample 3 Only
Q8TBX8	PI42C_HUMAN Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens GN=PIP4K2C PE=1 SV=3	20.60	1.98	3.96	4.95	2.97	2.97	6.93	2.20 E-08	1.76 E-07	2.67 E-07	6.90 E-08	1.34 E-07	4.06 E-07	3.14	6.09	18.47

Q9UBV2	SE1L1_HUMAN Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3	6.90		3.00	4.00	2.00	4.00	3.00		5.85E-08	6.35E-08	1.57E-08	4.16E-08	3.30E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
G3V5T0	G3V5T0_HUMAN Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=2 SV=1	55.00	24.57	22.56	22.62	23.53	22.56	21.59	3.83E-06	1.06E-05	9.70E-06	3.11E-06	7.98E-06	8.41E-06	0.81	2.08	2.20
P61247	RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	61.40	20.37	0.98	0.96	23.28	2.91	5.82	9.38E-07	2.38E-07	1.32E-07	1.10E-06	2.08E-07	3.73E-07	1.18	0.22	0.40
P00966	ASSY_HUMAN Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	19.20	3.00	7.00	4.00	3.00	9.00	10.00	7.82E-08	9.34E-07	5.19E-07	6.45E-08	9.17E-07	9.81E-07	0.82	11.73	12.55
P23258	TBG1_HUMAN Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	10.00	2.00	2.00	4.00	3.00	3.00	5.00	9.24E-08	1.34E-07	3.78E-07	9.62E-08	2.58E-07	4.29E-07	1.04	2.80	4.64
O15269	SPTC1_HUMAN Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1	38.50	10.00	11.00	17.00	9.00	11.00	14.00	4.51E-07	1.57E-06	2.20E-06	3.48E-07	1.18E-06	1.81E-06	0.77	2.63	4.01
Q00839	HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	3.20	1.00	1.00	1.00			2.00	4.33E-08	5.68E-09	7.75E-09			4.10E-08	Control 1 Only	Control 1 Only	0.95
C9J2Y9	C9J2Y9_HUMAN DNA-directed RNA polymerase OS=Homo sapiens GN=POLR2B PE=2 SV=2	5.00		3.00	1.00	1.00	3.00	2.00		1.61E-08	7.57E-09	3.69E-09	1.63E-08	1.29E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P12830	CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	8.70	0.99	3.97	2.98	1.98	4.97	1.99	2.17E-08	6.75E-08	4.96E-08	2.54E-08	5.37E-08	2.47E-08	1.17	2.47	1.14
F8VQE1	F8VQE1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=2 SV=1	9.30		1.00	1.00	2.00		1.00		1.75E-08	2.31E-08	2.34E-08		6.21E-09	Sample 1 Only		Sample 3 Only
Q9BUH6	CI142_HUMAN Uncharacterized protein C9orf142 OS=Homo sapiens GN=C9orf142 PE=1 SV=2	46.10	6.00	5.00	4.00	10.00	4.00	5.00	6.75E-07	9.21E-07	9.42E-07	5.75E-07	6.57E-07	7.73E-07	0.85	0.97	1.15
Q9ULE0	WWC3_HUMAN Protein WWC3 OS=Homo sapiens GN=WWC3 PE=1 SV=3	4.30	2.00	1.00	2.00	1.00		2.00	5.13E-09	1.07E-08	1.26E-08	6.11E-09		1.43E-08	1.19	Control 1 Only	2.80
E9PJD9	E9PJD9_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1	23.10	2.00			3.00	1.00	1.00	1.23E-06			1.03E-06	2.48E-07	2.85E-07	0.83	0.20	0.23
Q9NV79	PCMD2_HUMAN Protein-L-isoaspartate O-methyltransferase domain-containing protein 2 OS=Homo sapiens GN=PCMTD2 PE=2 SV=2	39.30	45.60	27.76	33.72	36.68	30.76	34.71	2.21E-06	5.03E-06	6.23E-06	1.54E-06	4.38E-06	5.00E-06	0.70	1.99	2.27
P78527	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	12.90	19.00	45.96	44.96	16.00	27.98	42.99	2.20E-08	9.87E-08	1.18E-07	1.92E-08	6.25E-08	9.98E-08	0.87	2.84	4.54
J3KNL6	J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=2 SV=1	20.10	58.96	1.00	1.00	42.97	1.00	1.00	2.67E-07	2.46E-09	7.57E-10	1.99E-07	1.80E-09	5.23E-09	0.74	0.01	0.02
P04792	HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	94.10	111.00	119.00	118.00	138.00	117.00	104.00	5.44E-05	1.33E-04	1.22E-04	5.14E-05	1.12E-04	9.76E-05	0.95	2.06	1.79
O95822	DCMC_HUMAN Malonyl-CoA decarboxylase, mitochondrial OS=Homo sapiens GN=MLYCD PE=1 SV=3	24.90	2.00	7.00	9.00		8.00	8.00	5.50E-08	5.63E-07	7.14E-07		4.97E-07	5.47E-07	Control 1 Only	9.03	9.94
Q9H4H8	FA83D_HUMAN Protein FAM83D OS=Homo sapiens GN=FAM83D PE=1 SV=3	17.00	3.00	1.00	8.00	3.00	2.00	5.00	7.69E-08	4.44E-08	1.11E-07	6.51E-08	3.81E-08	7.37E-08	0.85	0.50	0.96
Q96MG8	PCMD1_HUMAN Protein-L-isoaspartate O-methyltransferase domain-containing protein 1 OS=Homo sapiens GN=PCMTD1 PE=2 SV=2	36.40	41.79	24.86	32.85	33.85	25.88	32.83	3.32E-06	6.04E-06	8.79E-06	2.35E-06	5.29E-06	7.17E-06	0.71	1.59	2.16
Q9H4L5	OSBL3_HUMAN Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 PE=1 SV=1	4.40	0.99		0.99	0.99		0.99	3.61E-09		9.03E-09	3.58E-09		5.44E-09	0.99	Control 1 Only	1.51
P55735	SEC13_HUMAN Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=3	14.90	2.98	0.99	2.98	3.97	0.99	0.99	1.65E-07	1.02E-07	1.78E-07	1.65E-07	8.74E-08	9.16E-08	1.00	0.53	0.55

O95573	ACSL3_HUMAN Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3	5.40		1.00	1.00		2.00	2.00		1.54 E-08	1.06 E-08		1.98 E-08	1.54 E-08		Sample 2 Only	Sample 3 Only
P08237	K6PF_HUMAN 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	41.20	11.76	29.50	35.43	9.82	33.48	38.31	2.75 E-07	8.85 E-07	1.09 E-06	1.83 E-07	7.13 E-07	8.90 E-07	0.67	2.59	3.24
D6RAN4	D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1	34.60	10.89			12.87	0.99	1.98	1.15 E-06			1.19 E-06	1.07 E-07	1.57 E-07	1.03	0.09	0.14
Q5VY93	Q5VY93_HUMAN Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=2 SV=1	6.10	1.00	4.00	3.00	1.00	3.00	3.00	5.76 E-09	3.41 E-08	4.54 E-08	5.90 E-09	2.50 E-08	3.34 E-08	1.02	4.34	5.80
Q6P2Q9	PRP8_HUMAN Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	24.60	66.00			50.00		3.00	1.81 E-07			1.35 E-07		3.58 E-09	0.75	Control 1 Only	0.02
F5GY37	F5GY37_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=2 SV=1	30.00	3.97		2.98	2.98		6.95	1.07 E-07		2.08 E-07	5.73 E-08		3.47 E-07	0.54	Control 1 Only	3.25
Q15031	SYLM_HUMAN Probable leucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=LARS2 PE=1 SV=2	3.40		2.00	1.00		4.00	2.00		3.10 E-08	1.61 E-08		3.59 E-08	2.66 E-08		Sample 2 Only	Sample 3 Only
D6RAA6	D6RAA6_HUMAN Transmembrane protein 33 (Fragment) OS=Homo sapiens GN=TMEM33 PE=2 SV=1	9.00	2.00	1.00	1.00	4.00	3.00	2.00	2.57 E-07	2.97 E-07	2.65 E-07	2.47 E-07	4.26 E-07	3.61 E-07	0.96	1.66	1.41
F5GZS6	F5GZS6_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=2 SV=1	21.90	1.00	7.98	7.98		7.97	4.98	3.21 E-08	2.08 E-07	2.81 E-07		2.29 E-07	1.78 E-07	Control 1 Only	7.12	5.54
O95373	IPO7_HUMAN Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	6.80	5.00	4.00	4.00	5.00	2.00	4.00	7.42 E-08	5.28 E-08	6.45 E-08	6.73 E-08	2.63 E-08	5.37 E-08	0.91	0.35	0.72
Q96P70	IPO9_HUMAN Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	11.80	6.00	6.00	8.00	6.00	3.00	7.00	7.16 E-08	8.71 E-08	1.12 E-07	2.07 E-07	4.50 E-08	9.43 E-08	2.89	0.63	1.32
B7ZA04	B7ZA04_HUMAN Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1	17.50	2.98	3.99	8.92	2.96	6.93	4.96	6.30 E-08	6.41 E-08	2.10 E-07	5.21 E-08	1.07 E-07	1.03 E-07	0.83	1.70	1.63
B3KSH1	B3KSH1_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1	9.80	0.99	0.99	0.99		1.98		1.31 E-08	7.41 E-08	9.24 E-08		1.38 E-07		Control 1 Only	10.57	Control 1 Only
P40926	MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	52.10	11.92	11.93	9.94	12.92	16.90	4.98	4.38 E-07	9.47 E-07	8.98 E-07	4.58 E-07	9.79 E-07	3.97 E-07	1.05	2.23	0.90
Q01813	K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	55.00	53.54	102.09	100.59	47.08	96.64	93.16	1.44 E-06	4.36 E-06	4.45 E-06	1.14 E-06	3.52 E-06	3.75 E-06	0.79	2.45	2.61
Q15149-3	PLEC_HUMAN Isoform 3 of Plectin OS=Homo sapiens GN=PLEC	71.20	852.29	16.83	30.69	755.25	32.67	107.89	4.00 E-06	3.67 E-08	5.14 E-08	3.07 E-06	6.02 E-08	1.84 E-07	0.77	0.02	0.05
Q13200	PSMD2_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	48.90	22.79	75.28	65.37	14.86	64.38	64.38	4.11 E-07	2.16 E-06	2.23 E-06	2.41 E-07	1.81 E-06	1.85 E-06	0.59	4.41	4.50
Q8TEM1	PO210_HUMAN Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3	15.70	23.00	1.00		20.00			7.48 E-08	1.35 E-09		5.76 E-08			0.77	Control 1 Only	Control 1 Only
P06576	ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	59.40	38.59	46.48	43.54	37.60	44.51	46.50	2.32 E-06	8.47 E-06	7.22 E-06	1.81 E-06	6.79 E-06	6.30 E-06	0.78	2.93	2.72
Q5T196	Q5T196_HUMAN Fad1, flavin adenine dinucleotide synthetase, homolog (Yeast), isoform CRA_e OS=Homo sapiens GN=FLAD1	11.40	1.00	1.00	2.00	1.00	1.00	1.00	2.14 E-08	5.12 E-08	9.56 E-08	1.63 E-08	1.15 E-07	8.43 E-08	0.76	5.39	3.94

	PE=2 SV=1																
Q9BSJ8	ESYT1_HUMAN Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	10.70	1.00	4.00	2.00		3.00	3.00	6.99E-09	6.62E-08	2.96E-08		3.46E-08	4.40E-08	Control 1 Only	4.95	6.29
Q15365	PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	25.30	3.00	2.00	2.98	5.00	2.00	2.00	9.35E-08	1.45E-07	2.40E-07	1.31E-07	1.19E-07	1.27E-07	1.40	1.27	1.35
Q15437	SC23B_HUMAN Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	40.80	5.00	18.00	32.00	3.00	25.00	25.00	1.03E-07	4.49E-07	9.39E-07	2.42E-08	5.14E-07	6.58E-07	0.24	5.00	6.40
Q9BYN8	RT26_HUMAN 28S ribosomal protein S26, mitochondrial OS=Homo sapiens GN=MRPS26 PE=1 SV=1	15.10	2.00			2.00		1.00	1.01E-07			4.09E-08		3.69E-08	0.41	Control 1 Only	0.37
P49411	EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	60.20	40.00	46.00	51.00	46.00	47.00	51.00	2.77E-06	1.01E-05	1.05E-05	2.62E-06	7.99E-06	8.85E-06	0.95	2.89	3.20
O43242	PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	36.50	3.00	12.98	13.00	2.00	18.98	18.99	6.70E-08	8.25E-07	7.83E-07	2.13E-08	1.18E-06	8.65E-07	0.32	17.61	12.93
O15270	SPTC2_HUMAN Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1	20.80	5.00	3.00	5.00	3.00	5.00	6.00	7.51E-08	1.34E-07	1.70E-07	3.45E-08	1.12E-07	1.52E-07	0.46	1.50	2.03
B3KQ95	B3KQ95_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1	22.50	4.95	2.97	3.96	5.94	3.96	6.93	2.19E-07	2.53E-07	3.15E-07	1.73E-07	3.43E-07	4.62E-07	0.79	1.57	2.11
Q9NTJ5	SAC1_HUMAN Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=1 SV=2	4.30		0.99	0.99		1.98			2.98E-08	5.99E-08		6.90E-08			Sample 2 Only	
E7ENZ3	E7ENZ3_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	25.90	7.00	2.00	3.00	7.00	2.00	4.00	3.31E-07	1.37E-07	4.12E-07	2.00E-07	1.82E-07	3.26E-07	0.60	0.55	0.98
P05388	RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	52.10	23.34	9.68	10.70	27.23	11.66	12.63	2.15E-06	1.10E-06	1.38E-06	2.08E-06	1.55E-06	1.96E-06	0.97	0.72	0.91
Q96RQ3	MCCA_HUMAN Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3	29.10	2.95	19.70	22.64	3.95	18.69	21.64	7.43E-08	5.65E-07	5.79E-07	7.04E-08	4.28E-07	4.87E-07	0.95	5.75	6.56
B7Z817	B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1	14.10	2.00	8.97	9.97	3.99	7.98	8.98	4.71E-08	8.92E-07	1.00E-06	6.23E-08	7.66E-07	7.51E-07	1.32	16.28	15.97
B9A067	B9A067_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=2 SV=2	65.70	68.70	2.94	0.98	57.89	0.98	4.92	1.98E-06	7.68E-08	5.42E-08	1.65E-06	1.33E-08	6.43E-08	0.84	0.01	0.03
Q96RS6	NUDC1_HUMAN NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2	8.30	2.00	2.00	1.00	2.00	2.00	2.00	5.81E-08	7.19E-08	3.01E-08	4.63E-08	5.17E-08	1.03E-07	0.80	0.89	1.77
H3BUR4	H3BUR4_HUMAN RNA-binding protein NOB1 OS=Homo sapiens GN=NOB1 PE=2 SV=1	78.80	4.00	2.00	1.00	6.00	1.00	1.00	1.20E-06	1.23E-06	4.51E-07	1.15E-06	6.11E-07	6.11E-07	0.96	0.51	0.51
P61160	ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	14.70	1.00	1.00	1.00	3.00	1.00	3.00	1.73E-08	1.47E-07	1.56E-07	5.14E-08	1.34E-07	2.12E-07	2.98	7.75	12.27
E9PKL9	E9PKL9_HUMAN GDP-L-fucose synthase (Fragment) OS=Homo sapiens GN=TSTA3 PE=2 SV=1	22.70	1.00	1.00	1.00	1.00	1.00	1.00	3.58E-08	1.07E-07	1.09E-07	2.60E-08	8.15E-08	9.36E-08	0.73	2.28	2.61
Q9UNF1	MAGD2_HUMAN Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2	24.40	6.48	5.02	8.00	3.51	3.04	9.00	1.11E-07	9.60E-08	1.38E-07	5.64E-08	5.39E-08	1.67E-07	0.51	0.49	1.51
P51148	RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	22.70	1.99	1.99	3.98	1.99	3.98	1.99	6.90E-08	1.82E-07	2.78E-07	8.35E-08	1.88E-07	1.57E-07	1.21	2.73	2.28
P54619	AAKG1_HUMAN 5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=1 SV=1	26.40	3.96	3.96	6.93	2.97	3.96	5.94	1.57E-07	4.67E-07	1.18E-06	7.86E-08	5.99E-07	8.09E-07	0.50	3.83	5.17

P30050	RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	57.60	14.00			17.00	2.00	1.00	2.02E-06			2.09E-06	2.10E-07	1.33E-07	1.03	0.10	0.07
O00767	ACOD_HUMAN Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2	13.90	2.00	1.00	1.00	2.00	1.00	1.00	9.30E-08	1.08E-07	1.21E-07	4.88E-08	1.22E-07	8.85E-08	0.52	1.31	0.95
O95163	ELP1_HUMAN Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	12.60	1.00	7.00	9.00	3.00	8.00	5.00	9.30E-09	6.56E-08	8.33E-08	1.23E-08	5.07E-08	6.34E-08	1.32	5.45	6.82
K7EIN2	K7EIN2_HUMAN Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=4 SV=1	36.90	6.97	1.00	2.99	4.98	3.00	2.00	5.30E-07	1.58E-07	4.57E-07	2.98E-07	3.48E-07	2.95E-07	0.56	0.66	0.56
P56192	SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	22.20	6.94	22.81	23.80	9.91	18.85	18.85	1.02E-07	3.73E-07	3.41E-07	1.29E-07	2.60E-07	2.79E-07	1.27	2.56	2.75
Q96QK1	VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	8.50		5.00	5.00		4.00	7.00		6.80E-08	7.30E-08		6.01E-08	1.15E-07		Sample 2 Only	Sample 3 Only
Q96QR8	PURB_HUMAN Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3	10.30	3.00		2.00	1.00	1.00	2.00	4.06E-08		5.33E-08	1.93E-08	8.29E-09	8.99E-08	0.47	0.20	2.21
P46940	IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	47.30	63.95	92.85	78.89	66.91	60.90	81.87	2.66E-07	7.35E-07	4.81E-07	3.50E-07	3.85E-07	4.91E-07	1.31	1.45	1.84
P13639	EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	42.90	12.00	32.00	34.00	12.00	37.00	33.00	2.38E-07	8.98E-07	9.37E-07	2.13E-07	6.81E-07	8.28E-07	0.89	2.86	3.48
P61163	ACTZ_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	29.50	1.99	7.93	5.95	1.99	5.96	6.94	2.25E-08	9.11E-07	8.96E-07	2.84E-08	9.83E-07	1.18E-06	1.27	43.73	52.51
O00571	DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	29.60	17.00	4.00	9.00	18.00	6.00	9.00	5.36E-07	2.03E-07	2.02E-07	4.64E-07	1.07E-07	2.06E-07	0.87	0.20	0.38
O43592	XPOT_HUMAN Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	5.60	5.00	3.00	2.00	3.00	2.00	2.00	6.51E-08	4.59E-08	3.44E-08	3.39E-08	3.35E-08	4.97E-08	0.52	0.51	0.76
P12236	ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	53.00	5.00	3.50	5.50	5.00	3.50	4.50	7.08E-07	7.63E-07	1.64E-06	3.64E-07	6.44E-07	1.60E-06	0.51	0.91	2.26
P21266	GSTM3_HUMAN Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	76.00	32.96	32.96	33.97	28.97	32.96	36.95	5.40E-06	1.58E-05	1.58E-05	4.57E-06	1.47E-05	1.26E-05	0.85	2.72	2.34
P35908	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	95.60	9.00	16.00	14.00	9.00	13.00	11.00	3.02E-07	1.13E-06	9.37E-07	4.85E-07	8.10E-07	6.87E-07	1.61	2.69	2.28
Q5XUX0	FBX31_HUMAN F-box only protein 31 OS=Homo sapiens GN=FBXO31 PE=1 SV=2	24.60	12.00	13.00	13.00	9.00	16.00	15.00	3.06E-07	8.62E-07	8.48E-07	1.87E-07	7.58E-07	7.40E-07	0.61	2.48	2.42
Q71U36	TBA1A_HUMAN Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	82.00	2.94	0.98	2.96	1.96	2.94	2.95	6.48E-07	8.33E-07	1.19E-06	4.23E-07	9.18E-07	9.00E-07	0.65	1.42	1.39
P25705	ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	67.10	60.92	89.36	82.56	60.89	87.42	93.36	3.66E-06	2.05E-05	1.93E-05	3.11E-06	1.83E-05	1.62E-05	0.85	5.01	4.44
Q9Y230	RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	50.10	31.75	14.89	20.85	20.84	12.92	23.81	1.44E-06	1.38E-06	2.14E-06	8.59E-07	1.18E-06	2.16E-06	0.60	0.82	1.50
P06493	CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	64.00	12.90	14.92	18.90	13.91	16.91	12.94	8.05E-07	2.75E-06	2.96E-06	6.53E-07	2.58E-06	2.30E-06	0.81	3.21	2.86
Q8NC69	KCTD6_HUMAN BTB/POZ domain-containing protein KCTD6 OS=Homo sapiens GN=KCTD6 PE=2 SV=2	87.80	83.50	54.00	66.00	89.50	60.50	68.50	3.78E-05	5.94E-05	7.84E-05	2.94E-05	5.60E-05	6.86E-05	0.78	1.48	1.81
E9PF10	E9PF10_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=2 SV=1	7.40	1.00	2.00	2.00	1.00		4.00	6.39E-09	1.28E-08	1.15E-08	3.17E-09		2.09E-08	0.50	Control 1 Only	3.27
P60174	TPIS_HUMAN Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	15.00	2.00	1.00		2.00	3.00		7.84E-08	8.76E-08		6.03E-08	7.48E-08		0.77	0.95	Control 1 Only

P17858	K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	55.30	41.00	55.50	66.50	39.00	54.50	64.00	1.09E-06	2.12E-06	2.49E-06	8.76E-07	1.87E-06	2.10E-06	0.80	1.72	1.92
Q96KP4	CNDP2_HUMAN Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	11.40	1.99	3.98	2.00	1.99	2.99	2.99	1.76E-08	1.80E-07	1.79E-07	3.73E-08	1.29E-07	1.44E-07	2.11	7.33	8.17
O75643	U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	24.20	79.00			63.00	1.00	1.00	3.01E-07			2.45E-07	1.53E-09	1.94E-09	0.82	0.01	0.01
F5H7I0	F5H7I0_HUMAN BTB/POZ domain-containing protein KCTD6 (Fragment) OS=Homo sapiens GN=KCTD6 PE=2 SV=1	86.50	9.00	5.00	5.00	8.00	6.00	7.00	9.26E-06	1.23E-05	1.32E-05	6.87E-06	1.02E-05	1.31E-05	0.74	1.10	1.42
P53007	TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	18.00	5.00	3.00	4.00	4.00	3.00	4.00	2.84E-07	3.77E-07	6.00E-07	1.83E-07	3.43E-07	5.33E-07	0.64	1.21	1.88
Q7Z6Z7	HUWE1_HUMAN E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	2.90	0.99	5.94	4.95	0.99	6.93	5.94	9.16E-10	7.99E-09	4.93E-09	7.87E-10	8.20E-09	8.35E-09	0.86	8.96	9.12
B4E1G6	B4E1G6_HUMAN Galactokinase OS=Homo sapiens GN=GALK1 PE=2 SV=1	42.10	6.99	7.99	11.97	10.99	13.98	13.98	2.61E-07	7.26E-07	1.06E-06	2.67E-07	9.62E-07	1.18E-06	1.02	3.69	4.53
F8W9B4	F8W9B4_HUMAN Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=2 SV=1	38.00	6.99	2.99	6.99	7.00	6.98	8.98	4.04E-07	3.43E-07	1.05E-06	2.51E-07	8.56E-07	1.01E-06	0.62	2.12	2.50
P58107	EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	64.50	145.50	1.00	0.50	120.00	0.50	3.50	5.58E-07	4.44E-10	2.95E-10	4.62E-07	3.48E-10	4.20E-09	0.83	0.00	0.01
P24539	AT5F1_HUMAN ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2	26.20	3.00	5.00	5.00	6.00	9.00	5.00	1.71E-07	8.94E-07	1.01E-06	3.02E-07	1.48E-06	6.53E-07	1.77	8.69	3.82
P36578	RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	26.50	13.93	1.00	2.00	13.93	2.00	7.98	5.85E-07	9.31E-09	3.22E-08	5.99E-07	1.89E-08	1.26E-07	1.02	0.03	0.22
P05089	ARGI1_HUMAN Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	23.90	5.00	3.00	5.00	4.00	4.00	2.00	3.58E-08	5.18E-08	9.79E-08	6.03E-08	1.13E-07	4.97E-08	1.68	3.15	1.39
Q14204	DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	26.50	65.00	92.00	75.00	77.00	64.00	106.00	6.82E-08	1.63E-07	1.12E-07	9.76E-08	1.26E-07	1.86E-07	1.43	1.85	2.72
P05141	ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	64.40	8.50	4.50	6.50	7.50	5.50	9.00	7.85E-07	9.40E-07	1.64E-06	4.80E-07	1.16E-06	2.27E-06	0.61	1.47	2.89
P38646	GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	77.20	155.87	291.65	322.66	138.89	305.66	328.66	1.18E-05	3.57E-05	3.65E-05	7.72E-06	3.18E-05	3.46E-05	0.66	2.70	2.94
Q92616	GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	9.80	11.00	8.00	9.00	8.00	5.00	8.00	3.78E-08	2.99E-08	4.78E-08	2.75E-08	2.97E-08	3.81E-08	0.73	0.79	1.01
P07437	TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	84.20	67.32	47.52	47.52	73.26	52.47	49.50	1.32E-05	2.83E-05	2.56E-05	1.17E-05	2.45E-05	2.30E-05	0.89	1.85	1.74
Q4VXZ8	Q4VXZ8_HUMAN Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=2 SV=1	12.70			2.00	1.00	1.00	2.00			1.22E-07	9.89E-09	2.20E-08	6.97E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4DF41	B4DF41_HUMAN DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=2 SV=1	13.90	7.99	8.99	7.99	7.98	5.99	5.99	2.41E-08	6.07E-08	6.25E-08	3.75E-08	4.29E-08	4.20E-08	1.56	1.78	1.74
B4DGU4	B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1	14.10	3.50	1.00	3.00	3.50	2.50	4.00	3.32E-08	5.98E-09	2.33E-08	2.53E-08	2.13E-08	2.89E-08	0.76	0.64	0.87
Q9Y678	COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	11.90	1.00	4.00	5.00	1.00	4.00	3.99	2.64E-08	7.05E-08	1.61E-07	2.34E-08	1.12E-07	1.71E-07	0.89	4.22	6.49
P62888	RL30_HUMAN 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	66.10	9.97			9.97	1.99	1.99	1.90E-06			1.47E-06	3.09E-07	4.29E-07	0.78	0.16	0.23
Q9H3P7	GCP60_HUMAN Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4	10.00			3.00		1.00	2.00			5.39E-08		1.33E-08	3.12E-08		Sample 2 Only	Sample 3 Only

P10398	ARAF_HUMAN Serine/threonine-protein kinase A-Raf OS=Homo sapiens GN=ARAF PE=1 SV=2	5.60	2.04	1.56	2.56	3.60	1.56	2.08	3.41E-08	7.07E-08	1.05E-07	4.19E-08	6.68E-08	6.67E-08	1.23	1.96	1.96
Q8IYB1	M21D2_HUMAN Protein MB21D2 OS=Homo sapiens GN=MB21D2 PE=1 SV=3	28.70	7.00	7.00	10.00	4.00	9.00	11.00	1.51E-07	5.06E-07	6.06E-07	7.08E-08	4.85E-07	5.26E-07	0.47	3.22	3.49
P46109	CRKL_HUMAN Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1	39.30	10.00	6.00	12.00	8.00	10.00	11.00	5.09E-07	1.53E-06	2.08E-06	3.00E-07	1.50E-06	1.77E-06	0.59	2.94	3.49
P52597	HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	44.30	30.00	10.00	17.00	28.00	9.00	15.00	1.76E-06	1.14E-06	1.24E-06	1.54E-06	7.84E-07	1.27E-06	0.87	0.45	0.72
J3KNW4	J3KNW4_HUMAN Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=2 SV=1	43.70	11.00	13.00	21.00	9.00	14.00	20.00	1.07E-06	2.54E-06	4.20E-06	7.45E-07	2.69E-06	3.39E-06	0.70	2.51	3.16
P33993	MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	58.70	19.89	56.79	68.74	16.93	62.78	60.81	5.38E-07	1.85E-06	2.46E-06	3.89E-07	1.86E-06	1.97E-06	0.72	3.47	3.67
P68371	TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	83.10	7.00	7.00	7.00	6.00	8.00	9.00	2.51E-06	5.50E-06	5.48E-06	2.08E-06	4.82E-06	4.96E-06	0.83	1.92	1.98
P26641	EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	36.60	17.00	25.00	26.00	16.00	28.00	28.00	8.47E-07	3.85E-06	3.67E-06	6.35E-07	3.23E-06	3.47E-06	0.75	3.81	4.10
P02786	TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	52.00	35.75	149.10	136.14	33.78	139.16	122.24	5.81E-07	7.04E-06	6.07E-06	5.00E-07	6.04E-06	5.52E-06	0.86	10.40	9.51
Q15645	PCH2_HUMAN Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	34.50	24.92	23.91	25.89	19.93	23.89	21.93	8.18E-07	2.46E-06	2.90E-06	6.79E-07	3.05E-06	1.68E-06	0.83	3.73	2.06
Q9NZB2	F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	2.80	1.00	2.00	1.00	1.00	2.00	2.00	4.56E-09	6.30E-09	6.28E-09	4.06E-09	5.70E-09	1.09E-08	0.89	1.25	2.39
P41091	IF2G_HUMAN Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	32.40	5.96	3.96	3.97	5.95	1.98	8.95	1.84E-07	3.11E-07	2.97E-07	1.84E-07	1.27E-07	6.05E-07	1.00	0.69	3.29
P20700	LMNB1_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	68.10	65.49		1.00	71.49		1.00	2.25E-06		3.65E-08	2.61E-06		6.48E-09	1.16	Control 1 Only	0.00
P52272	HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	71.90	50.55			54.47		6.94	2.11E-06			1.75E-06		8.63E-08	0.83	Control 1 Only	0.04
Q9Y285	SYFA_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3	40.00	0.98	11.83	16.75	0.99	15.77	22.65	8.36E-10	1.32E-06	1.85E-06	2.62E-08	1.64E-06	1.95E-06	31.29	1964.11	2331.34
P47755	CAZA2_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	27.30	4.00	3.00	4.00	4.00	4.00	4.00	2.33E-07	6.02E-07	7.57E-07	1.91E-07	5.77E-07	6.14E-07	0.82	2.48	2.64
Q9NTJ3	SMC4_HUMAN Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2	14.60	10.98	9.99	9.99	4.00	11.98	10.99	3.65E-08	4.29E-08	4.55E-08	1.69E-08	7.66E-08	5.33E-08	0.46	2.10	1.46
P68032	ACTC_HUMAN Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	48.80	16.66	10.79	9.80	24.50	9.81	10.79	1.42E-06	4.19E-06	3.11E-06	2.79E-06	1.52E-06	3.38E-06	1.97	1.07	2.39
Q9BTE3	MCMBP_HUMAN Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2	21.20	6.00	13.00	17.00	8.00	13.00	14.00	1.52E-07	5.81E-07	5.96E-07	1.60E-07	4.60E-07	5.33E-07	1.05	3.03	3.51
P63151	2ABA_HUMAN Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1	8.10		2.98	1.99		2.98	2.98		2.60E-07	2.55E-07		2.62E-07	3.34E-07		Sample 2 Only	Sample 3 Only
G3V1R4	G3V1R4_HUMAN NOL1/NOP2/Sun domain family, member 2, isoform CRA_b OS=Homo	12.40		3.00	5.00		3.00	3.00		4.98E-08	6.22E-08		4.35E-08	5.15E-08		Sample 2 Only	Sample 3 Only

	sapiens GN=NSUN2 PE=2 SV=1																
Q14126	DSG2_HUMAN Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2	20.00	18.00			13.00		1.00	1.35 E-07			1.09 E-07		6.07 E-09	0.80	Control 1 Only	0.04
P62269	RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	57.90	18.00	1.00		19.00		1.00	2.51 E-06	1.90 E-08		2.03 E-06		1.84 E-07	0.81	Control 1 Only	0.07
Q0VDF9	HSP7E_HUMAN Heat shock 70 kDa protein 14 OS=Homo sapiens GN=HSPA14 PE=1 SV=1	4.50			2.00		2.00	1.00			5.60 E-08		3.82 E-08	9.28 E-09		Sample 2 Only	Sample 3 Only
B4DFA2	B4DFA2_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1	8.70		1.00	4.00		1.00	3.00		8.49 E-09	6.91 E-08		1.46 E-08	5.11 E-08		Sample 2 Only	Sample 3 Only
C9JJ19	C9JJ19_HUMAN 28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=2 SV=2	16.50	6.00	1.00	2.00	5.00	2.00	2.00	5.21 E-07	7.93 E-08	2.20 E-07	3.31 E-07	1.35 E-07	2.46 E-07	0.63	0.26	0.47
Q9Y266	NUDC_HUMAN Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	10.60	1.00	1.00	1.00	2.00	1.00	1.00	3.15 E-08	1.23 E-07	1.35 E-07	4.32 E-08	8.37 E-08	1.22 E-07	1.37	2.65	3.87
H0Y818	H0Y818_HUMAN DNA mismatch repair protein Mlh1 (Fragment) OS=Homo sapiens GN=MLH1 PE=4 SV=1	10.90	0.99	2.97	2.96	0.99	3.96	4.94	1.03 E-08	1.03 E-07	2.78 E-08	6.88 E-09	7.06 E-08	8.68 E-08	0.67	6.83	8.39
P62917	RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	33.50	15.80	0.99	0.99	20.74	0.99	1.98	2.04 E-06	1.46 E-07	2.17 E-07	2.15 E-06	1.98 E-07	3.78 E-07	1.06	0.10	0.18
Q9NPD3	EXOS4_HUMAN Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3	18.80	1.00	2.00	2.00		3.00	2.00	3.92 E-08	3.56 E-07	3.34 E-07		3.99 E-07	2.34 E-07	Control 1 Only	10.18	5.96
J3KN55	J3KN55_HUMAN Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial OS=Homo sapiens GN=MMAB PE=2 SV=1	12.60	2.00			1.00		1.00	1.25 E-07			6.81 E-08		7.79 E-08	0.55	Control 1 Only	0.62
H0Y566	H0Y566_HUMAN BTB/POZ domain-containing protein KCTD3 (Fragment) OS=Homo sapiens GN=KCTD3 PE=4 SV=1	8.50		1.00	1.00		1.00	2.00		5.58 E-08	4.11 E-08		1.10 E-08	7.15 E-08		Sample 2 Only	Sample 3 Only
C9JAB2	C9JAB2_HUMAN Serine/arginine-rich-splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=2 SV=1	31.10	5.50			4.50	1.00	1.00	4.17 E-07			4.00 E-07	4.07 E-08	3.99 E-08	0.96	0.10	0.10
P39656	OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	16.40	3.98	3.99	6.97	3.98	6.96	5.98	9.60 E-08	3.38 E-07	5.59 E-07	6.24 E-08	4.55 E-07	3.49 E-07	0.65	4.74	3.64
P61353	RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	55.10	17.90			15.89	0.99	1.99	3.82 E-06			2.65 E-06	2.13 E-07	5.13 E-07	0.69	0.06	0.13
P01833	PIGR_HUMAN Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4	4.10		2.00	1.00	1.00	1.00	1.00		1.82 E-08	1.02 E-08	9.85 E-09	6.02 E-09	8.33 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P31153	METK2_HUMAN S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	25.30	4.00	10.98	12.98	5.00	13.97	13.97	1.54 E-07	1.96 E-06	2.18 E-06	1.73 E-07	2.00 E-06	1.63 E-06	1.12	12.99	10.60
P50990	TCPQ_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	30.50	13.86	4.95	8.92	13.86	7.92	10.89	4.60 E-07	3.08 E-07	6.40 E-07	3.40 E-07	3.38 E-07	5.58 E-07	0.74	0.74	1.21
P11021	GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	78.40	254.00	525.00	539.00	223.00	569.00	552.00	3.18 E-05	1.19 E-04	1.20 E-04	2.10 E-05	1.08 E-04	1.18 E-04	0.66	3.39	3.72
F5H8J2	F5H8J2_HUMAN Uncharacterized protein OS=Homo sapiens GN=P4HB PE=3 SV=1	26.80	4.95	2.96	6.92	4.94	7.91	5.94	7.59 E-08	2.02 E-07	3.47 E-07	8.39 E-08	2.41 E-07	2.20 E-07	1.11	3.17	2.91
G8JLB6	G8JLB6_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	30.30	10.72	1.94	2.91	11.70	1.94	3.88	4.83 E-07	1.16 E-07	2.12 E-07	4.10 E-07	1.08 E-07	1.92 E-07	0.85	0.22	0.40

Q9NXV2	KCTD5_HUMAN BTB/POZ domain-containing protein KCTD5 OS=Homo sapiens GN=KCTD5 PE=1 SV=1	12.00	1.00		2.00	2.00	1.00	2.00	4.96 E-08		2.03 E-07	4.28 E-08	9.74 E-08	1.50 E-07	0.86	1.96	3.01
P07686	HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	16.50	5.97	2.99	5.95	5.96	3.00	3.98	1.36 E-07	2.28 E-07	2.67 E-07	1.38 E-07	1.64 E-07	2.50 E-07	1.02	1.21	1.84
H7C1F6	H7C1F6_HUMAN ES1 protein homolog, mitochondrial (Fragment) OS=Homo sapiens GN=C21orf33 PE=4 SV=1	27.40		0.99	0.99	1.99		1.99		7.14 E-08	7.89 E-08	5.31 E-08		1.20 E-07	Sample 1 Only		Sample 3 Only
P62277	RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	45.00	15.94			16.92	1.00	1.00	2.55 E-06			2.36 E-06	2.51 E-07	2.55 E-07	0.92	0.10	0.10
P04264	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	73.60	246.00	272.00	297.50	248.50	298.00	262.00	3.17 E-05	7.36 E-05	9.32 E-05	3.05 E-05	1.21 E-04	6.51 E-05	0.96	3.83	2.05
Q9NP72	RAB18_HUMAN Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1	30.10	5.95	1.98	0.99	4.95	0.99	1.99	3.69 E-07	2.05 E-07	1.19 E-07	2.38 E-07	1.36 E-07	2.34 E-07	0.65	0.37	0.63
P49327	FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	53.10	176.00	247.00	218.00	134.00	173.00	224.00	9.11 E-07	2.01 E-06	1.52 E-06	7.14 E-07	1.51 E-06	1.74 E-06	0.78	1.65	1.91
P12004	PCNA_HUMAN Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	65.10	11.00	8.00	8.00	13.00	10.00	7.00	6.87 E-07	1.43 E-06	1.18 E-06	5.87 E-07	1.32 E-06	1.03 E-06	0.85	1.93	1.49
Q5D862	FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	6.60	8.00	9.00	11.00	11.00	11.00	9.00	2.73 E-08	4.66 E-08	6.08 E-08	2.02 E-08	6.63 E-08	3.04 E-08	0.74	2.42	1.11
B3KSQ1	B3KSQ1_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=2 SV=1	12.00	4.00		1.00	2.00	1.00	1.00	9.39 E-08		1.82 E-07	4.36 E-08	1.26 E-07	1.45 E-07	0.46	1.34	1.54
H0Y368	H0Y368_HUMAN Dolichol-phosphate mannosyltransferase (Fragment) OS=Homo sapiens GN=DPM1 PE=4 SV=1	66.90	18.89	7.98	12.95	24.87	16.94	12.95	1.57 E-06	1.88 E-06	2.54 E-06	1.60 E-06	2.87 E-06	2.19 E-06	1.02	1.83	1.39
E5RIF2	E5RIF2_HUMAN Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=2 SV=1	5.70	1.49	0.99	1.98	0.50	0.99	1.98	1.08 E-08	1.10 E-08	9.10 E-09	2.62 E-09	9.65 E-09	1.42 E-08	0.24	0.90	1.31
D3DQ30	D3DQ30_HUMAN HCG40295, isoform CRA_d OS=Homo sapiens GN=TTC39A PE=2 SV=1	8.20	2.97	1.98	0.99	0.99	0.99	1.98	3.08 E-08	7.19 E-08	1.56 E-08	7.13 E-09	3.84 E-08	5.74 E-08	0.23	1.25	1.86
Q99714	HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	73.60	27.80	25.79	23.82	28.80	26.80	26.81	3.00 E-06	6.38 E-06	5.49 E-06	2.35 E-06	5.40 E-06	5.69 E-06	0.78	1.80	1.90
F8WEF7	F8WEF7_HUMAN Deleted in malignant brain tumors 1 protein OS=Homo sapiens GN=DMBT1 PE=2 SV=1	7.30	2.00	3.00	2.00	2.00	2.00	1.00	2.43 E-08	3.26 E-08	2.19 E-08	1.74 E-08	2.57 E-08	2.53 E-08	0.72	1.06	1.04
P60228	EIF3E_HUMAN Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	4.30		1.98	1.98		1.98	1.98		1.28 E-07	1.12 E-07		1.23 E-07	1.49 E-07		Sample 2 Only	Sample 3 Only
Q14694	UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2	4.00	0.99	0.99	2.97		1.98	2.97	4.71 E-09	2.11 E-08	3.88 E-08		2.12 E-08	3.46 E-08	Control 1 Only	4.49	7.34
P81605	DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	42.70	5.00	9.00	7.00	8.00	4.00	9.00	4.27 E-07	1.12 E-06	9.92 E-07	3.73 E-07	7.40 E-07	1.16 E-06	0.87	1.73	2.72
F5GX33	F5GX33_HUMAN Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=2 SV=1	14.30	1.00	1.00	2.00		1.00	4.00	2.32 E-08	2.25 E-08	3.20 E-08		1.72 E-08	7.13 E-08	Control 1 Only	0.74	3.07
P30040	ERP29_HUMAN Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	41.00	3.00	5.00	6.00	11.00	5.00	5.00	1.54 E-07	6.24 E-07	1.01 E-06	5.13 E-07	5.51 E-07	5.34 E-07	3.34	3.59	3.48
Q00325	MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	38.50	18.95	10.98	18.95	20.95	18.94	26.92	1.76 E-06	3.93 E-06	5.87 E-06	1.37 E-06	5.19 E-06	6.15 E-06	0.78	2.95	3.49

Q96TA1	NIBL1_HUMAN Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3	7.00		2.00	5.00		5.00	3.00		2.23E-08	6.36E-08		4.23E-08	3.28E-08		Sample 2 Only	Sample 3 Only
P62424	RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	41.70	17.97	0.99	0.99	21.95		2.99	1.17E-06	1.08E-08	6.61E-09	1.20E-06		1.21E-07	1.03	Control 1 Only	0.10
P08729	K2C7_HUMAN Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	73.60	79.50		3.00	74.50	3.00	7.00	8.49E-06		6.07E-08	7.38E-06	6.88E-08	3.10E-07	0.87	0.01	0.04
Q13155	AIMP2_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2	23.10	3.00	6.00	6.00	3.00	6.00	8.00	1.50E-07	4.98E-07	7.91E-07	1.06E-07	6.75E-07	8.17E-07	0.70	4.51	5.45
P54886	P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	18.50	3.00	9.00	12.00	3.00	8.00	8.00	8.61E-08	9.91E-07	8.25E-07	8.92E-08	9.26E-07	6.94E-07	1.04	10.75	8.06
P62633	CNBP_HUMAN Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	31.80	4.96	1.00	2.98	2.98	1.98	3.97	3.34E-07	1.26E-07	2.23E-07	1.65E-07	1.97E-07	4.00E-07	0.49	0.59	1.20
Q8WVX9	FACR1_HUMAN Fatty acyl-CoA reductase 1 OS=Homo sapiens GN=FAR1 PE=1 SV=1	15.00	5.00	3.00	5.00	5.00	5.00	6.00	1.35E-07	2.91E-07	3.03E-07	1.16E-07	2.37E-07	2.98E-07	0.86	1.76	2.21
J3KN39	J3KN39_HUMAN NACHT, LRR and PYD domains-containing protein 2 OS=Homo sapiens GN=NLRP2 PE=2 SV=1	12.10		6.00	6.00		8.00	7.00		7.40E-08	7.45E-08		9.80E-08	6.94E-08		Sample 2 Only	Sample 3 Only
Q13608	PEX6_HUMAN Peroxisome assembly factor 2 OS=Homo sapiens GN=PEX6 PE=1 SV=2	3.70		1.00	1.00		1.00	1.00		3.27E-09	5.90E-09		5.07E-09	5.55E-09		Sample 2 Only	Sample 3 Only
Q96AB3	ISOC2_HUMAN Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1	47.40	2.98	1.00	2.00	2.98	2.99	2.98	2.16E-07	3.56E-07	3.82E-07	1.56E-07	3.95E-07	5.05E-07	0.72	1.83	2.34
P22695	QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	49.00	9.91	26.72	30.68	10.89	26.70	32.67	1.59E-07	3.21E-06	3.14E-06	2.43E-07	2.60E-06	3.09E-06	1.52	16.30	19.39
Q08211	DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	15.40	11.00	12.00	9.00	11.00	7.00	11.00	6.41E-08	1.07E-07	9.09E-08	7.85E-08	4.15E-08	1.14E-07	1.23	0.65	1.78
Q99456	K1C12_HUMAN Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	10.70	1.00	3.00	4.00	1.00	4.00	3.00	5.14E-09	3.87E-08	3.07E-08	5.45E-09	3.50E-08	2.55E-08	1.06	6.80	4.96
Q16401	PSMD5_HUMAN 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3	25.80	5.00	3.00	8.00	6.00	5.00	8.00	1.82E-07	2.73E-07	5.45E-07	1.59E-07	3.17E-07	4.26E-07	0.88	1.74	2.34
B3KY94	B3KY94_HUMAN CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Homo sapiens GN=CDIPT PE=2 SV=1	13.70	2.00			1.00		1.00	1.41E-07			4.16E-08		8.43E-08	0.30	Control 1 Only	0.60
Q92804	RBP56_HUMAN TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1	13.10	5.94			6.93		0.99	2.05E-07			1.70E-07		1.53E-08	0.83	Control 1 Only	0.07
E9PFW3	E9PFW3_HUMAN AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=2 SV=1	28.60	1.99	6.96	7.97	1.98	6.96	8.94	8.79E-08	5.26E-07	6.45E-07	1.03E-07	5.31E-07	7.37E-07	1.18	6.04	8.38
Q9UBM7	DHCR7_HUMAN 7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	8.60	1.00	2.00	2.00	1.00	2.00	4.00	5.96E-08	2.48E-07	1.98E-07	4.49E-08	2.29E-07	2.79E-07	0.75	3.84	4.69
F8W9U3	F8W9U3_HUMAN Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=2 SV=1	33.70	4.95	0.99	0.99	4.95	0.99	0.99	3.05E-07	1.89E-07	1.82E-07	3.45E-07	2.00E-07	1.92E-07	1.13	0.65	0.63
P05023	AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	5.30		0.99	2.96		2.96	1.98		1.22E-08	3.17E-08		1.83E-08	2.11E-08		Sample 2 Only	Sample 3 Only
Q15046	SYK_HUMAN Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3	13.20		1.00	3.00			3.00		4.60E-09	4.04E-08			4.96E-08			Sample 3 Only

E9PIX6	E9PIX6_HUMAN Protein arginine N-methyltransferase 1 (Fragment) OS=Homo sapiens GN=PRMT1 PE=2 SV=1	30.60	1.00	3.00	4.00	1.00	4.00	6.00	9.61E-08	6.72E-07	7.67E-07	9.02E-08	6.06E-07	9.68E-07	0.94	6.31	10.07
P30101	PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	25.00	5.98	5.98	9.97	9.96	10.96	7.98	2.66E-07	4.18E-07	6.44E-07	2.65E-07	4.89E-07	4.66E-07	1.00	1.84	1.75
E7ETB3	E7ETB3_HUMAN Aspartyl aminopeptidase OS=Homo sapiens GN=DNPEP PE=2 SV=1	27.80	3.93	5.89	7.87	4.92	4.92	7.87	2.32E-07	5.40E-07	8.76E-07	2.04E-07	5.53E-07	7.60E-07	0.88	2.38	3.27
Q04695	K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	66.20	0.99	1.97	19.89	1.98	20.85	3.95	2.21E-09	2.10E-08	8.59E-07	1.43E-08	8.76E-07	6.58E-08	6.48	395.84	29.71
E7EQ69	E7EQ69_HUMAN N-alpha-acetyltransferase 50 OS=Homo sapiens GN=NAA50 PE=2 SV=1	63.10	27.63	13.82	12.82	27.63	20.76	20.74	4.37E-06	3.48E-06	2.64E-06	3.03E-06	4.43E-06	3.75E-06	0.69	1.01	0.86
B1AK13	B1AK13_HUMAN 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (Hydroxymethylglutaricaciduria), isoform CRA_b OS=Homo sapiens GN=HMGCL PE=2 SV=1	16.30	2.00	2.00	4.00	3.00	4.00	4.00	4.71E-08	1.78E-07	5.03E-07	6.87E-08	2.81E-07	4.38E-07	1.46	5.96	9.30
P04183	KITH_HUMAN Thymidine kinase, cytosolic OS=Homo sapiens GN=TK1 PE=1 SV=2	65.40	15.86	11.89	15.86	15.86	13.87	21.83	2.86E-06	3.57E-06	4.75E-06	1.75E-06	3.48E-06	5.21E-06	0.61	1.22	1.82
P28072	PSB6_HUMAN Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	8.80	1.00			1.00	1.00		7.24E-08			4.21E-08	2.40E-08		0.58	0.33	Control 1 Only
C9JJP5	C9JJP5_HUMAN Protein TFG (Fragment) OS=Homo sapiens GN=TFG PE=2 SV=1	14.10	1.00		1.00	1.00		2.00	8.73E-08		1.85E-07	9.18E-08		2.04E-07	1.05	Control 1 Only	2.34
B0UX83	B0UX83_HUMAN HLA-B associated transcript 3, isoform CRA_a OS=Homo sapiens GN=BAG6 PE=4 SV=1	2.50		1.00	0.99			0.99		4.78E-09	9.89E-09			1.29E-08			Sample 3 Only
P62937	PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	79.40	47.47	17.78	15.81	45.51	27.68	18.78	1.29E-05	7.33E-06	6.21E-06	9.82E-06	9.07E-06	5.94E-06	0.76	0.70	0.46
O15397	IPO8_HUMAN Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2	2.10	1.00		2.00	1.00		2.00	7.80E-09		9.70E-09	6.65E-09		9.21E-09	0.85	Control 1 Only	1.18
A0FGR8-2	ESYT2_HUMAN Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2	3.30	1.00	1.00	2.00	1.00	2.00	2.00	3.24E-09	4.05E-09	1.06E-08	3.24E-09	4.45E-09	1.19E-08	1.00	1.38	3.68
P62913	RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	50.60	13.93	2.98	4.98	14.90	6.96	6.97	2.09E-06	3.38E-07	6.34E-07	1.31E-06	1.09E-06	8.66E-07	0.63	0.52	0.41
Q92973	TNPO1_HUMAN Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	5.40	2.98	0.99	3.96	1.98	3.96	3.96	6.51E-08	1.66E-08	8.91E-08	4.50E-08	8.53E-08	5.41E-08	0.69	1.31	0.83
Q96S55	WRIP1_HUMAN ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 PE=1 SV=2	21.20	1.98	5.95	10.93	1.00	8.94	8.94	2.39E-08	1.40E-07	2.73E-07	2.16E-08	1.61E-07	2.23E-07	0.90	6.73	9.32
Q9NQH7	XPP3_HUMAN Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPNPEP3 PE=1 SV=1	19.40	4.00	7.00	7.00	3.00	7.00	8.00	1.25E-07	7.35E-07	5.95E-07	9.16E-08	5.83E-07	6.86E-07	0.73	4.68	5.50
H0Y6C3	H0Y6C3_HUMAN Pyrroline-5-carboxylate reductase 3 (Fragment) OS=Homo sapiens GN=PYCRL PE=2 SV=1	42.50	6.61	2.02	2.53	4.06	2.55	2.53	4.01E-07	3.08E-07	3.17E-07	2.22E-07	4.32E-07	3.05E-07	0.55	1.08	0.76
H0Y4R1	H0Y4R1_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=3 SV=1	50.60	23.50	19.50	20.00	42.50	15.50	20.00	1.42E-06	2.70E-06	2.53E-06	3.14E-06	1.73E-06	2.16E-06	2.21	1.21	1.52
Q9Y3Z3	SAMH1_HUMAN Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2	11.30		2.97	3.96		5.94	2.97		1.33E-07	9.61E-08		1.76E-07	6.93E-08		Sample 2 Only	Sample 3 Only
Q9BW92	SYTM_HUMAN Threonine--tRNA ligase, mitochondrial OS=Homo sapiens GN=TARS2 PE=1 SV=1	3.10	1.00	1.00	1.00			1.00	8.66E-09	7.02E-09	9.36E-09			2.25E-08	Control 1 Only	Control 1 Only	2.59
K7EJ81	K7EJ81_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo	21.50	17.97	3.00	2.00	16.98	2.00	1.00	3.07E-07	2.51E-08	1.18E-08	2.99E-07	1.15E-08	1.10E-08	0.97	0.04	0.04

	sapiens GN=EFTUD2 PE=2 SV=1																
P08727	K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	87.00	464.25	56.42	71.13	458.83	96.58	115.83	3.51E-04	1.08E-05	2.01E-05	3.22E-04	2.78E-05	4.78E-05	0.92	0.08	0.14
P53621	COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	19.90	19.00	29.00	31.00	14.00	31.00	32.00	8.12E-08	2.97E-07	2.84E-07	6.85E-08	2.36E-07	3.18E-07	0.84	2.90	3.91
P27348	1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	18.80		1.00	1.00	1.00	1.00	1.00		1.09E-07	1.22E-07	3.92E-08	1.13E-07	9.42E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E9PFG1	E9PFG1_HUMAN Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=2 SV=1	3.00	4.00	1.00	2.00	2.00	1.00	3.00	1.47E-08	7.23E-09	1.40E-08	1.03E-08	7.58E-09	1.55E-08	0.70	0.52	1.05
J3KN82	J3KN82_HUMAN Methylthioribulose-1-phosphate dehydratase OS=Homo sapiens GN=APIP PE=2 SV=1	36.00	5.00	5.00	5.00	5.00	5.00	5.00	1.76E-07	4.71E-07	4.53E-07	1.35E-07	5.18E-07	3.85E-07	0.77	2.94	2.18
B9ZVX0	B9ZVX0_HUMAN Diaphanous homolog 1 (Drosophila), isoform CRA_a OS=Homo sapiens GN=DIAPH1 PE=2 SV=1	17.90	2.00	27.00	20.99	1.00	18.99	18.00	4.02E-09	1.46E-07	9.94E-08	3.05E-09	1.26E-07	1.05E-07	0.76	31.36	26.13
Q9UL46	PSME2_HUMAN Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	41.80	8.98			7.99		1.00	4.48E-07			4.04E-07		7.07E-08	0.90	Control 1 Only	0.16
O43143	DHX15_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	9.60	5.00		2.00	5.00	1.00	3.00	8.14E-08		3.20E-08	6.51E-08	6.11E-09	3.53E-08	0.80	0.08	0.43
A1L0T0	ILVBL_HUMAN Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2	17.10	3.99	4.96	3.97	5.98	2.98	4.98	4.50E-08	1.74E-07	6.80E-08	3.93E-08	1.15E-07	1.50E-07	0.87	2.55	3.32
B4DLW8	B4DLW8_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=2 SV=1	15.30	3.00		0.50	4.00			9.89E-08		1.03E-08	1.02E-07			1.04	Control 1 Only	Control 1 Only
G5E9V5	G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1	26.00	3.00	4.00	5.00	6.00	6.99	4.99	1.02E-07	4.90E-07	4.51E-07	1.50E-07	5.74E-07	3.74E-07	1.47	5.65	3.68
F5H7M3	F5H7M3_HUMAN Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLAT PE=2 SV=1	5.50	0.99	0.99	2.98		1.98	2.98	1.76E-08	1.26E-08	1.01E-07		3.83E-08	8.48E-08	Control 1 Only	2.18	4.82
Q13616	CUL1_HUMAN Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2	6.10		2.00	4.00	1.00	2.00	2.00		2.91E-08	6.77E-08	7.24E-09	2.84E-08	5.57E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P51571	SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1	30.60	5.00			2.00	1.00	1.00	3.38E-07			9.97E-08	1.38E-07	8.25E-08	0.29	0.41	0.24
P13807	GYS1_HUMAN Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2	6.80		1.00	3.99	1.00	1.99	1.99		1.45E-08	5.55E-08	1.12E-08	1.85E-08	3.64E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P11498	PYC_HUMAN Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2	2.90		1.00	2.00		2.00	2.00		1.28E-08	2.37E-08		1.71E-08	2.17E-08		Sample 2 Only	Sample 3 Only
E5RHW4	E5RHW4_HUMAN Erlin-2 (Fragment) OS=Homo sapiens GN=ERLIN2 PE=2 SV=1	17.80	4.95		0.99	5.95	0.99	0.99	2.94E-07		9.66E-08	2.07E-07	9.06E-08	1.14E-07	0.71	0.31	0.39
E7EPB3	E7EPB3_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=2 SV=1	54.80	8.00	2.00	2.00	10.00	1.00	2.00	3.57E-06	4.16E-07	4.64E-07	3.75E-06	3.79E-07	5.20E-07	1.05	0.11	0.15
H0YEN5	H0YEN5_HUMAN 40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=2 SV=1	39.00	9.90	1.98	2.97	8.91	2.97	3.96	1.01E-06	2.44E-07	3.82E-07	7.65E-07	4.58E-07	4.90E-07	0.76	0.46	0.49

Q8TE77	SSH3_HUMAN Protein phosphatase Slingshot homolog 3 OS=Homo sapiens GN=SSH3 PE=1 SV=2	10.80		4.95	4.96		6.94	3.97		8.51E-08	6.39E-08		9.07E-08	6.65E-08		Sample 2 Only	Sample 3 Only
P05783	K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	87.40	430.91	37.99	56.97	403.92	72.99	93.97	2.25E-04	5.53E-06	1.07E-05	2.08E-04	1.52E-05	2.61E-05	0.93	0.07	0.12
P01834	IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	80.20	7.00	11.00	13.00	4.00	12.00	8.00	8.98E-07	3.90E-06	4.38E-06	5.31E-07	5.03E-06	3.24E-06	0.59	5.60	3.60
Q9BVQ7	SPA5L_HUMAN Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens GN=SPATA5L1 PE=1 SV=2	4.00	2.97		0.99	2.97			1.07E-07		4.20E-09	1.05E-07			0.98	Control 1 Only	Control 1 Only
Q13509	TBB3_HUMAN Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	40.70	10.00	5.00	4.00	9.00	7.00	6.00	5.25E-07	9.01E-07	8.71E-07	2.97E-07	9.66E-07	9.34E-07	0.56	1.84	1.78
K7EJT5	K7EJT5_HUMAN 60S ribosomal protein L22 (Fragment) OS=Homo sapiens GN=RPL22 PE=2 SV=1	51.10	3.00	1.00		3.00	1.00	1.00	2.31E-06	4.54E-07		1.36E-06	5.52E-07	7.44E-07	0.59	0.24	0.32
Q96HS1	PGAM5_HUMAN Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	22.70	4.00			5.00		1.00	2.62E-07			2.50E-07		2.40E-08	0.95	Control 1 Only	0.09
P61978	HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	21.40	5.00		2.00	4.00	1.00	3.00	1.01E-07		9.73E-08	7.44E-08	2.52E-08	1.08E-07	0.74	0.25	1.07
P43490	NAMPT_HUMAN Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	15.70	2.00	2.00	2.00	2.00	3.00	2.00	2.79E-08	1.63E-07	1.74E-07	2.41E-08	1.87E-07	1.38E-07	0.86	6.72	4.96
A8MXP9	A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	31.60	21.63		0.99	23.62		0.99	3.85E-07		3.56E-09	3.97E-07		7.55E-09	1.03	Control 1 Only	0.02
H3BRF5	H3BRF5_HUMAN KIAA1970 protein, isoform CRA_c OS=Homo sapiens GN=EARS2 PE=2 SV=1	5.50	2.00	2.00	1.00		1.00	3.00	1.11E-08	3.98E-08	2.43E-08		1.98E-08	5.16E-08	Control 1 Only	1.78	4.64
B4DR61	B4DR61_HUMAN Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=2 SV=1	7.80	1.98	3.96	2.97	0.99	2.97	3.96	4.15E-08	3.42E-07	2.01E-07	3.34E-08	2.14E-07	3.59E-07	0.81	5.17	8.65
O75367	H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	63.60	51.57			59.52		0.99	6.24E-06			6.41E-06		2.84E-08	1.03	Control 1 Only	0.00
E9PH29	E9PH29_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=2 SV=1	18.50	4.00	2.00	2.00	6.00	2.00	3.00	2.73E-07	3.32E-07	3.96E-07	4.00E-07	3.23E-07	3.11E-07	1.46	1.18	1.14
Q93100	KPBB_HUMAN Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB PE=1 SV=3	3.50		1.00	2.00		1.00	2.00		1.06E-08	1.75E-08		9.05E-09	2.02E-08		Sample 2 Only	Sample 3 Only
Q14980	NUMA1_HUMAN Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2	6.10	6.99	1.00	3.00	1.00	1.00	5.00	7.95E-09	1.26E-09	4.06E-09	1.35E-09	1.69E-09	9.65E-09	0.17	0.21	1.21
P09211	GSTP1_HUMAN Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	61.40	18.86	14.90	17.87	17.87	15.89	20.85	3.27E-06	7.95E-06	9.69E-06	2.42E-06	9.01E-06	1.00E-05	0.74	2.75	3.05
F5H355	F5H355_HUMAN Rab GTPase-binding effector protein 1 OS=Homo sapiens GN=RABEP1 PE=2 SV=1	9.80		4.00	2.50		3.50	2.00		3.35E-08	2.16E-08		2.97E-08	2.34E-08		Sample 2 Only	Sample 3 Only
P18085	ARF4_HUMAN ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	56.10	5.94		0.99	3.96	1.98	0.99	7.64E-07		1.61E-07	4.11E-07	3.60E-07	1.79E-07	0.54	0.47	0.23
P61981	1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	25.90	2.00	1.00	2.00	2.00	1.00	3.00	1.77E-07	1.52E-07	3.40E-07	1.33E-07	1.85E-07	3.32E-07	0.75	1.04	1.87
J3QT28	J3QT28_HUMAN Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=2 SV=1	18.70	0.99	0.99	1.98	0.99		3.96	3.63E-08	1.61E-07	1.98E-07	2.24E-08		3.61E-07	0.62	Control 1 Only	9.97

A8MUB1	A8MUB1_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1	58.20	8.99	7.00	6.99	6.99	8.99	7.98	7.62 E-07	1.91 E-06	1.88 E-06	5.81 E-07	2.02 E-06	2.05 E-06	0.76	2.65	2.69
P05787	K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	96.90	628.67	59.49	107.97	618.79	134.74	179.43	3.66 E-04	7.95 E-06	1.74 E-05	3.14 E-04	2.63 E-05	4.43 E-05	0.86	0.07	0.12
Q9NRR5	UBQL4_HUMAN Ubiquilin-4 OS=Homo sapiens GN=UBQLN4 PE=1 SV=2	12.10	2.97		1.98	3.97		1.98	7.23 E-08		4.33 E-08	7.58 E-08		4.29 E-08	1.05	Control 1 Only	0.59
H3BQZ7	H3BQZ7_HUMAN HCG2044799 OS=Homo sapiens GN=hCG_2044799 PE=4 SV=1	21.70	16.00	3.00	3.00	18.00	2.00	4.00	3.34 E-07	2.65 E-08	3.73 E-08	3.33 E-07	1.51 E-08	5.91 E-08	1.00	0.05	0.18
M0QZM1	M0QZM1_HUMAN Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens GN=HNRNPM PE=4 SV=1	77.80	13.00			12.00		1.00	1.04 E-06			9.79 E-07		3.71 E-08	0.94	Control 1 Only	0.04
Q7L576	CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	13.60	0.97	9.82	8.87	1.00	8.86	9.83	7.02 E-09	8.39 E-08	8.43 E-08	4.27 E-09	7.92 E-08	8.72 E-08	0.61	11.28	12.42
P18827	SDC1_HUMAN Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3	11.90	5.00		2.00	4.00		2.00	2.48 E-07		1.73 E-08	1.95 E-07		6.39 E-08	0.79	Control 1 Only	0.26
Q9UKM9-2	RALY_HUMAN Isoform 1 of RNA-binding protein Raly OS=Homo sapiens GN=RALY	52.40	35.34			48.15		1.95	4.50 E-06			4.33 E-06		8.52 E-08	0.96	Control 1 Only	0.02
Q9Y6Q5	AP1M2_HUMAN AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2 PE=1 SV=4	43.50	1.50	3.99	6.49	1.00	4.99	7.99	4.90 E-08	4.08 E-07	6.45 E-07	3.33 E-08	4.04 E-07	6.83 E-07	0.68	8.25	13.95
Q7Z3Y8	K1C27_HUMAN Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	19.60		3.98	4.98	6.98	1.00	2.99		6.51 E-08	1.01 E-07	8.32 E-08	1.91 E-08	6.09 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7ETK5	E7ETK5_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=2 SV=1	33.70	7.50	5.50	5.00	11.50	4.50	5.00	8.55 E-07	1.15 E-06	1.06 E-06	1.49 E-06	7.33 E-07	8.86 E-07	1.75	0.86	1.04
F8VPD4	F8VPD4_HUMAN CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1	31.90	48.00	65.00	53.00	28.00	52.00	55.00	1.77 E-07	3.78 E-07	3.13 E-07	1.19 E-07	3.99 E-07	3.38 E-07	0.67	2.26	1.91
B7Z955	B7Z955_HUMAN 6-phosphofructo-2-kinase OS=Homo sapiens GN=PFKFB3 PE=2 SV=1	13.40		1.98	0.99		1.00	1.99		8.59 E-08	9.40 E-09		4.13 E-08	5.27 E-08		Sample 2 Only	Sample 3 Only
P67809	YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	70.70	21.78	11.88	6.93	21.78	11.88	10.89	1.26 E-06	8.68 E-07	5.05 E-07	1.19 E-06	7.75 E-07	6.42 E-07	0.95	0.62	0.51
O00743	PPP6_HUMAN Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1	19.70	3.96	1.98	1.98	1.98	2.97	3.96	9.48 E-08	1.69 E-07	1.26 E-07	3.55 E-08	1.60 E-07	1.90 E-07	0.37	1.69	2.01
O14828	SCAM3_HUMAN Secretory carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 PE=1 SV=3	9.00	1.00	1.00	1.00	1.00	2.00	1.00	2.18 E-08	9.38 E-08	1.08 E-07	2.85 E-08	1.11 E-07	8.16 E-08	1.31	5.08	3.75
P35250	RFC2_HUMAN Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3	12.20	3.00		1.00	2.00	1.00	1.00	9.49 E-08		1.05 E-07	5.22 E-08	6.59 E-08	8.36 E-08	0.55	0.69	0.88
P22087	FBRL_HUMAN rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2	46.70	21.81	0.99	2.97	22.80	2.97	2.97	1.72 E-06	3.97 E-08	2.63 E-07	1.63 E-06	1.75 E-07	2.30 E-07	0.95	0.10	0.13
E7EWK3	E7EWK3_HUMAN Probable ATP-dependent RNA helicase DHX36 (Fragment) OS=Homo sapiens GN=DHX36 PE=2 SV=1	9.90	1.00	3.00	3.00		6.00	3.00	6.26 E-09	2.07 E-08	2.08 E-08		2.48 E-08	2.22 E-08	Control 1 Only	3.96	3.54
E9PC52	E9PC52_HUMAN Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=2 SV=1	14.20	1.00		4.93	2.96	1.98	3.96	4.18 E-08		4.47 E-07	7.93 E-08	1.52 E-07	2.54 E-07	1.90	3.63	6.08
Q8N1F7	NUP93_HUMAN Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2	9.80	0.98	1.97	4.95	0.98	3.95	5.93	8.82 E-09	2.08 E-08	6.31 E-08	5.81 E-09	3.45 E-08	5.30 E-08	0.66	3.91	6.01
B7Z4B8	B7Z4B8_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=2 SV=1	5.60	2.97			2.97		0.99	8.72 E-08			7.43 E-08		1.36 E-08	0.85	Control 1 Only	0.16

P62750	RL23A_HUMAN 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	50.00	12.89		0.99	15.86		0.99	1.73E-06		1.27E-07	1.66E-06		1.90E-07	0.96	Control 1 Only	0.11
B8ZZ50	B8ZZ50_HUMAN Eukaryotic translation initiation factor 4E type 2 OS=Homo sapiens GN=EIF4E2 PE=2 SV=1	30.50	2.97	4.95	4.95	1.98	5.94	4.95	4.13E-08	2.69E-07	2.74E-07	2.30E-08	3.00E-07	2.59E-07	0.56	7.27	6.27
P07384	CAN1_HUMAN Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	13.00	2.00	1.00	8.00	1.99	3.99	4.99	2.34E-08	8.52E-09	1.18E-07	2.47E-08	5.71E-08	6.75E-08	1.06	2.45	2.89
Q13085	ACACA_HUMAN Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	25.50	21.79	48.60	46.65	12.86	39.71	51.61	4.29E-08	1.73E-07	1.27E-07	2.35E-08	1.58E-07	1.62E-07	0.55	3.67	3.77
P62258	1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	36.90	4.96	4.95	5.95	7.93	5.94	6.94	2.32E-07	6.06E-07	6.24E-07	3.22E-07	4.63E-07	6.74E-07	1.39	1.99	2.90
E9PAV3	E9PAV3_HUMAN Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=2 SV=1	69.00	8.95	3.00	3.00	9.95	5.98	5.98	1.08E-07	1.10E-07	1.24E-07	9.85E-08	1.05E-07	1.38E-07	0.91	0.97	1.28
P38919	IF4A3_HUMAN Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	49.90	27.89			33.93			1.48E-06			1.93E-06			1.30	Control 1 Only	Control 1 Only
Q9H583	HEAT1_HUMAN HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3	13.70	31.96			19.97			1.36E-07			9.55E-08			0.70	Control 1 Only	Control 1 Only
P62995	TRA2B_HUMAN Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1	35.40	19.87			23.82			1.33E-06			1.73E-06			1.30	Control 1 Only	Control 1 Only
Q6FI13	H2A2A_HUMAN Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3	70.80	12.68			22.42			2.81E-05			4.80E-05			1.70	Control 1 Only	Control 1 Only
Q01546	K22O_HUMAN Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2	51.30			1.00			33.00			1.17E-08			1.07E-06			Sample 3 Only
O00567	NOP56_HUMAN Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4	36.00	16.90			15.89			5.22E-07			4.33E-07			0.83	Control 1 Only	Control 1 Only
Q9UKD2	MRT4_HUMAN mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2	54.00	15.00			17.00			6.13E-07			7.30E-07			1.19	Control 1 Only	Control 1 Only
Q9Y2X3	NOP58_HUMAN Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1	17.40	16.00			14.00			7.06E-07			5.59E-07			0.79	Control 1 Only	Control 1 Only
Q9Y512	SAM50_HUMAN Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3	24.30	16.00			14.00			8.17E-07			6.28E-07			0.77	Control 1 Only	Control 1 Only
P18077	RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	57.30	14.96			14.95			1.98E-06			1.48E-06			0.75	Control 1 Only	Control 1 Only
P61254	RL26_HUMAN 60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	57.20	10.75			16.63			1.54E-06			1.78E-06			1.15	Control 1 Only	Control 1 Only
P40429	RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	39.90	11.97			13.96			1.42E-06			1.64E-06			1.16	Control 1 Only	Control 1 Only
P50402	EMD_HUMAN Emerin OS=Homo sapiens GN=EMD PE=1 SV=1	37.80	12.00			14.00			1.16E-06			1.20E-06			1.04	Control 1 Only	Control 1 Only
M0R117	M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=2 SV=1	57.10	13.87			12.88			2.06E-06			1.44E-06			0.70	Control 1 Only	Control 1 Only
P07305	H10_HUMAN Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	27.30	10.00			14.00			9.75E-07			1.31E-06			1.34	Control 1 Only	Control 1 Only
J9JID7	J9JID7_HUMAN Lamin B2, isoform CRA_a OS=Homo sapiens GN=LMNB2 PE=2 SV=1	21.50	7.50			10.50			1.56E-07			2.30E-07			1.48	Control 1 Only	Control 1 Only
C9JRZ6	C9JRZ6_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=2 SV=1	38.30	11.97			8.98			9.03E-07			6.47E-07			0.72	Control 1 Only	Control 1 Only

P04908	H2A1B_HUMAN Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	70.80	4.95			14.85			2.18 E-06			5.80 E-06			2.65	Control 1 Only	Control 1 Only
Q9Y446	PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	13.30	8.99			9.98			1.39 E-07			1.36 E-07			0.98	Control 1 Only	Control 1 Only
P09493-10	TPM1_HUMAN Isoform 10 of Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1	86.60	2.88			15.35			1.56 E-07			8.22 E-07			5.28	Control 1 Only	Control 1 Only
B1AN48	B1AN48_HUMAN Small proline-rich protein 3 (Fragment) OS=Homo sapiens GN=SPRR3 PE=2 SV=1	70.40						18.00						2.81 E-06			Sample 3 Only
P02452	CO1A1_HUMAN Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	7.90		18.00						3.13 E-07							
O76021	RL1D1_HUMAN Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3	19.20	7.91			9.88			2.12 E-07			3.66 E-07			1.73	Control 1 Only	Control 1 Only
Q6DN03	H2B2C_HUMAN Putative histone H2B type 2-C OS=Homo sapiens GN=HIST2H2BC PE=5 SV=3	28.70	7.98			7.98			1.23 E-06			9.14 E-07			0.74	Control 1 Only	Control 1 Only
P31431	SDC4_HUMAN Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2	32.00	10.00			8.00			3.23 E-07			2.74 E-07			0.85	Control 1 Only	Control 1 Only
P62244	RS15A_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	70.80	8.92			7.93			1.06 E-06			7.18 E-07			0.68	Control 1 Only	Control 1 Only
Q9UMS4	PRP19_HUMAN Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	21.20	9.99			5.99			3.69 E-07			1.52 E-07			0.41	Control 1 Only	Control 1 Only
O15230	LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	4.40	12.00			4.00			1.07 E-08			3.22 E-09			0.30	Control 1 Only	Control 1 Only
P24928	RPB1_HUMAN DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2	8.70	11.00			5.00			2.27 E-08			1.15 E-08			0.51	Control 1 Only	Control 1 Only
B4E241	B4E241_HUMAN Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SFRS3 PE=2 SV=1	37.90	6.50			7.50			2.41 E-06			2.46 E-06			1.02	Control 1 Only	Control 1 Only
B7Z7A3	B7Z7A3_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=2 SV=1	17.50	6.93			7.92			2.10 E-07			1.98 E-07			0.94	Control 1 Only	Control 1 Only
O75340	PDCD6_HUMAN Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	36.60	6.98			7.98			3.75 E-07			3.85 E-07			1.03	Control 1 Only	Control 1 Only
O75955	FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	23.90	6.96			7.95			1.56 E-07			1.49 E-07			0.96	Control 1 Only	Control 1 Only
B5MCF9	B5MCF9_HUMAN Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1	13.00	7.92			5.94			2.12 E-07			1.46 E-07			0.69	Control 1 Only	Control 1 Only
P56537	IF6_HUMAN Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	27.30	8.00			6.00			6.81 E-07			4.58 E-07			0.67	Control 1 Only	Control 1 Only
P62241	RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	32.40	6.00			7.00			4.36 E-07			5.16 E-07			1.18	Control 1 Only	Control 1 Only
J3KTL2	J3KTL2_HUMAN Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=2 SV=1	32.30	5.94			6.93			2.34 E-07			2.33 E-07			1.00	Control 1 Only	Control 1 Only
E7EMK3	E7EMK3_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=2 SV=1	25.20	6.00			7.00			1.45 E-07			1.69 E-07			1.16	Control 1 Only	Control 1 Only
O60306	AQR_HUMAN Intron-binding protein aquarius OS=Homo sapiens GN=AQR PE=1 SV=4	7.50	9.00			4.00			2.51 E-08			9.90 E-09			0.40	Control 1 Only	Control 1 Only

Q9C075	K1C23_HUMAN Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2	24.40	6.98			5.98			1.38 E-07			9.81 E-08			0.71	Control 1 Only	Control 1 Only
P16104	H2AX_HUMAN Histone H2AX OS=Homo sapiens GN=H2AFX PE=1 SV=2	72.00	3.50			6.50			1.53 E-06			2.35 E-06			1.53	Control 1 Only	Control 1 Only
Q9Y277	VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	37.80	6.90			4.93			3.15 E-07			1.37 E-07			0.43	Control 1 Only	Control 1 Only
P21796	VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	30.40	7.00			5.00			3.02 E-07			1.96 E-07			0.65	Control 1 Only	Control 1 Only
O75531	BAF_HUMAN Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1	50.60	4.00			7.00			1.57 E-06			2.11 E-06			1.34	Control 1 Only	Control 1 Only
Q8TDN6	BRX1_HUMAN Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens GN=BRIX1 PE=1 SV=2	20.70	4.00			7.00			1.13 E-07			1.58 E-07			1.40	Control 1 Only	Control 1 Only
P46087	NOP2_HUMAN Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2	11.10	4.99			5.99			9.00 E-08			8.61 E-08			0.96	Control 1 Only	Control 1 Only
P05387	RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	56.50	6.00			5.00			8.27 E-07			5.89 E-07			0.71	Control 1 Only	Control 1 Only
P57053	H2BFS_HUMAN Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2	83.30	4.94			5.93			5.11 E-07			4.35 E-07			0.85	Control 1 Only	Control 1 Only
Q12788	TBL3_HUMAN Transducin beta-like protein 3 OS=Homo sapiens GN=TBL3 PE=1 SV=2	13.50	7.00			4.00			9.26 E-08			5.36 E-08			0.58	Control 1 Only	Control 1 Only
Q92522	H1X_HUMAN Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1	30.50	6.00			4.00			4.35 E-07			2.94 E-07			0.68	Control 1 Only	Control 1 Only
P68431	H31_HUMAN Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	88.20	3.50			3.50			2.11 E-06			1.93 E-06			0.92	Control 1 Only	Control 1 Only
P46783	RS10_HUMAN 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	32.10	3.99			5.99			4.65 E-07			5.62 E-07			1.21	Control 1 Only	Control 1 Only
Q8N257	H2B3B_HUMAN Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3	73.00	4.97			4.97			5.30 E-06			4.65 E-06			0.88	Control 1 Only	Control 1 Only
P62263	RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	18.50	5.00			5.00			9.36 E-07			4.92 E-07			0.52	Control 1 Only	Control 1 Only
P62753	RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	20.90	3.99			5.99			2.75 E-07			3.66 E-07			1.33	Control 1 Only	Control 1 Only
P08708	RS17_HUMAN 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	31.10	3.99			5.98			3.51 E-07			4.29 E-07			1.22	Control 1 Only	Control 1 Only
Q14137	BOP1_HUMAN Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2	9.00	4.98			4.97			1.07 E-07			9.37 E-08			0.88	Control 1 Only	Control 1 Only
Q6DKI1	RL7L_HUMAN 60S ribosomal protein L7-like 1 OS=Homo sapiens GN=RPL7L1 PE=1 SV=1	24.00	4.97			4.97			2.64 E-07			2.74 E-07			1.04	Control 1 Only	Control 1 Only
Q9BUP0	EFHD1_HUMAN EF-hand domain-containing protein D1 OS=Homo sapiens GN=EFHD1 PE=1 SV=1	37.20	2.00			7.99			5.14 E-08			3.34 E-07			6.50	Control 1 Only	Control 1 Only
Q9H7B2	RPF2_HUMAN Ribosome production factor 2 homolog OS=Homo sapiens GN=RPF2 PE=1 SV=2	26.50	3.00			7.00			1.68 E-07			3.32 E-07			1.97	Control 1 Only	Control 1 Only
B5MC59	B5MC59_HUMAN Replication protein A 14 kDa subunit OS=Homo sapiens GN=RPA3 PE=2 SV=1	32.90	4.00			5.00			7.32 E-07			6.17 E-07			0.84	Control 1 Only	Control 1 Only
Q9UBG3	CRNN_HUMAN Cornulin OS=Homo sapiens GN=CRNN PE=1 SV=1	26.10						9.00						9.45 E-08			Sample 3 Only

Q9UNX4	WDR3_HUMAN WD repeat-containing protein 3 OS=Homo sapiens GN=WDR3 PE=1 SV=1	8.20	5.00			4.00			6.19E-08			4.48E-08			0.72	Control 1 Only	Control 1 Only
J3KTE4	J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=2 SV=1	26.90	3.00			6.00			3.41E-07			6.11E-07			1.79	Control 1 Only	Control 1 Only
C9J6C5	C9J6C5_HUMAN MKI67 FHA domain-interacting nucleolar phosphoprotein (Fragment) OS=Homo sapiens GN=NIFK PE=2 SV=1	25.30	5.00			4.00			3.95E-07			3.17E-07			0.80	Control 1 Only	Control 1 Only
B4DJP7	B4DJP7_HUMAN Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=2 SV=1	15.80	4.00			4.00			6.28E-07			2.37E-07			0.38	Control 1 Only	Control 1 Only
P49207	RL34_HUMAN 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	21.40	3.00			5.00			5.33E-07			7.43E-07			1.39	Control 1 Only	Control 1 Only
P62851	RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	20.80	4.00			4.00			1.15E-06			9.70E-07			0.85	Control 1 Only	Control 1 Only
K7EK07	K7EK07_HUMAN Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=2 SV=1	90.90	3.98			3.98			3.26E-06			4.53E-06			1.39	Control 1 Only	Control 1 Only
O00468-3	AGRIN_HUMAN Isoform 3 of Agrin OS=Homo sapiens GN=AGRN	4.20	5.98			2.00			1.26E-08			5.26E-09			0.42	Control 1 Only	Control 1 Only
P42766	RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	26.00	3.00			5.00			3.75E-07			5.38E-07			1.44	Control 1 Only	Control 1 Only
P48729	KC1A_HUMAN Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=2	15.70	4.95			3.96			1.39E-07			1.18E-07			0.85	Control 1 Only	Control 1 Only
Q06323	PSME1_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	25.30	2.97			4.97			2.04E-07			2.53E-07			1.24	Control 1 Only	Control 1 Only
P09661	RU2A_HUMAN U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2	20.00	3.97			4.97			2.03E-07			1.91E-07			0.94	Control 1 Only	Control 1 Only
Q13148	TADBP_HUMAN TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1	12.10	3.96			4.96			5.44E-08			7.87E-08			1.45	Control 1 Only	Control 1 Only
Q15061	WDR43_HUMAN WD repeat-containing protein 43 OS=Homo sapiens GN=WDR43 PE=1 SV=3	8.30	4.00			4.00			4.40E-08			6.38E-08			1.45	Control 1 Only	Control 1 Only
Q8NI36	WDR36_HUMAN WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1	6.60	3.99			4.00			3.23E-08			2.54E-08			0.79	Control 1 Only	Control 1 Only
B4DFJ5	B4DFJ5_HUMAN 28S ribosomal protein S25, mitochondrial OS=Homo sapiens GN=MRPS25 PE=2 SV=1	47.30	4.00			3.00			3.27E-07			1.80E-07			0.55	Control 1 Only	Control 1 Only
F5H315	F5H315_HUMAN Pre-mRNA-splicing factor SYF1 OS=Homo sapiens GN=XAB2 PE=2 SV=1	6.70	5.00			2.00			3.70E-08			8.10E-09			0.22	Control 1 Only	Control 1 Only
Q9NV31	IMP3_HUMAN U3 small nucleolar ribonucleoprotein protein IMP3 OS=Homo sapiens GN=IMP3 PE=1 SV=1	27.70	3.00			4.00			2.91E-07			2.53E-07			0.87	Control 1 Only	Control 1 Only
B3KVR1	B3KVR1_HUMAN Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPN PE=2 SV=1	21.90	3.00			4.00			2.20E-07			2.59E-07			1.18	Control 1 Only	Control 1 Only
Q9Y5S9	RBM8A_HUMAN RNA-binding protein 8A OS=Homo sapiens GN=RBM8A PE=1 SV=1	27.00	3.00			5.00			4.44E-07			4.45E-07			1.00	Control 1 Only	Control 1 Only
Q71DI3	H32_HUMAN Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	88.20	3.00			4.00			8.23E-06			8.49E-06			1.03	Control 1 Only	Control 1 Only
C9JBJ6	C9JBJ6_HUMAN DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens GN=POLR2H PE=2 SV=1	39.50	4.00			3.00			3.45E-07			1.84E-07			0.53	Control 1 Only	Control 1 Only

Q12965	MYO1E_HUMAN Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2	5.80	1.00			6.00			6.56 E-09			4.51 E-08			6.88	Control 1 Only	Control 1 Only
O75569	PRKRA_HUMAN Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA PE=1 SV=1	27.80	1.98			4.95			9.60 E-08			1.32 E-07			1.38	Control 1 Only	Control 1 Only
P04083	ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	20.80						6.99						2.97 E-07			Sample 3 Only
P62266	RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	23.80	2.00			4.99			2.59 E-07			3.84 E-07			1.48	Control 1 Only	Control 1 Only
Q07065	CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	11.30	4.00			3.00			4.85 E-08			3.02 E-08			0.62	Control 1 Only	Control 1 Only
Q15269	PWP2_HUMAN Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2	5.10	4.00			3.00			7.44 E-08			4.35 E-08			0.59	Control 1 Only	Control 1 Only
Q96A72	MGN2_HUMAN Protein mago nashi homolog 2 OS=Homo sapiens GN=MAGOHB PE=1 SV=1	52.00	3.92			2.95			4.09 E-07			1.55 E-07			0.38	Control 1 Only	Control 1 Only
Q14690	RRP5_HUMAN Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3	4.80	6.00						1.04 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q96A35	RM24_HUMAN 39S ribosomal protein L24, mitochondrial OS=Homo sapiens GN=MRPL24 PE=1 SV=1	17.60	3.00			3.00			1.13 E-07			1.29 E-07			1.14	Control 1 Only	Control 1 Only
Q9GZL7	WDR12_HUMAN Ribosome biogenesis protein WDR12 OS=Homo sapiens GN=WDR12 PE=1 SV=2	5.70	3.00			3.00			6.36 E-08			5.83 E-08			0.92	Control 1 Only	Control 1 Only
Q9NP55	BPIA1_HUMAN BPI fold-containing family A member 1 OS=Homo sapiens GN=BPIFA1 PE=1 SV=1	13.70	3.00			3.00			1.02 E-07			8.85 E-08			0.87	Control 1 Only	Control 1 Only
Q9Y2P8	RCL1_HUMAN RNA 3'-terminal phosphate cyclase-like protein OS=Homo sapiens GN=RCL1 PE=1 SV=3	13.70	4.00			2.00			9.55 E-08			5.01 E-08			0.52	Control 1 Only	Control 1 Only
F5GYQ1	F5GYQ1_HUMAN V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=2 SV=1	8.20	3.00			3.00			1.19 E-07			1.15 E-07			0.97	Control 1 Only	Control 1 Only
C9J4Z3	C9J4Z3_HUMAN 60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=2 SV=1	61.80	3.99			2.00			4.21 E-07			1.40 E-07			0.33	Control 1 Only	Control 1 Only
B4DQI6	B4DQI6_HUMAN Transformer-2 protein homolog alpha OS=Homo sapiens GN=TRA2A PE=2 SV=1	28.30	1.98			3.96			1.73 E-07			1.72 E-07			0.99	Control 1 Only	Control 1 Only
Q9H552	Q9H552_HUMAN Uncharacterized protein OS=Homo sapiens PE=4 SV=1	29.90	4.00			2.00			5.96 E-08			1.99 E-08			0.33	Control 1 Only	Control 1 Only
Q86Y46	K2C73_HUMAN Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	17.80	2.00			4.00			4.09 E-08			5.27 E-08			1.29	Control 1 Only	Control 1 Only
P20290	BTF3_HUMAN Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1	29.60	2.00			4.00			1.61 E-07			1.80 E-07			1.12	Control 1 Only	Control 1 Only
Q8TED0	UTP15_HUMAN U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens GN=UTP15 PE=1 SV=3	10.00	3.96			1.98			9.34 E-08			5.49 E-08			0.59	Control 1 Only	Control 1 Only
A6NJD9	A6NJD9_HUMAN 39S ribosomal protein L23, mitochondrial OS=Homo sapiens GN=MRPL23 PE=2 SV=1	31.40	2.00			3.00			2.37 E-07			1.83 E-07			0.77	Control 1 Only	Control 1 Only
Q96GQ7	DDX27_HUMAN Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens GN=DDX27 PE=1 SV=2	4.60	3.00			2.00			6.88 E-08			4.48 E-08			0.65	Control 1 Only	Control 1 Only

Q96PK6	RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	7.00	2.00			3.00			3.53E-08			5.19E-08			1.47	Control 1 Only	Control 1 Only
A4D2Q0	A4D2Q0_HUMAN SUN domain-containing protein 1 OS=Homo sapiens GN=UNC84A PE=2 SV=1	6.70	2.00			3.00			1.87E-08			2.67E-08			1.43	Control 1 Only	Control 1 Only
H7BYN3	H7BYN3_HUMAN Transcription factor A, mitochondrial (Fragment) OS=Homo sapiens GN=TFAM PE=4 SV=1	20.10	2.00			3.00			1.59E-07			1.04E-07			0.66	Control 1 Only	Control 1 Only
F8WCF6	F8WCF6_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=2 SV=1	16.80	2.97			1.98			2.08E-07			1.62E-07			0.78	Control 1 Only	Control 1 Only
O00566	MPP10_HUMAN U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=1 SV=2	3.20	2.00			3.00			3.23E-08			4.39E-08			1.36	Control 1 Only	Control 1 Only
Q969X6	CIR1A_HUMAN Cirhin OS=Homo sapiens GN=CIRH1A PE=1 SV=1	3.70	1.98			2.97			4.22E-08			4.50E-08			1.07	Control 1 Only	Control 1 Only
O15213	WDR46_HUMAN WD repeat-containing protein 46 OS=Homo sapiens GN=WDR46 PE=1 SV=3	7.20	2.00			3.00			7.53E-08			8.95E-08			1.19	Control 1 Only	Control 1 Only
E7EMB3	E7EMB3_HUMAN Calmodulin OS=Homo sapiens GN=CALM2 PE=2 SV=1	22.10	1.98			2.97			8.58E-08			1.77E-07			2.06	Control 1 Only	Control 1 Only
E7ETA6	E7ETA6_HUMAN Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=2 SV=1	1.80	3.00			2.00			5.84E-09			6.28E-09			1.07	Control 1 Only	Control 1 Only
Q9HD33	RM47_HUMAN 39S ribosomal protein L47, mitochondrial OS=Homo sapiens GN=MRPL47 PE=1 SV=2	10.40	1.00			4.00			2.50E-08			1.21E-07			4.85	Control 1 Only	Control 1 Only
F8W6H6	F8W6H6_HUMAN Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=2 SV=1	4.90	2.00			3.00			1.53E-09			6.24E-09			4.08	Control 1 Only	Control 1 Only
B4DGD3	B4DGD3_HUMAN Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=2 SV=1	20.80	2.00			2.00			1.67E-07			1.14E-07			0.68	Control 1 Only	Control 1 Only
B4DQJ8	B4DQJ8_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1	23.10	2.00			2.00			4.49E-08			3.61E-08			0.80	Control 1 Only	Control 1 Only
C9J3L7	C9J3L7_HUMAN Replication initiator 1 OS=Homo sapiens GN=REPIN1 PE=2 SV=2	21.20	2.00			2.00			1.15E-08			1.08E-08			0.94	Control 1 Only	Control 1 Only
E7ETK0	E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1	20.80	2.00			2.00			5.99E-07			5.54E-07			0.92	Control 1 Only	Control 1 Only
K7EJ20	K7EJ20_HUMAN Glutathione peroxidase (Fragment) OS=Homo sapiens GN=GPX4 PE=3 SV=2	20.60	3.00			1.00			1.42E-07			1.72E-08			0.12	Control 1 Only	Control 1 Only
Q12905	ILF2_HUMAN Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	11.30	1.00			3.00			1.94E-08			6.06E-08			3.12	Control 1 Only	Control 1 Only
Q8IWA0	WDR75_HUMAN WD repeat-containing protein 75 OS=Homo sapiens GN=WDR75 PE=1 SV=1	4.90	2.00			2.00			1.37E-08			1.85E-08			1.35	Control 1 Only	Control 1 Only
Q9BVP2	GNL3_HUMAN Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2	8.80	1.00			3.00			2.50E-08			3.76E-08			1.51	Control 1 Only	Control 1 Only
B0QYD3	B0QYD3_HUMAN DNA dC->dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=2 SV=1	8.10	1.98			1.98			3.79E-08			4.05E-08			1.07	Control 1 Only	Control 1 Only
J3KQE0	J3KQE0_HUMAN SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=2 SV=1	6.70	2.00			2.00			1.50E-08			1.40E-08			0.93	Control 1 Only	Control 1 Only
Q99959	PKP2_HUMAN Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2	2.30	2.00			2.00			1.65E-08			1.57E-08			0.95	Control 1 Only	Control 1 Only

B5ME19	EIFCL_HUMAN Eukaryotic translation initiation factor 3 subunit C-like protein OS=Homo sapiens GN=EIF3CL PE=2 SV=1	4.40			3.00		1.00				2.00 E-08		5.72 E-09			Sample 2 Only	
P29373	RABP2_HUMAN Cellular retinoic acid-binding protein 2 OS=Homo sapiens GN=CRABP2 PE=1 SV=2	22.00	2.00			2.00			9.82 E-08			6.34 E-08			0.65	Control 1 Only	Control 1 Only
E7ENR5	E7ENR5_HUMAN U3 small nucleolar ribonucleoprotein protein IMP4 (Fragment) OS=Homo sapiens GN=IMP4 PE=2 SV=1	16.50	1.00			2.99			5.89 E-08			1.60 E-07			2.71	Control 1 Only	Control 1 Only
P56182	RRP1_HUMAN Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens GN=RRP1 PE=1 SV=1	6.70	2.00			2.00			3.44 E-08			5.89 E-08			1.71	Control 1 Only	Control 1 Only
P11388	TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	3.10	2.99					1.00	8.16 E-09					2.34 E-09	Control 1 Only	Control 1 Only	0.29
Q8IUE6	H2A2B_HUMAN Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3	66.20	1.98			1.98			5.99 E-06			6.77 E-06			1.13	Control 1 Only	Control 1 Only
E9PPU0	E9PPU0_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=4 SV=1	47.40	2.00			2.00			1.21 E-08			9.66 E-09			0.80	Control 1 Only	Control 1 Only
Q5JTH9	RRP12_HUMAN RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2	3.80	3.00			1.00			9.83 E-09			5.79 E-10			0.06	Control 1 Only	Control 1 Only
Q6SJ93	F111B_HUMAN Protein FAM111B OS=Homo sapiens GN=FAM111B PE=1 SV=1	7.70	3.00			1.00			5.48 E-08			1.64 E-08			0.30	Control 1 Only	Control 1 Only
Q96S19	CP013_HUMAN UPF0585 protein C16orf13 OS=Homo sapiens GN=C16orf13 PE=1 SV=2	27.00	1.99			1.99			5.93 E-08			1.08 E-07			1.83	Control 1 Only	Control 1 Only
E7ESU4	E7ESU4_HUMAN N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=2 SV=1	2.90	2.00			1.00			1.01 E-08			1.45 E-09			0.14	Control 1 Only	Control 1 Only
Q9NVP1	DDX18_HUMAN ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2	8.40	1.00			2.00			1.45 E-08			6.35 E-08			4.40	Control 1 Only	Control 1 Only
J3KPN6	J3KPN6_HUMAN Involucrin OS=Homo sapiens GN=IVL PE=2 SV=1	6.80						3.00						5.66 E-08			Sample 3 Only
O75934	SPF27_HUMAN Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1	11.60	1.00			2.00			4.21 E-08			6.48 E-08			1.54	Control 1 Only	Control 1 Only
Q9Y3Y2	CHTOP_HUMAN Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2	12.90				3.00						6.58 E-08			Sample 1 Only		
Q9Y5J1	UTP18_HUMAN U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3	5.80	1.99			1.00			6.34 E-08			1.82 E-08			0.29	Control 1 Only	Control 1 Only
H7BZ20	H7BZ20_HUMAN Thymidylate kinase (Fragment) OS=Homo sapiens GN=DTYMK PE=4 SV=1	10.90	1.99			0.99			9.03 E-08			3.78 E-08			0.42	Control 1 Only	Control 1 Only
Q9Y676	RT18B_HUMAN 28S ribosomal protein S18b, mitochondrial OS=Homo sapiens GN=MRPS18B PE=1 SV=1	9.70	2.00			1.00			8.71 E-08			4.51 E-08			0.52	Control 1 Only	Control 1 Only
E9PJM3	E9PJM3_HUMAN F-box only protein 3 OS=Homo sapiens GN=FBXO3 PE=2 SV=1	7.80			2.00			1.00			1.03 E-07			6.78 E-08			Sample 3 Only
J3QLQ6	J3QLQ6_HUMAN Nucleolar protein 11 (Fragment) OS=Homo sapiens GN=NOL11 PE=2 SV=1	13.60	2.00			1.00			1.97 E-07			4.30 E-08			0.22	Control 1 Only	Control 1 Only
P38117	ETFB_HUMAN Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3	8.20	2.00			1.00			9.53 E-08			3.67 E-08			0.39	Control 1 Only	Control 1 Only

Q10589	BST2_HUMAN Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1	14.90	2.00			1.00			2.04 E-07			6.84 E-08			0.33	Control 1 Only	Control 1 Only
Q9H0U3	MAGT1_HUMAN Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1 PE=1 SV=1	5.70	2.00			1.00			1.04 E-07			2.03 E-08			0.20	Control 1 Only	Control 1 Only
E9PCV0	E9PCV0_HUMAN Beta-glucuronidase OS=Homo sapiens GN=GUSB PE=2 SV=1	6.90			1.00			2.00			1.59 E-08			5.08 E-08			Sample 3 Only
G3V5X4	G3V5X4_HUMAN Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=2 SV=1	0.70	1.00			2.00			8.47 E-10			1.18 E-09			1.39	Control 1 Only	Control 1 Only
P22531	SPR2E_HUMAN Small proline-rich protein 2E OS=Homo sapiens GN=SPRR2E PE=2 SV=2	43.10						2.98						1.49 E-07			Sample 3 Only
Q13637	RAB32_HUMAN Ras-related protein Rab-32 OS=Homo sapiens GN=RAB32 PE=1 SV=3	9.80	2.00			1.00			4.79 E-08			9.12 E-09			0.19	Control 1 Only	Control 1 Only
K7ERN7	K7ERN7_HUMAN Notchless protein homolog 1 OS=Homo sapiens GN=NLE1 PE=2 SV=1	18.90	2.00			1.00			1.61 E-07			8.70 E-08			0.54	Control 1 Only	Control 1 Only
C9JMC5	C9JMC5_HUMAN Aldehyde dehydrogenase, dimeric NADP-preferring (Fragment) OS=Homo sapiens GN=ALDH3A1 PE=2 SV=1	12.90						2.99						4.45 E-08			Sample 3 Only
B4DXW1	B4DXW1_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=2 SV=1	8.70				3.00						9.78 E-08			Sample 1 Only		
K4DI93	K4DI93_HUMAN Cullin 4B, isoform CRA_e OS=Homo sapiens GN=CUL4B PE=2 SV=1	4.60			2.98						2.99 E-08						
P11047	LAMC1_HUMAN Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	2.50	2.00			1.00			3.23 E-09			2.02 E-09			0.63	Control 1 Only	Control 1 Only
P28074	PSB5_HUMAN Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	8.40	1.98				0.99		4.68 E-08				2.73 E-08		Control 1 Only	0.58	Control 1 Only
E7EN32	E7EN32_HUMAN Menin OS=Homo sapiens GN=MEN1 PE=2 SV=1	6.70			2.00			1.00			2.10 E-08			1.79 E-08			Sample 3 Only
O43818	U3IP2_HUMAN U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens GN=RRP9 PE=1 SV=1	4.40	2.00			1.00			8.29 E-08			4.61 E-08			0.56	Control 1 Only	Control 1 Only
B1AVQ5	B1AVQ5_HUMAN Mucin-1 subunit alpha OS=Homo sapiens GN=MUC1 PE=2 SV=1	12.50	1.98			0.99			4.17 E-08			2.08 E-08			0.50	Control 1 Only	Control 1 Only
M0QXB4	M0QXB4_HUMAN Coatomer protein complex, subunit epsilon, isoform CRA_g OS=Homo sapiens GN=COPE PE=2 SV=1	25.80			1.00	2.00					6.54 E-08	4.44 E-08			Sample 1 Only		
P42224	STAT1_HUMAN Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2	3.30			0.99			1.99			1.11 E-08			2.46 E-08			Sample 3 Only
O15144	ARPC2_HUMAN Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1	11.30				3.00						8.69 E-08			Sample 1 Only		
F8WF69	F8WF69_HUMAN Clathrin light chain A OS=Homo sapiens GN=CLTA PE=2 SV=1	4.60			2.00			1.00			1.25 E-07			4.29 E-08			Sample 3 Only
O60506	HNRPQ_HUMAN Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	6.30				2.97						4.27 E-08			Sample 1 Only		
P33778	H2B1B_HUMAN Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	83.30	0.50			1.00			1.93 E-08			2.30 E-08			1.19	Control 1 Only	Control 1 Only
Q99877	H2B1N_HUMAN Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3	83.30	0.50			1.00			1.93 E-08			2.30 E-08			1.19	Control 1 Only	Control 1 Only
P07737	PROF1_HUMAN Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	31.40	1.00				2.00		6.44 E-08				8.66 E-08		Control 1 Only	1.35	Control 1 Only

Q5XKE5	K2C79_HUMAN Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	25.20	1.00			2.00			6.72 E-09			2.86 E-08			4.25	Control 1 Only	Control 1 Only
P24390	ERD21_HUMAN ER lumen protein retaining receptor 1 OS=Homo sapiens GN=KDELR1 PE=1 SV=1	14.60	2.00			1.00			7.23 E-08			1.69 E-08			0.23	Control 1 Only	Control 1 Only
Q15382	RHEB_HUMAN GTP-binding protein Rheb OS=Homo sapiens GN=RHEB PE=1 SV=1	18.50	4.00		1.00				2.03 E-07						Control 1 Only	Control 1 Only	Control 1 Only
Q6YP21	KAT3_HUMAN Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens GN=CCBL2 PE=1 SV=1	5.70			2.00			1.00			1.29 E-07			6.36 E-08			Sample 3 Only
Q8WVV4	POF1B_HUMAN Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3	4.90					3.00						4.22 E-08			Sample 2 Only	
F8VQX6	F8VQX6_HUMAN Methyltransferase-like protein 7A (Fragment) OS=Homo sapiens GN=METTL7A PE=2 SV=1	16.70	2.00						1.51 E-07						Control 1 Only	Control 1 Only	Control 1 Only
G3V2K7	G3V2K7_HUMAN Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=2 SV=1	15.00	2.00						7.01 E-08						Control 1 Only	Control 1 Only	Control 1 Only
P08574	CY1_HUMAN Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3	8.60		1.00			1.00			8.57 E-08			7.34 E-08			Sample 2 Only	
Q5JR04	Q5JR04_HUMAN Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=MOV10 PE=2 SV=1	2.80				2.00						1.68 E-08			Sample 1 Only		
Q5JY65	Q5JY65_HUMAN Crooked neck-like protein 1 OS=Homo sapiens GN=CRNKL1 PE=2 SV=1	3.30	2.00						3.05 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q9NYH9	UTP6_HUMAN U3 small nucleolar RNA-associated protein 6 homolog OS=Homo sapiens GN=UTP6 PE=1 SV=2	4.90				2.00						2.40 E-08			Sample 1 Only		
C9J381	C9J381_HUMAN Inosine-5'-monophosphate dehydrogenase 1 OS=Homo sapiens GN=IMPDH1 PE=2 SV=1	5.90				2.00						1.85 E-08			Sample 1 Only		
B4DT74	B4DT74_HUMAN Mannose-P-dolichol utilization defect 1 protein OS=Homo sapiens GN=MPDU1 PE=2 SV=1	22.00	1.99						5.50 E-08						Control 1 Only	Control 1 Only	Control 1 Only
H7BZW6	H7BZW6_HUMAN Histone deacetylase complex subunit SAP18 (Fragment) OS=Homo sapiens GN=SAP18 PE=4 SV=2	25.20	1.00			1.00			2.12 E-07			1.27 E-08			0.06	Control 1 Only	Control 1 Only
Q9Y6Q5-2	AP1M2_HUMAN Isoform 2 of AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2	44.20	1.00			1.00			8.67 E-09			7.82 E-09			0.90	Control 1 Only	Control 1 Only
B1AHC8	B1AHC8_HUMAN X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa), isoform CRA_b OS=Homo sapiens GN=XRCC6 PE=2 SV=1	4.40	1.99						3.15 E-08						Control 1 Only	Control 1 Only	Control 1 Only
O76094	SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3	3.40			1.00			1.00			2.85 E-09			6.28 E-09			Sample 3 Only
Q96BQ5	CC127_HUMAN Coiled-coil domain-containing protein 127 OS=Homo sapiens GN=CCDC127 PE=1 SV=1	7.30	1.00			1.00			3.96 E-08			2.73 E-08			0.69	Control 1 Only	Control 1 Only
A8K8E1	A8K8E1_HUMAN TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 PE=2 SV=1	4.70				1.99						5.30 E-08			Sample 1 Only		

Q9Y6K5	OAS3_HUMAN 2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3	1.70			1.00			1.00			2.90 E-08			3.76 E-08			Sample 3 Only
B4DTC3	B4DTC3_HUMAN Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=2 SV=1	19.60				1.98						8.44 E-08			Sample 1 Only		
P49247	RPIA_HUMAN Ribose-5-phosphate isomerase OS=Homo sapiens GN=RPIA PE=1 SV=3	8.70						2.00						1.79 E-07			Sample 3 Only
Q5VZM2-2	RRAGB_HUMAN Isoform 2 of Ras-related GTP-binding protein B OS=Homo sapiens GN=RRAGB	7.70			0.99			0.99			4.54 E-08			5.72 E-08			Sample 3 Only
P02649	APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	7.60	1.00			1.00			3.63 E-08			1.35 E-08			0.37	Control 1 Only	Control 1 Only
C9JWG9	C9JWG9_HUMAN Williams-Beuren syndrome chromosomal region 16 protein (Fragment) OS=Homo sapiens GN=WBSCR16 PE=2 SV=1	22.90		1.00		1.00				1.38 E-07		5.51 E-08			Sample 1 Only		
H3BTH6	H3BTH6_HUMAN F-box only protein 22 (Fragment) OS=Homo sapiens GN=FBXO22 PE=2 SV=1	10.00			0.99			1.00			8.07 E-08			1.20 E-07			Sample 3 Only
Q9NUP9	LIN7C_HUMAN Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1	14.70	2.00						1.30 E-07						Control 1 Only	Control 1 Only	Control 1 Only
B4DXZ6	B4DXZ6_HUMAN Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=2 SV=1	13.90	1.00			1.00			1.87 E-08			1.68 E-09			0.09	Control 1 Only	Control 1 Only
Q15050	RRS1_HUMAN Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2	8.20	1.00			1.00			1.09 E-08			1.27 E-08			1.16	Control 1 Only	Control 1 Only
P04279	SEMG1_HUMAN Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2	7.40						2.00						1.23 E-07			Sample 3 Only
Q9NV06	DCA13_HUMAN DDB1- and CUL4-associated factor 13 OS=Homo sapiens GN=DCAF13 PE=1 SV=2	3.80				2.00						5.12 E-08			Sample 1 Only		
Q9BVG4	PBDC1_HUMAN Protein PBDC1 OS=Homo sapiens GN=PBDC1 PE=1 SV=1	10.70			2.00						1.42 E-07						
Q14692	BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	1.50	1.00			1.00			7.78 E-09			7.65 E-09			0.98	Control 1 Only	Control 1 Only
Q5W0U4	BSPRY_HUMAN B box and SPRY domain-containing protein OS=Homo sapiens GN=BSPRY PE=2 SV=1	9.80			1.00			1.00			2.39 E-08			2.36 E-08			Sample 3 Only
Q9Y3U8	RL36_HUMAN 60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	21.90	2.00						2.87 E-07						Control 1 Only	Control 1 Only	Control 1 Only
B4DEU5	B4DEU5_HUMAN L-fucose kinase OS=Homo sapiens GN=FUK PE=2 SV=1	35.80			1.00			1.00			4.62 E-08			3.32 E-08			Sample 3 Only
O14818	PSA7_HUMAN Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	14.00			1.00		1.00				9.38 E-08		6.97 E-08			Sample 2 Only	
Q9Y3C6	PPIL1_HUMAN Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens GN=PPIL1 PE=1 SV=1	24.70	1.00			1.00			5.88 E-08			3.37 E-08			0.57	Control 1 Only	Control 1 Only
F5GWK3	F5GWK3_HUMAN Pre-mRNA-splicing factor RBM22 OS=Homo sapiens GN=RBM22 PE=2 SV=1	5.40				2.00						2.92 E-08			Sample 1 Only		
Q02790	FKBP4_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	7.60					1.99						4.85 E-08			Sample 2 Only	
B3KVN2	B3KVN2_HUMAN Farnesyltransferase, CAAX box, alpha, isoform CRA_c OS=Homo sapiens	11.40			1.00			1.00			2.58 E-08			1.22 E-08			Sample 3 Only

	GN=FNTA PE=2 SV=1																
P13010	XRCC5_HUMAN X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	4.80			1.00	1.00					1.88 E-09	9.05 E-09			Sample 1 Only		
P14735	IDE_HUMAN Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4	2.50			1.00			1.00			3.91 E-09			4.09 E-09			Sample 3 Only
A6NIT2	A6NIT2_HUMAN Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform OS=Homo sapiens GN=PHKA1 PE=2 SV=1	0.70	1.00			1.00			5.97 E-09			1.11 E-08			1.87	Control 1 Only	Control 1 Only
D3YTB1	D3YTB1_HUMAN 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=2 SV=1	15.00	1.00			1.00			5.15 E-08			2.23 E-07			4.34	Control 1 Only	Control 1 Only
E9PE17	E9PE17_HUMAN 28S ribosomal protein S17, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS17 PE=2 SV=1	14.00	1.00			1.00			1.13 E-07			8.59 E-08			0.76	Control 1 Only	Control 1 Only
Q6PIK3	Q6PIK3_HUMAN HCG1995540, isoform CRA_b OS=Homo sapiens GN=RAB4B PE=2 SV=1	19.80	1.98						8.20 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q9H0U4	RAB1B_HUMAN Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1	18.40	0.99			0.99			2.68 E-08			3.06 E-08			1.14	Control 1 Only	Control 1 Only
P05386	RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	28.90	1.00			1.00			5.60 E-07			4.06 E-07			0.73	Control 1 Only	Control 1 Only
B4DR52	B4DR52_HUMAN Histone H2B OS=Homo sapiens GN=HIST2H2BF PE=2 SV=1	64.50				1.99						4.84 E-08			Sample 1 Only		
Q9Y2T7	YBOX2_HUMAN Y-box-binding protein 2 OS=Homo sapiens GN=YBX2 PE=1 SV=2	15.10	1.00			1.00			1.06 E-08			1.75 E-08			1.65	Control 1 Only	Control 1 Only
E7EPA1	E7EPA1_HUMAN Phosphoribosyl pyrophosphate synthase-associated protein 2 (Fragment) OS=Homo sapiens GN=PRPSAP2 PE=2 SV=1	13.40			0.99			0.99			1.02 E-07			8.18 E-08			Sample 3 Only
F8W1S1	F8W1S1_HUMAN Keratin, type II cytoskeletal 74 OS=Homo sapiens GN=KRT74 PE=2 SV=1	14.20	1.00			1.00			6.35 E-08			3.67 E-08			0.58	Control 1 Only	Control 1 Only
Q86UD0	SAPC2_HUMAN Suppressor APC domain-containing protein 2 OS=Homo sapiens GN=SAPCD2 PE=2 SV=2	4.60						1.00						4.15 E-08			Sample 3 Only
Q9Y5V3	MAGD1_HUMAN Melanoma-associated antigen D1 OS=Homo sapiens GN=MAGED1 PE=1 SV=3	3.00						1.00						5.79 E-09			Sample 3 Only
Q8NB90	SPAT5_HUMAN Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3	3.00				1.00						9.56 E-09			Sample 1 Only		
O75489	NDUS3_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1	7.60	1.00						3.88 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q9BPX5	ARP5L_HUMAN Actin-related protein 2/3 complex subunit 5-like protein OS=Homo sapiens GN=ARPC5L PE=1 SV=1	13.10				1.00						5.24 E-08			Sample 1 Only		
Q9HCN8	SDF2L_HUMAN Stromal cell-derived factor 2-like protein 1 OS=Homo sapiens GN=SDF2L1 PE=1 SV=2	13.60	1.00						6.30 E-08						Control 1 Only	Control 1 Only	Control 1 Only
B7Z6B8	B7Z6B8_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=2 SV=1	17.20	1.00						1.32 E-08						Control 1 Only	Control 1 Only	Control 1 Only

E9PF18	E9PF18_HUMAN Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=2 SV=1	7.30			1.00						1.52 E-08						
Q9Y3A2	UTP11_HUMAN Probable U3 small nucleolar RNA-associated protein 11 OS=Homo sapiens GN=UTP11L PE=1 SV=2	12.60	1.00						4.34 E-08						Control 1 Only	Control 1 Only	Control 1 Only
A6NKB8	A6NKB8_HUMAN Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=2 SV=1	4.30			1.00						1.31 E-08						
Q9P0M6	H2AW_HUMAN Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3	10.20	1.00						3.27 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q92673	SORL_HUMAN Sortilin-related receptor OS=Homo sapiens GN=SORL1 PE=1 SV=2	1.20					1.00						1.72 E-09			Sample 2 Only	
Q92626	PXDN_HUMAN Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	2.20			1.00						1.07 E-09						
Q13601	KRR1_HUMAN KRR1 small subunit processome component homolog OS=Homo sapiens GN=KRR1 PE=1 SV=4	5.90	1.00						2.05 E-08						Control 1 Only	Control 1 Only	Control 1 Only
O75165	DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5	1.00						1.00						8.14 E-10			Sample 3 Only
A6NG51	A6NG51_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=2 SV=2	1.00						1.00						1.23 E-09			Sample 3 Only
P31949	S10AB_HUMAN Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	15.20					1.00						6.90 E-08			Sample 2 Only	
P61106	RAB14_HUMAN Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	12.10				1.00						1.72 E-08			Sample 1 Only		
Q562R1	ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	21.50					1.00						1.52 E-07			Sample 2 Only	
Q13243	SRSF5_HUMAN Serine/arginine-rich splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=1 SV=1	8.90				1.00						1.93 E-08			Sample 1 Only		
Q8WXF1	PSPC1_HUMAN Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1	4.60			1.00						6.17 E-08						

Table A3. FLAG candidates from cytoplasmic immunoprecipitations that had been treated with RNase.

			SPECTRAL COUNTS						SPECTRAL INDEX (MIC SIn)						RATIOS		
Prot	Description	% Cover	C1	C2	C3	S1	S2	S3	C1	C2	C3	S1	S2	S3	S1/C1	S2/C1	S3/C1
Q9UKV8	AGO2_HUMAN Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	89.90	36.00	3.00		961.76	764.87	832.79	3.47E-07	4.33E-09		1.22E-04	6.59E-05	7.48E-05	350.65	190.27	215.84
P35579	MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	79.70	101.90	227.33	699.31	246.25	235.77	579.95	5.72E-07	9.45E-07	9.46E-06	1.73E-06	7.56E-07	6.83E-06	3.02	1.32	11.94
O14744	ANM5_HUMAN Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	66.20	443.49	201.81	257.88	334.52	245.20	237.38	1.09E-04	1.77E-05	3.14E-05	5.77E-05	1.74E-05	2.36E-05	0.53	0.16	0.22
P52732	KIF11_HUMAN Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	72.10	444.00	172.00	351.00	246.00	132.00	255.00	2.20E-05	3.18E-06	8.22E-06	6.00E-06	1.08E-06	4.61E-06	0.27	0.05	0.21
Q14204	DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	57.60	196.00	60.00	116.00	303.00	251.00	634.00	3.94E-07	3.24E-08	1.03E-07	6.83E-07	2.20E-07	1.61E-06	1.73	0.56	4.09
P04264	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	71.10	256.00	200.00	320.00	184.00	201.00	193.00	2.48E-05	7.03E-06	2.27E-05	1.11E-05	7.25E-06	6.98E-06	0.45	0.29	0.28
P06310	KV206_HUMAN Ig kappa chain V-II region RPMI 6410 OS=Homo sapiens PE=4 SV=1	18.00	112.86	177.21	319.79	127.71	192.06	260.38	5.43E-03	6.92E-03	5.79E-03	4.67E-03	6.35E-03	4.37E-03	0.86	1.17	0.81
P35527	K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	82.30	163.83	150.91	239.21	104.28	144.03	121.11	9.79E-06	3.85E-06	1.23E-05	3.83E-06	3.14E-06	2.90E-06	0.39	0.32	0.30
P60709	ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	79.70	85.28	174.67	222.79	145.18	98.12	164.84	4.93E-05	6.28E-05	1.55E-04	1.11E-04	2.05E-05	1.02E-04	2.24	0.42	2.07
P13645	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	66.40	178.57	130.82	162.78	126.84	110.83	110.90	1.52E-05	5.15E-06	8.50E-06	9.61E-06	2.88E-06	4.31E-06	0.63	0.19	0.28
P35908	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	89.00	85.50	53.00	76.50	67.00	54.00	55.50	4.21E-06	1.25E-06	2.87E-06	2.80E-06	7.61E-07	1.45E-06	0.67	0.18	0.34
P05787	K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	82.80	78.09	12.46	204.33	110.96	21.39	252.03	4.31E-06	1.06E-07	1.78E-05	7.75E-06	2.60E-07	3.15E-05	1.80	0.06	7.30
Q9BQA1	MEP50_HUMAN Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	60.20	112.70	108.70	116.71	107.69	103.67	91.78	4.90E-05	1.63E-05	2.64E-05	2.95E-05	1.24E-05	1.65E-05	0.60	0.25	0.34
Q9UPY3	DICER_HUMAN Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	53.40				177.49	215.39	237.28				1.00E-06	8.36E-07	1.28E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q15208	STK38_HUMAN Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1	68.40	106.00	73.00	119.00	120.00	106.00	103.00	7.53E-06	2.63E-06	7.01E-06	1.01E-05	3.63E-06	6.67E-06	1.34	0.48	0.88
P49327	FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	50.10	198.50	38.00	46.00	77.50	83.00	129.50	1.50E-06	4.43E-08	6.61E-08	2.59E-07	1.19E-07	3.81E-07	0.17	0.08	0.25
F5H012	F5H012_HUMAN E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=2 SV=1	64.20	94.91	57.88	88.85	125.88	82.80	94.85	5.11E-06	1.46E-06	3.08E-06	5.98E-06	4.53E-06	5.24E-06	1.17	0.89	1.03
P08727	K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	85.80	78.79	13.93	150.66	72.86	15.98	190.59	5.12E-06	1.18E-07	2.04E-05	5.80E-06	2.21E-07	3.93E-05	1.13	0.04	7.68
F8VPD4	F8VPD4_HUMAN CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1	48.70	45.00	14.00	24.00	114.00	79.00	177.00	2.41E-07	1.74E-08	3.29E-08	6.44E-07	1.84E-07	1.22E-06	2.67	0.76	5.05
P04792	HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	94.10	44.00	34.00	54.00	73.00	90.00	153.00	2.27E-05	3.19E-06	8.47E-06	3.14E-05	1.19E-05	6.11E-05	1.39	0.53	2.70
P11142	HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	53.60	35.98	16.54	36.03	109.85	61.28	125.43	5.62E-07	1.73E-07	6.40E-07	3.84E-06	1.06E-06	5.13E-06	6.84	1.89	9.13
P05783	K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	87.00	34.00	9.00	118.96	53.00	13.00	160.96	1.85E-06	6.28E-08	8.76E-06	3.34E-06	2.34E-07	2.19E-05	1.80	0.13	11.84

P36578	RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	63.20	10.95	8.98	28.84	70.69	103.57	145.32	1.52E-07	5.91E-08	5.37E-07	3.81E-06	5.18E-06	9.43E-06	25.08	34.17	62.16
P78527	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	25.90	25.99	30.98	30.99	69.94	57.97	135.91	3.06E-08	1.37E-08	1.97E-08	8.83E-08	3.28E-08	1.79E-07	2.88	1.07	5.86
P49411	EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	58.80	44.00	23.00	51.00	49.00	53.00	109.00	3.14E-06	7.42E-07	2.19E-06	3.56E-06	2.72E-06	7.52E-06	1.13	0.87	2.40
Q9UPQ9	TNR6B_HUMAN Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	38.30	1.00			84.15	159.41	74.25	2.37E-08			3.86E-07	5.70E-07	2.95E-07	16.29	24.05	12.43
Q9UH99	SUN2_HUMAN SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	58.30	52.82	34.88	44.82	100.66	36.88	50.79	1.19E-06	3.04E-07	8.44E-07	2.66E-06	4.32E-07	7.30E-07	2.25	0.36	0.62
P23396	RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	84.80	4.89	15.60	47.89	52.80	69.36	119.28	3.07E-07	3.59E-07	3.78E-06	7.72E-06	4.21E-06	1.80E-05	25.14	13.73	58.62
Q00610	CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	44.60	61.71	27.92	54.76	65.72	34.88	69.74	4.30E-07	4.27E-08	1.36E-07	3.28E-07	6.21E-08	2.46E-07	0.76	0.14	0.57
P08238	HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	72.50	195.27	19.47	23.98	16.97	11.50	29.94	1.05E-05	2.25E-07	3.96E-07	2.42E-07	6.22E-08	5.08E-07	0.02	0.01	0.05
Q7Z406-2	MYH14_HUMAN Isoform 2 of Myosin-14 OS=Homo sapiens GN=MYH14	54.30	4.90	4.90	112.77	16.66	11.77	146.12	1.34E-08	3.27E-09	3.02E-07	2.97E-08	7.62E-09	5.22E-07	2.22	0.57	38.96
F5H5D3	F5H5D3_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1	76.40	53.40	23.22	23.16	70.94	47.66	56.31	1.21E-05	4.43E-06	4.27E-06	2.71E-06	7.07E-06	2.30E-05	2.24	0.58	1.90
Q01813	K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	47.70	56.02	13.87	21.30	52.08	33.72	80.81	7.95E-07	7.46E-08	2.41E-07	6.80E-07	2.25E-07	1.69E-06	0.86	0.28	2.13
O00159-3	MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	55.70	4.93	9.88	25.71	114.49	45.45	67.23	2.11E-08	1.90E-08	7.45E-08	1.62E-06	1.81E-07	4.76E-07	76.96	8.58	22.59
P02786	TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	42.00	85.38	38.71	47.63	20.82	25.83	42.68	2.01E-06	2.57E-07	4.66E-07	1.77E-07	1.24E-07	5.14E-07	0.09	0.06	0.26
P39023	RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	60.00	5.91	1.97	27.73	48.45	83.06	88.10	8.35E-08	1.74E-08	6.65E-07	3.94E-06	3.04E-06	6.04E-06	47.21	36.45	72.38
E7EW20	E7EW20_HUMAN Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=2 SV=1	49.20	1.00	29.94	144.78	14.97		64.91	1.25E-09	5.05E-08	9.07E-07	3.98E-08		2.18E-07	31.85	Control 1 Only	174.68
P07437	TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	84.90	40.59	15.84	20.79	74.25	41.58	58.41	6.13E-06	1.90E-06	3.06E-06	2.29E-05	1.02E-05	2.13E-05	3.73	1.66	3.48
Q13200	PSMD2_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	42.40	57.44	21.80	31.71	27.74	24.78	78.27	6.89E-07	9.84E-08	2.81E-07	1.74E-07	9.12E-08	6.40E-07	0.25	0.13	0.93
P17858	K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	51.40	32.00	6.00	16.00	62.00	44.00	81.00	3.93E-07	2.11E-08	1.73E-07	1.04E-06	3.81E-07	1.73E-06	2.65	0.97	4.40
P61247	RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	76.10	0.99	4.86	28.16	32.09	48.60	117.73	3.54E-09	6.92E-08	1.04E-06	2.98E-06	1.69E-06	1.07E-05	841.87	477.23	3018.39
P63244	GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	62.80	8.66	16.34	38.40	31.64	60.43	72.89	6.47E-07	3.03E-07	1.57E-06	3.45E-06	1.87E-06	6.95E-06	5.33	2.89	10.75
P23458	JAK1_HUMAN Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2	43.80	12.00	19.00	35.00	31.00	49.00	89.00	8.08E-08	4.30E-08	1.22E-07	1.51E-07	1.13E-07	4.60E-07	1.87	1.40	5.69
E7EMH5	E7EMH5_HUMAN Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=2 SV=1	44.20	12.96	14.94	37.91	54.81	48.83	59.87	2.55E-07	1.12E-07	6.71E-07	2.26E-06	9.47E-07	1.46E-06	8.86	3.71	5.70
P53621	COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	36.80	75.99	19.99	18.00	22.99	26.99	61.96	5.92E-07	3.37E-08	3.69E-08	1.02E-07	5.18E-08	3.51E-07	0.17	0.09	0.59

P05388	RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	66.90	10.65	4.82	20.31	55.25	55.09	71.41	6.54E-07	8.49E-08	1.53E-06	1.01E-05	1.07E-05	1.51E-05	15.45	16.33	23.05
P18124	RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	56.50	6.98	6.99	31.88	50.80	53.84	69.74	7.56E-07	1.49E-07	2.34E-06	1.25E-05	4.16E-06	1.40E-05	16.50	5.50	18.52
P46777	RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	52.50		1.00	19.00	48.00	65.00	89.00		7.63E-09	5.39E-07	4.19E-06	3.21E-06	6.72E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P11021	GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	60.10	21.00	9.00	22.00	52.00	26.00	73.00	2.88E-07	8.82E-08	2.62E-07	1.11E-06	3.27E-07	1.60E-06	3.85	1.14	5.58
P25705	ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	55.90	80.52	26.51	31.43	19.73	16.71	35.44	4.42E-06	3.37E-07	7.01E-07	2.80E-07	1.43E-07	1.11E-06	0.06	0.03	0.25
Q9P219	DAPLE_HUMAN Protein Daple OS=Homo sapiens GN=CCDC88C PE=1 SV=3	32.20	45.00	27.00	29.00	42.00	21.00	48.00	1.34E-07	2.99E-08	4.74E-08	9.89E-08	2.00E-08	9.08E-08	0.74	0.15	0.68
P68104	EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	33.80	29.95	19.96	34.90	34.92	28.93	58.86	2.52E-06	6.25E-07	1.08E-06	2.61E-06	1.10E-06	3.34E-06	1.04	0.44	1.33
Q16531	DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	42.70	22.61	12.80	28.58	42.33	34.50	58.12	1.46E-07	2.46E-08	8.73E-08	2.51E-07	9.88E-08	3.01E-07	1.72	0.68	2.07
P62701	RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	67.30		4.98	32.91	28.89	38.84	87.75		6.06E-08	1.79E-06	5.24E-06	1.51E-06	1.32E-05	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q13085	ACACA_HUMAN Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	31.10	77.76	16.74	20.71	11.79	9.84	54.19	2.94E-07	1.12E-08	2.12E-08	1.87E-08	6.88E-09	9.81E-08	0.06	0.02	0.33
C9J9K3	C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	71.60	5.00	12.97	24.91	32.89	46.86	70.80	6.30E-07	5.90E-07	2.56E-06	5.94E-06	5.55E-06	1.43E-05	9.43	8.81	22.75
P13647	K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	58.30	31.87	19.87	53.68	30.88	20.87	24.86	5.74E-07	1.42E-07	7.12E-07	4.99E-07	1.69E-07	2.51E-07	0.87	0.29	0.44
P35580	MYH10_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	51.50		8.82	106.84	6.87	2.94	56.85		6.26E-09	2.76E-07	1.02E-08	2.93E-09	1.12E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P46940	IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	30.80	26.00	15.49	51.48	24.00	12.00	42.98	8.64E-08	2.19E-08	1.71E-07	6.31E-08	1.37E-08	1.50E-07	0.73	0.16	1.74
P15924	DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	30.50	26.00	3.00	51.99	17.00	6.00	75.00	4.13E-08	1.63E-09	5.94E-08	2.50E-08	3.29E-09	1.16E-07	0.61	0.08	2.82
P48735	IDHP_HUMAN Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	59.50	64.47	10.89	20.79	12.89	10.89	45.61	4.64E-06	1.53E-07	3.98E-07	3.49E-07	1.60E-07	1.48E-06	0.08	0.03	0.32
P07814	SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	31.80	55.00	10.00	20.00	12.00	6.00	51.00	2.91E-07	1.15E-08	3.08E-08	3.79E-08	1.05E-08	1.74E-07	0.13	0.04	0.60
P50416	CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	37.00	33.92	6.98	5.98	40.85	29.90	40.86	3.50E-07	2.09E-08	2.83E-08	4.29E-07	1.44E-07	4.74E-07	1.22	0.41	1.35
P62424	RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	45.10	0.99		13.94	18.94	54.89	72.88	1.16E-08		6.40E-07	1.78E-06	1.82E-06	7.18E-06	153.18	156.80	618.24
Q6ZRV2	FA83H_HUMAN Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3	38.00	4.00			32.00	40.00	85.00	1.34E-08			2.05E-07	1.03E-07	6.51E-07	15.23	7.66	48.46
E9PLK3	E9PLK3_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1	46.60	105.59	15.86	9.87	6.96	1.00	7.92	1.63E-06	8.49E-08	4.10E-08	2.40E-08	6.84E-10	3.05E-08	0.01	0.00	0.02
P62917	RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	51.40	4.94	5.93	21.75	27.66	44.46	50.41	3.15E-07	1.01E-07	1.79E-06	7.53E-06	2.84E-06	1.06E-05	23.89	9.01	33.75
Q02878	RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	40.30	2.98	2.98	11.97	28.44	44.36	60.30	7.11E-08	4.74E-08	5.54E-07	2.67E-06	2.67E-06	6.67E-06	37.47	37.54	93.74

P33993	MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	51.70	69.72	2.00	8.96	23.89	6.94	43.76	1.30E-06	5.81E-09	1.06E-07	2.21E-07	4.89E-08	7.38E-07	0.17	0.04	0.57
P06576	ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	55.60	68.24	22.77	15.86	4.94	5.95	35.63	4.34E-06	3.45E-07	3.31E-07	6.58E-08	5.49E-08	1.11E-06	0.02	0.01	0.26
Q5T4S7	UBR4_HUMAN E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	13.40	15.99	2.00	4.99	17.98	18.98	90.90	1.42E-08	3.51E-10	6.71E-09	5.66E-08	6.35E-09	8.52E-08	3.99	0.45	6.02
P46781	RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	66.00	1.00	6.98	23.94	21.93	32.90	61.85	1.33E-07	3.24E-07	2.90E-06	8.00E-06	2.09E-06	1.35E-05	60.14	15.72	101.80
O15230	LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	19.50			1.00	45.00	38.00	66.00			5.18E-10	7.81E-08	2.73E-08	8.16E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P07900	HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	46.30	62.87	14.94	14.94	17.95	11.94	22.92	1.54E-06	8.12E-08	2.03E-07	1.87E-07	7.36E-08	3.11E-07	0.12	0.05	0.20
Q9ULV0	MYO5B_HUMAN Unconventional myosin-Vb OS=Homo sapiens GN=MYO5B PE=1 SV=3	31.50	100.37	23.95	18.98	1.00			5.25E-07	3.47E-08	2.80E-08	1.11E-09			0.00	Control 1 Only	Control 1 Only
J3KNL6	J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=2 SV=1	23.30	6.00	1.00	2.00	27.00	21.00	86.00	1.37E-08	6.86E-10	7.59E-10	7.82E-08	2.62E-08	2.57E-07	5.69	1.90	18.73
Q02543	RL18A_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	62.50		1.98	15.84	38.62	33.71	45.57		3.83E-08	1.96E-06	7.76E-06	3.35E-06	1.06E-05	Sample 1 Only	Sample 2 Only	Sample 3 Only
P13639	EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	35.90	63.00	5.00	10.00	21.00	11.00	32.00	8.32E-07	1.25E-08	5.95E-08	1.80E-07	3.34E-08	2.98E-07	0.22	0.04	0.36
P02533	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	71.00	25.00	20.50	33.00	14.50	13.50	21.00	6.27E-07	1.68E-07	5.01E-07	2.20E-07	1.11E-07	1.87E-07	0.35	0.18	0.30
P40429	RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	60.10	2.00	1.00	12.95	26.88	37.79	56.70	4.72E-08	1.66E-08	1.04E-06	6.18E-06	3.00E-06	9.30E-06	131.04	63.51	197.12
Q14974	IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	20.40	28.00	8.99	21.97	20.98	17.96	34.93	4.16E-07	2.74E-08	1.50E-07	3.15E-07	6.48E-08	4.33E-07	0.76	0.16	1.04
P15880	RS2_HUMAN 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	47.10		2.95	15.75	18.70	38.39	55.17		2.09E-08	8.00E-07	2.12E-06	1.06E-06	6.28E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P62906	RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	54.80		5.00	11.00	15.00	36.00	65.00		9.14E-08	6.27E-07	2.65E-06	1.86E-06	5.90E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
O15084	ANR28_HUMAN Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A OS=Homo sapiens GN=ANKRD28 PE=1 SV=5	35.90	38.55	10.84	12.81	20.76	19.74	25.67	3.12E-07	1.96E-08	4.30E-08	1.04E-07	5.01E-08	1.01E-07	0.33	0.16	0.32
Q9C0C2	TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	31.20	3.00			8.00	20.00	98.00	8.07E-09			2.07E-08	3.22E-08	4.53E-07	2.57	3.99	56.13
Q9Y2H1	ST38L_HUMAN Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3	46.80	24.81	19.87	17.89	23.85	15.93	20.84	6.27E-07	1.90E-07	2.99E-07	6.49E-07	1.75E-07	4.21E-07	1.04	0.28	0.67
P26373	RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	59.20	1.99	1.00	11.96	22.86	32.82	52.72	4.99E-08	1.46E-08	8.90E-07	3.02E-06	1.75E-06	1.11E-05	60.45	34.94	222.87
J3KMW7	J3KMW7_HUMAN E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=2 SV=1	23.30	2.99	2.99	5.97	15.97	33.95	58.85	9.79E-09	1.52E-08	7.10E-08	6.19E-08	3.17E-08	1.14E-07	6.33	3.24	11.60
P53618	COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	33.50	14.00	2.00	4.00	41.98	26.99	37.00	9.20E-08	4.39E-09	2.42E-08	3.71E-07	9.72E-08	3.27E-07	4.03	1.06	3.55
E7ESA8	E7ESA8_HUMAN U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=2 SV=1	40.90	15.70	16.68	24.54	16.71	21.62	25.54	7.70E-07	5.31E-07	1.13E-06	7.34E-07	7.99E-07	1.14E-06	0.95	1.04	1.48
B4D	B4DF41_HUMAN DNA mismatch repair protein	34.40	9.00	3.00	3.99	33.0	21.0	45.9	2.78	2.08	7.30	1.24	5.14	1.70	4.48	1.85	6.12

F41	Msh6 OS=Homo sapiens GN=MSH6 PE=2 SV=1					0	0	9	E-08	E-09	E-09	E-07	E-08	E-07			
P27635	RL10_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	57.00		1.98	14.80	13.86	37.58	46.55		4.70 E-08	7.93 E-07	4.95 E-06	1.42 E-06	9.15 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9H552	Q9H552_HUMAN Uncharacterized protein OS=Homo sapiens PE=4 SV=1	22.40	6.50	2.50	17.50	11.50	2.50	18.50	3.49 E-07	8.87 E-08	1.53 E-06	8.17 E-07	2.92 E-08	3.02 E-06	2.34	0.08	8.65
Q92673	SORL_HUMAN Sortilin-related receptor OS=Homo sapiens GN=SORL1 PE=1 SV=2	22.00	2.00			16.93	29.89	65.76	3.08 E-09			3.20 E-08	3.53 E-08	1.86 E-07	10.39	11.44	60.29
P06493	CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	63.30	6.65	8.59	28.96	7.54	11.03	40.86	9.74 E-07	3.07 E-07	1.92 E-06	6.18 E-07	4.25 E-07	2.50 E-06	0.64	0.44	2.57
A8MUB1	A8MUB1_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1	64.90	13.69	8.82	8.79	26.49	27.48	28.47	1.18 E-06	5.53 E-07	7.55 E-07	3.31 E-06	2.29 E-06	3.39 E-06	2.82	1.95	2.88
P68032	ACTC_HUMAN Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	37.10	10.85	8.82	27.45	31.56	7.84	25.55	1.20 E-06	4.21 E-07	5.54 E-06	7.49 E-06	2.94 E-07	4.01 E-06	6.25	0.25	3.35
P30050	RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	69.10	2.00	4.00	17.00	20.00	33.00	31.00	2.41 E-07	6.17 E-08	1.16 E-06	6.25 E-06	2.18 E-06	6.81 E-06	25.95	9.07	28.30
O95163	ELP1_HUMAN Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	37.20	7.00	1.00	2.00	24.00	21.99	51.93	3.69 E-08	1.11 E-09	2.85 E-09	1.10 E-07	4.25 E-08	2.17 E-07	2.97	1.15	5.88
F8VSC5	F8VSC5_HUMAN SCY1-like protein 2 (Fragment) OS=Homo sapiens GN=SCYL2 PE=2 SV=1	37.00	71.00	2.00	14.00			22.00	2.39 E-06	1.43 E-08	1.60 E-07			3.97 E-07	Control 1 Only	Control 1 Only	0.17
Q99460	PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	35.70	15.98	7.99	4.99	16.98	17.99	39.95	1.61 E-07	1.55 E-08	2.40 E-08	1.15 E-07	3.74 E-08	1.75 E-07	0.72	0.23	1.09
C9J2Y9	C9J2Y9_HUMAN DNA-directed RNA polymerase OS=Homo sapiens GN=POLR2B PE=2 SV=2	35.80	9.99	2.00	1.00	21.99	22.00	48.00	3.61 E-08	9.26 E-10	1.73 E-09	1.05 E-07	4.21 E-08	1.76 E-07	2.92	1.17	4.87
P00338	LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	37.70	49.01	13.71	17.64	3.92	6.89	10.81	1.06 E-05	3.32 E-07	5.20 E-07	2.16 E-07	7.63 E-08	2.84 E-07	0.02	0.01	0.03
Q86YZ3	HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	23.40	25.00	11.00	33.00	14.00	10.00	12.00	6.53 E-08	7.55 E-09	5.83 E-08	3.15 E-08	1.39 E-08	1.21 E-08	0.48	0.21	0.18
P17655	CAN2_HUMAN Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6	36.70	4.00		1.00	31.00	25.00	42.08	5.18 E-08		7.91 E-09	4.50 E-07	1.51 E-07	7.87 E-07	8.70	2.91	15.21
Q13263	TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	36.90	9.92		1.98	23.81	40.70	23.82	9.94 E-08		9.19 E-09	1.71 E-07	2.28 E-07	1.72 E-07	1.72	2.29	1.73
P62805	H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	54.40	6.00	8.00	26.00	11.00	9.00	41.00	7.26 E-07	5.56 E-07	1.28 E-05	3.87 E-06	5.33 E-07	3.20 E-05	5.33	0.73	44.05
Q7Z6Z7	HUWE1_HUMAN E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	13.30	51.73	3.99	4.96	1.00	0.99	35.81	7.22 E-08	1.39 E-09	1.90 E-09	7.97 E-10	2.02 E-10	2.55 E-08	0.01	0.00	0.35
P61353	RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	61.80	0.99	1.00	9.96	21.89	27.84	35.81	1.62 E-07	1.82 E-08	2.17 E-06	8.38 E-06	2.90 E-06	1.17 E-05	51.82	17.93	72.37
P62753	RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	37.30			12.97	12.00	26.96	44.93			6.20 E-07	1.14 E-06	1.47 E-06	4.64 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P62277	RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	55.60	1.00	1.99	11.95	17.93	23.92	38.86	1.44 E-07	7.51 E-08	1.79 E-06	5.23 E-06	1.76 E-06	1.09 E-05	36.28	12.18	75.87
Q92900	RENT1_HUMAN Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	37.90				20.00	38.99	35.99				7.16 E-08	8.16 E-08	1.23 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8N257	H2B3B_HUMAN Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3	57.90	12.66	6.80	16.58	25.35	7.77	25.39	1.07 E-06	1.37 E-06	7.60 E-06	4.87 E-06	1.40 E-06	2.22 E-05	4.56	1.31	20.80
B4DUC5	B4DUC5_HUMAN Exportin-2 OS=Homo sapiens GN=CSE1L PE=2 SV=1	24.40	5.00	11.00	22.00	13.00	25.00	18.00	7.17 E-08	5.56 E-08	2.58 E-07	1.79 E-07	1.17 E-07	3.67 E-07	2.49	1.64	5.12

Q5VY93	Q5VY93_HUMAN Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=2 SV=1	32.80	8.00		3.00	7.00	26.00	45.00	5.11E-08		1.13E-08	3.24E-08	9.11E-08	4.04E-07	0.63	1.78	7.90
P08779	K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	68.10	17.50	4.00	36.00	2.00	7.00	23.00	3.94E-07	1.97E-08	4.52E-07	2.46E-08	2.37E-08	2.41E-07	0.06	0.06	0.61
P62280	RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	67.10	1.00	4.97	13.92	15.91	19.90	33.84	1.50E-07	1.41E-07	1.76E-06	5.11E-06	1.34E-06	7.07E-06	34.10	8.92	47.25
M0R0F0	M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=2 SV=1	59.50		3.97	9.91	18.84	18.87	36.75		9.71E-08	5.50E-07	1.72E-06	1.49E-06	4.14E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P56192	SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	29.80	22.81	1.98	2.97	15.86	10.91	34.68	1.35E-07	2.35E-09	1.53E-08	9.42E-08	2.16E-08	2.16E-07	0.70	0.16	1.60
P16615	AT2A2_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	25.80	20.80	8.92	9.91	15.86	6.94	24.72	1.60E-07	2.52E-08	4.79E-08	8.85E-08	2.15E-08	1.40E-07	0.55	0.13	0.87
Q15645	PCH2_HUMAN Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	30.30	9.95	9.95	11.94	14.94	13.94	28.94	2.83E-07	1.26E-07	2.05E-07	3.93E-07	1.63E-07	6.46E-07	1.39	0.58	2.28
P41252	SYIC_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	25.20	37.86	5.98	16.93	5.00	1.00	18.92	2.31E-07	7.26E-09	4.04E-08	1.35E-08	8.57E-10	5.83E-08	0.06	0.00	0.25
P50914	RL14_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	34.40	2.00	4.00	11.00	21.00	21.00	27.00	5.65E-08	1.49E-07	1.21E-06	1.01E-05	2.61E-06	8.67E-06	178.70	46.13	153.36
O43242	PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	43.60	20.98	11.99	13.98	9.98	13.99	17.98	6.02E-07	1.04E-07	1.65E-07	2.33E-07	1.25E-07	2.82E-07	0.39	0.21	0.47
E9PDF6	E9PDF6_HUMAN Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=2 SV=1	41.30		12.91	8.96	45.76	6.98	11.97		2.93E-08	2.17E-08	3.37E-07	1.59E-08	3.93E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q16875	F263_HUMAN 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1	47.20	27.59	11.82	7.86	14.77	10.82	10.83	1.01E-06	1.02E-07	9.35E-08	2.88E-07	1.37E-07	1.70E-07	0.29	0.14	0.17
Q08211	DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	23.80	5.00	10.00	6.00	11.00	19.00	35.00	2.48E-08	1.50E-08	9.84E-09	3.74E-08	5.47E-08	1.53E-07	1.51	2.21	6.18
F5H1Z7	F5H1Z7_HUMAN Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=2 SV=1	28.20				56.00	18.00	10.00				8.86E-07	1.00E-07	7.12E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P61313	RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	44.60	1.97		1.97	16.74	25.67	33.52	4.21E-08		1.42E-07	1.66E-06	1.47E-06	4.85E-06	39.38	35.01	115.34
P62241	RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	57.70	1.00	1.00	17.00	4.00	25.00	36.00	1.31E-08	9.01E-09	7.72E-07	6.63E-07	1.23E-06	5.05E-06	50.63	94.20	385.50
P62269	RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	55.30	1.00	2.00	11.00	15.00	18.00	35.99	1.02E-07	1.28E-07	1.31E-06	3.90E-06	1.66E-06	9.73E-06	38.08	16.27	95.09
P62081	RS7_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	63.90	2.00	2.00	12.00	16.00	20.00	29.00	4.04E-07	7.19E-08	1.97E-06	4.02E-06	1.74E-06	6.47E-06	9.96	4.31	16.04
P52272	HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	54.60	0.50	2.48	2.97	12.35	9.90	29.67	4.46E-09	8.16E-09	1.23E-08	1.30E-07	5.90E-08	5.21E-07	29.11	13.24	116.97
P62888	RL30_HUMAN 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	66.10	1.00	1.00	11.95	15.97	18.97	31.94	1.50E-07	1.83E-08	1.16E-06	5.72E-06	2.25E-06	8.08E-06	38.26	15.04	54.06
J3QRN6	J3QRN6_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=2 SV=1	35.10		12.92	14.91	30.88	4.97	12.92		3.47E-08	4.27E-08	2.01E-07	9.38E-09	4.13E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q86VP6	CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	28.20	10.97	2.00	15.99	14.99	10.00	24.96	5.09E-08	1.90E-09	5.24E-08	8.09E-08	1.66E-08	1.16E-07	1.59	0.33	2.27
F5H2F4	F5H2F4_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens	30.60	36.98	3.00		12.00	6.00	19.00	2.56E-07	2.01E-09		4.67E-08	9.27E-09	8.39E-08	0.18	0.04	0.33

	GN=MTHFD1 PE=2 SV=1																
P46779	RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	58.40		1.00	11.81	17.72	19.66	27.54		1.64E-08	1.89E-06	1.17E-05	4.04E-06	7.94E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P62249	RS16_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	74.00	1.98	1.00	9.87	16.79	14.83	30.66	3.55E-07	3.04E-08	3.39E-06	9.38E-06	1.89E-06	1.29E-05	26.44	5.32	36.43
P62913	RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	61.80		1.53	7.12	8.36	17.01	17.95		4.13E-08	4.40E-07	2.94E-06	1.84E-06	3.65E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P26641	EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	32.30	23.00	8.00	7.00	10.00	11.00	15.00	1.07E-06	1.29E-07	1.07E-07	2.88E-07	1.10E-07	4.36E-07	0.27	0.10	0.41
Q9NYL9	TMOD3_HUMAN Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1	44.90	3.99	8.97	25.94	15.95	5.99	12.96	1.53E-07	1.77E-07	8.36E-07	8.20E-07	1.16E-07	2.91E-07	5.37	0.76	1.91
P55884	EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	29.50	39.96	10.00	3.99	4.00	5.99	9.99	5.78E-07	3.03E-08	2.03E-08	1.34E-08	1.42E-08	4.30E-08	0.02	0.02	0.07
P54136	SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	34.50	22.81	5.94	13.91	2.97	0.99	24.80	3.73E-07	2.88E-08	1.22E-07	2.21E-08	5.63E-09	3.60E-07	0.06	0.02	0.96
P43686	PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	46.90	11.00	9.00	6.00	5.00	10.00	30.00	3.68E-07	6.23E-08	1.21E-07	1.63E-07	1.22E-07	7.83E-07	0.44	0.33	2.13
P52597	HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	51.60	4.94	2.96	3.96	9.90	19.89	27.85	1.81E-07	2.93E-08	5.78E-08	3.29E-07	4.36E-07	1.64E-06	1.82	2.41	9.04
H7BXY3	H7BXY3_HUMAN Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=2 SV=1	37.40				16.00	28.00	24.00				4.91E-08	5.77E-08	8.59E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q14697	GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	40.40	62.36			0.99		4.94	6.88E-07			5.77E-09		1.75E-08	0.01	Control 1 Only	0.03
Q14152	EIF3A_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1	22.60	42.97	4.00	6.00	1.00	2.00	9.99	2.19E-07	1.03E-08	8.45E-09	1.67E-09	1.72E-09	2.77E-08	0.01	0.01	0.13
Q92616	GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	11.90	7.00		5.00	18.00	18.00	20.00	1.21E-08		4.93E-09	2.48E-08	1.12E-08	3.41E-08	2.06	0.93	2.83
B4DER1	B4DER1_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1	31.90	44.00	4.00	7.00	2.00		11.00	3.76E-07	5.95E-09	1.49E-08	4.51E-09		3.27E-08	0.01	Control 1 Only	0.09
Q14766-3	LTBP1_HUMAN Isoform 3 of Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1	23.70	0.99	2.95	3.95	6.89	24.56	27.53	4.94E-09	4.05E-09	1.01E-08	2.12E-08	5.14E-08	1.05E-07	4.29	10.39	21.18
B7Z6Z4	B7Z6Z4_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	65.50	1.97	3.93	27.55	8.86	0.99	21.64	3.94E-07	1.02E-07	7.99E-06	2.10E-06	2.58E-08	3.42E-06	5.32	0.07	8.69
E9PFW3	E9PFW3_HUMAN AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=2 SV=1	50.80	0.99	2.00	3.97	13.92	18.89	24.86	1.46E-08	7.23E-09	5.59E-08	3.71E-07	3.03E-07	1.03E-06	25.42	20.78	70.87
P46778	RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	35.00			3.00	11.00	19.00	29.00			6.18E-07	5.04E-06	1.36E-06	7.51E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9UJW0	DCTN4_HUMAN Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1	36.30	10.97	12.96	21.94	11.96	2.99	4.96	2.28E-07	1.11E-07	4.89E-07	3.82E-07	2.42E-08	4.40E-08	1.67	0.11	0.19
Q9Y230	RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	48.20	1.99	1.99	1.99	10.92	10.91	36.72	5.46E-08	1.25E-08	2.08E-08	2.65E-07	1.48E-07	1.34E-06	4.85	2.70	24.51
P0CG38	POTEI_HUMAN POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1	10.30	6.93	5.95	18.81	11.88	3.95	16.80	1.19E-07	2.74E-08	2.03E-07	3.99E-07	1.32E-08	1.68E-07	3.35	0.11	1.41
P62244	RS15A_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	77.70			9.90	9.91	14.86	26.75			1.02E-06	3.47E-06	1.08E-06	8.11E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6P	LARP1_HUMAN La-related protein 1	19.50		0.99	0.99	5.94	15.8	37.5		1.20	4.56	2.30	5.55	2.39	Sample	Sample	Sample

KG0	OS=Homo sapiens GN=LARP1 PE=1 SV=2						3	9		E-09	E-09	E-08	E-08	E-07	1 Only	2 Only	3 Only
Q9Y3Z3	SAMH1_HUMAN Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2	35.10	5.94		2.97	14.83	5.94	29.67	6.67 E-08		2.28 E-08	2.14 E-07	3.25 E-08	6.20 E-07	3.21	0.49	9.30
P35998	PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	50.30	11.00	5.00	12.00	2.00	4.00	27.00	3.78 E-07	4.56 E-08	1.71 E-07	3.12 E-08	2.85 E-08	7.69 E-07	0.08	0.08	2.03
Q13045	FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	21.50	16.92	3.97	3.00	11.95	5.00	19.89	1.17 E-07	5.66 E-09	1.62 E-08	6.15 E-08	8.64 E-09	1.61 E-07	0.53	0.07	1.38
O00571	DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	25.70	7.99	1.00	3.00	11.00	11.49	20.50	8.05 E-08	2.26 E-09	2.59 E-08	1.74 E-07	8.32 E-08	4.23 E-07	2.16	1.03	5.26
Q8NDV7	TNR6A_HUMAN Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	13.50				11.00	20.50	18.50				5.35 E-08	5.18 E-08	5.98 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q12965	MYO1E_HUMAN Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2	21.60		7.99	16.95	21.99	3.98	9.96		2.28 E-08	5.24 E-08	9.24 E-08	4.30 E-09	3.14 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O43175	SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	29.30	8.98	5.99	7.99	11.98	8.99	16.98	1.55 E-07	3.50 E-08	6.93 E-08	3.33 E-07	8.88 E-08	4.05 E-07	2.14	0.57	2.60
Q13610	PWP1_HUMAN Periodic tryptophan protein 1 homolog OS=Homo sapiens GN=PWP1 PE=1 SV=1	38.30			1.99	17.99	20.98	19.98			2.24 E-08	5.34 E-07	3.33 E-07	5.54 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q93077	H2A1C_HUMAN Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3	40.80	3.96	3.00	8.37	8.13	3.96	11.37	3.27 E-07	1.24 E-07	3.48 E-06	2.09 E-06	2.14 E-07	8.70 E-06	6.40	0.65	26.65
O75165	DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5	18.30	3.00		1.00	9.00	15.00	32.00	4.81 E-09		6.06 E-10	1.26 E-08	1.12 E-08	5.41 E-08	2.62	2.32	11.23
P62750	RL23A_HUMAN 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	55.80		2.97	6.93	2.97	14.85	30.70		8.89 E-08	9.89 E-07	1.61 E-06	1.27 E-06	4.87 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q00325	MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	18.30	12.99	7.00	7.99	6.99	7.99	15.97	1.56 E-06	9.64 E-08	2.56 E-07	4.43 E-07	8.07 E-08	8.23 E-07	0.28	0.05	0.53
Q9BUF5	TBB6_HUMAN Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	70.20	2.00	0.99	0.99	12.96	14.94	20.90	6.22 E-08	5.77 E-09	5.79 E-09	5.04 E-07	8.33 E-07	1.05 E-06	8.11	13.39	16.86
Q9Y265	RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	49.30	7.97	3.98	2.00	6.93	4.96	32.71	1.39 E-07	1.41 E-08	2.08 E-08	2.39 E-07	4.94 E-08	9.68 E-07	1.72	0.36	6.96
P62191	PRS4_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	48.40	19.00	7.00	9.00	5.00	5.00	13.99	8.17 E-07	7.00 E-08	2.00 E-07	1.88 E-07	7.34 E-08	6.21 E-07	0.23	0.09	0.76
D6RAN4	D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1	47.30		2.97	6.93	10.89	17.82	17.82		6.14 E-08	7.62 E-07	2.18 E-06	1.95 E-06	4.06 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P50502	F10A1_HUMAN Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	23.30	7.92	6.93	6.93	13.87	6.93	11.89	3.13 E-07	1.87 E-07	4.33 E-07	6.15 E-07	1.57 E-07	6.75 E-07	1.96	0.50	2.16
J3KTE4	J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=2 SV=1	39.90		1.00	3.00	17.00	17.00	18.00		2.27 E-08	2.49 E-07	1.86 E-06	5.76 E-07	1.74 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JNW5	C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1	52.90	1.00	2.00	9.00	12.00	11.00	20.00	4.92 E-08	2.63 E-08	6.48 E-07	1.46 E-06	7.06 E-07	5.13 E-06	29.73	14.35	104.29
Q9Y285	SYFA_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3	33.70	3.95		1.98	13.81	8.86	21.70	9.26 E-08		9.60 E-09	4.89 E-07	1.11 E-07	5.86 E-07	5.28	1.20	6.33
P43490	NAMPT_HUMAN Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	25.10		2.00	3.00	6.99	7.99	33.96		9.29 E-09	1.88 E-08	1.44 E-07	6.55 E-08	8.47 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only

P46783	RS10_HUMAN 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	68.50	1.00		6.97	6.99	13.97	23.94	2.25E-07		4.15E-07	1.26E-06	1.07E-06	3.97E-06	5.62	4.74	17.64
G5E9V5	G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1	51.40				3.00	16.92	34.82				9.71E-08	2.62E-07	1.17E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q14CN4	K2C72_HUMAN Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2	18.10	3.48	11.74	6.38	4.64	6.80	1.74	5.80E-08	1.93E-07	1.02E-07	9.38E-08	7.02E-08	9.55E-09	1.62	1.21	0.16
P61163	ACTZ_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	39.40	3.96	4.96	9.92	13.88	5.95	9.92	9.38E-08	6.44E-08	2.90E-07	8.02E-07	1.49E-07	3.53E-07	8.55	1.59	3.76
Q96P70	IPO9_HUMAN Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	13.60	4.00	3.00	1.00	12.00	13.00	19.00	1.70E-08	4.42E-09	1.78E-09	6.42E-08	4.79E-08	8.21E-08	3.78	2.82	4.84
P18077	RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	55.50			3.98	13.93	11.92	19.86			4.97E-07	5.68E-06	7.06E-07	8.18E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P47897	SYQ_HUMAN Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	24.10	38.73	1.98	4.97			3.98	4.97E-07	2.65E-09	3.34E-08			3.34E-08	Control 1 Only	Control 1 Only	0.07
Q9UHL4	DPP2_HUMAN Dipeptidyl peptidase 2 OS=Homo sapiens GN=DPP7 PE=1 SV=3	20.50	3.98	5.97	6.96	9.94	11.94	10.94	6.74E-08	5.49E-08	1.09E-07	2.16E-07	1.45E-07	3.07E-07	3.21	2.15	4.55
Q15633	TRBP2_HUMAN RISC-loading complex subunit TARBP2 OS=Homo sapiens GN=TARBP2 PE=1 SV=3	36.20				6.97	19.87	20.89				3.28E-07	4.11E-07	7.67E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4DRT2	B4DRT2_HUMAN 28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=2 SV=1	45.50	1.99		1.00	4.98	19.87	19.89	2.90E-08		1.27E-08	1.15E-07	3.99E-07	6.99E-07	3.95	13.74	24.10
B4DEB1	B4DEB1_HUMAN Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1	29.30	3.00	4.00	11.00	5.00	3.00	14.00	2.17E-07	2.94E-07	3.63E-06	1.00E-06	4.24E-07	9.00E-06	4.61	1.95	41.46
P01625	KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	14.00	9.00	8.00	7.00	8.00	8.00	7.00	4.48E-06	8.54E-07	2.45E-06	4.82E-06	7.33E-07	1.88E-06	1.07	0.16	0.42
B9ZVX0	B9ZVX0_HUMAN Diaphanous homolog 1 (Drosophila), isoform CRA_a OS=Homo sapiens GN=DIAPH1 PE=2 SV=1	21.90	9.98		4.00	2.00	10.00	19.99	3.71E-08		7.81E-09	3.39E-09	1.62E-08	5.97E-08	0.09	0.44	1.61
P68371	TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	84.70	8.00	5.00	7.00	9.00	9.00	9.00	1.32E-06	3.55E-07	7.26E-07	5.12E-06	2.48E-06	5.53E-06	3.89	1.88	4.20
Q9NQX4	MYO5C_HUMAN Unconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	19.20		12.91	27.89	1.99		0.99		1.72E-08	5.86E-08	2.74E-09		1.53E-09	Sample 1 Only		Sample 3 Only
B3KXW5	B3KXW5_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=2 SV=1	15.00	4.00	0.50	1.50	7.00	3.00	6.50	2.63E-08	5.91E-10	7.38E-09	4.65E-08	4.80E-09	4.37E-08	1.77	0.18	1.66
J3KQU9	J3KQU9_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=2 SV=1	14.90	4.00	0.50	1.50	7.00	3.00	6.50	2.70E-08	6.05E-10	7.56E-09	4.76E-08	4.92E-09	4.47E-08	1.77	0.18	1.66
P58107	EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	13.70	6.00		15.76	3.94		17.76	5.12E-09		1.25E-08	2.75E-09		2.23E-08	0.54	Control 1 Only	4.35
P33992	MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	21.50	29.94	1.00	5.00			6.99	3.97E-07	1.83E-09	2.98E-08			6.43E-08	Control 1 Only	Control 1 Only	0.16
P39019	RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	70.30			6.00	8.00	11.00	19.00			2.72E-07	1.41E-06	5.10E-07	4.37E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q16822	PCKGM_HUMAN Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3	18.80	16.79	2.97	3.96	2.95	0.99	15.80	2.93E-07	5.74E-09	2.65E-08	3.35E-08	3.77E-09	2.61E-07	0.11	0.01	0.89
P14868	SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	39.30	12.89	5.96	6.96	1.00		13.91	2.55E-07	2.66E-08	1.08E-07	8.52E-09		1.69E-07	0.03	Control 1 Only	0.66
H3BRG4	H3BRG4_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=2 SV=1	36.20		3.98	0.99		7.95	29.89		3.39E-08	1.54E-08		8.05E-08	8.54E-07		Sample 2 Only	Sample 3 Only

G3XAB8	G3XAB8_HUMAN Trinucleotide repeat containing 6C, isoform CRA_a OS=Homo sapiens GN=TNRC6C PE=2 SV=1	14.90				4.00	22.00	15.00				1.01E-08	3.84E-08	2.82E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P60866	RS20_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	36.10	0.99	1.98	3.96	10.89	9.90	12.87	2.57E-07	4.42E-08	7.87E-07	3.80E-06	4.95E-07	3.52E-06	14.79	1.93	13.68
P08729	K2C7_HUMAN Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	66.30			12.50		1.00	27.50			2.22E-07		1.81E-08	9.23E-07		Sample 2 Only	Sample 3 Only
Q5JR04	Q5JR04_HUMAN Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=MOV10 PE=2 SV=1	24.30				9.00	19.00	14.00				3.56E-08	3.87E-08	5.72E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q15075	EEA1_HUMAN Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	1.30	11.00		1.00	21.00	1.00	1.00	2.36E-08		8.46E-10	3.97E-08	6.98E-10	1.18E-09	1.68	0.03	0.05
P43246	MSH2_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	16.00	3.98	2.99	1.99	9.92	6.96	13.91	1.48E-08	3.83E-09	4.46E-09	3.18E-08	1.01E-08	3.56E-08	2.15	0.68	2.41
H0Y368	H0Y368_HUMAN Dolichol-phosphate mannosyltransferase (Fragment) OS=Homo sapiens GN=DPM1 PE=4 SV=1	43.80	2.00	2.00	4.97	4.99	6.95	17.90	7.93E-08	6.70E-09	1.52E-07	2.48E-07	1.03E-07	1.22E-06	3.12	1.30	15.34
P50748	KNTC1_HUMAN Kinetochore-associated protein 1 OS=Homo sapiens GN=KNTC1 PE=1 SV=1	11.40	2.00		2.00	8.00	5.00	22.00	2.42E-09		1.51E-09	1.49E-08	2.23E-09	4.72E-08	6.18	0.92	19.51
O75340	PDCD6_HUMAN Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	29.80	8.96	2.98	7.97	6.97	3.98	8.97	3.25E-06	4.33E-08	5.98E-07	1.44E-06	8.30E-08	6.48E-07	0.44	0.03	0.20
Q5SWX8	ODR4_HUMAN Protein odr-4 homolog OS=Homo sapiens GN=ODR4 PE=2 SV=1	27.80	2.97	8.91	7.92	4.95	7.92	7.92	7.92E-08	7.69E-08	1.40E-07	1.18E-07	1.03E-07	1.81E-07	1.49	1.30	2.28
Q9NZB2	F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	21.60	1.00			8.97	10.92	19.88	4.36E-09			4.49E-08	1.55E-08	7.91E-08	10.29	3.56	18.15
B4DL14	B4DL14_HUMAN ATP synthase subunit gamma OS=Homo sapiens GN=ATP5C1 PE=2 SV=1	36.80	7.00	1.00	9.00	1.00	3.00	19.00	1.07E-06	1.46E-08	3.46E-07	9.59E-08	6.83E-08	1.18E-06	0.09	0.06	1.10
J3KPZ3	J3KPZ3_HUMAN Probable E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens GN=MYCBP2 PE=2 SV=1	7.30	1.00	1.00	2.00	2.00	7.00	27.00	5.57E-09	1.02E-09	1.69E-09	1.75E-09	2.20E-09	1.66E-08	0.32	0.39	2.98
P62195	PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	39.40	6.98	1.00	3.99	4.96	6.94	15.88	1.29E-07	2.22E-08	6.40E-08	1.46E-07	1.86E-07	4.78E-07	1.13	1.44	3.71
P08237	K6PF_HUMAN 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	17.90	6.90	1.97	3.96	6.92	2.97	16.80	6.73E-08	4.11E-09	3.00E-08	6.59E-08	2.64E-08	2.48E-07	0.98	0.39	3.69
P08107	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	34.50	0.99	1.97	3.95	10.84	7.91	12.85	1.11E-08	7.11E-09	4.21E-08	1.79E-07	5.48E-08	2.55E-07	16.12	4.94	22.92
Q93008	USP9X_HUMAN Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	8.70	8.99	2.00	4.00	6.00	3.00	14.98	1.81E-08	6.37E-10	3.87E-09	8.38E-09	2.71E-09	1.72E-08	0.46	0.15	0.95
Q92538	GBF1_HUMAN Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2	12.30	3.50	1.50	1.00	6.00	8.50	14.00	3.00E-08	1.34E-09	8.38E-10	1.06E-08	7.51E-09	3.02E-08	0.35	0.25	1.01
Q9Y6D6	BIG1_HUMAN Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2	13.70	3.96	0.99	0.99	9.90	7.93	13.86	1.30E-08	2.11E-10	1.06E-09	3.12E-08	8.55E-09	3.43E-08	2.40	0.66	2.63
F5H897	F5H897_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=2 SV=1	33.20	24.90	1.99	1.00	4.99		4.98	3.68E-07	9.05E-09	6.85E-09	3.26E-08		4.61E-08	0.09	Control 1 Only	0.13

P42704	LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	12.60	17.91	5.99	3.98	2.00	1.00	6.95	5.85 E-08	6.06 E-09	8.04 E-09	4.55 E-09	6.34 E-10	1.25 E-08	0.08	0.01	0.21
M0QZM1	M0QZM1_HUMAN Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens GN=HNRNPM PE=4 SV=1	71.30	0.50	0.50	1.00	3.50	4.00	10.00	8.49 E-09	5.73 E-09	1.12 E-08	7.87 E-08	4.94 E-08	3.81 E-07	9.26	5.82	44.88
P82930	RT34_HUMAN 28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=1 SV=2	42.70	1.99		1.00	2.99	9.98	15.95	9.79 E-08		3.16 E-08	2.38 E-07	2.31 E-07	1.01 E-06	2.43	2.36	10.32
Q8NHQ1	CEP70_HUMAN Centrosomal protein of 70 kDa OS=Homo sapiens GN=CEP70 PE=1 SV=2	17.90	0.99	4.95	7.92	2.97	2.97	9.90	3.34 E-08	3.86 E-08	6.72 E-08	3.47 E-08	1.35 E-08	1.07 E-07	1.04	0.40	3.22
Q9NZ32	ARP10_HUMAN Actin-related protein 10 OS=Homo sapiens GN=ACTR10 PE=1 SV=1	29.50	5.97	7.96	11.98	5.97	3.99	2.00	2.67 E-07	8.43 E-08	3.86 E-07	2.78 E-07	4.02 E-08	5.41 E-08	1.04	0.15	0.20
Q9UNF1	MAGD2_HUMAN Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2	26.60	3.97	0.99	3.95	6.92	1.99	17.83	4.04 E-08	7.85 E-09	3.82 E-08	8.02 E-08	6.57 E-09	4.20 E-07	1.98	0.16	10.38
P14923	PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	22.10	7.98	1.00	11.94	4.00		10.48	3.81 E-08	6.20 E-10	5.95 E-08	1.40 E-08		6.67 E-08	0.37	Control 1 Only	1.75
Q9UKD2	MRT4_HUMAN mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2	47.70			1.00	5.00	10.00	20.00			7.88 E-09	2.38 E-07	1.56 E-07	8.78 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P12004	PCNA_HUMAN Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	41.80	4.00	1.00	7.00	3.00	2.00	17.00	6.15 E-07	8.80 E-09	1.56 E-07	1.47 E-07	1.37 E-08	1.00 E-06	0.24	0.02	1.63
E9PKF6	E9PKF6_HUMAN Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=2 SV=1	20.40	2.95		2.96	5.94	0.99	19.72	2.83 E-08		2.34 E-08	2.94 E-07	3.85 E-09	1.67 E-07	10.38	0.14	5.90
E9PLL6	E9PLL6_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1	50.90			4.96	3.98	5.97	20.84			5.09 E-07	1.39 E-06	6.05 E-07	5.21 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P49207	RL34_HUMAN 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	37.60			4.00	8.00	9.00	13.00			9.74 E-07	3.00 E-06	7.10 E-07	4.91 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P22102	PUR2_HUMAN Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	19.80	15.97	2.00	2.00	2.99		9.99	9.45 E-08	2.17 E-09	4.03 E-09	8.44 E-09		3.34 E-08	0.09	Control 1 Only	0.35
P62851	RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	31.20	1.00	1.00	4.00	3.00	8.00	17.00	1.51 E-07	1.89 E-08	6.75 E-07	1.21 E-06	5.21 E-07	6.72 E-06	7.97	3.44	44.43
P23258	TBG1_HUMAN Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	35.00	0.99	0.99		2.97	5.96	22.85	1.53 E-08	5.14 E-09		6.13 E-08	6.74 E-08	7.98 E-07	4.01	4.41	52.16
P67809	YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	64.80				4.96	18.87	8.94				1.36 E-07	6.60 E-07	3.36 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q08J23	NSUN2_HUMAN tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2	23.20	28.00		1.00	1.00		4.00	4.49 E-07		1.24 E-08	1.50 E-09		3.00 E-08	0.00	Control 1 Only	0.07
P08708	RS17_HUMAN 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	65.90			4.97	4.98	6.96	16.91			4.11 E-07	9.64 E-07	6.43 E-07	2.99 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8N0W3	FUK_HUMAN L-fucose kinase OS=Homo sapiens GN=FUK PE=2 SV=2	19.30	3.50			9.50	5.50	6.50	1.59 E-08			5.49 E-08	8.28 E-09	3.01 E-08	3.46	0.52	1.90
Q9H4A4	AMPB_HUMAN Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2	27.40	31.93		2.00				5.25 E-07		1.28 E-08				Control 1 Only	Control 1 Only	Control 1 Only
P62829	RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	43.60	1.98		1.99	6.93	4.96	16.87	1.79 E-07		1.08 E-07	9.27 E-07	1.78 E-07	1.92 E-06	5.17	0.99	10.68
O00743	PPP6_HUMAN Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1	28.60			8.94	1.98	3.98	16.87			1.68 E-07	7.57 E-08	3.24 E-08	5.61 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only

O15269	SPTC1_HUMAN Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1	32.60	1.00	3.00	9.00	2.00	3.00	14.00	2.43 E-08	2.22 E-08	1.12 E-07	6.22 E-08	3.01 E-08	3.31 E-07	2.56	1.24	13.62
P62266	RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	32.20		0.99	5.99	3.00	6.00	14.96		3.00 E-08	7.62 E-07	4.92 E-07	2.64 E-07	3.69 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P14625	ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	19.40	13.99	1.00	5.00	2.00	1.00	9.00	1.45 E-07	3.45 E-09	2.62 E-08	4.34 E-09	1.68 E-09	4.50 E-08	0.03	0.01	0.31
Q6ZNJ1	NBEL2_HUMAN Neurobeachin-like protein 2 OS=Homo sapiens GN=NBEAL2 PE=1 SV=2	10.10	2.98			2.99	4.97	20.84	3.91 E-09			8.48 E-09	2.82 E-09	2.58 E-08	2.17	0.72	6.60
E9PG35	E9PG35_HUMAN Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=MCCC1 PE=2 SV=1	20.70	13.88	2.98	1.98		0.99	8.92	2.44 E-07	1.44 E-08	1.63 E-08		5.87 E-09	1.29 E-07	Control 1 Only	0.02	0.53
P11216	PYGB_HUMAN Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	26.00	22.00		1.00	3.00		5.00	1.80 E-07		6.61 E-09	1.31 E-08		3.17 E-08	0.07	Control 1 Only	0.18
Q6DD88	ATLA3_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1	20.30	3.96	0.99	4.95	2.96	1.98	15.87	6.29 E-08	3.86 E-09	3.92 E-08	4.28 E-08	8.36 E-09	2.72 E-07	0.68	0.13	4.33
P42766	RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	35.80			3.00	6.00	8.00	10.00			3.20 E-07	9.99 E-07	4.49 E-07	3.40 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
J3QRS3	J3QRS3_HUMAN Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=2 SV=1	71.30		2.00	11.00	3.00	1.00	12.00		1.24 E-07	3.06 E-06	5.03 E-07	3.48 E-08	2.19 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7ETK0	E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1	32.30			1.00	10.00	3.00	13.00			9.82 E-08	6.31 E-07	1.77 E-07	1.31 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y2I8	WDR37_HUMAN WD repeat-containing protein 37 OS=Homo sapiens GN=WDR37 PE=1 SV=2	25.30			1.00	4.00	8.00	14.95			3.67 E-09	7.68 E-08	2.12 E-08	2.57 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y6G9	DC1L1_HUMAN Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3	25.80			1.99	6.00	7.99	10.99			1.20 E-08	6.93 E-08	4.67 E-08	2.05 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
E5KLJ5	E5KLJ5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1	15.20	15.00	2.00	4.00	2.00		3.00	7.12 E-08	3.34 E-09	1.52 E-08	1.07 E-08		1.06 E-08	0.15	Control 1 Only	0.15
P41743	KPCI_HUMAN Protein kinase C iota type OS=Homo sapiens GN=PRKCI PE=1 SV=2	20.60	16.00	1.00	3.00	3.00	1.00	4.00	3.40 E-07	6.52 E-09	2.97 E-08	3.44 E-08	1.19 E-08	4.32 E-08	0.10	0.03	0.13
G3V529	G3V529_HUMAN ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=2 SV=1	21.90				5.00	14.00	9.00				1.95 E-08	4.59 E-08	3.06 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P62263	RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	39.70	1.00	1.00	4.00	2.00	8.00	12.00	2.36 E-07	2.55 E-08	3.07 E-07	7.97 E-07	3.53 E-07	2.12 E-06	3.38	1.50	8.98
Q9BXJ9	NAA15_HUMAN N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1	17.70	26.93						1.88 E-07						Control 1 Only	Control 1 Only	Control 1 Only
Q9H2M9	RBGPR_HUMAN Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1	12.10	10.00		1.00	2.00	2.00	13.00	3.33 E-08		1.64 E-09	3.67 E-09	2.71 E-09	2.82 E-08	0.11	0.08	0.85
O43592	XPOT_HUMAN Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	17.00	0.99		1.00	10.99	5.99	8.00	4.07 E-09		2.57 E-09	9.86 E-08	1.38 E-08	7.09 E-08	24.23	3.39	17.42
P62333	PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	37.50	5.96	1.99	1.99	1.00		12.92	1.85 E-07	1.31 E-08	3.02 E-08	2.16 E-08		3.38 E-07	0.12	Control 1 Only	1.83
P62854	RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	50.40		1.00	3.00	4.00	6.00	13.00		4.91 E-08	1.10 E-06	2.08 E-06	9.23 E-07	7.23 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9H9T3	ELP3_HUMAN Elongator complex protein 3 OS=Homo sapiens GN=ELP3 PE=1 SV=2	18.40	1.98			10.89	2.97	7.92	1.96 E-08			1.87 E-07	2.23 E-08	1.74 E-07	9.53	1.14	8.88
F8W6H6	F8W6H6_HUMAN Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=2 SV=1	12.90	0.50	3.99	20.00			2.00	1.52 E-09	2.94 E-09	2.68 E-08			1.03 E-09	Control 1 Only	Control 1 Only	0.68

H7C269	H7C269_HUMAN Trinucleotide repeat-containing gene 6A protein (Fragment) OS=Homo sapiens GN=TNRC6A PE=2 SV=1	12.60				3.00	3.50	8.50				2.15 E-08	2.61 E-08	3.54 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B7ZA04	B7ZA04_HUMAN Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1	12.30	2.00		1.00	6.97	3.97	10.93	2.87 E-08		3.89 E-09	9.40 E-08	2.90 E-08	1.24 E-07	3.28	1.01	4.32
P33991	MCM4_HUMAN DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5	19.00	16.97	1.00		1.00		6.00	1.16 E-07	1.61 E-09		6.27 E-09		3.82 E-08	0.05	Control 1 Only	0.33
D3YTB1	D3YTB1_HUMAN 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=2 SV=1	40.60			2.00	4.00	7.00	11.00			1.41 E-07	1.04 E-06	3.09 E-07	2.08 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
H0Y6C3	H0Y6C3_HUMAN Pyrroline-5-carboxylate reductase 3 (Fragment) OS=Homo sapiens GN=PYCRL PE=2 SV=1	21.80	0.99		1.99	1.99	3.98	15.94	4.32 E-08		1.88 E-08	1.10 E-07	8.02 E-08	5.19 E-07	2.55	1.86	12.01
P02538	K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	57.30	4.98	2.98	6.97	3.98	2.98	3.98	6.45 E-08	1.77 E-08	7.45 E-08	4.00 E-08	2.03 E-08	4.38 E-08	0.62	0.31	0.68
Q8WUM4	PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	17.50	23.99					1.00	1.47 E-07					1.29 E-09	Control 1 Only	Control 1 Only	0.01
P17987	TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	16.90	10.85		1.97	1.98	1.98	6.91	1.99 E-07		1.82 E-08	3.04 E-08	8.17 E-09	1.05 E-07	0.15	0.04	0.53
F6SBX2	F6SBX2_HUMAN Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=2 SV=1	16.00	5.00			1.00	3.00	15.00	3.28 E-08			1.88 E-09	4.19 E-09	6.60 E-08	0.06	0.13	2.01
Q14692	BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	8.80				7.00	10.00	7.00				4.13 E-08	2.21 E-08	3.06 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9BYN8	RT26_HUMAN 28S ribosomal protein S26, mitochondrial OS=Homo sapiens GN=MRPS26 PE=1 SV=1	31.70				2.00	6.00	16.00				1.21 E-07	2.13 E-07	8.87 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P21964	COMT_HUMAN Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2	45.20			4.97	4.98	1.99	11.95			1.98 E-07	6.28 E-07	1.63 E-08	5.78 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
O95373	IPO7_HUMAN Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	8.80			3.00	6.00	5.00	9.00			8.95 E-09	2.61 E-08	1.17 E-08	4.38 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q92973	TNPO1_HUMAN Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	14.80	0.99	1.98	0.99	6.95	7.93	4.94	9.43 E-09	4.37 E-09	1.33 E-08	5.54 E-08	2.44 E-08	3.43 E-08	5.87	2.59	3.63
Q9BVA1	TBB2B_HUMAN Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	77.50	0.50	0.50	1.50	4.00	3.50	6.50	4.89 E-09	6.19 E-09	2.44 E-08	2.10 E-07	6.57 E-08	2.06 E-07	42.91	13.42	42.01
A1L0T0	ILVBL_HUMAN Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2	23.60	1.99		1.00	1.99	1.99	14.89	2.63 E-08		2.55 E-09	1.75 E-08	1.85 E-08	2.56 E-07	0.67	0.70	9.73
F5GXC8	F5GXC8_HUMAN Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=2 SV=1	30.10	0.99			2.96	2.97	13.86	9.23 E-09			4.62 E-08	2.46 E-08	2.85 E-07	5.01	2.66	30.91
Q13464	ROCK1_HUMAN Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	15.20	15.00	2.00	3.00			3.00	6.21 E-08	1.26 E-09	4.03 E-09			4.66 E-09	Control 1 Only	Control 1 Only	0.08
Q1KMD3	HNRL2_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1	21.00	2.00	2.00		2.00	11.00	1.00	9.52 E-07	6.05 E-08		1.18 E-08	4.12 E-08	3.41 E-09	0.01	0.04	0.00
Q6DT37	MRCKG_HUMAN Serine/threonine-protein kinase MRCK gamma OS=Homo sapiens GN=CDC42BPG PE=1 SV=2	8.80	2.00			5.00	3.00	13.00	4.67 E-09			1.03 E-08	3.70 E-09	3.32 E-08	2.21	0.79	7.12
Q9H	AGO3_HUMAN Protein argonaute-3 OS=Homo	17.20				10.0	6.00	7.00				5.78	2.60	4.92	Sample	Sample	Sample

9G7	sapiens GN=AGO3 PE=1 SV=2					0						E-07	E-07	E-07	1 Only	2 Only	3 Only
B7Z4C8	B7Z4C8_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=2 SV=1	43.50			4.00	3.00	4.00	9.00			6.75 E-07	1.19 E-06	7.49 E-07	3.05 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
B9EGP5	B9EGP5_HUMAN MON2 protein OS=Homo sapiens GN=MON2 PE=2 SV=1	6.00	3.00		2.00	5.00	3.00	9.00	6.62 E-09		4.20 E-09	9.72 E-09	3.77 E-09	2.92 E-08	1.47	0.57	4.41
C9J3L7	C9J3L7_HUMAN Replication initiator 1 OS=Homo sapiens GN=REPIN1 PE=2 SV=2	18.70				8.98	6.97	5.99				7.31 E-08	6.07 E-08	9.11 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
J3KN39	J3KN39_HUMAN NACHT, LRR and PYD domains-containing protein 2 OS=Homo sapiens GN=NLRP2 PE=2 SV=1	9.40	8.94	2.97	1.00	1.00	1.98	5.95	4.97 E-08	3.60 E-09	5.72 E-09	2.35 E-09	1.77 E-09	1.48 E-08	0.05	0.04	0.30
O00231	PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	27.30		3.00	1.00	4.00	2.00	12.00		2.85 E-08	2.61 E-08	5.35 E-08	1.33 E-08	2.49 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P05141	ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	32.60	1.00	1.00	5.00	4.00	1.00	10.00	5.98 E-08	2.39 E-08	1.44 E-07	1.75 E-07	4.84 E-09	4.70 E-07	2.92	0.08	7.86
Q8IY17	PLPL6_HUMAN Neuropathy target esterase OS=Homo sapiens GN=PNPLA6 PE=1 SV=2	10.60	2.00			3.99	1.00	14.95	4.33 E-09			9.79 E-09	8.49 E-10	3.58 E-08	2.26	0.20	8.27
M0R2B7	M0R2B7_HUMAN DNA polymerase OS=Homo sapiens GN=POLD1 PE=2 SV=1	14.50	8.95		2.99	0.99		8.97	2.74 E-08		2.80 E-09	1.83 E-09		2.44 E-08	0.07	Control 1 Only	0.89
P22087	FBRL_HUMAN rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2	32.40			2.97		1.98	15.86			4.08 E-08		1.68 E-08	3.92 E-07		Sample 2 Only	Sample 3 Only
E9PM69	E9PM69_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=2 SV=1	29.70	7.94		1.97	0.99		6.97	2.14 E-07		4.07 E-08	1.72 E-08		1.66 E-07	0.08	Control 1 Only	0.78
F5H1X8	F5H1X8_HUMAN Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=2 SV=1	4.60	2.98	0.99		5.99	3.98	6.97	3.79 E-09	1.99 E-10		6.96 E-09	2.27 E-09	6.21 E-09	1.84	0.60	1.64
P50454	SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	28.00	2.98		1.99	0.99	2.99	11.91	9.40 E-08		2.70 E-08	1.08 E-08	2.04 E-08	2.50 E-07	0.11	0.22	2.66
O75382	TRIM3_HUMAN Tripartite motif-containing protein 3 OS=Homo sapiens GN=TRIM3 PE=1 SV=2	21.40				0.99	0.98	18.79				1.06 E-08	8.60 E-09	2.24 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q07960	RHG01_HUMAN Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1	17.50	4.00	1.99	4.98	1.00	1.00	7.96	7.22 E-08	9.64 E-09	5.15 E-08	7.87 E-09	3.88 E-09	1.28 E-07	0.11	0.05	1.78
Q13608	PEX6_HUMAN Peroxisome assembly factor 2 OS=Homo sapiens GN=PEX6 PE=1 SV=2	15.70	3.00			5.00	2.00	11.00	9.94 E-09			1.86 E-08	2.96 E-09	3.90 E-08	1.87	0.30	3.93
O95625	ZBT11_HUMAN Zinc finger and BTB domain-containing protein 11 OS=Homo sapiens GN=ZBTB11 PE=1 SV=2	11.90				3.00	14.00	3.00				1.83 E-08	3.52 E-08	1.38 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P18085	ARF4_HUMAN ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	26.70	1.97	0.99	4.92	1.97	1.97	7.88	2.26 E-07	1.60 E-08	2.72 E-07	2.00 E-07	2.05 E-08	4.58 E-07	0.88	0.09	2.02
O15270	SPTC2_HUMAN Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1	31.00	1.00			1.00	3.00	14.99	9.89 E-09			3.98 E-09	1.74 E-08	3.37 E-07	0.40	1.76	34.06
O75367	H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	31.20			4.00			15.99			5.80 E-08			4.15 E-07			Sample 3 Only
P00966	ASSY_HUMAN Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	18.00	17.00		1.00			2.00	6.64 E-07		7.18 E-09			2.91 E-08	Control 1 Only	Control 1 Only	0.04
P05387	RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	95.70			1.00	3.00	6.00	10.00			1.64 E-07	6.53 E-07	3.96 E-07	3.28 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q13501	SQSTM_HUMAN Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1	25.20				1.98	3.96	12.89				3.76 E-08	4.41 E-08	3.92 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q4ZG55	GREB1_HUMAN Protein GREB1 OS=Homo sapiens GN=GREB1 PE=2 SV=1	7.50	2.00			2.00	4.00	12.00	1.92 E-09			2.19 E-09	2.59 E-09	2.14 E-08	1.14	1.35	11.13

Q9P2R3	ANFY1_HUMAN Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2	11.80	9.00	5.98	3.00		1.00	1.00	4.30 E-08	5.85 E-09	1.19 E-09		3.43 E-10	1.68 E-09	Control 1 Only	0.01	0.04
Q9UBV2	SE1L1_HUMAN Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3	12.60	4.00	1.00		3.00	3.00	8.00	4.23 E-08	4.11 E-09		2.88 E-08	1.57 E-08	5.94 E-08	0.68	0.37	1.40
P40939	ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	12.50	15.00	1.00	2.00	1.00			2.22 E-07	4.81 E-09	2.15 E-08	8.65 E-09			0.04	Control 1 Only	Control 1 Only
A6NFI3	ZN316_HUMAN Zinc finger protein 316 OS=Homo sapiens GN=ZNF316 PE=1 SV=1	11.60				7.00	7.00	5.00				5.31 E-08	1.53 E-08	9.01 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y3U8	RL36_HUMAN 60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	30.50			1.00	1.99	2.99	8.98			3.69 E-08	2.90 E-07	1.67 E-07	1.15 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4E0X2	B4E0X2_HUMAN RAF proto-oncogene serine/threonine-protein kinase OS=Homo sapiens GN=RAF1 PE=2 SV=1	38.30				4.00	2.99	11.99				6.50 E-08	2.28 E-08	1.70 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P24928	RPB1_HUMAN DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2	10.30	2.00				1.00	16.00	3.51 E-09				1.85 E-10	2.30 E-08	Control 1 Only	0.05	6.54
K7EKS7	K7EKS7_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=2 SV=1	52.10	1.00	1.00	3.00	3.00	3.00	8.00	1.26 E-06	1.28 E-07	1.01 E-06	3.00 E-06	5.79 E-07	2.76 E-06	2.39	0.46	2.20
Q9H4Y5	GSTO2_HUMAN Glutathione S-transferase omega-2 OS=Homo sapiens GN=GSTO2 PE=1 SV=1	23.90		1.96	3.94	5.89	2.94	3.94		3.25 E-08	1.41 E-07	6.99 E-07	6.98 E-08	1.71 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
G8JLH9	G8JLH9_HUMAN Signal transducer and activator of transcription OS=Homo sapiens GN=STAT3 PE=2 SV=1	15.80	6.00	1.00	5.00	1.00	1.00	4.00	7.27 E-08	4.63 E-09	4.64 E-08	5.97 E-09	5.84 E-09	3.87 E-08	0.08	0.08	0.53
P25398	RS12_HUMAN 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	34.10			1.00	4.00	4.00	8.00			1.38 E-07	1.28 E-06	1.75 E-07	1.02 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
A8MXP9	A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	16.20				0.98	3.94	12.82				3.84 E-09	1.62 E-08	5.83 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P38646	GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	15.50	2.00		3.00	5.00	1.00	7.00	9.84 E-09		2.71 E-08	4.38 E-08	4.44 E-09	9.33 E-08	4.45	0.45	9.48
P49368	TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	23.70	3.96		2.97	2.97		7.91	4.87 E-08		2.55 E-08	3.98 E-08		1.24 E-07	0.82	Control 1 Only	2.54
O95347	SMC2_HUMAN Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	14.30	4.99	2.00	1.00		1.00	8.98	2.24 E-08	8.07 E-09	6.42 E-10		4.84 E-09	2.35 E-08	Control 1 Only	0.22	1.05
B7Z817	B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1	5.90	3.00	2.00	2.00	1.00	2.00	6.00	7.29 E-08	9.78 E-09	2.43 E-08	1.15 E-08	2.53 E-08	9.57 E-08	0.16	0.35	1.31
F8W9B4	F8W9B4_HUMAN Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=2 SV=1	40.40				2.00		14.95				8.03 E-08		8.12 E-07	Sample 1 Only		Sample 3 Only
I3L2C7	I3L2C7_HUMAN Gem-associated protein 4 OS=Homo sapiens GN=GEMIN4 PE=2 SV=1	3.20			1.98	2.97	4.98	5.95			3.57 E-08	2.10 E-07	7.53 E-09	2.34 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
O75083	WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	22.40	16.96						3.46 E-07						Control 1 Only	Control 1 Only	Control 1 Only
P07996	TSP1_HUMAN Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	10.80				5.00	3.00	9.00				1.38 E-08	4.61 E-09	4.87 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q86TG7	PEG10_HUMAN Retrotransposon-derived protein PEG10 OS=Homo sapiens GN=PEG10 PE=1 SV=2	19.40				1.00	6.00	10.00				4.72 E-09	2.27 E-08	9.77 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
J3KSP6	J3KSP6_HUMAN Fucokinase, isoform CRA_d OS=Homo sapiens GN=FUK PE=2 SV=1	20.20	1.50		1.00	3.00	0.50	2.50	5.93 E-09		7.38 E-09	2.66 E-08	1.70 E-09	2.45 E-08	4.48	0.29	4.14
Q9NYU2	UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens	11.20	14.00		1.00	1.00		1.00	5.22 E-08		9.80 E-10	7.25 E-10		9.81 E-10	0.01	Control 1 Only	0.02

	GN=UGGT1 PE=1 SV=3																
B4DWW1	B4DWW1_HUMAN ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=2 SV=1	20.70			2.97	2.97	2.97	6.93			2.01E-07	2.00E-07	4.86E-08	8.77E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4DXM1	B4DXM1_HUMAN FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=2 SV=1	20.30	6.00	2.00	5.00		1.00	2.00	2.69E-07	1.48E-08	1.51E-07		9.92E-09	7.84E-08	Control 1 Only	0.04	0.29
E9PMI6	E9PMI6_HUMAN Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=2 SV=1	44.30	1.99	3.00	4.99	1.00	2.00	3.00	1.05E-06	1.25E-07	6.36E-07	3.24E-07	9.81E-08	4.97E-07	0.31	0.09	0.47
G3V3G9	G3V3G9_HUMAN DDB1- and CUL4-associated factor 8 OS=Homo sapiens GN=DCAF8 PE=2 SV=1	8.00	2.99		2.00	5.98	1.99	2.98	3.46E-08		1.81E-08	8.55E-08	3.36E-09	2.38E-08	2.47	0.10	0.69
P49748	ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	17.20	10.99	1.00	1.99		1.00	1.00	1.66E-07	3.22E-09	1.42E-08		1.53E-09	6.34E-09	Control 1 Only	0.01	0.04
Q14566	MCM6_HUMAN DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	24.00	15.00						1.37E-07						Control 1 Only	Control 1 Only	Control 1 Only
E9PD53	E9PD53_HUMAN Structural maintenance of chromosomes protein OS=Homo sapiens GN=SMC4 PE=2 SV=1	8.50	5.00	1.00	1.00	2.00		6.00	1.97E-08	5.80E-10	8.80E-10	5.01E-09		1.04E-08	0.25	Control 1 Only	0.53
F5H4B6	F5H4B6_HUMAN Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=2 SV=1	19.30	14.99						1.34E-07						Control 1 Only	Control 1 Only	Control 1 Only
F8WCY5	F8WCY5_HUMAN Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=2 SV=1	24.30					5.94	7.92					1.93E-07	3.98E-07		Sample 2 Only	Sample 3 Only
H3BTN5	H3BTN5_HUMAN Pyruvate kinase (Fragment) OS=Homo sapiens GN=PKM PE=2 SV=1	28.20	10.90	0.99		1.98		0.99	1.81E-07	5.42E-09		2.30E-08		1.30E-08	0.13	Control 1 Only	0.07
P04259	K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	59.90	5.00	1.00	5.00		2.00	2.00	6.01E-08	2.60E-09	4.46E-08		4.91E-09	1.21E-08	Control 1 Only	0.08	0.20
Q04695	K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	41.70	0.99	1.00	4.98		2.00	4.97	5.45E-09	9.92E-09	3.34E-08		7.18E-09	3.41E-08	Control 1 Only	1.32	6.26
B3KSH1	B3KSH1_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1	28.80	4.00	1.00	1.00	1.00	1.00	6.00	1.11E-07	1.08E-08	1.26E-08	7.58E-09	8.36E-09	1.20E-07	0.07	0.08	1.08
B4DQI4	B4DQI4_HUMAN Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=2 SV=1	30.30	2.00		1.00		1.00	9.99	3.77E-07		1.77E-08		2.44E-08	6.07E-07	Control 1 Only	0.06	1.61
B4E1G6	B4E1G6_HUMAN Galactokinase OS=Homo sapiens GN=GALK1 PE=2 SV=1	18.10	3.00	1.00	1.00			9.00	1.06E-07	5.52E-09	1.39E-08			1.67E-07	Control 1 Only	Control 1 Only	1.59
P40227	TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	20.30	2.97			2.97		7.92	4.73E-08			3.93E-08		1.03E-07	0.83	Control 1 Only	2.17
P51659	DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	11.30		3.97	3.97	2.98		2.97		1.52E-08	3.06E-08	3.06E-08		2.00E-08	Sample 1 Only		Sample 3 Only
J3KR97	J3KR97_HUMAN Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=2 SV=1	4.30	1.98		2.97	1.98		5.94	9.76E-09		9.41E-09	6.83E-09		1.37E-08	0.70	Control 1 Only	1.41
O60884	DNJA2_HUMAN DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	11.20				2.00	4.00	5.00				9.41E-08	5.24E-08	1.06E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P61513	RL37A_HUMAN 60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2	66.30				2.99	2.98	6.96				1.14E-06	1.85E-07	1.16E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q5QPL9	Q5QPL9_HUMAN RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1	19.30				0.98	2.96	9.88				3.39E-08	3.80E-08	3.34E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only

Q9923	SORT_HUMAN Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3	6.70	4.00			4.00	3.00	2.00	2.24E-08			1.54E-08	5.31E-09	1.15E-08	0.69	0.24	0.51
Q13509	TBB3_HUMAN Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	48.20	1.00			3.99	4.00	4.99	3.58E-08			1.35E-07	5.11E-08	5.84E-07	3.77	1.43	16.33
Q9H3U1-2	UN45A_HUMAN Isoform 2 of Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A	11.90	5.00		1.00	2.00		5.99	2.07E-08		4.42E-09	5.55E-09		4.12E-08	0.27	Control 1 Only	1.99
Q14258	TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	17.30	1.00				3.00	9.00	1.04E-08				1.49E-08	1.29E-07	Control 1 Only	1.42	12.31
Q5D862	FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	7.10	6.00		3.00	2.00	1.00	1.00	1.12E-08		3.15E-09	5.01E-09	7.66E-10	7.68E-10	0.45	0.07	0.07
Q9Y6D5	BIG2_HUMAN Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Homo sapiens GN=ARFGEF2 PE=1 SV=3	9.30				3.00	0.50	8.00				6.61E-09	2.66E-10	1.16E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E5RJ68	E5RJ68_HUMAN AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=2 SV=1	7.00	1.00		1.00	1.00		10.00	3.41E-09		5.08E-09	5.95E-09		7.20E-08	1.75	Control 1 Only	21.15
E9PEZ1	E9PEZ1_HUMAN Cullin-9 OS=Homo sapiens GN=CUL9 PE=2 SV=1	3.10				2.00	2.00	9.00				2.38E-09	7.69E-10	1.29E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
F8W845	F8W845_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=2 SV=1	11.70	0.98				0.99	10.86	3.65E-09				1.51E-09	5.65E-08	Control 1 Only	0.42	15.50
H0Y4R1	H0Y4R1_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=3 SV=1	19.60	6.99		3.99			1.99	1.89E-07		5.80E-08			3.46E-08	Control 1 Only	Control 1 Only	0.18
P53597	SUCA_HUMAN Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4	17.30				1.00		12.00				9.15E-08		3.49E-07	Sample 1 Only		Sample 3 Only
P81605	DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	42.70	2.00		6.00			3.00	5.49E-08		1.87E-07			6.66E-08	Control 1 Only	Control 1 Only	1.21
Q16401	PSMD5_HUMAN 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3	21.50	3.00	2.00	3.00			5.00	4.31E-08	1.12E-08	3.64E-08			9.14E-08	Control 1 Only	Control 1 Only	2.12
Q7L576	CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	6.90	5.91	3.94	1.97			1.00	3.50E-08	4.57E-09	4.54E-09			1.76E-09	Control 1 Only	Control 1 Only	0.05
Q9BRS2	RIOK1_HUMAN Serine/threonine-protein kinase RIO1 OS=Homo sapiens GN=RIOK1 PE=1 SV=2	15.00	1.00	1.00	1.00		1.00	7.00	2.70E-08	4.26E-09	1.26E-08		7.81E-09	1.08E-07	Control 1 Only	0.29	4.00
O00232	PSD12_HUMAN 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	11.20		1.00	1.00	2.00	2.00	6.00		2.33E-09	1.28E-08	3.41E-08	1.13E-08	9.51E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P49257	LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	9.60	5.00	2.00	1.00	1.00	1.00	1.00	1.82E-07	1.60E-08	1.61E-08	1.16E-08	1.08E-08	2.94E-08	0.06	0.06	0.16
B4DN45	B4DN45_HUMAN S-adenosylmethionine synthase OS=Homo sapiens GN=MAT2A PE=2 SV=1	20.10	4.00	2.00			1.00	4.00	2.56E-07	3.79E-08			1.59E-08	1.39E-07	Control 1 Only	0.06	0.54
P25205	MCM3_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	16.00	10.92						6.94E-08						Control 1 Only	Control 1 Only	Control 1 Only
P31689	DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	14.40				2.99	1.99	6.97				5.13E-08	2.80E-08	1.82E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
D3DQ30	D3DQ30_HUMAN HCG40295, isoform CRA_d OS=Homo sapiens GN=TTC39A PE=2 SV=1	13.60	0.99		1.98	2.97	1.98	3.97	4.50E-09		1.57E-08	4.74E-08	1.70E-08	7.14E-08	10.55	3.79	15.89
P35	AHR_HUMAN Aryl hydrocarbon receptor	7.90				3.00	4.00	5.00				2.62	1.38	4.77	Sample	Sample	Sample

869	OS=Homo sapiens GN=AHR PE=1 SV=2											E-08	E-08	E-08	1 Only	2 Only	3 Only
P42338	PK3CB_HUMAN Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit beta isoform OS=Homo sapiens GN=PIK3CB PE=1 SV=1	7.70				0.99	2.99	7.96				2.32 E-09	5.23 E-09	2.20 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6KB66	K2C80_HUMAN Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	21.30			4.00			7.00			2.13 E-08			9.06 E-08			Sample 3 Only
P12236	ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	32.20	2.00	1.00	2.00	2.00	1.00	4.00	1.16 E-07	1.24 E-08	7.80 E-08	8.71 E-08	1.54 E-08	2.21 E-07	0.75	0.13	1.90
Q02413	DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	8.90	2.00		5.00	2.00	1.00	2.00	9.80 E-09		1.93 E-08	4.20 E-09	1.46 E-09	3.41 E-09	0.43	0.15	0.35
Q14764	MVP_HUMAN Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	7.80				3.00	5.00	3.00				5.33 E-08	7.56 E-09	5.34 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9UPN7	PP6R1_HUMAN Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5	7.20	1.00		1.00	1.00	1.00	8.00	1.13 E-09		3.33 E-09	1.77 E-09	1.22 E-09	4.17 E-08	1.57	1.08	37.09
Q9Y678	COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	5.90	2.00	1.00		2.00		2.00	1.52 E-08	1.47 E-09		2.05 E-08		1.53 E-08	1.34	Control 1 Only	1.00
F5GWF6	F5GWF6_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=2 SV=2	22.10	1.00			1.00		9.00	9.35 E-09			1.21 E-08		9.51 E-08	1.30	Control 1 Only	10.18
O43933	PEX1_HUMAN Peroxisome biogenesis factor 1 OS=Homo sapiens GN=PEX1 PE=1 SV=1	7.80		1.00		3.00		7.00		2.92 E-09		1.33 E-08		1.92 E-08	Sample 1 Only		Sample 3 Only
P05023	AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	10.50	10.85						7.56 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q14139	UBE4A_HUMAN Ubiquitin conjugation factor E4 A OS=Homo sapiens GN=UBE4A PE=1 SV=2	7.60	2.00			5.00	1.00	3.00	8.46 E-09			1.51 E-08	1.43 E-09	7.67 E-09	1.78	0.17	0.91
Q6R327	RICTR_HUMAN Rapamycin-insensitive companion of mTOR OS=Homo sapiens GN=RICTOR PE=1 SV=1	5.40				1.00	5.00	5.00				3.54 E-09	4.76 E-09	8.28 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8N3C0	ASCC3_HUMAN Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3	3.60	1.00				2.00	8.00	1.93 E-09				1.33 E-09	9.90 E-09	Control 1 Only	0.69	5.13
Q92947	GCDH_HUMAN Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=GCDH PE=1 SV=1	16.40				0.99	0.99	8.91				1.54 E-08	5.16 E-09	1.69 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9P2M7	CING_HUMAN Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	4.40		1.00	3.00			4.98		1.60 E-09	8.76 E-09			1.27 E-08			Sample 3 Only
Q9NUQ8	ABCF3_HUMAN ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2	9.00	7.00		1.00	2.00			6.48 E-08		3.68 E-09	1.53 E-08			0.24	Control 1 Only	Control 1 Only
B4DK71	B4DK71_HUMAN Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=2 SV=1	8.10	2.97	0.99		1.98		3.96	4.92 E-08	2.72 E-09		1.88 E-08		7.10 E-08	0.38	Control 1 Only	1.44
P21266	GSTM3_HUMAN Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	25.30	0.99	4.98	2.99			0.99	1.22 E-07	1.34 E-07	1.03 E-07			3.53 E-08	Control 1 Only	Control 1 Only	0.29
E9PAV3	E9PAV3_HUMAN Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=2 SV=1	59.20	1.00		4.00		1.00	4.00	2.85 E-09		1.92 E-08		5.47 E-09	2.15 E-08	Control 1 Only	1.92	7.54
O75306	NDUS2_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=1 SV=2	15.50			1.00		2.00	7.00			6.58 E-09		1.68 E-08	1.57 E-07		Sample 2 Only	Sample 3 Only
P61254	RL26_HUMAN 60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	55.20			0.98	1.00	1.50	3.46			5.85 E-08	3.17 E-07	4.75 E-07	1.80 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only

Q15293	RCN1_HUMAN Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1	15.40					3.00	7.00					3.02 E-08	2.02 E-07		Sample 2 Only	Sample 3 Only
Q93100-3	KPBB_HUMAN Isoform 3 of Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB	8.40	1.98					6.93	3.54 E-09					2.41 E-08	Control 1 Only	Control 1 Only	6.81
Q99714	HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	14.20			2.99	2.00		4.98			6.71 E-08	8.40 E-08		1.37 E-07	Sample 1 Only		Sample 3 Only
E5RHU3	E5RHU3_HUMAN Syndecan-2 (Fragment) OS=Homo sapiens GN=SDC2 PE=2 SV=2	16.80				1.00		8.00				3.18 E-08		3.21 E-07	Sample 1 Only		Sample 3 Only
E9PE17	E9PE17_HUMAN 28S ribosomal protein S17, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS17 PE=2 SV=1	14.00	1.00			3.00	2.00	3.00	5.84 E-08			2.95 E-07	4.03 E-08	3.67 E-07	5.05	0.69	6.28
Q8NF37	PCAT1_HUMAN Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2	11.80	1.00	1.00				7.00	5.63 E-09	1.00 E-09				9.97 E-08	Control 1 Only	Control 1 Only	17.71
A0FGR8-2	ESYT2_HUMAN Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2	5.80	2.00			2.00		4.97	4.59 E-09			4.19 E-09		3.42 E-08	0.91	Control 1 Only	7.44
Q9ULX6	AKP8L_HUMAN A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L PE=1 SV=3	5.00				3.00	2.00	4.00				1.71 E-08	3.53 E-09	3.78 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4DMU0	B4DMU0_HUMAN Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYCR1 PE=2 SV=1	12.90	0.99	0.99	2.97	0.99		2.97	4.02 E-08	7.84 E-09	5.15 E-08	3.90 E-08		5.93 E-08	0.97	Control 1 Only	1.48
H7C3T4	H7C3T4_HUMAN Peroxiredoxin-4 (Fragment) OS=Homo sapiens GN=PRDX4 PE=4 SV=1	16.10	1.00	0.50	1.00	1.00		1.50	2.59 E-07	9.70 E-09	4.27 E-08	9.16 E-08		4.50 E-08	0.35	Control 1 Only	0.17
B4DZI8	B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	4.60	1.00			1.00	1.00	5.98	6.00 E-09			3.26 E-09	1.90 E-09	2.29 E-08	0.54	0.32	3.82
P10398	ARAF_HUMAN Serine/threonine-protein kinase A-Raf OS=Homo sapiens GN=ARAF PE=1 SV=2	18.00				1.00	2.00	6.00				1.69 E-08	1.52 E-08	7.94 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7ERK9	E7ERK9_HUMAN Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=2 SV=1	14.60				3.00	3.00	3.00				3.63 E-08	1.49 E-08	5.33 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
F5GZS6	F5GZS6_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=2 SV=1	8.70	6.93					0.99	1.32 E-07					1.76 E-08	Control 1 Only	Control 1 Only	0.13
P42224	STAT1_HUMAN Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2	7.50	7.98			1.00			6.15 E-08			6.40 E-09			0.10	Control 1 Only	Control 1 Only
P56537	IF6_HUMAN Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	17.10			2.00		1.00	6.00			4.78 E-08		1.90 E-08	2.28 E-07		Sample 2 Only	Sample 3 Only
Q53G59	KLH12_HUMAN Kelch-like protein 12 OS=Homo sapiens GN=KLHL12 PE=1 SV=2	7.40	4.95			2.97		0.99	7.90 E-08			2.89 E-08		1.59 E-08	0.37	Control 1 Only	0.20
Q8TE77	SSH3_HUMAN Protein phosphatase Slingshot homolog 3 OS=Homo sapiens GN=SSH3 PE=1 SV=2	11.30	6.93					0.99	5.32 E-08					1.53 E-08	Control 1 Only	Control 1 Only	0.29
Q8WUY1	THEM6_HUMAN Protein THEM6 OS=Homo sapiens GN=THEM6 PE=1 SV=2	29.30	1.00		1.00			7.00	5.12 E-08		2.29 E-08			2.70 E-07	Control 1 Only	Control 1 Only	5.27
P04350	TBB4A_HUMAN Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	81.30	0.99		1.00	4.00	1.00	1.98	4.15 E-08		2.66 E-08	1.37 E-06	5.79 E-09	1.26 E-07	32.91	0.14	3.02
Q9BUP0	EFHD1_HUMAN EF-hand domain-containing protein D1 OS=Homo sapiens GN=EFHD1	33.50			9.00						2.71 E-07						

	PE=1 SV=1																
Q9BV44	THUM3_HUMAN THUMP domain-containing protein 3 OS=Homo sapiens GN=THUMPD3 PE=1 SV=1	12.20	1.00					7.00	9.29 E-09					8.33 E-08	Control 1 Only	Control 1 Only	8.97
Q9UN37	VPS4A_HUMAN Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1	16.70	0.99			1.00		7.00	4.22 E-09			1.99 E-08		1.59 E-07	4.72	Control 1 Only	37.64
Q9Y5V3	MAGD1_HUMAN Melanoma-associated antigen D1 OS=Homo sapiens GN=MAGED1 PE=1 SV=3	7.80				1.00		7.99				4.71 E-09		1.07 E-07	Sample 1 Only		Sample 3 Only
B4E241	B4E241_HUMAN Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SFRS3 PE=2 SV=1	30.60			1.00	2.00	3.00	2.00			1.56 E-07	3.56 E-07	1.80 E-07	7.51 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
A2AE48	A2AE48_HUMAN Tripartite motif-containing protein 26 (Fragment) OS=Homo sapiens GN=TRIM26 PE=2 SV=1	19.00				1.00	2.99	4.00				3.03 E-08	3.53 E-08	1.68 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4DEM7	B4DEM7_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1	13.80	0.99			3.96	0.99	1.98	8.99 E-09			4.35 E-08	6.66 E-09	2.46 E-08	4.84	0.74	2.73
E9PPM8	E9PPM8_HUMAN Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=2 SV=1	7.30	0.99		0.99	0.99	0.99	3.96	1.02 E-08		1.01 E-08	1.05 E-08	3.04 E-09	8.01 E-08	1.03	0.30	7.84
B4DFJ5	B4DFJ5_HUMAN 28S ribosomal protein S25, mitochondrial OS=Homo sapiens GN=MRPS25 PE=2 SV=1	50.00					4.00	4.00					1.26 E-07	3.55 E-07		Sample 2 Only	Sample 3 Only
B4E2W0	B4E2W0_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1	6.00	0.99	1.97	1.97	1.98		0.99	2.47 E-08	1.30 E-08	4.17 E-08	3.55 E-08		1.04 E-08	1.44	Control 1 Only	0.42
Q9Y6Q5	AP1M2_HUMAN AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2 PE=1 SV=4	51.80	0.50			1.99	0.50	1.99	1.18 E-08			1.04 E-07	4.35 E-09	9.30 E-08	8.84	0.37	7.91
P38935	SMBP2_HUMAN DNA-binding protein SMUBP-2 OS=Homo sapiens GN=IGHMBP2 PE=1 SV=3	6.30					0.99	6.98					1.24 E-09	3.00 E-08		Sample 2 Only	Sample 3 Only
P50991	TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	7.70	1.00	1.00	1.00	1.00		3.00	8.89 E-09	3.29 E-09	3.34 E-09	1.54 E-08		4.01 E-08	1.73	Control 1 Only	4.51
P53396	ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	7.10	4.96			0.99		1.99	1.91 E-08			9.39 E-10		8.22 E-09	0.05	Control 1 Only	0.43
Q6ZN55	ZN574_HUMAN Zinc finger protein 574 OS=Homo sapiens GN=ZNF574 PE=1 SV=2	9.60				2.00	6.00					6.43 E-09	1.48 E-08		Sample 1 Only	Sample 2 Only	
Q96HS1	PGAM5_HUMAN Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	11.40					1.00	6.00					1.38 E-08	2.10 E-07		Sample 2 Only	Sample 3 Only
H0Y653	H0Y653_HUMAN Nucleolar protein 56 (Fragment) OS=Homo sapiens GN=NOP56 PE=4 SV=1	22.40						6.00						2.60 E-07			Sample 3 Only
O00487	PSDE_HUMAN 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	11.00			1.00	2.00	1.00	3.00			2.10 E-08	7.36 E-08	1.14 E-08	6.94 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O14802	RPC1_HUMAN DNA-directed RNA polymerase III subunit RPC1 OS=Homo sapiens GN=POLR3A PE=1 SV=2	3.90	1.00			1.00	1.00	4.00	3.72 E-09			2.31 E-09	9.04 E-10	1.06 E-08	0.62	0.24	2.84
Q7Z3Y8	K1C27_HUMAN Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	17.00				1.00	4.98					1.55 E-08	2.12 E-08		Sample 1 Only	Sample 2 Only	
Q96CS3	FAF2_HUMAN FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2	14.60	1.00		1.00			5.00	1.62 E-08		5.53 E-09			6.94 E-08	Control 1 Only	Control 1 Only	4.29

Q9Y676	RT18B_HUMAN 28S ribosomal protein S18b, mitochondrial OS=Homo sapiens GN=MRPS18B PE=1 SV=1	26.40					2.00	5.00					3.05 E-08	1.13 E-07		Sample 2 Only	Sample 3 Only
O15397	IPO8_HUMAN Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2	2.10	4.00			1.00	1.00		1.26 E-08			3.71 E-09	5.57 E-10		0.29	0.04	Control 1 Only
P04207	KV308_HUMAN Ig kappa chain V-III region CLL OS=Homo sapiens PE=1 SV=2	19.40	1.98		2.98		0.99	0.99	7.58 E-07		1.83 E-07		2.06 E-08	6.94 E-08	Control 1 Only	0.03	0.09
P47914	RL29_HUMAN 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	14.50				1.00	4.00	2.00				1.06 E-08	1.79 E-07	8.80 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4DVY1	B4DVY1_HUMAN Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=2 SV=1	12.60	5.00					2.00	7.61 E-08					2.05 E-08	Control 1 Only	Control 1 Only	0.27
B7Z1R5	B7Z1R5_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=2 SV=1	7.40	4.00	1.00				2.00	5.08 E-08	2.00 E-09				2.44 E-08	Control 1 Only	Control 1 Only	0.48
C9JA93	C9JA93_HUMAN TBC1 domain family member 15 (Fragment) OS=Homo sapiens GN=TBC1D15 PE=2 SV=1	15.80	3.96					2.97	8.44 E-08					6.89 E-08	Control 1 Only	Control 1 Only	0.82
C9JAB2	C9JAB2_HUMAN Serine/arginine-rich-splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=2 SV=1	37.90					1.00	6.00					1.35 E-08	2.02 E-07		Sample 2 Only	Sample 3 Only
E7EWT1	E7EWT1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=2 SV=1	7.40		3.00	1.00	1.00		2.00		1.72 E-08	5.09 E-09	6.92 E-09		2.76 E-08	Sample 1 Only		Sample 3 Only
K7ELC2	K7ELC2_HUMAN 40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=2 SV=1	34.80						7.00						9.12 E-07			Sample 3 Only
Q8NB90	SPAT5_HUMAN Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3	7.20				0.99	1.99	3.98				4.60 E-09	3.69 E-09	1.75 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P62714	PP2AB_HUMAN Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1	23.90						6.92						2.43 E-07			Sample 3 Only
P11388	TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	2.20			1.99	1.00	2.00	1.99			2.22 E-09	1.49 E-09	2.06 E-09	5.34 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P12830	CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	6.60	1.00					5.99	3.59 E-09					3.00 E-08	Control 1 Only	Control 1 Only	8.35
Q8IWV7	UBR1_HUMAN E3 ubiquitin-protein ligase UBR1 OS=Homo sapiens GN=UBR1 PE=1 SV=1	3.70			1.00		1.00	4.99			1.23 E-09		9.87 E-10	7.23 E-09		Sample 2 Only	Sample 3 Only
Q99832	TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	8.20	2.97			1.98		1.98	3.06 E-08			2.38 E-08		1.98 E-08	0.78	Control 1 Only	0.65
Q9BRZ2	TRI56_HUMAN E3 ubiquitin-protein ligase TRIM56 OS=Homo sapiens GN=TRIM56 PE=1 SV=3	7.40				2.00	1.99	2.99				7.98 E-09	6.91 E-09	3.26 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9BSJ8	ESYT1_HUMAN Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	4.50				1.00	1.00	4.00				2.19 E-09	1.62 E-09	1.01 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9BYK8	HELZ2_HUMAN Helicase with zinc finger domain 2 OS=Homo sapiens GN=HELZ2 PE=1 SV=6	3.10						7.00						5.93 E-09			Sample 3 Only
J3KNW4	J3KNW4_HUMAN Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=2 SV=1	13.60		1.00			2.00	3.00		9.13 E-09			1.94 E-08	5.38 E-08		Sample 2 Only	Sample 3 Only
P06702	S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	31.60	1.00		3.00		2.00		2.75 E-08		1.70 E-07		4.51 E-08		Control 1 Only	1.64	Control 1 Only
P10	CH60_HUMAN 60 kDa heat shock protein,	7.90	2.00	2.00				1.00	2.70	4.95				9.29	Control	Control	0.34

809	mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2								E-08	E-09				E-09	1 Only	1 Only	
P14174	MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	23.50			1.00	3.00					4.83 E-08	2.87 E-07			Sample 1 Only		
Q96A35	RM24_HUMAN 39S ribosomal protein L24, mitochondrial OS=Homo sapiens GN=MRPL24 PE=1 SV=1	16.20					1.00	4.00					8.49 E-09	1.50 E-07		Sample 2 Only	Sample 3 Only
B4DYD8	B4DYD8_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	8.30			1.00	2.00		2.00			1.43 E-08	4.31 E-08		4.00 E-08	Sample 1 Only		Sample 3 Only
F8VZ44	F8VZ44_HUMAN Aladin OS=Homo sapiens GN=AAAS PE=2 SV=1	6.40	1.99	0.99	0.99			1.99	3.34 E-08	4.27 E-09	9.55 E-09			2.39 E-08	Control 1 Only	Control 1 Only	0.71
P52292	IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	5.90	3.00		1.00	1.00		1.00	4.69 E-08		1.04 E-08	9.66 E-09		1.09 E-08	0.21	Control 1 Only	0.23
P18583	SON_HUMAN Protein SON OS=Homo sapiens GN=SON PE=1 SV=4	4.60				0.99		4.97				1.23 E-09		4.33 E-09	Sample 1 Only		Sample 3 Only
B7Z909	B7Z909_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=2 SV=1	6.30	1.00			3.99		1.00	4.39 E-09			4.12 E-08		1.01 E-08	9.38	Control 1 Only	2.29
Q5T749	KPRP_HUMAN Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	4.70	1.00	1.00	1.00	1.00	2.00		4.30 E-09	3.62 E-09	1.41 E-08	5.21 E-09	6.41 E-09		1.21	1.49	Control 1 Only
P35749	MYH11_HUMAN Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	15.20		0.50	2.00	0.50		0.50		4.24 E-10	3.21 E-09	5.95 E-10		8.87 E-10	Sample 1 Only		Sample 3 Only
E7ENA9	E7ENA9_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=2 SV=2	11.30	1.98					3.96	2.61 E-08					2.98 E-08	Control 1 Only	Control 1 Only	1.14
E7ENJ6	E7ENJ6_HUMAN AP-1 complex subunit mu-1 OS=Homo sapiens GN=AP1M1 PE=2 SV=1	29.50				0.99	1.98	2.97				6.55 E-09	2.06 E-08	6.76 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E9PBF6	E9PBF6_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=2 SV=1	15.20			2.97			2.97			4.66 E-08			6.13 E-08			Sample 3 Only
E9PJN0	E9PJN0_HUMAN Acyl-coenzyme A thioesterase 8 OS=Homo sapiens GN=ACOT8 PE=2 SV=1	11.50			1.00	1.00	1.00	3.00			2.50 E-08	1.92 E-08	6.03 E-09	1.68 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
F5H0N7	F5H0N7_HUMAN CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1 PE=2 SV=1	8.40						6.00						1.44 E-08			Sample 3 Only
P48729	KC1A_HUMAN Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=2	17.80						5.94						1.38 E-07			Sample 3 Only
H0YMV8	H0YMV8_HUMAN 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=2 SV=1	25.00						2.97						4.10 E-07			Sample 3 Only
H7BZJ3	H7BZJ3_HUMAN Thioredoxin (Fragment) OS=Homo sapiens GN=PDIA3 PE=2 SV=1	20.30	3.00	1.00			1.00	1.00	1.22 E-07	1.58 E-08			2.92 E-08	6.18 E-08	Control 1 Only	0.24	0.51
P52907	CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	8.70			4.00			2.00			7.43 E-08			3.27 E-08			Sample 3 Only
Q562R1	ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	27.40			3.00	1.00	2.00				5.03 E-06	4.58 E-08	3.94 E-08		Sample 1 Only	Sample 2 Only	
P63220	RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	45.70				1.00		5.00				5.52 E-07		7.70 E-07	Sample 1 Only		Sample 3 Only
P04844	RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	31.10	1.00	1.00				3.00	1.70 E-08	6.70 E-09				4.30 E-08	Control 1 Only	Control 1 Only	2.53
Q08378	GOGA3_HUMAN Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2	2.70			0.99	1.99	0.99	1.98			5.03 E-10	2.78 E-09	4.19 E-10	3.35 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q13011	ECH1_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo	9.80			2.99			3.00			1.04 E-07			9.25 E-08			Sample 3 Only

	sapiens GN=ECH1 PE=1 SV=2																
Q53GQ0	DHB12_HUMAN Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2	18.90				1.00	0.99	3.99				5.41 E-08	4.38 E-09	1.42 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6YN16	HSDL2_HUMAN Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	14.20	1.00		2.00	1.00		1.00	2.36 E-08		2.67 E-08	2.06 E-08		8.76 E-09	0.87	Control 1 Only	0.37
Q92734	TFG_HUMAN Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=2	13.90				1.00		4.00				1.29 E-08		7.77 E-08	Sample 1 Only		Sample 3 Only
Q96FS4	SIPA1_HUMAN Signal-induced proliferation-associated protein 1 OS=Homo sapiens GN=SIPA1 PE=1 SV=1	5.10						6.00						4.17 E-08			Sample 3 Only
Q13885	TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	68.80				2.00	1.00	3.00				4.60 E-08	1.82 E-08	1.07 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9UNM6	PSD13_HUMAN 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2	12.20			0.99			4.94			8.38 E-09			7.25 E-08			Sample 3 Only
H0Y9R3	H0Y9R3_HUMAN WD repeat-containing protein 26 (Fragment) OS=Homo sapiens GN=WDR26 PE=4 SV=1	10.50				1.00		3.00				2.32 E-08		9.73 E-08	Sample 1 Only		Sample 3 Only
P05109	S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	23.70			3.00		2.00				1.24 E-07		6.12 E-08			Sample 2 Only	
P13807	GYS1_HUMAN Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2	6.80	2.98			0.99			4.06 E-08			4.51 E-09			0.11	Control 1 Only	Control 1 Only
Q9Y2T2	AP3M1_HUMAN AP-3 complex subunit mu-1 OS=Homo sapiens GN=AP3M1 PE=1 SV=1	10.50				1.00		4.00				6.57 E-09		6.30 E-08	Sample 1 Only		Sample 3 Only
Q9Y2X3	NOP58_HUMAN Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1	11.90						5.00						8.70 E-08			Sample 3 Only
B1AJY5	B1AJY5_HUMAN 26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens GN=PSMD10 PE=2 SV=1	29.20	1.00					4.00	6.15 E-08					1.43 E-07	Control 1 Only	Control 1 Only	2.33
F5H8J2	F5H8J2_HUMAN Uncharacterized protein OS=Homo sapiens GN=P4HB PE=3 SV=1	14.50	2.97			0.99		0.99	1.84 E-08			3.25 E-09		1.25 E-08	0.18	Control 1 Only	0.68
B4DLV4	B4DLV4_HUMAN Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT2 PE=2 SV=1	15.40	3.96		0.99				1.80 E-07		2.39 E-09				Control 1 Only	Control 1 Only	Control 1 Only
B4DZ67	B4DZ67_HUMAN Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=2 SV=1	5.50		0.99				3.97		1.11 E-09				1.26 E-08			Sample 3 Only
Q15057	ACAP2_HUMAN Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ACAP2 PE=1 SV=3	4.80	3.00			1.00		1.00	2.43 E-08			9.66 E-09		1.19 E-08	0.40	Control 1 Only	0.49
P42858	HD_HUMAN Huntingtin OS=Homo sapiens GN=HTT PE=1 SV=2	1.90	1.00			2.00		2.00	1.90 E-09			1.71 E-09		2.62 E-09	0.90	Control 1 Only	1.38
P30153	2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	7.10			0.99		0.99	2.97			4.51 E-09		2.30 E-09	2.19 E-08		Sample 2 Only	Sample 3 Only
E7ESC6	E7ESC6_HUMAN Exportin-7 OS=Homo sapiens GN=XPO7 PE=2 SV=1	2.80				3.00	1.00	1.00				9.95 E-09	1.32 E-09	1.73 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
E9PET8	E9PET8_HUMAN Kinesin heavy chain isoform 5C OS=Homo sapiens GN=KIF5C PE=2 SV=2	2.70	1.99			0.99	1.99		1.23 E-08			6.33 E-09	2.81 E-09		0.52	0.23	Control 1 Only
E9PJN1	E9PJN1_HUMAN Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA4 PE=2 SV=1	6.40						4.94						3.37 E-08			Sample 3 Only

P48047	ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	22.50	4.00		1.00				4.43 E-07		2.33 E-08				Control 1 Only	Control 1 Only	Control 1 Only
P05386	RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	28.90			1.00	1.00	1.00	2.00			3.43 E-07	3.34 E-07	1.98 E-07	1.24 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q13057	COASY_HUMAN Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4	5.70	2.97		0.99			0.99	5.11 E-08		4.51 E-09			5.74 E-09	Control 1 Only	Control 1 Only	0.11
P09960	LKHA4_HUMAN Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2	7.70	5.00						6.79 E-08						Control 1 Only	Control 1 Only	Control 1 Only
P11498	PYC_HUMAN Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2	7.70	5.00						2.16 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q6P2Q9	PRP8_HUMAN Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	2.10						5.00						3.78 E-09			Sample 3 Only
Q96RQ1	ERGI2_HUMAN Endoplasmic reticulum-Golgi intermediate compartment protein 2 OS=Homo sapiens GN=ERGIC2 PE=1 SV=2	9.00					1.98	1.98					1.73 E-08	5.44 E-08		Sample 2 Only	Sample 3 Only
Q9H4M9	EHD1_HUMAN EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2	10.30	4.94						9.13 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q9H6S0	YTDC2_HUMAN Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=1 SV=2	3.10						4.99						7.79 E-09			Sample 3 Only
Q9ULT8	HECD1_HUMAN E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3	3.00	3.00					2.00	3.93 E-09					9.63 E-10	Control 1 Only	Control 1 Only	0.24
E9PNW8	E9PNW8_HUMAN Fatty acyl-CoA reductase 1 (Fragment) OS=Homo sapiens GN=FAR1 PE=2 SV=1	11.30	1.00	1.00		1.00		1.00	1.69 E-08	1.52 E-08		9.65 E-09		2.03 E-08	0.57	Control 1 Only	1.20
J3QLR8	J3QLR8_HUMAN 28S ribosomal protein S23, mitochondrial OS=Homo sapiens GN=MRPS23 PE=2 SV=1	19.70					1.00	3.00					2.62 E-08	1.63 E-07		Sample 2 Only	Sample 3 Only
O95714	HERC2_HUMAN E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2	0.80						4.00						1.63 E-09			Sample 3 Only
P59665	DEF1_HUMAN Neutrophil defensin 1 OS=Homo sapiens GN=DEFA1 PE=1 SV=1	19.10		2.00			2.00			4.13 E-08			2.95 E-08			Sample 2 Only	
Q9H4L5	OSBL3_HUMAN Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 PE=1 SV=1	3.90			1.00			3.00			2.43 E-09			7.73 E-09			Sample 3 Only
Q9Y6N5	SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	5.80	2.00	1.00			1.00		1.38 E-07	1.54 E-08			3.06 E-08		Control 1 Only	0.22	Control 1 Only
G3V2A4	G3V2A4_HUMAN Telomerase protein component 1 OS=Homo sapiens GN=TEP1 PE=2 SV=1	3.20				1.00	1.00	2.00				1.95 E-09	7.79 E-10	2.55 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
O43837	IDH3B_HUMAN Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2	7.30						3.98						9.18 E-08			Sample 3 Only
P46977	STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	4.10	2.00					2.00	3.71 E-08					1.82 E-08	Control 1 Only	Control 1 Only	0.49
Q05086	UBE3A_HUMAN Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A PE=1 SV=4	4.30	2.00			1.00		1.00	1.44 E-08			7.43 E-09		6.23 E-09	0.52	Control 1 Only	0.43

J3QRD1	J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=2 SV=1	5.60	1.00		1.00			1.00	5.07 E-09		1.57 E-08			1.48 E-08	Control 1 Only	Control 1 Only	2.92
P18827	SDC1_HUMAN Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3	11.90			1.00			3.00			7.33 E-09			3.10 E-08			Sample 3 Only
P41240	CSK_HUMAN Tyrosine-protein kinase CSK OS=Homo sapiens GN=CSK PE=1 SV=1	5.30	1.99	1.00	1.00				8.12 E-08	8.10 E-09	7.48 E-09				Control 1 Only	Control 1 Only	Control 1 Only
Q3KQU3	MA7D1_HUMAN MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1	3.10					2.00	1.00					3.10 E-09	5.31 E-09		Sample 2 Only	Sample 3 Only
O00767	ACOD_HUMAN Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2	7.00			1.00		1.00	2.00			1.33 E-08		1.35 E-08	5.81 E-08		Sample 2 Only	Sample 3 Only
Q3LXA3	DHAK_HUMAN Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2	4.20	0.99			1.99		0.99	4.07 E-09			1.58 E-08		4.57 E-09	3.88	Control 1 Only	1.12
K7EJC1	K7EJC1_HUMAN 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=2 SV=1	9.30			1.00	1.00		2.00			4.36 E-08	7.90 E-08		1.02 E-07	Sample 1 Only		Sample 3 Only
B7ZLZ2	B7ZLZ2_HUMAN ER degradation-enhancing alpha-mannosidase-like protein 3 OS=Homo sapiens GN=EDEM3 PE=2 SV=1	6.10					1.00	3.00					1.97 E-09	7.46 E-09		Sample 2 Only	Sample 3 Only
E7EX29	E7EX29_HUMAN 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1	16.70	0.99		0.99			1.98	1.45 E-07		1.93 E-08			4.46 E-08	Control 1 Only	Control 1 Only	0.31
F5GYR8	F5GYR8_HUMAN General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=2 SV=1	5.20	3.00					1.00	1.50 E-08					1.23 E-09	Control 1 Only	Control 1 Only	0.08
H0YL92	H0YL92_HUMAN Importin-4 OS=Homo sapiens GN=IPO4 PE=2 SV=1	18.40			1.00		1.00	2.00			2.25 E-08		1.54 E-08	1.14 E-07		Sample 2 Only	Sample 3 Only
P51665	PSMD7_HUMAN 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	16.40				0.99	1.99	1.00				1.68 E-08	2.27 E-08	1.85 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P24844	MYL9_HUMAN Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4	70.90			3.00			1.00			2.63 E-07			7.08 E-08			Sample 3 Only
K7EPU3	K7EPU3_HUMAN Chitobiosyldiphosphodolichol beta-mannosyltransferase (Fragment) OS=Homo sapiens GN=ALG1 PE=2 SV=1	15.80	1.00			1.00		2.00	9.45 E-08			6.42 E-08		9.76 E-08	0.68	Control 1 Only	1.03
O43615	TIM44_HUMAN Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2	8.20						4.00						4.76 E-08			Sample 3 Only
O60264	SMCA5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1	2.80						3.00						6.57 E-09			Sample 3 Only
O75643	U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	1.50	1.00					3.00	2.92 E-09					3.31 E-09	Control 1 Only	Control 1 Only	1.13
P01876	IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	15.60	3.00	1.00					3.49 E-08	1.69 E-08					Control 1 Only	Control 1 Only	Control 1 Only
Q01546	K22O_HUMAN Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2	15.50		3.97						4.14 E-08							
P10	RO60_HUMAN 60 kDa SS-A/Ro	6.40	1.00			1.00	1.00	1.00	1.00			1.25	6.95	9.72	1.25	0.69	0.97

155	ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=1 SV=2								E-08			E-08	E-09	E-09			
P10412	H14_HUMAN Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	16.90						4.00						1.80 E-07			Sample 3 Only
B0FLL2	B0FLL2_HUMAN 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 2 transcript variant 3 OS=Homo sapiens GN=PFKFB2 PE=2 SV=1	15.10	0.99					2.97	2.50 E-08					2.58 E-08	Control 1 Only	Control 1 Only	1.03
Q75MJ1	Q75MJ1_HUMAN ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=2 SV=1	9.80						4.00						6.76 E-08			Sample 3 Only
B4DFA2	B4DFA2_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1	5.00	1.00		1.00	1.00		1.00	1.17 E-08		3.77 E-09	7.64 E-09		5.56 E-09	0.65	Control 1 Only	0.48
Q96HJ9-2	CG055_HUMAN Isoform 2 of UPF0562 protein C7orf55 OS=Homo sapiens GN=C7orf55	8.20					1.00	3.00					7.11 E-09	3.75 E-08		Sample 2 Only	Sample 3 Only
Q9BZK7	TBL1R_HUMAN F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens GN=TBL1XR1 PE=1 SV=1	8.00					2.00	2.00					6.02 E-09	1.05 E-08		Sample 2 Only	Sample 3 Only
Q9UBB4	ATX10_HUMAN Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1	14.40					0.99	2.97					3.86 E-09	4.86 E-08		Sample 2 Only	Sample 3 Only
K7EJ81	K7EJ81_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=2 SV=1	5.40						3.00						7.30 E-09			Sample 3 Only
Q8NFQ8	TOIP2_HUMAN Torsin-1A-interacting protein 2 OS=Homo sapiens GN=TOR1AIP2 PE=1 SV=1	8.50						3.00						5.58 E-08			Sample 3 Only
B4DET3	B4DET3_HUMAN Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=2 SV=1	2.60		2.00			1.00			6.70 E-09			1.21 E-09			Sample 2 Only	
B4DEK7	B4DEK7_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=2 SV=1	23.90					0.99	1.98					1.07 E-08	8.58 E-08		Sample 2 Only	Sample 3 Only
B4E0R6	B4E0R6_HUMAN Importin-5 OS=Homo sapiens GN=IPO5 PE=2 SV=1	3.30				1.00		2.00				4.98 E-09		1.36 E-08	Sample 1 Only		Sample 3 Only
P55072	TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	3.00	2.00			1.00			6.09 E-09			3.60 E-09			0.59	Control 1 Only	Control 1 Only
Q9Y657	SPIN1_HUMAN Spindlin-1 OS=Homo sapiens GN=SPIN1 PE=1 SV=3	8.80	1.00		2.00				6.69 E-08		7.88 E-08				Control 1 Only	Control 1 Only	Control 1 Only
H7C1E4	H7C1E4_HUMAN AP-1 complex subunit sigma-1A (Fragment) OS=Homo sapiens GN=AP1S1 PE=4 SV=1	15.80					1.00	2.00					1.09 E-08	8.36 E-08		Sample 2 Only	Sample 3 Only
B4DGU4	B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1	3.10						2.50						1.60 E-08			Sample 3 Only
P53007	TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	10.30	1.00					2.00	3.08 E-08					3.82 E-08	Control 1 Only	Control 1 Only	1.24
Q02790	FKBP4_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	7.60						3.00						4.59 E-08			Sample 3 Only
Q8IZT6	ASPM_HUMAN Abnormal spindle-like microcephaly-associated protein OS=Homo sapiens GN=ASPM PE=1 SV=2	1.00						3.00						1.83 E-09			Sample 3 Only
Q9BW92	SYTM_HUMAN Threonine--tRNA ligase, mitochondrial OS=Homo sapiens GN=TARS2 PE=1 SV=1	5.60	2.99						1.75 E-08						Control 1 Only	Control 1 Only	Control 1 Only
B5ME19	EIFCL_HUMAN Eukaryotic translation initiation factor 3 subunit C-like protein OS=Homo	2.40	2.00					1.00	1.02 E-08					2.69 E-09	Control 1 Only	Control 1 Only	0.26

	sapiens GN=EIF3CL PE=2 SV=1																
H0Y FP3	H0YFP3_HUMAN Protoporphyrinogen oxidase (Fragment) OS=Homo sapiens GN=PPOX PE=4 SV=1	9.60	1.00		1.00			1.00	4.57 E-08		1.60 E-08			2.39 E-08	Control 1 Only	Control 1 Only	0.52
P47 929	LEG7_HUMAN Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	14.00			3.00						6.75 E-08						
P31 431	SDC4_HUMAN Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2	15.70						2.00						2.27 E-08			Sample 3 Only
Q9H 497	TOR3A_HUMAN Torsin-3A OS=Homo sapiens GN=TOR3A PE=1 SV=1	8.30						2.97						4.26 E-08			Sample 3 Only
B3K QC5	B3KQC5_HUMAN Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase OS=Homo sapiens GN=MAN1B1 PE=2 SV=1	9.50				2.00		1.00				1.69 E-08		3.08 E-09	Sample 1 Only		Sample 3 Only
J3Q KW2	J3QKW2_HUMAN 28S ribosomal protein S7, mitochondrial OS=Homo sapiens GN=MRPS7 PE=2 SV=1	14.20					2.00	1.00					2.43 E-08	2.61 E-08		Sample 2 Only	Sample 3 Only
C9J 1V9	C9J1V9_HUMAN HCG2043275 OS=Homo sapiens GN=hCG_2043275 PE=4 SV=2	13.20			0.99			1.98			2.03 E-08			8.30 E-08			Sample 3 Only
Q96 EY7	PTCD3_HUMAN Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3	3.60						3.00						3.39 E-08			Sample 3 Only
C9IZ E4	C9IZE4_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=2 SV=1	10.30					2.00	1.00					1.08 E-08	1.36 E-08		Sample 2 Only	Sample 3 Only
E9P C74	E9PC74_HUMAN Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=2 SV=1	4.50				1.00		2.00				1.30 E-08		1.98 E-08	Sample 1 Only		Sample 3 Only
Q9Y 4R8	TELO2_HUMAN Telomere length regulation protein TEL2 homolog OS=Homo sapiens GN=TELO2 PE=1 SV=2	3.00						3.00						1.81 E-08			Sample 3 Only
I3L1 P8	I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens GN=SLC25A11 PE=2 SV=1	12.20						3.00						5.89 E-08			Sample 3 Only
O60 678	ANM3_HUMAN Protein arginine N-methyltransferase 3 OS=Homo sapiens GN=PRMT3 PE=1 SV=3	4.50	3.00						5.50 E-08						Control 1 Only	Control 1 Only	Control 1 Only
G3V 198	G3V198_HUMAN Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=2 SV=1	1.50				0.99		1.99				2.65 E-09		4.23 E-09	Sample 1 Only		Sample 3 Only
E7E MB6	E7EMB6_HUMAN Aspartyl aminopeptidase OS=Homo sapiens GN=DNPEP PE=2 SV=1	6.30	1.00					2.00	2.33 E-08					3.50 E-08	Control 1 Only	Control 1 Only	1.50
B3K VR1	B3KVR1_HUMAN Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPN PE=2 SV=1	8.90			0.99	0.99		0.99			1.84 E-09	1.31 E-08		2.70 E-08	Sample 1 Only		Sample 3 Only
C9K 0G7	C9K0G7_HUMAN D-beta-hydroxybutyrate dehydrogenase, mitochondrial (Fragment) OS=Homo sapiens GN=BDH1 PE=2 SV=1	13.20	0.99					1.99	5.90 E-08					7.61 E-08	Control 1 Only	Control 1 Only	1.29
B7Z 418	B7Z418_HUMAN Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=2 SV=1	7.20						2.97						4.87 E-08			Sample 3 Only
Q96 9Z0	TBRG4_HUMAN Protein TBRG4 OS=Homo sapiens GN=TBRG4 PE=1 SV=1	3.00	2.97						2.54 E-08						Control 1 Only	Control 1 Only	Control 1 Only
P26 640	SYVC_HUMAN Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4	4.00	3.00						1.09 E-08						Control 1 Only	Control 1 Only	Control 1 Only
F5H 5Y3	F5H5Y3_HUMAN Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68	7.00					1.00	2.00					7.55 E-09	4.59 E-08		Sample 2 Only	Sample 3 Only

	PE=2 SV=1																
P46939	UTRO_HUMAN Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2	1.30						3.00						2.77 E-09			Sample 3 Only
H3BR94	H3BR94_HUMAN Dynactin subunit 5 OS=Homo sapiens GN=DCTN5 PE=2 SV=1	13.80			1.99			0.99			1.26 E-07			3.31 E-08			Sample 3 Only
Q8NB46	ANR52_HUMAN Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit C OS=Homo sapiens GN=ANKRD52 PE=1 SV=3	4.80	1.00					2.00	7.65 E-09					5.63 E-09	Control 1 Only	Control 1 Only	0.73
O75489	NDUS3_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1	20.10						3.00						1.36 E-07			Sample 3 Only
P62913-2	RL11_HUMAN Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11	61.60					1.00	2.00					1.33 E-08	4.75 E-08		Sample 2 Only	Sample 3 Only
P16401	H15_HUMAN Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	8.80					1.00	2.00					1.29 E-08	1.20 E-07		Sample 2 Only	Sample 3 Only
Q9NVN8	GNL3L_HUMAN Guanine nucleotide-binding protein-like 3-like protein OS=Homo sapiens GN=GNL3L PE=1 SV=1	6.40						3.00						2.68 E-08			Sample 3 Only
Q9ULE0	WWC3_HUMAN Protein WWC3 OS=Homo sapiens GN=WWC3 PE=1 SV=3	1.80						3.00						9.13 E-09			Sample 3 Only
B4E1J0	B4E1J0_HUMAN Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens GN=PBXIP1 PE=2 SV=1	3.90						2.00						1.40 E-08			Sample 3 Only
P02765	FETUA_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	3.50	2.00						1.33 E-08						Control 1 Only	Control 1 Only	Control 1 Only
P62857	RS28_HUMAN 40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	30.40						2.00						4.72 E-07			Sample 3 Only
Q9Y3D8	KAD6_HUMAN Adenylate kinase isoenzyme 6 OS=Homo sapiens GN=AK6 PE=1 SV=1	10.70						2.00						1.26 E-07			Sample 3 Only
B3KQ95	B3KQ95_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1	11.40						2.00						4.23 E-08			Sample 3 Only
A3KMH1	VWA8_HUMAN von Willebrand factor A domain-containing protein 8 OS=Homo sapiens GN=VWA8 PE=1 SV=2	1.90						2.00						3.28 E-09			Sample 3 Only
F5H4R9	F5H4R9_HUMAN Dynamin-2 OS=Homo sapiens GN=DNM2 PE=2 SV=1	2.30						1.99						1.49 E-08			Sample 3 Only
H0YDS0	H0YDS0_HUMAN Ubiquilin-1 (Fragment) OS=Homo sapiens GN=UBQLN1 PE=2 SV=1	16.60	0.99					0.99	3.81 E-08					3.14 E-08	Control 1 Only	Control 1 Only	0.82
Q9NZ01	TECR_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1	8.40						2.00						4.63 E-08			Sample 3 Only
Q70IA6	MOB2_HUMAN MOB kinase activator 2 OS=Homo sapiens GN=MOB2 PE=1 SV=1	12.70	1.00		1.00				5.05 E-08		3.97 E-08				Control 1 Only	Control 1 Only	Control 1 Only
Q96EK5	KBP_HUMAN KIF1-binding protein OS=Homo sapiens GN=KIAA1279 PE=1 SV=1	4.00	2.00						1.68 E-08						Control 1 Only	Control 1 Only	Control 1 Only
B3KY94	B3KY94_HUMAN CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Homo sapiens GN=CDIPT PE=2 SV=1	20.20						1.99						1.39 E-07			Sample 3 Only
D6RDY6	D6RDY6_HUMAN Signal recognition particle subunit SRP72 (Fragment) OS=Homo sapiens GN=SRP72 PE=2 SV=2	6.20						2.00						2.83 E-08			Sample 3 Only
F8WAG2	F8WAG2_HUMAN Serine/threonine-protein kinase Nek7 (Fragment) OS=Homo sapiens GN=NEK7 PE=2 SV=1	22.00						2.00						1.25 E-07			Sample 3 Only

Q09666	AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	1.10						2.00						6.83 E-10			Sample 3 Only
A6H8Z3	A6H8Z3_HUMAN RAB3GAP1 protein OS=Homo sapiens GN=RAB3GAP1 PE=2 SV=1	3.20						2.00						5.18 E-09			Sample 3 Only
B3KP49	B3KP49_HUMAN RAN binding protein 10, isoform CRA_b OS=Homo sapiens GN=RANBP10 PE=2 SV=1	5.40						2.00						3.34 E-08			Sample 3 Only
Q96DV4	RM38_HUMAN 39S ribosomal protein L38, mitochondrial OS=Homo sapiens GN=MRPL38 PE=1 SV=2	4.70						2.00						3.30 E-08			Sample 3 Only
E9PC52	E9PC52_HUMAN Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=2 SV=1	10.10				0.99		0.99				1.19 E-08		1.49 E-08	Sample 1 Only		Sample 3 Only
M0QXB4	M0QXB4_HUMAN Coatomer protein complex, subunit epsilon, isoform CRA_g OS=Homo sapiens GN=COPE PE=2 SV=1	8.20						1.99						6.71 E-08			Sample 3 Only
O43390	HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	3.60				0.99		0.99				6.11 E-09		1.23 E-08	Sample 1 Only		Sample 3 Only
H0Y2W2	H0Y2W2_HUMAN ATPase family AAA domain-containing protein 3A (Fragment) OS=Homo sapiens GN=ATAD3A PE=4 SV=1	4.10						1.98						1.61 E-08			Sample 3 Only
P04080	CYTB_HUMAN Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	24.50				2.00						3.41 E-07			Sample 1 Only		
P30041	PRDX6_HUMAN Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	12.50	1.00		1.00				1.82 E-07		2.22 E-08				Control 1 Only	Control 1 Only	Control 1 Only
Q01081	U2AF1_HUMAN Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3	8.80					2.00						6.90 E-08			Sample 2 Only	
I3L2B0	I3L2B0_HUMAN Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=2 SV=1	5.50	1.99						1.32 E-08						Control 1 Only	Control 1 Only	Control 1 Only
E7ENR4	E7ENR4_HUMAN Hexokinase-1 OS=Homo sapiens GN=HK1 PE=2 SV=1	2.10						2.00						6.06 E-09			Sample 3 Only
Q14126	DSG2_HUMAN Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2	1.70			1.00			1.00			2.17 E-09			2.84 E-09			Sample 3 Only
Q8NCM8	DYHC2_HUMAN Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4	0.60						2.00						1.17 E-09			Sample 3 Only
Q5JTZ9	SYAM_HUMAN Alanine--tRNA ligase, mitochondrial OS=Homo sapiens GN=AARS2 PE=1 SV=1	3.90	2.00						6.47 E-09						Control 1 Only	Control 1 Only	Control 1 Only
Q96QK1	VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	4.30	2.00						2.72 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q9NW08	RPC2_HUMAN DNA-directed RNA polymerase III subunit RPC2 OS=Homo sapiens GN=POLR3B PE=1 SV=2	1.80						2.00						3.48 E-09			Sample 3 Only
Q08380	LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	3.60						1.99						1.41 E-08			Sample 3 Only
P54886	P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	2.60	2.00						1.03 E-08						Control 1 Only	Control 1 Only	Control 1 Only

G3XAB3	G3XAB3_HUMAN Tetratricopeptide repeat domain 17, isoform CRA_c OS=Homo sapiens GN=TTC17 PE=2 SV=1	2.60						2.00						4.87 E-09			Sample 3 Only
Q7Z7G8	VP13B_HUMAN Vacuolar protein sorting-associated protein 13B OS=Homo sapiens GN=VPS13B PE=1 SV=2	0.60						2.00						8.10 E-10			Sample 3 Only
F5H7B0	F5H7B0_HUMAN Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=2 SV=1	3.40				1.00	0.99					2.41 E-09	1.67 E-09		Sample 1 Only	Sample 2 Only	
Q00839	HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	2.90				1.00	1.00					6.57 E-09	3.51 E-09		Sample 1 Only	Sample 2 Only	
Q9Y4C2	F115A_HUMAN Protein FAM115A OS=Homo sapiens GN=FAM115A PE=1 SV=3	2.30						2.00						3.89 E-09			Sample 3 Only
F5H6T1	F5H6T1_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=2 SV=1	8.50						2.00						6.12 E-08			Sample 3 Only
Q13470	TNK1_HUMAN Non-receptor tyrosine-protein kinase TNK1 OS=Homo sapiens GN=TNK1 PE=1 SV=3	2.40						2.00						2.55 E-08			Sample 3 Only
C9JBJ6	C9JBJ6_HUMAN DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens GN=POLR2H PE=2 SV=1	23.70						1.98						1.04 E-07			Sample 3 Only
E7EUT5	E7EUT5_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=2 SV=1	10.40			1.00		1.00				9.99 E-09		3.22 E-09			Sample 2 Only	
A1A528	A1A528_HUMAN Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=2 SV=1	3.00				1.00		1.00				7.19 E-09		1.18 E-08	Sample 1 Only		Sample 3 Only
Q13347	EIF3I_HUMAN Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	9.80		1.00	1.00					5.29 E-09	1.45 E-08						
H3BLU6	H3BLU6_HUMAN E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=2 SV=1	0.80				1.00		1.00				8.45 E-10		8.96 E-10	Sample 1 Only		Sample 3 Only
H0Y3Y9	H0Y3Y9_HUMAN 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens GN=PSMD4 PE=4 SV=1	9.80	0.99					0.99	3.43 E-08					2.92 E-08	Control 1 Only	Control 1 Only	0.85
Q96I99	SUCB2_HUMAN Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2	9.70	1.98						1.67 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q9Y6Q5-2	AP1M2_HUMAN Isoform 2 of AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2	52.50					1.00	1.00					5.40 E-09	2.19 E-08		Sample 2 Only	Sample 3 Only
H7C3E9	H7C3E9_HUMAN Probable ATP-dependent RNA helicase DDX56 (Fragment) OS=Homo sapiens GN=DDX56 PE=4 SV=1	6.10						1.98						1.94 E-08			Sample 3 Only
B4DLW8	B4DLW8_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=2 SV=1	3.90					1.00	1.00					1.00 E-08	1.34 E-08		Sample 2 Only	Sample 3 Only
E5RIT6	E5RIT6_HUMAN 60S ribosomal protein L26-like 1 (Fragment) OS=Homo sapiens GN=RPL26L1 PE=2 SV=1	56.20					0.99	0.99					2.06 E-08	5.10 E-08		Sample 2 Only	Sample 3 Only
P61978	HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	8.20						2.00						1.83 E-08			Sample 3 Only
Q15751	HERC1_HUMAN Probable E3 ubiquitin-protein ligase HERC1 OS=Homo sapiens GN=HERC1	0.70	1.00					1.00	8.79 E-10					2.23 E-10	Control 1 Only	Control 1 Only	0.25

	PE=1 SV=2																
Q7Z794	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	10.60			1.51						3.38 E-09						
Q5XKE5	K2C79_HUMAN Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	18.10		2.00						1.93 E-08							
Q8N1N4	K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	10.60			1.00						7.06 E-09						
Q9Y2T7	YBOX2_HUMAN Y-box-binding protein 2 OS=Homo sapiens GN=YBX2 PE=1 SV=2	15.90					1.00	1.00					1.33 E-08	8.77 E-09		Sample 2 Only	Sample 3 Only
Q13444	ADA15_HUMAN Disintegrin and metalloproteinase domain-containing protein 15 OS=Homo sapiens GN=ADAM15 PE=1 SV=4	3.90						1.98						1.07 E-08			Sample 3 Only
E9PK47	E9PK47_HUMAN Phosphorylase OS=Homo sapiens GN=PYGL PE=2 SV=1	8.60	2.00						1.18 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q7Z7A4	PXK_HUMAN PX domain-containing protein kinase-like protein OS=Homo sapiens GN=PXK PE=1 SV=1	5.20						1.98						2.30 E-08			Sample 3 Only
Q3ZCM7	TBB8_HUMAN Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2	28.60				1.98						6.13 E-08			Sample 1 Only		
Q9NRF8	PYRG2_HUMAN CTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1	5.50	2.00						1.41 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q5TA58	Q5TA58_HUMAN Protein argonaute-1 OS=Homo sapiens GN=AGO1 PE=2 SV=1	19.10				1.00		1.00				5.01 E-09		3.37 E-09	Sample 1 Only		Sample 3 Only
O75843	AP1G2_HUMAN AP-1 complex subunit gamma-like 2 OS=Homo sapiens GN=AP1G2 PE=1 SV=1	3.70						1.00						7.01 E-09			Sample 3 Only
P07384	CAN1_HUMAN Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	2.20						0.99						9.56 E-09			Sample 3 Only
Q969Q0	RL36L_HUMAN 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3	17.00					1.00						1.16 E-07			Sample 2 Only	
Q9NUL7	DDX28_HUMAN Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens GN=DDX28 PE=1 SV=2	4.30						1.00						1.06 E-08			Sample 3 Only
D6RCE2	D6RCE2_HUMAN Tetratricopeptide repeat protein 37 (Fragment) OS=Homo sapiens GN=TTC37 PE=2 SV=1	3.60				1.00						5.49 E-09			Sample 1 Only		
E7EMM2	E7EMM2_HUMAN AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=2 SV=1	2.90						1.00						2.74 E-09			Sample 3 Only
O14980	XPO1_HUMAN Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	1.10					1.00						3.16 E-09			Sample 2 Only	
B7Z1N3	B7Z1N3_HUMAN GPI transamidase component PIG-T OS=Homo sapiens GN=PIGT PE=2 SV=1	9.50						1.00						1.13 E-08			Sample 3 Only
E9PG15	E9PG15_HUMAN 14-3-3 protein theta (Fragment) OS=Homo sapiens GN=YWHAQ PE=2 SV=1	24.80						1.00						2.38 E-08			Sample 3 Only
P61981	1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	19.00						1.00						2.30 E-08			Sample 3 Only
P62258	1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	15.30						0.99						2.08 E-08			Sample 3 Only
F2Z2E2	F2Z2E2_HUMAN Ras GTPase-activating-like protein IQGAP3 OS=Homo sapiens GN=IQGAP3 PE=2 SV=1	2.10						1.00						1.76 E-09			Sample 3 Only
Q86	K2C73_HUMAN Keratin, type II cytoskeletal 73	10.70						0.99						8.64			Sample

Y46	OS=Homo sapiens GN=KRT73 PE=1 SV=1												E-09			3 Only
F8V TV8	F8VTV8_HUMAN Cyclin-dependent kinase 4 OS=Homo sapiens GN=CDK4 PE=2 SV=1	11.80						0.99					4.51 E-08			Sample 3 Only
Q58 FF6	H90B4_HUMAN Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1	17.00	1.00						1.90 E-08					Control 1 Only	Control 1 Only	Control 1 Only
Q8I UE6	H2A2B_HUMAN Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3	37.70						0.99					1.65 E-07			Sample 3 Only
Q9H 4B7	TBB1_HUMAN Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	11.80	1.00						1.40 E-08					Control 1 Only	Control 1 Only	Control 1 Only
Q9H CK5	AGO4_HUMAN Protein argonaute-4 OS=Homo sapiens GN=AGO4 PE=1 SV=2	14.10				1.00						4.13 E-08		Sample 1 Only		

Table A4. Endogenous candidates from cytoplasmic immunoprecipitations that had been treated with RNase.

			SPECTRAL COUNTS						SPECTRAL INDEX (MIC SIn)						RATIOS		
Prot	**Description**	**% Cover**	**C1**	**C2**	**C3**	**S1**	**S2**	**S3**	**C1**	**C2**	**C3**	**S1**	**S2**	**S3**	**S1/C1**	**S2/C1**	**S3/C1**
Q9UKV8	AGO2_HUMAN Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	77.40				149.96	145.97	90.50				2.67E-05	1.73E-05	7.05E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9H9G7	AGO3_HUMAN Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	51.00				45.47	35.45	15.97				3.45E-06	2.15E-06	7.55E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P01859	IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	4.90				3.00	4.00	3.00				1.46E-06	8.16E-07	3.58E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P46736	BRCC3_HUMAN Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=2	37.50				10.89	3.96	2.97				1.69E-06	5.03E-07	1.84E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9UL18	AGO1_HUMAN Protein argonaute-1 OS=Homo sapiens GN=AGO1 PE=1 SV=3	46.20				16.95	11.96	5.99				1.18E-06	4.34E-07	1.94E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q15018	F175B_HUMAN BRISC complex subunit Abro1 OS=Homo sapiens GN=FAM175B PE=1 SV=2	25.30				7.00	5.00	1.00				6.14E-07	2.13E-07	2.54E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9J050	C9J050_HUMAN Choline-phosphate cytidylyltransferase A (Fragment) OS=Homo sapiens GN=PCYT1A PE=2 SV=1	13.90				0.99	2.97	0.99				2.28E-07	4.96E-07	1.28E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
F5H6T1	F5H6T1_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=2 SV=1	13.40				1.00	1.00	3.00				2.09E-07	7.70E-08	2.01E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9UPY3	DICER_HUMAN Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	19.40	0.99	1.00		30.92	36.91	10.00	2.26E-09	3.24E-09		4.03E-07	3.32E-07	9.03E-08	178.36	147.08	39.94
Q8NDV7	TNR6A_HUMAN Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	5.40				7.99	9.98	5.99				1.55E-07	1.08E-07	9.44E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9NTJ5	SAC1_HUMAN Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=1 SV=2	11.10				1.98	2.96	1.97				7.00E-08	9.43E-08	7.81E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
H0Y720	H0Y720_HUMAN Trinucleotide repeat-containing gene 6B protein (Fragment) OS=Homo sapiens GN=TNRC6B PE=4 SV=1	5.70				4.00	2.00	3.00				7.39E-08	1.98E-08	7.19E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P01605	KV113_HUMAN Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1	25.00	15.00	12.00	3.00		2.00	6.00	1.46E-05	4.08E-05	1.35E-06		5.58E-07	2.62E-06	Control 1 Only	0.04	0.18
E9PC52	E9PC52_HUMAN Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=2 SV=1	18.50	1.00			4.97	2.00	1.00	2.68E-08			4.95E-07	8.38E-08	2.29E-08	18.47	3.13	0.85
F5GX33	F5GX33_HUMAN Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=2 SV=1	4.90		1.00		1.99	2.98	1.99		9.73E-09		6.75E-08	1.06E-07	6.11E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P01614	KV201_HUMAN Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	20.40	6.50	4.50	2.00	0.50		3.50	9.47E-06	5.54E-05	2.05E-06	1.34E-06		3.37E-06	0.14	Control 1 Only	0.36
B4DJV5	B4DJV5_HUMAN Periodic tryptophan protein 1 homolog OS=Homo sapiens GN=PWP1 PE=2 SV=1	5.70	2.00	1.00				5.00	5.97E-08	2.47E-08				1.37E-06	Control 1 Only	Control 1 Only	22.91
G3XAB8	G3XAB8_HUMAN Trinucleotide repeat containing 6C, isoform CRA_a OS=Homo sapiens GN=TNRC6C PE=2 SV=1	3.80				1.00	4.00	3.00				4.49E-09	1.80E-08	1.92E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q7L775	EPMIP_HUMAN EPM2A-interacting protein 1 OS=Homo sapiens GN=EPM2AIP1 PE=1 SV=1	10.70		1.00			6.00	2.00		1.80E-08			2.72E-07	4.63E-08		Sample 2 Only	Sample 4:Set8 Only
P12035	K2C3_HUMAN Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3	29.90	3.00	2.00			1.00		1.32E-07	3.11E-08			8.74E-09		Control 1 Only	0.07	Control1 Only

Q9UHD2	TBK1_HUMAN Serine/threonine-protein kinase TBK1 OS=Homo sapiens GN=TBK1 PE=1 SV=1	10.40	2.00	6.00			1.00		2.35E-08	1.36E-07			8.61E-09		Control 1 Only	0.37	Control1 Only
P01625	KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	14.00	4.00	7.00	2.00	1.00	2.00	2.00	1.23E-05	4.87E-05	5.77E-07	3.26E-07	1.67E-06	3.99E-06	0.03	0.14	0.33
H0YKU1	H0YKU1_HUMAN Tropomodulin-3 (Fragment) OS=Homo sapiens GN=TMOD3 PE=4 SV=1	33.70	3.00	6.00	5.00			2.00	2.94E-07	2.16E-06	1.15E-06			4.00E-07	Control 1 Only	Control 1 Only	1.36
P01620	KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	29.40	1.00	2.99		0.99			3.06E-07	1.94E-06		2.78E-07			0.91	Control 1 Only	Control1 Only
E7EQD7	E7EQD7_HUMAN Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=2 SV=1	5.20		1.00		3.00	3.00			1.60E-08		9.11E-08	4.69E-08		Sample 1 Only	Sample 2 Only	
P19013	K2C4_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	51.10		3.97		9.98		2.00		9.45E-08		5.57E-07		1.30E-07	Sample 1 Only		Sample 3 Only
O14950	ML12B_HUMAN Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	83.70	3.00	8.00	12.00			6.00	8.18E-07	7.15E-06	4.98E-06			1.95E-06	Control 1 Only	Control 1 Only	2.38
J3KTE4	J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=2 SV=1	14.00		1.00	1.00			4.00		2.34E-07	8.70E-08			2.08E-06			Sample 3 Only
P06310	KV206_HUMAN Ig kappa chain V-II region RPMI 6410 OS=Homo sapiens PE=4 SV=1	17.30	4.50	3.50	1.00	1.50		3.50	5.38E-06	4.48E-05	1.00E-06	6.01E-06		2.62E-06	1.12	Control 1 Only	0.49
P41250	SYG_HUMAN Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	6.80	2.00	4.00		1.00			5.15E-08	6.80E-08		1.80E-08			0.35	Control 1 Only	Control1 Only
Q9HCC0	MCCB_HUMAN Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	17.90		2.00		4.00	4.00	1.00		8.67E-08		2.61E-07	1.71E-07	4.55E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8N163	CCAR2_HUMAN Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2	16.10	3.96	0.99		8.91	10.89		5.49E-08	1.08E-08		1.68E-07	1.91E-07		3.07	3.47	Control1 Only
J3QRN6	J3QRN6_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=2 SV=1	8.70	5.00	4.99	3.00			3.00	2.08E-07	1.40E-07	4.40E-08			7.24E-08	Control 1 Only	Control 1 Only	0.35
P22830	HEMH_HUMAN Ferrochelatase, mitochondrial OS=Homo sapiens GN=FECH PE=1 SV=2	21.50	1.98	1.98		6.93	3.96		7.16E-08	1.14E-07		6.87E-07	2.58E-07		9.60	3.60	Control1 Only
Q13085	ACACA_HUMAN Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	2.20	0.99	2.97				0.99	4.27E-09	2.39E-08				3.87E-09	Control 1 Only	Control 1 Only	0.91
Q9H4H8	FA83D_HUMAN Protein FAM83D OS=Homo sapiens GN=FAM83D PE=1 SV=3	6.50	1.00	1.00		3.00	2.00	1.00	2.60E-08	3.49E-08		2.18E-07	6.38E-08	3.50E-08	8.38	2.45	1.35
Q9BTE3	MCMBP_HUMAN Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2	8.40		1.00		1.00	1.00	3.00		2.72E-08		3.04E-08	1.52E-08	9.81E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q14139	UBE4A_HUMAN Ubiquitin conjugation factor E4 A OS=Homo sapiens GN=UBE4A PE=1 SV=2	4.70	1.00	3.00		1.00			3.54E-08	7.83E-08		2.15E-08			0.61	Control 1 Only	Control1 Only
P05023	AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	4.80		0.99		1.98	2.97			8.42E-09		2.34E-08	2.43E-08		Sample 1 Only	Sample 2 Only	
Q7Z3Y8	K1C27_HUMAN Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	18.70	1.99			4.96	1.00		5.07E-08			2.01E-07	3.10E-08		3.95	0.61	Control1 Only
P36578	RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	27.60	7.98	8.97		2.99	1.99	24.88	6.48E-07	1.04E-06		8.75E-08	7.51E-08	6.82E-06	0.14	0.12	10.52
E9PJM3	E9PJM3_HUMAN F-box only protein 3 OS=Homo sapiens GN=FBXO3 PE=2 SV=1	12.60	1.00	3.00		1.00		1.00	3.67E-08	5.20E-07		9.24E-08		3.92E-08	2.52	Control 1 Only	1.07
Q9UBS4	DJB11_HUMAN DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1	24.60	1.00	9.00		1.00	2.00	4.00	9.53E-08	3.67E-06		1.25E-07	3.34E-07	4.65E-07	1.31	3.51	4.88
Q92616	GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	8.80	5.00	17.00		1.00	5.00	1.00	4.21E-08	1.66E-07		3.51E-09	4.18E-08	4.89E-09	0.08	0.99	0.12

P22626	ROA2_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	27.60	2.00			1.00		7.00	1.51 E-07			3.45 E-08		5.73 E-07	0.23	Control 1 Only	3.79
O00159-3	MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	15.10	4.86	4.24	4.24			4.24	1.40 E-07	1.27 E-07	8.43 E-08			8.89 E-08	Control 1 Only	Control 1 Only	0.64
O60547	GMDS_HUMAN GDP-mannose 4,6 dehydratase OS=Homo sapiens GN=GMDS PE=1 SV=1	21.30		1.00		7.00	1.00	1.00		1.71 E-07		5.75 E-07	5.31 E-08	3.02 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JSQ1	C9JSQ1_HUMAN Creatine kinase U-type, mitochondrial (Fragment) OS=Homo sapiens GN=CKMT1B PE=2 SV=1	24.10		4.94		2.97	1.98	0.99		2.05 E-06		2.85 E-07	1.86 E-07	7.57 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y3I0	RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	20.20	1.00	3.00		6.00	10.00	3.00	5.48 E-08	2.43 E-07		4.07 E-07	5.68 E-07	1.29 E-07	7.43	10.37	2.36
E7ESC6	E7ESC6_HUMAN Exportin-7 OS=Homo sapiens GN=XPO7 PE=2 SV=1	3.60	1.00	3.00		1.00			8.80 E-09	5.03 E-08		1.42 E-08			1.62	Control 1 Only	Control1 Only
P0CG38	POTEI_HUMAN POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1	9.60	0.99	2.98	4.00			3.00	2.77 E-08	1.87 E-07	2.86 E-07			1.35 E-07	Control 1 Only	Control 1 Only	4.88
O43242	PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	17.80		1.00		2.00	4.00	3.00		9.86 E-08		5.24 E-08	2.24 E-07	7.67 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8IYB1	M21D2_HUMAN Protein MB21D2 OS=Homo sapiens GN=MB21D2 PE=1 SV=3	15.50		1.00		4.00	4.00	1.00		9.08 E-08		1.75 E-07	1.13 E-07	2.38 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P62424	RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	22.90	2.97	3.97	0.99	1.98		15.95	2.78 E-07	7.46 E-07	8.46 E-08	8.92 E-08		3.52 E-06	0.32	Control 1 Only	12.66
P60709	ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	80.80	124.78	90.63	121.02	46.68	43.80	141.30	9.68 E-05	2.27 E-04	1.63 E-04	1.63 E-05	1.59 E-05	1.23 E-04	0.17	0.16	1.27
P35579	MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	77.80	208.81	424.57	318.79	15.00	36.98	336.80	8.07 E-06	2.38 E-05	2.54 E-05	1.75 E-07	5.02 E-07	1.74 E-05	0.02	0.06	2.16
P30101	PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	17.20	0.99	0.99		0.99	2.98	4.98	4.40 E-08	7.89 E-08		4.59 E-08	1.89 E-07	1.64 E-07	1.04	4.30	3.73
Q13247	SRSF6_HUMAN Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2	7.50	0.99	0.99				7.94	1.03 E-07	1.31 E-07				7.47 E-07	Control 1 Only	Control 1 Only	7.26
O95822	DCMC_HUMAN Malonyl-CoA decarboxylase, mitochondrial OS=Homo sapiens GN=MLYCD PE=1 SV=3	20.70	1.00	1.00		3.00	5.00	1.00	4.67 E-08	8.90 E-08		1.60 E-07	2.21 E-07	5.56 E-08	3.44	4.74	1.19
E9PG35	E9PG35_HUMAN Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=MCCC1 PE=2 SV=1	16.70		4.97		1.00		0.99		1.35 E-07		1.71 E-08		2.42 E-08	Sample 1 Only		Sample 3 Only
J3KN67	J3KN67_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=2 SV=1	71.60	7.80	20.40	23.48	19.44	5.88	16.62	2.71 E-06	1.15 E-05	7.84 E-06	3.57 E-06	6.94 E-07	2.90 E-06	1.32	0.26	1.07
P39023	RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	48.60	5.94	9.89	6.94	1.98		39.57	8.83 E-07	1.59 E-06	7.50 E-07	5.47 E-08		9.86 E-06	0.06	Control 1 Only	11.17
Q01081	U2AF1_HUMAN Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3	8.80		1.00	1.00	1.00		3.00		1.56 E-07	2.79 E-08	7.19 E-08		4.97 E-07	Sample 1 Only		Sample 3 Only
P48735	IDHP_HUMAN Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	35.40	2.97	8.91	1.98	10.90	7.93	11.89	1.46 E-07	1.25 E-06	6.59 E-08	1.39 E-06	1.40 E-06	1.55 E-06	9.48	9.56	10.62
P51659	DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	39.40	20.79	32.65		15.85	9.91	2.97	1.01 E-06	1.80 E-06		5.72 E-07	3.06 E-07	8.45 E-08	0.57	0.30	0.08

Q02878	RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	26.00	10.00	8.50	2.50	4.00		23.00	8.11E-07	9.68E-07	2.82E-07	2.54E-07		5.69E-06	0.31	Control 1 Only	7.01
F8W6L6	F8W6L6_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=2 SV=1	29.10	5.00	31.00	29.00			22.00	4.17E-08	2.99E-07	4.49E-07			2.73E-07	Control 1 Only	Control 1 Only	6.55
P10809	CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	20.90	3.00	3.00		4.00	7.00	5.00	5.77E-08	2.01E-07		2.17E-07	3.90E-07	1.35E-07	3.76	6.76	2.34
Q8NF37	PCAT1_HUMAN Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2	7.10		3.00			2.00	1.00		3.52E-07			6.12E-08	6.17E-08		Sample 2 Only	Sample 3 Only
H7C1M2	H7C1M2_HUMAN Protein SON (Fragment) OS=Homo sapiens GN=SON PE=4 SV=1	5.60	1.00	1.00		1.00	6.00	2.00	1.22E-08	4.70E-09		9.28E-09	2.85E-08	1.15E-08	0.76	2.32	0.94
B7Z4C8	B7Z4C8_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=2 SV=1	21.50	1.00	1.00	1.00	1.00		3.00	2.54E-07	2.14E-07	2.15E-07	2.33E-07		1.61E-06	0.92	Control 1:Set1 Only	6.34
P28482	MK01_HUMAN Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3	22.50	2.00	2.61		4.61	3.61	2.61	6.87E-07	8.89E-07		2.18E-06	1.52E-06	5.06E-07	3.18	Control 1 Only	0.74
C9JDV8	C9JDV8_HUMAN Protein NipSnap homolog 1 (Fragment) OS=Homo sapiens GN=NIPSNAP1 PE=2 SV=1	23.20	1.00	2.00		3.00	2.00	4.00	4.85E-07	1.36E-06		2.72E-06	9.31E-07	1.22E-06	5.61	1.92	2.52
Q9NXH9	TRM1_HUMAN tRNA (guanine(26)-N(2))-dimethyltransferase OS=Homo sapiens GN=TRMT1 PE=1 SV=1	5.40	1.00	2.99		1.00		1.00	2.36E-08	7.31E-08		2.33E-08		1.29E-08	0.98	Control 1 Only	0.55
B0AZV0	B0AZV0_HUMAN Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=2 SV=1	17.60	1.00	2.00		5.00	1.00		1.56E-07	3.25E-07		1.06E-06	1.52E-07		6.81	0.97	Control1 Only
P58107	EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	6.00	0.98				1.00	2.98	1.36E-09				7.57E-10	5.94E-09	Control 1 Only	0.56	4.36
Q15365	PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	6.20		3.00	1.00	1.00	1.00	2.00		5.30E-07	2.86E-08	5.94E-08	7.19E-08	8.96E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P62714	PP2AB_HUMAN Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1	23.90	0.99	4.95		2.97	1.98	0.99	9.65E-08	1.29E-06		3.55E-07	1.88E-07	2.58E-08	3.68	1.95	0.27
P26373	RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	49.30		3.97		1.00		9.95		1.23E-06		2.46E-08		2.95E-06	Sample 1 Only		Sample 3 Only
P14868	SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	51.90	5.95	10.92	0.99	12.89	18.83	10.93	2.44E-07	1.11E-06	1.02E-08	1.39E-06	1.27E-06	5.91E-07	5.68	5.21	2.42
P60866	RS20_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	31.10	0.99	0.99		0.99		2.97	9.42E-08	2.81E-07		1.51E-07		7.40E-07	1.61	Control 1 Only	7.85
P40429	RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	24.10	4.99	3.00	2.00	6.99	2.00	12.97	1.87E-06	3.00E-06	2.08E-06	1.52E-06	4.80E-07	1.40E-05	0.81	0.26	7.50
J3KRX5	J3KRX5_HUMAN 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=2 SV=1	35.50		4.95	0.99	1.98	1.98	5.94		4.20E-06	1.17E-07	6.33E-07	1.10E-07	1.13E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JNW5	C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1	17.40		3.00		2.00		3.00		2.89E-06		3.89E-07		8.67E-07	Sample 1 Only		Sample 3 Only
P52597	HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	24.30	2.96	4.95		8.91	6.95	9.92	1.76E-07	7.51E-07		1.05E-06	5.32E-07	5.30E-07	5.98	3.03	3.02
C9JEH3	C9JEH3_HUMAN Angio-associated migratory cell protein OS=Homo sapiens GN=AAMP PE=2 SV=1	12.50		2.97		1.98	1.98	1.98		1.63E-07		1.76E-07	1.03E-07	9.73E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4D	B4DR63_HUMAN 26S protease regulatory	38.40	1.00	6.00		6.00	7.00	5.00	4.84	7.44		5.89	7.53	4.50	12.17	15.57	9.30

R63	subunit 4 OS=Homo sapiens GN=PSMC1 PE=2 SV=1								E-08	E-07		E-07	E-07	E-07			
Q13509	TBB3_HUMAN Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	39.30		5.00		2.00	2.00	2.00		1.13 E-06		1.99 E-07	1.08 E-07	1.90 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P61313	RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	14.70	3.00	4.00	3.00	2.00	3.00	9.97	5.00 E-07	8.93 E-07	5.85 E-07	1.25 E-07	2.90 E-07	4.00 E-06	0.25	0.58	7.99
F5H365	F5H365_HUMAN Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=2 SV=1	15.60	3.96	10.89		5.93	3.96		1.42 E-07	3.98 E-07		1.86 E-07	5.40 E-08		1.32	0.38	Control1 Only
B4DY08	B4DY08_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=2 SV=1	26.30	2.97	1.97		0.99	0.99	8.91	1.86 E-07	1.54 E-07		1.28 E-08	6.51 E-08	6.76 E-07	0.07	0.35	3.63
F2Z2E1	F2Z2E1_HUMAN Constitutive coactivator of peroxisome proliferator-activated receptor gamma OS=Homo sapiens GN=FAM120B PE=2 SV=1	11.70	1.98	3.96		1.98		0.99	3.20 E-08	6.89 E-08		2.74 E-08		1.75 E-08	0.86	Control 1 Only	0.55
P63220	RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	30.90	1.00		1.00			3.00	2.37 E-07		1.37 E-07			8.14 E-07	Control 1 Only	Control 1 Only	3.44
B4DRT2	B4DRT2_HUMAN 28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=2 SV=1	20.40	1.00	1.99	1.00	4.98	0.99	3.99	8.86 E-08	1.50 E-07	5.16 E-08	3.52 E-07	4.35 E-08	2.21 E-07	3.97	0.49	2.50
P08779	K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	71.70	51.00	24.50	17.50	43.00	83.50	36.50	4.40 E-06	1.43 E-06	9.50 E-07	2.70 E-06	8.31 E-06	3.09 E-06	0.61	1.89	0.70
P52907	CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	30.40	1.00	5.00		7.00	5.00	1.00	1.24 E-07	7.59 E-07		1.21 E-06	5.05 E-07	1.28 E-07	9.75	4.08	1.03
P02786	TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	28.90	13.86	15.86		18.86	19.85	7.93	3.38 E-07	5.54 E-07		1.03 E-06	5.34 E-07	2.92 E-07	3.03	1.58	0.87
P07954	FUMH_HUMAN Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3	14.80		1.00		1.00	3.00			1.30 E-07		1.45 E-07	1.30 E-07		Sample 1 Only	Sample 2 Only	
F5H012	F5H012_HUMAN E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=2 SV=1	14.10		3.00		5.98		2.98		2.15 E-07		3.69 E-07		8.28 E-08	Sample 1 Only		Sample 3 Only
P02538	K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	68.30	10.95	8.96	7.98	13.95	15.94	11.96	8.19 E-07	7.03 E-07	4.95 E-07	1.23 E-06	1.99 E-06	9.43 E-07	1.50	2.43	1.15
J3KNW4	J3KNW4_HUMAN Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=2 SV=1	15.80	1.00	3.00		5.00	1.00	2.00	1.01 E-07	5.89 E-07		1.12 E-06	8.63 E-08	2.22 E-07	11.07	0.86	2.20
B5MC07	B5MC07_HUMAN Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=2 SV=1	10.30	1.98	2.97	0.99	0.99	1.98	0.99	3.76 E-07	7.13 E-07	1.23 E-07	2.52 E-07	2.51 E-07	8.36 E-08	0.67	0.67	0.22
Q00325	MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	34.60	2.00	6.99	3.00	10.98	4.99	10.00	1.48 E-07	1.36 E-06	2.62 E-07	2.27 E-06	4.82 E-07	8.60 E-07	15.31	3.25	5.80
E5RJR5	E5RJR5_HUMAN S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=2 SV=1	27.00	1.00	0.99		3.00	0.99		1.21 E-07	2.67 E-07		6.92 E-07	1.04 E-07		5.74	0.86	Control1 Only
E9PHH5	E9PHH5_HUMAN Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=2 SV=1	23.50	1.00	4.00		3.00			8.78 E-08	7.42 E-07		4.08 E-07			4.64	Control 1:Set1 Only	Control1 Only
E9PHS0	E9PHS0_HUMAN LanC-like protein 1 (Fragment) OS=Homo sapiens GN=LANCL1 PE=2 SV=1	21.90		2.00		2.00	1.00	3.00		4.02 E-07		2.63 E-07	1.53 E-07	3.90 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P06493	CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	26.90		2.98	0.99	4.98		2.97		5.12 E-07	1.96 E-07	1.00 E-06		4.07 E-07	Sample 1 Only		Sample 3 Only

K7EK07	K7EK07_HUMAN Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=2 SV=1	25.80	11.81	5.92	4.93	9.84	3.93	19.71	3.86E-06	2.07E-06	1.89E-06	2.65E-06	5.71E-07	1.21E-05	0.69	0.15	3.14
H0YEN5	H0YEN5_HUMAN 40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=2 SV=1	45.60	3.93	8.84	2.96	1.96	0.98	17.73	5.71E-07	2.94E-06	7.27E-07	3.46E-07	1.46E-07	7.83E-06	0.61	0.26	13.69
P62906	RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	29.50	2.00	5.00	3.00	3.00	2.00	6.00	2.87E-07	1.34E-06	3.93E-07	5.12E-07	1.64E-07	3.30E-06	1.79	0.57	11.52
P04259	K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	68.30	9.00	5.00	4.00	5.00	15.00	7.00	6.42E-07	1.51E-07	1.39E-07	2.56E-07	1.19E-06	3.74E-07	0.40	1.86	0.58
P61962	DCAF7_HUMAN DDB1- and CUL4-associated factor 7 OS=Homo sapiens GN=DCAF7 PE=1 SV=1	13.70		3.00		4.00	3.00			3.99E-07		5.01E-07	2.76E-07		Sample 1 Only	Sample 2 Only	
P35249	RFC4_HUMAN Replication factor C subunit 4 OS=Homo sapiens GN=RFC4 PE=1 SV=2	11.00		3.98		1.00	1.00	0.99		3.18E-07		5.83E-08	3.72E-08	7.09E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P06702	S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	28.10	1.00	4.00		2.00	2.00		8.97E-08	7.15E-07		2.28E-07	1.30E-06		2.54	14.43	Control1 Only
P00966	ASSY_HUMAN Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	9.70	1.00	5.00		1.00	2.00	1.00	4.64E-08	4.60E-07		1.04E-07	9.45E-08	6.73E-08	2.25	2.04	1.45
Q1KMD3	HNRL2_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1	19.10	4.00	9.00		8.00	10.00	3.00	1.06E-07	2.23E-07		3.60E-07	1.96E-07	6.68E-08	3.41	1.86	0.63
H3BMH7	H3BMH7_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1	18.10	2.00	3.00		1.00	1.00	1.00	1.31E-07	5.47E-07		7.64E-08	1.54E-07	1.29E-07	0.59	1.18	0.99
F2Z2U8	F2Z2U8_HUMAN Myosin-14 OS=Homo sapiens GN=MYH14 PE=2 SV=1	33.10	2.99	25.84	37.79	0.99		29.82	2.87E-08	2.98E-07	5.64E-07	3.28E-08		4.41E-07	1.14	Control 1 Only	15.35
O95486	SC24A_HUMAN Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2	3.00	1.00	3.00		1.00	2.00		7.84E-09	4.26E-08		1.35E-08	1.28E-08		1.73	1.63	Control1 Only
P67809	YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	36.10	0.99	2.98	0.99	0.99	1.98	3.97	2.81E-08	3.20E-07	1.31E-08	1.51E-07	2.34E-07	2.91E-07	5.38	8.31	10.35
B4DR61	B4DR61_HUMAN Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=2 SV=1	7.80	0.99	2.97		1.98	0.99	0.99	2.67E-08	5.06E-07		1.72E-07	5.02E-08	6.29E-08	6.43	1.88	2.35
Q6PKG0	LARP1_HUMAN La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	5.00	1.98	2.97			0.99	5.94	3.46E-08	6.55E-08			1.29E-08	1.75E-07	Control 1 Only	0.37	5.07
Q53GQ0	DHB12_HUMAN Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2	28.80	1.00	5.98		7.99	2.99	6.00	9.30E-08	1.18E-06		1.01E-06	2.69E-07	1.08E-06	10.88	2.89	11.59
P28799	GRN_HUMAN Granulins OS=Homo sapiens GN=GRN PE=1 SV=2	11.50	6.90	4.95		5.92	5.93	2.96	3.68E-07	2.72E-07		4.65E-07	5.91E-07	1.32E-07	1.26	1.61	0.36
Q7Z794	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	36.50	25.50	15.00	6.50	32.00	14.50	9.50	9.58E-07	5.34E-07	2.13E-07	2.00E-06	8.17E-07	3.12E-07	2.09	0.85	0.33
Q6UWP8	SBSN_HUMAN Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2	18.30	4.00		1.00	4.00	5.00		1.95E-07		1.19E-08	2.64E-07	1.19E-07		1.36	0.61	Control1 Only
P05198	IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	14.00	2.00	4.00	2.00	4.00	3.00	4.00	1.81E-07	6.35E-07	6.94E-08	9.25E-07	3.68E-07	3.27E-07	5.11	2.03	1.81
P31153	METK2_HUMAN S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	13.40	2.00	3.00		5.00	6.00	3.00	9.14E-08	5.74E-07		6.73E-07	3.69E-07	1.65E-07	7.36	4.04	1.81
P26641	EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	30.00	8.00	13.00	3.00	16.00	11.00	18.00	8.07E-07	2.58E-06	1.50E-07	2.63E-06	1.74E-06	1.96E-06	3.26	2.15	2.43
P42704	LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo	19.20	8.00	13.00		12.53	16.00	7.00	8.38E-08	1.84E-07		2.36E-07	1.52E-07	9.41E-08	2.81	1.81	1.12

	sapiens GN=LRPPRC PE=1 SV=3																
B4DZI8	B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	6.40	2.00	3.00		1.00	3.00		2.78E-08	6.37E-08		2.00E-08	3.02E-08		0.72	1.09	Control1 Only
B5MCQ5	B5MCQ5_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=2 SV=1	9.60		1.00		3.00	1.00			9.87E-08		1.11E-07	6.84E-08		Sample 1 Only	Sample 2 Only	
P60842	IF4A1_HUMAN Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	11.30		0.99		1.98		2.97		2.26E-07		2.44E-07		1.63E-07	Sample 1 Only		Sample 3 Only
P39019	RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	31.70		2.00	2.00	2.00		3.00		5.76E-07	2.02E-07	3.73E-07		1.01E-06	Sample 1 Only		Sample 3 Only
G3V1R9	G3V1R9_HUMAN Inositol-3-phosphate synthase 1 OS=Homo sapiens GN=ISYNA1 PE=2 SV=1	16.20	3.96	4.95		5.94	7.92	1.98	1.56E-07	7.35E-07		7.45E-07	7.20E-07	1.13E-07	4.78	4.61	0.72
P52272	HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	36.00	20.75	25.67	2.97	4.95	13.81	20.74	9.47E-07	1.06E-06	2.72E-08	1.06E-07	3.23E-07	7.19E-07	0.11	0.34	0.76
B4E1G6	B4E1G6_HUMAN Galactokinase OS=Homo sapiens GN=GALK1 PE=2 SV=1	23.20		5.98		1.99	2.99	1.99		7.62E-07		8.33E-08	1.85E-07	1.62E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P07384	CAN1_HUMAN Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	5.30	2.00	3.00		2.00	1.00	1.00	6.98E-08	1.07E-07		5.02E-08	1.38E-08	3.65E-08	0.72	0.20	0.52
P54803	GALC_HUMAN Galactocerebrosidase OS=Homo sapiens GN=GALC PE=1 SV=2	27.20	6.87	8.85		21.60	6.88	8.84	6.47E-07	1.47E-06		2.49E-06	7.12E-07	4.86E-07	3.85	1.10	0.75
B7ZAR1	B7ZAR1_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	16.70		3.00		3.00	3.00	1.99		3.75E-07		3.56E-07	1.49E-07	1.52E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P05388	RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	54.90	26.40	19.46	2.92	23.46	12.64	74.14	5.21E-06	1.17E-05	4.09E-07	6.77E-06	2.02E-06	2.09E-05	1.30	0.39	4.00
O43707	ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	8.10	3.88	4.87		3.88	2.93	0.97	1.57E-07	1.54E-07		1.20E-07	4.34E-08	1.60E-08	0.76	0.28	0.10
P06576	ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	47.10	19.79	23.73	11.91	35.64	26.70	34.60	1.52E-06	3.65E-06	7.08E-07	4.49E-06	2.53E-06	3.06E-06	2.96	1.66	2.02
P20930	FILA_HUMAN Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	4.30	4.00			2.00	1.00		1.51E-08			3.29E-09	5.48E-09		0.22	0.36	Control1 Only
P62269	RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	31.60	6.00	8.00	5.00	7.00	4.00	15.00	1.20E-06	3.16E-06	9.73E-07	1.54E-06	5.87E-07	6.96E-06	1.29	0.49	5.82
Q9Y2A7	NCKP1_HUMAN Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	4.10	1.00	1.00		3.00			1.37E-08	1.47E-08		4.88E-08			3.57	Control 1 Only	Control1 Only
P55072	TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	4.50	2.00	1.00		3.00	1.00	1.00	4.89E-08	1.78E-08		6.93E-08	2.93E-08	1.74E-08	1.42	0.60	0.36
Q08188	TGM3_HUMAN Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	9.70	7.00	4.00	1.00	6.00	5.00	4.00	1.85E-07	7.56E-08	3.11E-08	2.23E-07	1.20E-07	1.45E-07	1.20	0.65	0.78
P23258	TBG1_HUMAN Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	6.70	1.00	3.00		3.00	2.00	2.00	1.35E-07	6.99E-07		1.99E-07	1.67E-07	1.33E-07	1.47	1.23	0.98
Q9NQH7	XPP3_HUMAN Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPNPEP3 PE=1 SV=1	32.20	8.00	9.00		4.00	7.00	6.00	5.83E-07	1.46E-06		3.78E-07	4.97E-07	3.54E-07	0.65	0.85	0.61
P22392	NDKB_HUMAN Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	39.00	2.97	5.94	0.99	3.96			8.95E-07	2.21E-06	1.06E-07	1.94E-06			2.17	Control 1 Only	Control1 Only
P39656	OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	14.90	0.99	4.99		4.98	3.98	1.99	8.34E-08	4.06E-07		4.78E-07	2.34E-07	9.89E-08	5.73	2.80	1.19

P54886	P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	9.60		8.00		3.00	2.00	1.00		2.25 E-07		1.15 E-07	1.66 E-07	9.42 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P12004	PCNA_HUMAN Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	28.70		5.00		5.00	2.00	2.00		8.90 E-07		9.71 E-07	3.43 E-07	1.44 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P49419	AL7A1_HUMAN Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5	29.90	2.95	5.93		5.92	5.92	3.95	2.56 E-07	5.54 E-07		6.44 E-07	4.29 E-07	2.46 E-07	2.52	1.68	0.96
P40939	ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	21.80	5.00	13.00		6.00	3.00	2.00	1.68 E-07	4.79 E-07		2.68 E-07	7.53 E-08	5.37 E-08	1.59	0.45	0.32
Q86VP6	CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	22.10	7.99	17.98		6.99	7.00	6.00	2.30 E-07	6.41 E-07		2.66 E-07	1.36 E-07	1.34 E-07	1.15	0.59	0.58
P62805	H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	53.40	22.00	15.00	9.00	22.00	9.00	42.00	1.29 E-05	6.97 E-06	4.67 E-06	7.42 E-06	1.62 E-06	3.04 E-05	0.57	0.13	2.35
Q93034	CUL5_HUMAN Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4	47.70	36.00	52.00	2.00	29.00	41.00	15.00	2.06 E-06	3.77 E-06	5.75 E-08	1.68 E-06	1.38 E-06	6.02 E-07	0.82	0.67	0.29
P17987	TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	24.30	5.93	8.93		6.93	10.92	3.96	1.91 E-07	5.91 E-07		4.87 E-07	5.85 E-07	1.89 E-07	2.55	3.06	0.99
B4DWJ2	B4DWJ2_HUMAN Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=2 SV=1	17.80	9.00	9.00		6.00	3.00	1.00	2.37 E-07	2.89 E-07		2.17 E-07	8.94 E-08	1.95 E-08	0.91	0.38	0.08
P78347	GTF2I_HUMAN General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	19.90	9.98	4.00		10.99	4.98		2.24 E-07	8.27 E-08		3.97 E-07	9.68 E-08		1.77	0.43	Control1 Only
P27694	RFA1_HUMAN Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2	37.30	19.98	17.98		23.98	22.98	1.00	7.99 E-07	9.85 E-07		1.56 E-06	1.25 E-06	4.50 E-08	1.95	1.56	0.06
Q13155	AIMP2_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2	10.00	2.00	3.00		3.00	1.00	1.00	1.14 E-07	6.08 E-07		3.07 E-07	1.00 E-07	4.36 E-08	2.70	0.88	0.38
G5E9V5	G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1	37.90	1.00	5.00		6.00	1.00	3.00	4.88 E-08	4.75 E-07		6.87 E-07	4.44 E-08	1.08 E-07	14.06	0.91	2.21
P62888	RL30_HUMAN 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	42.60	4.00	5.99	2.00	5.99	1.00	4.00	1.32 E-06	2.33 E-06	1.02 E-06	1.55 E-06	1.66 E-07	5.67 E-06	1.17	0.13	4.29
F8VWC5	F8VWC5_HUMAN 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=2 SV=1	37.10	0.99	5.94	2.97	1.98		15.84	1.70 E-07	1.80 E-06	7.51 E-07	5.30 E-07		3.76 E-06	3.13	Control 1 Only	22.17
E7EQ69	E7EQ69_HUMAN N-alpha-acetyltransferase 50 OS=Homo sapiens GN=NAA50 PE=2 SV=1	28.00		5.98		3.98		0.99		1.32 E-06		7.75 E-07		6.16 E-08	Sample 1 Only		Sample 3 Only
B4E022	B4E022_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=2 SV=1	22.20	4.00	4.00		3.00	6.00	1.00	8.86 E-08	1.48 E-07		8.18 E-08	2.63 E-07	2.87 E-08	0.92	2.97	0.32
Q9NZT2	OGFR_HUMAN Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3	28.20	16.00	19.00	2.00	25.00	27.00	20.00	7.57 E-07	1.80 E-06	1.41 E-08	1.52 E-06	1.35 E-06	1.11 E-06	2.01	1.78	1.46
Q08211	DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	8.40	2.00	8.00		4.00	6.00	6.00	1.31 E-08	1.30 E-07		4.09 E-08	5.02 E-08	1.30 E-07	3.12	3.83	9.95
P46779	RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	38.00	1.97	7.90	2.96	1.98		6.92	5.43 E-07	4.44 E-06	9.66 E-07	7.22 E-07		3.18 E-06	1.33	Control 1 Only	5.86
P43686	PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	27.10		7.00		2.00	4.00	4.00		8.51 E-07		1.34 E-07	2.60 E-07	1.63 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9H552	Q9H552_HUMAN Uncharacterized protein OS=Homo sapiens PE=4 SV=1	26.30	5.50	6.00	7.50	8.50	4.50	10.50	8.14 E-07	1.20 E-06	1.03 E-06	1.44 E-06	1.12 E-06	2.07 E-06	1.76	1.37	2.55
Q7L	CYFP1_HUMAN Cytoplasmic FMR1-interacting	2.40		2.99			0.99	0.99		3.32			9.64	1.22		Sample	Sample

576	protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1									E-08			E-09	E-08		2 Only	3 Only
P63244	GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	33.40	7.72	15.03	4.82	13.51	7.30	28.51	1.13 E-06	5.15 E-06	6.54 E-07	3.02 E-06	9.22 E-07	6.50 E-06	2.67	0.81	5.74
P23396	RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	87.20	21.32	28.19	12.64	22.40	16.51	60.20	6.52 E-06	1.61 E-05	3.64 E-06	1.16 E-05	3.20 E-06	2.46 E-05	1.77	0.49	3.77
P46777	RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	49.20	3.00	13.00		7.00	2.00	14.00	4.76 E-07	3.84 E-06		9.87 E-07	2.00 E-07	1.67 E-06	2.07	0.42	3.50
H7BXW3	H7BXW3_HUMAN Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=2 SV=1	13.40	3.98	6.94		2.98	2.97	1.99	3.22 E-07	2.78 E-07		2.23 E-07	9.02 E-08	8.27 E-08	0.69	0.28	0.26
E9PM69	E9PM69_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=2 SV=1	43.60	0.99	8.95		6.97	10.93	4.97	4.20 E-08	9.42 E-07		5.51 E-07	7.10 E-07	2.26 E-07	13.13	16.90	5.37
P49748	ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	10.30	0.99	2.97		0.99	2.98	0.99	2.24 E-08	8.22 E-08		1.33 E-08	1.23 E-07	2.33 E-08	0.59	5.50	1.04
P50991	TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	33.60	1.99	4.95		4.95	9.93	2.98	7.62 E-08	4.83 E-07		1.98 E-07	5.86 E-07	5.97 E-08	2.60	7.70	0.78
H3BRG4	H3BRG4_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=2 SV=1	25.70		3.97		3.97	2.00	1.98		3.56 E-07		2.99 E-07	9.98 E-08	1.39 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P46781	RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	51.50	1.00	9.99	1.00	4.00	2.00	10.97	1.53 E-07	2.62 E-06	4.34 E-07	7.67 E-07	2.33 E-07	3.78 E-06	5.01	1.52	24.67
J3KPS3	J3KPS3_HUMAN Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=2 SV=1	39.00	5.90	7.85		8.83	9.79	3.93	3.99 E-07	1.10 E-06		1.02 E-06	9.11 E-07	3.05 E-07	2.57	2.29	0.77
C9J7B1	C9J7B1_HUMAN Protein NipSnap homolog 2 (Fragment) OS=Homo sapiens GN=GBAS PE=2 SV=1	24.60		1.00		4.00		2.00		2.13 E-06		2.51 E-06		6.56 E-07	Sample 1 Only		Sample 3 Only
P62854	RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	20.90	1.00	2.00	1.00	2.00		5.00	1.31 E-06	2.41 E-06	5.63 E-07	1.17 E-06		5.18 E-06	0.89	Control 1 Only	3.95
Q99880	H2B1L_HUMAN Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3	57.90	28.44	22.54	13.73	23.53	10.78	45.10	1.48 E-05	1.16 E-05	5.63 E-06	7.45 E-06	2.82 E-06	3.70 E-05	0.50	0.19	2.51
M0QZC5	M0QZC5_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=2 SV=1	55.90	3.00	5.00	2.00	5.00	2.00	6.00	7.87 E-07	2.44 E-06	9.46 E-07	1.92 E-06	3.83 E-07	3.84 E-06	2.44	0.49	4.88
Q86YZ3	HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	34.30	84.00	64.00	56.00	99.00	90.00	59.00	1.86 E-06	7.59 E-07	5.36 E-07	1.90 E-06	1.66 E-06	1.08 E-06	1.03	0.89	0.58
B7Z817	B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1	8.80		3.97		0.99	1.98	1.98		3.69 E-07		1.05 E-07	7.47 E-08	7.21 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E9PLK3	E9PLK3_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1	11.00	6.93	6.93		3.96	3.96	0.99	1.23 E-07	1.61 E-07		1.03 E-07	6.85 E-08	2.21 E-08	0.84	0.56	0.18
Q8TEQ6	GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	5.00	3.00	2.00		3.00	4.00		5.04 E-08	6.11 E-09		3.69 E-08	4.67 E-08		0.73	0.93	Control1 Only
P78371	TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	44.30	8.93	11.91		11.90	14.86	4.95	5.24 E-07	1.44 E-06		8.54 E-07	1.57 E-06	4.47 E-07	1.63	3.00	0.85
P05783	K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	75.30	35.00	31.99	39.00	36.99	46.99	67.99	3.49 E-06	5.69 E-06	6.04 E-06	5.65 E-06	5.67 E-06	1.08 E-05	1.62	1.62	3.10
B4DQI4	B4DQI4_HUMAN Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=2 SV=1	25.50		3.00			1.00	3.00		6.98 E-07			1.36 E-07	8.86 E-07		Sample 2 Only	Sample 3 Only

P41252	SYIC_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	12.40	5.99	11.96		12.96	6.99	5.97	1.09 E-07	3.29 E-07		3.87 E-07	1.48 E-07	1.06 E-07	3.53	1.35	0.97
P04844	RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	23.70		4.98		4.98	1.99	1.99		6.80 E-07		6.44 E-07	1.05 E-07	2.42 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y230	RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	60.30	6.93	18.85		20.85	16.87	14.89	3.91 E-07	2.73 E-06		2.03 E-06	1.45 E-06	1.04 E-06	5.20	3.69	2.66
P62195	PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	20.40	1.00	3.99	1.00	2.00	3.00	4.00	9.07 E-08	6.12 E-07	2.31 E-08	2.31 E-07	1.30 E-07	1.38 E-07	2.54	1.44	1.52
P49257	LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	8.60	2.00	4.00		4.00	4.00	2.00	6.81 E-08	4.22 E-07		2.89 E-07	2.87 E-07	1.34 E-07	4.25	4.22	1.97
Q96P70	IPO9_HUMAN Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	17.60	8.00	12.00		11.00	7.00	6.00	2.47 E-07	4.72 E-07		5.61 E-07	2.22 E-07	2.54 E-07	2.27	0.90	1.03
P05787	K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	88.00	51.31	55.66	59.13	51.25	59.11	108.91	5.92 E-06	8.79 E-06	8.76 E-06	6.42 E-06	9.74 E-06	1.74 E-05	1.08	1.64	2.94
B4DEM7	B4DEM7_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1	29.50	7.97	8.96		12.93	8.96	4.98	4.19 E-07	6.63 E-07		9.13 E-07	4.73 E-07	1.59 E-07	2.18	1.13	0.38
Q9Y224	CN166_HUMAN UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	43.00	2.00	5.00	1.00	8.00	1.00	1.00	1.85 E-07	9.63 E-07	3.37 E-08	1.53 E-06	9.56 E-08	5.91 E-08	8.27	0.52	0.32
Q53GT1	KLH22_HUMAN Kelch-like protein 22 OS=Homo sapiens GN=KLHL22 PE=1 SV=2	14.70	0.99	4.98		5.98	1.00	1.00	2.44 E-08	1.58 E-07		1.85 E-07	4.83 E-08	2.81 E-08	7.58	1.98	1.15
M0R0F0	M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=2 SV=1	39.50	2.00	8.00	3.00	6.00	2.00	13.00	1.13 E-06	2.69 E-06	4.28 E-07	1.57 E-06	3.17 E-07	4.11 E-06	1.39	0.28	3.63
P23526	SAHH_HUMAN Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	32.40	5.00	11.00		13.16	7.00	6.00	5.21 E-07	1.65 E-06		1.87 E-06	7.20 E-07	4.78 E-07	3.59	1.38	0.92
E5KLJ5	E5KLJ5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1	10.20	3.00	7.00		8.00	4.00	2.00	3.61 E-08	1.39 E-07		1.73 E-07	6.05 E-08	1.61 E-08	4.79	1.68	0.45
P36542	ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	49.00	3.00	12.00	3.00	12.00	6.00	3.00	5.52 E-07	2.44 E-06	4.05 E-07	3.60 E-06	6.13 E-07	5.64 E-07	6.51	1.11	1.02
E9PBS1	E9PBS1_HUMAN Phosphoribosylaminoimidazole carboxylase (Fragment) OS=Homo sapiens GN=PAICS PE=2 SV=1	18.90		5.00		3.00	2.00			7.12 E-07		3.14 E-07	1.92 E-07		Sample 1 Only	Sample 2 Only	
B4E363	B4E363_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=2 SV=1	10.50	1.98	2.97		1.98	2.97	1.98	3.02 E-07	6.21 E-07		3.75 E-07	6.14 E-07	3.05 E-07	1.24	2.04	1.01
P18124	RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	45.20	3.98	13.93	7.95	7.96	5.96	18.91	4.40 E-07	4.45 E-06	1.44 E-06	1.99 E-06	7.30 E-07	6.10 E-06	4.52	1.66	13.87
P13646	K1C13_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	55.20	9.45	9.45	0.51	16.89	6.97	9.44	6.36 E-07	7.97 E-07	9.32 E-08	1.38 E-06	1.96 E-07	5.55 E-07	2.16	0.31	0.87
G3V5T0	G3V5T0_HUMAN Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=2 SV=1	55.40	1.99	3.98		1.99	1.00	1.99	4.42 E-07	1.54 E-06		9.28 E-07	1.95 E-07	2.99 E-07	2.10	0.44	0.68
Q9NV79	PCMD2_HUMAN Protein-L-isoaspartate O-methyltransferase domain-containing protein 2 OS=Homo sapiens GN=PCMTD2 PE=2 SV=2	24.70	3.96	17.87	0.99	11.91	7.94	7.94	9.31 E-07	4.63 E-06	1.10 E-07	1.75 E-06	1.33 E-06	1.00 E-06	1.88	1.43	1.08
P14625	ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	6.00	3.00	2.00		2.00	2.00	3.00	7.62 E-08	7.65 E-08		8.67 E-08	6.15 E-08	6.60 E-08	1.14	0.81	0.87
Q15	NONO_HUMAN Non-POU domain-containing	40.60	3.97	6.96		7.94	6.96	2.98	1.72	1.46		4.04	7.02	6.92	2.35	4.08	0.40

233	octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4								E-07	E-06		E-07	E-07	E-08			
Q9UJ70	NAGK_HUMAN N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4	23.30	1.98	2.96		5.93	1.98	0.98	3.61 E-07	3.89 E-07		7.73 E-07	2.36 E-07	3.25 E-08	2.14	0.66	0.09
Q01813	K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	35.20	13.86	24.75		17.82	17.84	6.93	6.19 E-07	1.40 E-06		7.94 E-07	4.08 E-07	2.57 E-07	1.28	0.66	0.42
O43592	XPOT_HUMAN Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	9.80	3.00	9.00		3.00	4.00	5.00	4.84 E-08	2.48 E-07		5.49 E-08	4.87 E-08	1.11 E-07	1.13	1.00	2.29
Q6YN16	HSDL2_HUMAN Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	23.20	1.99	4.98		3.00	4.99	2.99	1.47 E-07	8.17 E-07		2.25 E-07	3.27 E-07	1.47 E-07	1.53	2.23	1.00
B4DUR8	B4DUR8_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=2 SV=1	29.00	4.95	7.91		6.93	9.90	2.97	4.27 E-07	6.63 E-07		4.18 E-07	8.60 E-07	2.25 E-07	0.98	2.01	0.53
F5H7I0	F5H7I0_HUMAN BTB/POZ domain-containing protein KCTD6 (Fragment) OS=Homo sapiens GN=KCTD6 PE=2 SV=1	85.10	1.00	2.00		3.00	2.00	4.00	3.29 E-07	4.90 E-06		3.86 E-06	1.39 E-06	1.90 E-06	11.74	4.22	5.79
Q15437	SC23B_HUMAN Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	35.50	20.00	20.00		18.00	10.00	1.00	9.52 E-07	1.05 E-06		1.12 E-06	3.16 E-07	3.07 E-08	1.17	0.33	0.03
Q3SYB4	Q3SYB4_HUMAN SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1	14.30	11.00	4.00		10.00	5.00	5.00	5.55 E-07	1.32 E-07		6.63 E-07	1.20 E-07	1.51 E-07	1.20	0.22	0.27
P53621	COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	11.00	2.00	8.00		6.00	7.00	3.00	1.73 E-08	1.43 E-07		9.38 E-08	7.05 E-08	5.48 E-08	5.44	4.09	3.18
D6RFM5	D6RFM5_HUMAN Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=2 SV=1	7.00	1.98	1.98		2.97	2.98	0.99	2.92 E-07	4.53 E-07		4.01 E-07	4.59 E-07	1.50 E-07	1.38	1.57	0.51
O14965	AURKA_HUMAN Aurora kinase A OS=Homo sapiens GN=AURKA PE=1 SV=2	9.70		3.00		2.00	1.00			4.17 E-07		2.68 E-07	4.11 E-08		Sample 1 Only	Sample 2 Only	
Q13263	TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	21.70	6.95	11.91		8.92	12.91	6.95	2.11 E-07	3.75 E-07		2.87 E-07	2.52 E-07	2.52 E-07	1.36	1.19	1.20
P05089	ARGI1_HUMAN Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	39.80	9.00	4.00		12.00	9.00	2.00	8.86 E-07	2.45 E-07		7.86 E-07	6.00 E-07	1.36 E-07	0.89	0.68	0.15
C9J9K3	C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	70.50	23.94	18.95	11.98	18.97	17.96	50.88	1.24 E-05	2.07 E-05	3.43 E-06	9.22 E-06	7.69 E-06	3.19 E-05	0.75	0.62	2.58
B4DZH6	B4DZH6_HUMAN Histone deacetylase 6 OS=Homo sapiens GN=HDAC6 PE=2 SV=1	4.80	3.00	3.00		3.00	3.00	1.00	7.43 E-08	8.18 E-08		9.55 E-08	9.44 E-08	2.09 E-08	1.29	1.27	0.28
K7ERI7	K7ERI7_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=2 SV=1	41.10	1.98	2.97	1.98	1.98	0.99	3.97	8.40 E-07	1.51 E-06	3.86 E-07	8.95 E-07	2.50 E-07	2.51 E-06	1.07	0.30	2.99
P00390	GSHR_HUMAN Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2	15.20	2.98	5.96		5.96	6.96	0.99	1.41 E-07	5.42 E-07		4.11 E-07	4.89 E-07	1.43 E-08	2.91	3.46	0.10
P46940	IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	31.90	58.87	60.92		36.91	44.89	22.97	1.42 E-06	1.24 E-06		8.02 E-07	7.76 E-07	4.21 E-07	0.56	0.55	0.30
Q96S55	WRIP1_HUMAN ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 PE=1 SV=2	6.90	0.99	3.97		0.99	3.97		2.37 E-08	1.28 E-07		4.20 E-08	7.14 E-08		1.77	3.01	Control1 Only
P18085	ARF4_HUMAN ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	31.10	0.99	1.98	0.99	2.97	0.99	1.98	1.84 E-07	4.93 E-07	8.78 E-08	5.90 E-07	8.56 E-08	3.42 E-07	3.21	0.47	1.86
Q16401	PSMD5_HUMAN 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3	23.60	3.00	7.00		5.00	4.00	3.00	3.53 E-07	1.23 E-06		7.72 E-07	6.71 E-07	6.55 E-07	2.19	1.90	1.86
E9P	E9PH29_HUMAN Thioredoxin-dependent	15.50	1.00	2.00		3.00	2.00		1.27	8.37		9.38	3.37		7.38	2.65	Control1

H29	peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=2 SV=1								E-07	E-07		E-07	E-07				Only
P25398	RS12_HUMAN 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	24.20	3.00	4.00	3.00	1.00		6.00	3.78 E-06	6.87 E-06	2.47 E-06	1.32 E-06		1.59 E-05	0.35	Control 1 Only	4.20
C9JJ19	C9JJ19_HUMAN 28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=2 SV=2	10.10		2.53		2.52		0.99		5.83 E-07		6.23 E-07		1.47 E-07	Sample 1 Only		Sample 3 Only
P62913	RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	32.00	3.98	6.95	1.98	4.96	2.98	11.91	7.65 E-07	3.66 E-06	4.27 E-07	2.52 E-06	4.40 E-07	3.41 E-06	3.29	0.57	4.45
D6RAN4	D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1	40.10	1.98	3.96		2.97	0.99	3.96	5.87 E-07	2.00 E-06		1.08 E-06	1.29 E-07	7.67 E-07	1.84	0.22	1.31
F8W810	F8W810_HUMAN Uncharacterized protein OS=Homo sapiens PE=2 SV=1	9.90	1.99	1.99		2.98	4.97	3.98	1.73 E-07	4.17 E-07		3.33 E-07	3.01 E-07	1.41 E-07	1.93	1.74	0.82
P49189	AL9A1_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3	38.30	9.98	7.98	1.00	13.98	13.98	12.98	1.28 E-06	1.94 E-06	6.22 E-08	1.62 E-06	1.70 E-06	9.74 E-07	1.26	1.33	0.76
Q06210	GFPT1_HUMAN Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3	18.10	6.00	8.00		5.00	4.00	3.00	1.65 E-07	3.43 E-07		2.24 E-07	8.38 E-08	7.98 E-08	1.36	0.51	0.48
P25705	ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	64.40	19.59	39.27	9.77	37.33	30.42	28.42	1.75 E-06	7.60 E-06	3.41 E-07	5.62 E-06	3.66 E-06	3.35 E-06	3.21	2.09	1.92
P16615	AT2A2_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	22.30	12.95	20.89		15.94	23.92	14.94	1.87 E-07	4.59 E-07		3.57 E-07	3.11 E-07	1.77 E-07	1.91	1.66	0.95
Q13885	TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	67.60	1.00	1.00			3.00	1.00	5.52 E-08	7.63 E-08			1.46 E-07	2.64 E-08	Control 1 Only	2.63	0.48
P33993	MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	45.30	18.95	37.87		25.88	17.91	7.96	8.23 E-07	2.39 E-06		1.42 E-06	6.07 E-07	4.40 E-07	1.72	0.74	0.53
P68371	TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	75.70	18.58	16.67	11.79	14.67	15.70	18.61	5.58 E-06	1.35 E-05	1.43 E-06	9.52 E-06	7.57 E-06	9.47 E-06	1.71	1.36	1.70
P62753	RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	6.40	3.00	2.00	2.00		1.00	9.00	2.31 E-07	7.72 E-07	1.52 E-07		5.94 E-08	1.44 E-06	Control 1 Only	0.26	6.25
P62937	PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	55.20	7.90	10.87	1.98	14.82	7.92	4.94	6.34 E-06	9.78 E-06	8.86 E-07	7.33 E-06	2.56 E-06	3.28 E-06	1.16	0.40	0.52
H7BY58	H7BY58_HUMAN Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=2 SV=1	61.20	8.97	12.96	2.00	19.96	6.98	10.99	2.83 E-06	8.71 E-06	8.18 E-07	1.01 E-05	2.73 E-06	3.10 E-06	3.57	0.96	1.09
P23246	SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	15.80	5.00	6.00		7.99	6.99	3.00	2.78 E-07	1.98 E-07		2.88 E-07	2.33 E-07	9.61 E-08	1.04	0.84	0.35
Q15645	PCH2_HUMAN Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	18.30	4.00	11.00	7.00	11.00	7.00	13.00	2.43 E-06	2.22 E-06	7.21 E-07	4.92 E-06	9.83 E-07	1.00 E-06	2.03	0.41	0.41
P61247	RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	56.40	12.67	19.41	2.90	16.44	7.75	36.77	2.66 E-06	5.70 E-06	2.17 E-07	2.35 E-06	6.35 E-07	7.97 E-06	0.88	0.24	2.99
P61353	RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	33.80	2.00	5.00	1.00	3.00		3.00	7.60 E-07	2.91 E-06	4.74 E-07	1.64 E-06		1.61 E-06	2.15	Control 1 Only	2.11
E9PAV3	E9PAV3_HUMAN Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=2 SV=1	56.60	4.95	6.91	1.98	4.95	3.95	9.92	8.09 E-08	2.31 E-07	8.07 E-09	1.63 E-07	6.60 E-08	1.79 E-07	2.02	0.81	2.22
Q8N1N4	K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	49.20	26.97	16.96	9.00	27.94	22.97	7.99	1.50 E-06	8.35 E-07	2.39 E-07	1.79 E-06	1.20 E-06	2.76 E-07	1.19	0.80	0.18

Q9Y305	ACOT9_HUMAN Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2	36.70	8.98	8.98	1.99	10.97	10.98	4.98	9.64E-07	1.25E-06	9.89E-08	1.53E-06	1.10E-06	3.02E-07	1.59	1.14	0.31
P13647	K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	68.60	122.45	81.64	60.81	121.50	109.58	68.74	1.57E-05	7.22E-06	4.67E-06	1.56E-05	1.27E-05	6.41E-06	0.99	0.81	0.41
F5H6I7	F5H6I7_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=2 SV=1	17.80	1.00	3.00		5.00	3.00	3.00	4.68E-08	6.98E-07		4.19E-07	1.90E-07	3.33E-07	8.97	4.05	7.12
H0YDD8	H0YDD8_HUMAN 60S acidic ribosomal protein P2 (Fragment) OS=Homo sapiens GN=RPLP2 PE=3 SV=1	67.40	1.00	2.00		2.00		4.00	7.74E-07	1.12E-06		1.21E-06		1.18E-06	1.56	Control 1 Only	1.53
P62701	RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	62.70	9.98	22.96	6.99	13.96	5.99	32.92	1.24E-06	6.28E-06	6.93E-07	2.40E-06	5.59E-07	7.38E-06	1.95	0.45	5.98
Q562R1	ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	21.50	1.00	1.00	2.00			3.00	3.42E-07	4.33E-06	1.03E-05			1.19E-05	Control 1 Only	Control 1 Only	34.62
P52292	IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	10.80	1.00	5.00		3.00	4.00	4.00	2.36E-08	4.61E-07		1.70E-07	2.11E-07	2.31E-07	7.21	8.96	9.78
P62917	RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	32.70	5.91	11.85	5.91	2.96	0.99	15.80	1.40E-06	8.26E-06	1.81E-06	9.81E-07	4.68E-07	1.29E-05	0.70	0.33	9.20
Q9Y295	DRG1_HUMAN Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1	41.70	6.00	13.00		15.00	12.00	10.00	8.18E-07	3.14E-06		2.99E-06	1.20E-06	7.64E-07	3.65	1.46	0.93
P22735	TGM1_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=1 SV=4	17.50	7.99	4.99		4.99	7.00	1.00	1.44E-07	9.61E-08		6.54E-08	1.09E-07	1.75E-08	0.45	0.76	0.12
O15269	SPTC1_HUMAN Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1	17.10	3.00	3.00	1.00	5.00	5.00	4.00	2.37E-07	6.22E-07	3.62E-08	6.11E-07	3.37E-07	1.73E-07	2.58	1.42	0.73
B7ZA04	B7ZA04_HUMAN Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1	13.20	2.99	3.98		3.98	3.99	1.00	8.60E-08	1.29E-07		1.18E-07	7.99E-08	7.27E-08	1.38	0.93	0.85
P12830	CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	6.90	2.99	3.00		2.00	4.99	2.00	6.61E-08	4.74E-08		5.03E-08	6.78E-08	2.53E-08	0.76	1.02	0.38
P47755	CAZA2_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	25.20	1.00	4.00	1.00	5.00	1.00	1.00	1.36E-07	8.21E-07	3.64E-08	5.93E-07	1.24E-07	7.71E-08	4.37	0.91	0.57
G8JLH9	G8JLH9_HUMAN Signal transducer and activator of transcription OS=Homo sapiens GN=STAT3 PE=2 SV=1	17.90	3.00	7.00		5.00	1.00	3.00	9.57E-08	1.95E-07		2.12E-07	1.71E-08	1.35E-07	2.21	0.18	1.41
F5GZS6	F5GZS6_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=2 SV=1	15.50	0.99	1.98		2.98	1.98	0.99	3.33E-07	2.13E-07		4.10E-07	1.60E-07	1.11E-07	1.23	0.48	0.33
P25205	MCM3_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	35.50	17.84	14.88		14.88	16.85	0.99	6.43E-07	3.68E-07		4.39E-07	3.51E-07	2.50E-08	0.68	0.55	0.04
P21266	GSTM3_HUMAN Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	70.20	2.99	15.96	0.99	26.97	4.98	3.97	3.81E-07	1.05E-05	1.32E-07	1.19E-05	8.61E-07	8.23E-07	31.20	2.26	2.16
Q14974	IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	29.50	18.88	25.86	1.00	17.90	22.87	12.92	1.60E-06	2.28E-06	1.01E-08	1.50E-06	9.93E-07	6.60E-07	0.94	0.62	0.41
P49411	EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	53.10	15.00	42.00	8.00	28.00	28.00	36.00	1.62E-06	1.05E-05	8.05E-07	5.90E-06	3.86E-06	6.03E-06	3.65	2.39	3.73
P56192	SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	17.10	6.95	11.89		8.93	12.88	0.99	9.46E-08	2.62E-07		2.14E-07	1.94E-07	3.02E-08	2.26	2.05	0.32
Q05639	EF1A2_HUMAN Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	31.70	9.50	9.50	2.00	9.50	7.50	9.00	1.89E-06	4.91E-06	2.80E-07	3.18E-06	2.94E-06	2.53E-06	1.68	1.56	1.34

P07900	HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	26.50	10.96	10.97		9.98	6.00	6.99	3.84E-07	4.04E-07		5.11E-07	2.03E-07	2.51E-07	1.33	0.53	0.65
P30040	ERP29_HUMAN Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	19.90	1.00	2.00		3.00	1.00	1.00	1.25E-07	4.66E-07		5.23E-07	1.33E-07	6.82E-08	4.20	1.07	0.55
P50416	CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	37.00	23.93	27.92	2.00	21.92	18.93	8.97	7.40E-07	1.36E-06	2.74E-08	9.11E-07	5.06E-07	3.24E-07	1.23	0.68	0.44
J3KNL6	J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=2 SV=1	2.40		4.00			2.00	3.00		2.68E-08			1.02E-08	2.36E-08		Sample 2 Only	Sample 3 Only
I3L3P7	I3L3P7_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=2 SV=1	24.00	1.98	1.98	0.99	0.99		2.97	7.12E-07	1.96E-06	5.02E-07	8.15E-07		1.83E-06	1.14	Control 1 Only	2.57
O95373	IPO7_HUMAN Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	7.50	7.00	7.00		5.00	5.00	4.00	1.61E-07	2.28E-07		1.40E-07	9.21E-08	9.22E-08	0.87	0.57	0.57
P08727	K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	84.00	45.96	53.44	75.96	52.47	56.93	108.90	6.07E-06	1.31E-05	1.59E-05	9.53E-06	1.11E-05	2.13E-05	1.57	1.83	3.51
H7C378	H7C378_HUMAN 26S proteasome non-ATPase regulatory subunit 1 (Fragment) OS=Homo sapiens GN=PSMD1 PE=4 SV=1	22.90	1.00	3.00		2.00	3.00	2.00	7.09E-07	8.97E-07		7.03E-07	6.50E-07	5.73E-07	0.99	0.92	0.81
Q9H773	DCTP1_HUMAN dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1	20.60	2.00	3.00	1.00	3.00	2.00	3.00	3.13E-07	1.69E-06	1.86E-07	1.46E-06	6.17E-07	5.41E-07	4.66	1.97	1.73
Q14204	DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	2.60	2.00	6.00		2.00	3.00	4.00	5.01E-09	1.54E-08		3.64E-09	5.88E-09	1.59E-08	0.73	1.17	3.17
Q5D862	FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	12.00	19.00	8.00	9.00	23.00	14.00	8.00	4.44E-07	2.20E-07	1.75E-07	4.47E-07	3.01E-07	2.55E-07	1.01	0.68	0.57
Q13835	PKP1_HUMAN Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	10.30	2.00	3.00	1.00	3.00	5.00	1.00	6.55E-08	4.83E-08	4.35E-09	3.73E-08	8.76E-08	1.63E-08	0.57	1.34	0.25
E7EW34	E7EW34_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=2 SV=1	31.00	13.97	15.97	1.00	13.95	17.95	4.98	7.23E-07	7.33E-07	4.63E-09	9.44E-07	6.85E-07	1.10E-07	1.31	0.95	0.15
P02533	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	79.90	78.50	50.00	51.50	77.00	76.00	44.50	1.10E-05	5.09E-06	4.53E-06	9.08E-06	1.03E-05	5.05E-06	0.83	0.94	0.46
E5RIT6	E5RIT6_HUMAN 60S ribosomal protein L26-like 1 (Fragment) OS=Homo sapiens GN=RPL26L1 PE=2 SV=1	23.70	1.00	3.00	1.00			5.00	1.02E-07	8.18E-07	1.31E-07			8.85E-07	Control 1 Only	Control 1 Only	8.70
B4E2W0	B4E2W0_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1	14.20	1.97	1.97		2.97	0.99	1.97	1.92E-07	7.47E-07		3.48E-07	2.48E-07	1.97E-07	1.81	1.29	1.02
P06733	ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	48.20	5.97	14.93		13.97	14.95	5.99	3.86E-07	1.86E-06		1.51E-06	8.40E-07	3.10E-07	3.93	2.18	0.80
P50454	SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	30.60	2.95	8.87		7.87	6.87	2.95	1.82E-07	1.17E-06		7.91E-07	6.77E-07	1.33E-07	4.36	3.73	0.73
Q13162	PRDX4_HUMAN Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	32.10	2.00	7.96		5.99	4.00	2.00	2.32E-07	1.92E-06		1.80E-06	4.64E-07	2.72E-07	7.77	2.00	1.17
Q5T749	KPRP_HUMAN Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	17.40	23.00	8.00	9.00	20.00	23.00	12.00	1.50E-06	3.06E-07	2.66E-07	1.01E-06	8.07E-07	6.20E-07	0.67	0.54	0.41
M0R210	M0R210_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=2 SV=1	57.40	4.97	6.97	1.99	3.97		10.95	2.74E-06	4.76E-06	9.96E-07	2.25E-06		5.00E-06	0.82	Control 1 Only	1.82
O00231	PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	6.90		3.00		1.00	1.00	2.00		5.15E-07		3.00E-07	4.70E-08	2.59E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6ZRV2	FA83H_HUMAN Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3	5.30	1.00	4.00		1.00	2.00	2.00	1.10E-08	7.13E-08		1.53E-08	2.77E-08	2.77E-08	1.39	2.52	2.53

Q9Y678	COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	10.60	2.00	4.99		4.99	4.99	3.99	3.86 E-07	5.58 E-07		5.03 E-07	2.96 E-07	3.06 E-07	1.30	0.77	0.79
F8W9B4	F8W9B4_HUMAN Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=2 SV=1	37.30	1.00	3.99		6.98	4.99	2.00	5.81 E-08	1.12 E-06		8.24 E-07	3.69 E-07	1.80 E-07	14.18	6.35	3.10
Q5T750	XP32_HUMAN Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=1	8.40	8.00	4.00	3.00	6.00	3.00	4.00	1.75 E-06	4.60 E-07	3.28 E-07	1.20 E-06	4.64 E-07	5.19 E-07	0.69	0.27	0.30
P50502	F10A1_HUMAN Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	23.30	6.94	8.92	0.99	5.95	9.92	7.94	1.26 E-06	4.18 E-06	4.62 E-08	1.72 E-06	1.97 E-06	1.04 E-06	1.36	1.56	0.83
Q9BUF5	TBB6_HUMAN Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	39.50	4.99	5.97		3.97	3.99	5.97	1.83 E-07	5.87 E-07		1.83 E-07	4.40 E-07	2.73 E-07	1.00	2.40	1.49
P14174	MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	15.70	6.00	2.00		2.00		4.00	3.98 E-06	1.04 E-06		2.39 E-06		1.94 E-06	0.60	Control 1 Only	0.49
P49327	FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	28.20	46.00	68.00	1.00	40.00	48.00	36.00	5.50 E-07	8.61 E-07	7.96 E-09	4.03 E-07	3.99 E-07	4.22 E-07	0.73	0.72	0.77
P33992	MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	55.20	49.87	42.89	2.00	41.89	43.83	11.97	3.96 E-06	3.30 E-06	4.16 E-08	3.69 E-06	2.15 E-06	4.72 E-07	0.93	0.54	0.12
G3V4J7	G3V4J7_HUMAN DDB1- and CUL4-associated factor 5 OS=Homo sapiens GN=DCAF5 PE=2 SV=1	21.60	13.92	20.89	2.99	13.90	12.93	13.95	5.86 E-07	1.70 E-06	4.77 E-08	6.75 E-07	5.56 E-07	7.86 E-07	1.15	0.95	1.34
E9PNQ1	E9PNQ1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=2 SV=1	2.90	2.00	1.00		3.00			5.63 E-08	4.95 E-08		1.22 E-07			2.17	Control 1 Only	Control1 Only
Q3SY84	K2C71_HUMAN Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=3	23.70	10.00	9.50	7.00	16.51	11.00	6.00	3.84 E-06	1.71 E-06	5.28 E-07	3.05 E-06	1.67 E-06	5.57 E-07	0.79	0.44	0.15
P61978	HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	21.90	2.00	1.00		2.00	1.00	4.00	6.27 E-08	1.55 E-07		6.22 E-08	1.86 E-08	1.71 E-07	0.99	0.30	2.72
P40926	MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	28.40	2.98	4.98		6.97	0.99	1.98	1.61 E-07	1.03 E-06		7.90 E-07	1.19 E-07	1.27 E-07	4.91	0.74	0.79
Q16531	DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	52.40	92.60	94.61	1.97	88.63	71.93	61.05	6.42 E-06	6.97 E-06	3.34 E-08	6.03 E-06	3.18 E-06	2.57 E-06	0.94	0.50	0.40
P04843	RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	21.30	3.00	8.00		7.00	5.00		1.38 E-07	3.69 E-07		3.39 E-07	1.05 E-07		2.47	0.76	Control1 Only
B5MCP9	B5MCP9_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=2 SV=1	39.00	6.00	9.00	3.00	7.00	2.00	6.00	2.23 E-06	4.36 E-06	7.00 E-07	2.47 E-06	1.96 E-07	3.74 E-06	1.10	0.09	1.68
O43143	DHX15_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	11.40	7.00	3.00		2.00	2.00	4.00	3.59 E-07	1.59 E-07		1.89 E-07	9.33 E-08	1.73 E-07	0.53	0.26	0.48
P04406	G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	60.10	15.99	20.98	4.00	23.97	16.98	10.99	1.59 E-06	2.51 E-06	1.90 E-07	2.70 E-06	1.44 E-06	7.41 E-07	1.70	0.91	0.47
Q53FA7	QORX_HUMAN Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2	14.50	1.00	4.00		4.00	2.00	1.00	1.99 E-07	9.11 E-07		8.27 E-07	3.54 E-07	8.35 E-08	4.16	1.78	0.42
F5H5D3	F5H5D3_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1	66.60	39.36	31.90	14.46	37.74	25.09	38.45	1.39 E-05	5.29 E-05	2.16 E-06	2.92 E-05	1.58 E-05	1.59 E-05	2.10	1.14	1.15
P11021	GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	69.40	138.00	158.00	28.00	151.00	168.00	79.00	1.96 E-05	2.55 E-05	1.93 E-06	2.44 E-05	2.12 E-05	7.63 E-06	1.25	1.08	0.39
Q07065	CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	10.60		2.81		0.81	0.81	1.00		8.79 E-08		3.88 E-08	4.34 E-08	1.93 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only

Q02413	DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	30.00	37.00	21.00	8.00	41.00	28.00	11.00	9.20E-07	3.76E-07	1.43E-07	9.82E-07	4.72E-07	1.76E-07	1.07	0.51	0.19
B7Z5E2	B7Z5E2_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=2 SV=1	17.60	1.00	3.00	1.00	2.00	2.00	3.00	1.69E-07	6.90E-07	2.85E-08	3.45E-07	2.34E-07	4.25E-07	2.04	1.38	2.51
Q9NZT1	CALL5_HUMAN Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	15.10	2.00	5.00	3.00	4.00	5.00	3.00	3.02E-07	4.97E-07	4.30E-07	5.81E-07	5.06E-07	3.03E-07	1.92	1.67	1.00
O95881	TXD12_HUMAN Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	26.20	2.00	3.00		5.00	2.00	1.00	6.57E-07	1.70E-06		1.98E-06	3.96E-07	2.88E-07	3.02	0.60	0.44
P30153	2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	32.60	5.93	6.93		8.87	9.85	2.96	2.51E-07	7.31E-07		4.90E-07	4.90E-07	1.30E-07	1.95	1.95	0.52
P04792	HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	72.20	39.00	56.00	23.00	53.00	34.00	99.00	2.85E-05	1.24E-04	1.07E-05	6.30E-05	2.89E-05	5.33E-05	2.21	1.02	1.87
P11142	HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	80.00	109.08	122.69	9.74	106.11	119.68	47.70	1.39E-05	2.14E-05	3.92E-07	1.39E-05	1.36E-05	4.28E-06	1.00	0.98	0.31
P23921	RIR1_HUMAN Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1	7.70	1.99	1.00		3.98			9.79E-08	2.77E-08		1.41E-07			1.44	Control 1 Only	Control1 Only
E7EPB3	E7EPB3_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=2 SV=1	33.90	2.00	7.00	5.00	6.00	3.00	18.00	1.95E-06	1.18E-05	3.46E-06	3.18E-06	8.79E-07	1.52E-05	1.63	0.45	7.80
P05141	ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	52.00	4.00	5.00		8.50	3.00	3.00	7.42E-07	1.39E-06		1.31E-06	4.58E-07	6.21E-07	1.77	0.62	0.84
Q13011	ECH1_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	37.20	9.99	11.98	1.00	9.98	11.98	6.98	1.17E-06	2.94E-06	5.35E-08	2.01E-06	1.25E-06	4.62E-07	1.72	1.07	0.40
P08237	K6PF_HUMAN 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	27.70	8.88	13.83		7.90	10.86	7.89	2.53E-07	6.87E-07		4.22E-07	2.61E-07	3.70E-07	1.67	1.03	1.47
Q8TEX9	IPO4_HUMAN Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2	11.30		7.91		4.95	1.98	0.99		2.03E-07		2.01E-07	1.26E-08	1.39E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6KB66-3	K2C80_HUMAN Isoform 3 of Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80	21.60	5.00	3.00	3.00	4.50	4.00	4.00	1.89E-07	1.12E-07	9.13E-08	1.34E-07	1.49E-07	1.53E-07	0.71	0.78	0.81
Q6ZVX7	FBX50_HUMAN F-box only protein 50 OS=Homo sapiens GN=NCCRP1 PE=1 SV=1	10.90	4.00	3.00	1.00	5.00	3.00	1.00	3.68E-07	1.85E-07	5.27E-08	3.98E-07	2.29E-07	4.44E-08	1.08	0.62	0.12
Q9NRR5	UBQL4_HUMAN Ubiquilin-4 OS=Homo sapiens GN=UBQLN4 PE=1 SV=2	15.60	2.56	5.56		2.56	5.12	3.56	1.65E-07	2.26E-07		1.58E-07	1.74E-07	1.02E-07	0.96	1.05	0.62
Q99714	HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	78.50	10.94	16.89	1.98	17.87	13.90	10.93	2.21E-06	6.21E-06	7.16E-08	5.76E-06	1.91E-06	1.72E-06	2.61	0.86	0.78
Q6KB66	K2C80_HUMAN Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	24.90	5.00	3.00	3.00	4.50	4.00	4.00	2.04E-07	1.21E-07	9.84E-08	1.44E-07	1.60E-07	1.65E-07	0.71	0.79	0.81
P08238	HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	33.30	14.97	12.00	1.99	13.98	15.97	6.99	7.86E-07	8.31E-07	2.85E-08	9.78E-07	5.93E-07	2.44E-07	1.24	0.75	0.31
Q9NZB2	F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	10.70	3.00	9.00		5.00	3.00	1.00	3.16E-08	1.91E-07		1.25E-07	5.14E-08	2.64E-08	3.95	1.63	0.84
P68104	EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	40.30	21.49	26.45	4.00	24.45	21.46	23.96	2.78E-06	1.24E-05	3.67E-07	6.92E-06	5.50E-06	4.65E-06	2.49	1.98	1.68
M0R117	M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=2 SV=1	33.30	1.00	3.00	3.00			8.00	8.43E-08	1.04E-06	2.89E-07			1.55E-06	Control 1 Only	Control 1 Only	18.43
F8V	F8VYY9_HUMAN 5'-AMP-activated protein	25.90	1.00	2.00		3.00	2.00		5.56	3.51		3.64	8.15		6.54	1.47	Control1

YY9	kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=2 SV=1								E-08	E-07		E-07	E-08				Only
K7ERJ1	K7ERJ1_HUMAN Thymidine kinase (Fragment) OS=Homo sapiens GN=TK1 PE=2 SV=1	52.80	2.00	6.00		7.00	2.00	1.00	5.06 E-07	3.57 E-06		2.66 E-06	7.66 E-07	3.05 E-07	5.25	1.51	0.60
H0Y4R1	H0Y4R1_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=3 SV=1	12.60	7.99	5.99		5.99	6.99	4.00	1.43 E-06	1.32 E-06		8.72 E-07	1.26 E-06	3.92 E-07	0.61	0.88	0.27
P30050	RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	38.80	6.00	6.00	4.00	7.00	2.00	14.00	1.34 E-06	3.29 E-06	4.28 E-07	1.32 E-06	1.61 E-07	4.03 E-06	0.99	0.12	3.02
Q06323	PSME1_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	19.30	1.00	3.00		4.00	2.00	2.00	6.07 E-08	1.13 E-06		9.74 E-07	1.71 E-07	1.53 E-07	16.04	2.81	2.51
P31944	CASPE_HUMAN Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	17.80	6.00	2.00	1.00	3.00	5.00	1.00	2.83 E-07	6.76 E-08	6.86 E-08	9.04 E-08	2.28 E-07	6.67 E-08	0.32	0.81	0.24
Q96QK1	VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	9.50	5.00	4.00		6.00	4.00	1.00	1.51 E-07	1.36 E-07		2.08 E-07	8.47 E-08	2.08 E-08	1.38	0.56	0.14
O94952	FBX21_HUMAN F-box only protein 21 OS=Homo sapiens GN=FBXO21 PE=2 SV=2	13.40	3.96	2.97		1.98	3.96	1.98	3.07 E-07	2.64 E-07		1.85 E-07	2.22 E-07	1.19 E-07	0.60	0.72	0.39
Q8WVX9	FACR1_HUMAN Fatty acyl-CoA reductase 1 OS=Homo sapiens GN=FAR1 PE=1 SV=1	11.50	2.00	3.00		2.00	2.00	2.00	1.67 E-07	3.43 E-07		2.28 E-07	1.31 E-07	1.11 E-07	1.36	0.79	0.67
P78527	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	5.70	5.00	12.99		2.00	5.00	12.98	1.28 E-08	4.98 E-08		2.06 E-09	1.35 E-08	5.33 E-08	0.16	1.06	4.18
M0QZL1	M0QZL1_HUMAN Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=2 SV=1	23.40	1.00	4.00		4.00	1.00	2.00	1.79 E-07	1.01 E-06		9.07 E-07	1.74 E-07	2.09 E-07	5.07	0.97	1.17
F5H2F4	F5H2F4_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1	37.80	20.99	28.99		30.99	26.00	4.99	5.67 E-07	1.01 E-06		1.16 E-06	4.74 E-07	7.57 E-08	2.05	0.84	0.13
Q00839	HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	13.20	10.00	9.00		11.00	3.00	2.00	3.94 E-07	2.32 E-07		4.34 E-07	9.76 E-08	4.75 E-08	1.10	0.25	0.12
P62333	PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	22.10		4.97		5.95	3.97	0.99		6.34 E-07		4.41 E-07	2.03 E-07	4.41 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q00610	CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	32.80	36.87	48.82		25.90	44.82	26.89	8.48 E-07	1.01 E-06		4.43 E-07	7.51 E-07	5.28 E-07	0.52	0.89	0.62
P81605	DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	30.00	9.00	5.00	4.00	10.00	9.00	4.00	3.67 E-06	1.73 E-06	6.71 E-07	3.64 E-06	2.20 E-06	7.10 E-07	0.99	0.60	0.19
P62277	RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	25.80	2.00	7.98	1.99	4.99	1.00	3.98	6.49 E-07	4.15 E-06	7.50 E-07	2.28 E-06	1.42 E-07	2.73 E-06	3.52	0.22	4.22
O00571	DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	16.40	7.99	8.50	1.50	8.00	4.00	7.00	3.09 E-07	3.21 E-07	1.28 E-08	2.57 E-07	1.31 E-07	2.10 E-07	0.83	0.42	0.68
O43175	SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	30.00	7.00	15.98	2.00	13.99	11.99	12.00	1.04 E-06	3.16 E-06	7.53 E-08	1.83 E-06	1.09 E-06	1.67 E-06	1.77	1.05	1.62
P62851	RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	15.20	1.00	1.00				4.00	4.24 E-07	1.05 E-06				1.58 E-06	Control 1 Only	Control 1 Only	3.73
Q92734	TFG_HUMAN Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=2	40.20		24.81		1.98	9.92	30.77		5.56 E-06		2.36 E-07	1.03 E-06	4.69 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P53396	ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	23.30	16.85	17.84		11.89	15.87	5.97	2.92 E-07	4.00 E-07		3.51 E-07	2.34 E-07	6.18 E-08	1.20	0.80	0.21
Q04	K1C17_HUMAN Keratin, type I cytoskeletal 17	62.30	13.8	5.96	2.00	6.94	10.9	1.98	8.83	4.05	1.26	2.44	1.02	6.10	0.28	1.15	0.07

695	OS=Homo sapiens GN=KRT17 PE=1 SV=2		8				4		E-07	E-07	E-07	E-07	E-06	E-08			
P04264	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	74.80	540.00	384.00	360.00	461.00	470.00	470.00	3.56 E-04	1.90 E-04	2.08 E-04	2.81 E-04	2.37 E-04	1.91 E-04	0.79	0.67	0.54
H0YNW5	H0YNW5_HUMAN Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=2 SV=1	30.50	1.00	3.99		5.97	1.00	1.99	1.13 E-07	2.47 E-06		2.18 E-06	6.08 E-08	1.90 E-07	19.24	0.54	1.67
P07437	TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	75.90	23.76	31.68	6.93	24.75	24.75	29.70	3.49 E-06	1.57 E-05	5.62 E-07	6.70 E-06	6.13 E-06	8.14 E-06	1.92	1.76	2.33
B4DP52	B4DP52_HUMAN HCG2005638, isoform CRA_c OS=Homo sapiens GN=DDX39B PE=2 SV=1	12.80		2.00		1.00		3.00		2.25 E-07		9.56 E-08		1.17 E-07	Sample 1 Only		Sample 3 Only
P15924	DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	30.20	86.00	70.00	32.00	68.00	90.00	46.99	7.84 E-07	5.07 E-07	2.47 E-07	4.72 E-07	6.20 E-07	3.61 E-07	0.60	0.79	0.46
Q14566	MCM6_HUMAN DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	4.30	3.00	2.00		2.00	2.00		3.89 E-08	5.14 E-08		5.86 E-08	3.71 E-08		1.51	0.96	Control1 Only
Q8NC69	KCTD6_HUMAN BTB/POZ domain-containing protein KCTD6 OS=Homo sapiens GN=KCTD6 PE=2 SV=2	59.10	23.50	26.50	10.50	32.50	23.00	28.00	1.49 E-05	3.92 E-05	3.69 E-06	3.54 E-05	1.18 E-05	1.38 E-05	2.38	0.79	0.93
Q9HA64	KT3K_HUMAN Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2	26.50	1.98	5.95		6.93	4.96		2.82 E-07	1.77 E-06		1.18 E-06	7.65 E-07		4.18	2.71	Control1 Only
O43837	IDH3B_HUMAN Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2	11.20		2.00		3.00		1.00		2.57 E-07		1.99 E-07		4.55 E-08	Sample 1 Only		Sample 3 Only
F8W7C6	F8W7C6_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=2 SV=1	42.90	3.95	6.91	1.97	3.94	1.97	10.90	6.89 E-07	3.06 E-06	2.69 E-07	4.80 E-07	1.65 E-07	3.18 E-06	0.70	0.24	4.61
P22102	PUR2_HUMAN Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	8.70	2.99	5.98		4.99	3.98	1.99	8.14 E-08	2.24 E-07		1.83 E-07	7.95 E-08	2.89 E-08	2.24	0.98	0.36
P08107	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	37.40	14.85	23.74	0.99	17.77	22.71	7.91	9.30 E-07	2.03 E-06	1.37 E-08	1.11 E-06	1.39 E-06	3.60 E-07	1.19	1.49	0.39
E7EMH5	E7EMH5_HUMAN Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=2 SV=1	17.50	2.00	7.98		3.98	4.99	3.99	1.23 E-07	4.54 E-07		2.11 E-07	2.18 E-07	1.72 E-07	1.72	1.78	1.41
Q15067	ACOX1_HUMAN Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3	12.10	2.00	2.00		3.00	2.00	1.00	1.21 E-07	3.11 E-07		2.56 E-07	1.31 E-07	6.21 E-08	2.12	1.09	0.51
P00338	LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	34.30	4.92	5.89		6.89	4.91	3.93	7.71 E-07	2.08 E-06		1.23 E-06	1.15 E-06	5.78 E-07	1.59	1.49	0.75
P62241	RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	26.10	1.00	4.00	1.00	3.00	1.00	9.00	2.05 E-07	1.24 E-06	1.37 E-07	3.71 E-07	6.93 E-08	1.20 E-06	1.81	0.34	5.88
Q92499	DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	26.60	17.00	11.00		15.00	10.00	2.00	9.23 E-07	7.70 E-07		1.11 E-06	4.32 E-07	9.67 E-08	1.20	0.47	0.10
P13645	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	70.50	431.59	301.02	255.58	329.05	304.10	338.63	3.12 E-04	1.94 E-04	1.41 E-04	3.12 E-04	2.14 E-04	1.42 E-04	1.00	0.68	0.45
G5E9Q2	G5E9Q2_HUMAN Cold shock domain containing E1, RNA-binding, isoform CRA_d OS=Homo sapiens GN=CSDE1 PE=2 SV=1	18.50	8.98	5.99		14.93	5.98		3.35 E-07	1.96 E-07		3.98 E-07	1.17 E-07		1.19	0.35	Control1 Only
P55060	XPO2_HUMAN Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	36.20	26.73	41.58		31.68	28.71	21.78	1.26 E-06	2.48 E-06		1.50 E-06	1.11 E-06	1.02 E-06	1.19	0.87	0.81
P35527	K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	93.60	333.62	254.17	251.21	299.86	339.64	275.93	1.56 E-04	8.82 E-05	9.86 E-05	1.44 E-04	1.24 E-04	8.53 E-05	0.92	0.79	0.55

A8MUS3	A8MUS3_HUMAN 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=2 SV=1	47.10	2.00	2.00	1.00	1.00	1.00	6.00	6.32E-07	1.46E-06	1.97E-07	4.11E-07	2.50E-07	1.70E-06	0.65	0.40	2.69
Q9H3U1	UN45A_HUMAN Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1	12.50	3.00	4.00		3.00	2.00	2.00	3.16E-08	5.50E-08		5.10E-08	1.42E-08	2.49E-08	1.61	0.45	0.79
J3KR97	J3KR97_HUMAN Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=2 SV=1	7.10	3.00	2.00		2.00	1.00	2.00	3.90E-08	3.49E-08		3.41E-08	1.46E-08	2.83E-08	0.87	0.37	0.73
P53618	COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	18.60	10.00	12.00		12.00	6.00	2.00	2.77E-07	4.10E-07		4.82E-07	1.55E-07	7.13E-08	1.74	0.56	0.26
Q9NUQ8	ABCF3_HUMAN ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2	14.40	3.00	7.00		2.00	7.00	4.00	7.09E-08	2.13E-07		4.84E-08	1.45E-07	9.97E-08	0.68	2.04	1.41
Q9Y6N5	SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	8.20	0.99	1.00	1.00	2.98	1.00	1.00	2.49E-06	5.87E-08	4.35E-08	2.41E-06	1.57E-07	1.00E-07	0.97	0.06	0.04
P40227	TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	29.60	2.97	6.93		1.98	6.94	2.97	1.62E-07	5.60E-07		1.58E-07	4.68E-07	1.17E-07	0.97	2.89	0.72
Q9Y265	RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	46.10	3.97	19.79		12.89	15.83	10.87	1.88E-07	2.54E-06		8.67E-07	1.25E-06	6.87E-07	4.62	6.65	3.66
Q96MG8	PCMD1_HUMAN Protein-L-isoaspartate O-methyltransferase domain-containing protein 1 OS=Homo sapiens GN=PCMTD1 PE=2 SV=2	31.10	8.96	24.86	1.00	19.89	13.92	16.92	6.62E-07	4.89E-06	6.01E-08	2.21E-06	2.20E-06	1.34E-06	3.33	3.33	2.03
E7ERW2	E7ERW2_HUMAN Aspartate aminotransferase OS=Homo sapiens GN=GOT2 PE=2 SV=1	11.40	2.00	3.00		3.00	2.00		1.18E-07	3.60E-07		3.36E-07	1.31E-07		2.85	1.11	Control1 Only
J3QRD1	J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=2 SV=1	21.10	0.99	2.98		1.98	1.99	1.99	4.00E-08	3.36E-07		1.20E-07	1.37E-07	1.29E-07	3.00	3.42	3.21
P07814	SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	8.60	3.00	8.00		5.00	5.00	3.00	5.22E-08	1.37E-07		7.32E-08	8.36E-08	3.78E-08	1.40	1.60	0.72
Q92973	TNPO1_HUMAN Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	9.40	7.94	8.92		7.93	5.93	6.93	2.31E-07	4.35E-07		3.40E-07	1.54E-07	1.58E-07	1.48	0.67	0.69
P14618	KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	50.80	22.57	41.24	1.96	25.55	33.39	14.71	1.09E-06	4.07E-06	2.69E-08	1.70E-06	2.70E-06	9.07E-07	1.55	2.47	0.83
P35908	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	97.30	222.00	170.00	155.00	190.50	204.00	173.50	7.71E-05	4.70E-05	3.85E-05	6.14E-05	5.91E-05	3.87E-05	0.80	0.77	0.50
Q99456	K1C12_HUMAN Keratin, type I cytoskeletal 12 OS=Homo sapiens GN=KRT12 PE=1 SV=1	6.90	17.00	9.00	7.00	16.00	9.00	9.00	6.19E-07	3.29E-07	2.18E-07	5.15E-07	2.90E-07	3.87E-07	0.83	0.47	0.63
P32119	PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	54.50	14.00	13.50	3.50	11.00	9.00	4.50	1.00E-05	1.25E-05	2.01E-06	1.34E-05	7.83E-06	2.82E-06	1.34	0.78	0.28
Q08380	LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	12.80	0.99	6.98	0.99	0.99	3.98	4.98	4.34E-08	2.93E-07	5.52E-09	2.81E-08	8.97E-08	2.31E-07	0.65	2.07	5.32
F8VPD4	F8VPD4_HUMAN CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1	9.70	3.00	14.00		5.00	7.00	11.00	1.69E-08	2.63E-07		3.28E-08	5.77E-08	1.95E-07	1.94	3.42	11.52
P38646	GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	66.10	72.86	93.86	12.95	76.91	81.84	42.93	7.80E-06	1.22E-05	6.94E-07	9.44E-06	7.31E-06	3.65E-06	1.21	0.94	0.47
P13639	EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	25.30	15.50	13.50		12.50	13.00	8.50	3.27E-07	5.80E-07		3.75E-07	2.74E-07	2.72E-07	1.15	0.84	0.83
Q5T440	CAF17_HUMAN Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1	39.60	3.00	12.00	1.00	7.00	11.00	3.00	6.47E-07	4.70E-06	5.90E-08	3.08E-06	2.14E-06	2.52E-07	4.75	3.31	0.39
Q15	ELOB_HUMAN Transcription elongation factor	33.90	4.98	3.98	1.00	7.98	1.00	4.99	2.56	2.74	1.12	3.46	1.78	1.83	1.35	0.07	0.71

370	B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1								E-06	E-06	E-07	E-06	E-07	E-06			
P17858	K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	32.30	12.50	19.50		19.00	15.00	5.50	9.07 E-07	1.19 E-06		1.12 E-06	5.85 E-07	4.13 E-07	1.23	0.64	0.46
P14923	PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	41.70	36.85	27.89	9.95	33.91	39.88	14.95	2.14 E-06	1.11 E-06	1.95 E-07	1.69 E-06	1.20 E-06	5.88 E-07	0.79	0.56	0.27
E5RHG8	E5RHG8_HUMAN Transcription elongation factor B polypeptide 1 (Fragment) OS=Homo sapiens GN=TCEB1 PE=2 SV=1	74.20	1.98	3.96	0.99	5.94	0.99	3.96	8.86 E-07	2.34 E-06	2.09 E-07	2.18 E-06	1.24 E-07	1.11 E-06	2.46	0.14	1.25
P24752	THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	34.00	4.99	8.98		9.98	6.99	1.00	8.55 E-07	1.64 E-06		1.55 E-06	8.61 E-07	7.18 E-08	1.81	1.01	0.08
A8MUB1	A8MUB1_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1	61.40	1.94	7.86		8.81	2.95	4.91	7.63 E-08	1.36 E-06		9.10 E-07	2.02 E-07	3.31 E-07	11.93	2.65	4.34
E7EP00	E7EP00_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=2 SV=2	8.80	4.00	6.00		4.00	5.00	2.00	7.18 E-08	1.51 E-07		9.97 E-08	1.05 E-07	1.85 E-08	1.39	1.47	0.26
Q86X55	CARM1_HUMAN Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 PE=1 SV=3	7.30	0.99	0.99		0.99		2.97	7.29 E-08	1.48 E-07		1.46 E-07		7.46 E-08	2.00	Control 1 Only	1.02
P54136	SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	30.20	13.88	21.82		11.91	16.86	5.95	4.48 E-07	9.12 E-07		5.13 E-07	5.72 E-07	2.74 E-07	1.15	1.28	0.61
J3KS22	J3KS22_HUMAN L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=2 SV=1	21.90	1.00	1.00		2.00	1.00	1.00	1.68 E-07	3.05 E-07		6.02 E-07	1.63 E-07	1.35 E-07	3.58	0.97	0.80
A6NIW5	A6NIW5_HUMAN Peroxiredoxin 2, isoform CRA_a OS=Homo sapiens GN=PRDX2 PE=2 SV=2	62.50	0.50	1.00		1.00		0.50	6.96 E-08	2.92 E-07		6.70 E-07		4.51 E-08	9.63	Control 1 Only	0.65
H0Y6C3	H0Y6C3_HUMAN Pyrroline-5-carboxylate reductase 3 (Fragment) OS=Homo sapiens GN=PYCRL PE=2 SV=1	12.30		0.99		1.98	0.99	1.98		3.33 E-07		3.41 E-07	1.51 E-07	2.22 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P07686	HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	8.20	1.00	0.99		1.99		1.99	4.57 E-08	1.10 E-07		1.39 E-07		7.46 E-08	3.04	Control 1 Only	1.64
O43708	MAAI_HUMAN Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3	45.80	2.00	2.00		2.00	1.00	2.00	5.65 E-07	2.01 E-06		1.73 E-06	1.79 E-07	5.08 E-07	3.06	0.32	0.90
Q9BUH6	CI142_HUMAN Uncharacterized protein C9orf142 OS=Homo sapiens GN=C9orf142 PE=1 SV=2	10.30	1.00	2.00		2.00	1.00		9.72 E-08	5.43 E-07		4.91 E-07	9.45 E-08		5.05	0.97	Control1 Only
E7EMB6	E7EMB6_HUMAN Aspartyl aminopeptidase OS=Homo sapiens GN=DNPEP PE=2 SV=1	9.30		1.00		1.00	1.00	1.00		1.47 E-07		1.29 E-07	2.28 E-08	4.25 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P12236	ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	39.90	1.00	2.00		2.00	1.00	1.00	1.84 E-07	7.30 E-07		6.23 E-07	1.23 E-07	9.25 E-08	3.39	0.67	0.50
Q96KP4	CNDP2_HUMAN Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	10.10	0.99			1.00	1.99	0.99	3.94 E-08			9.55 E-08	1.12 E-07	3.75 E-08	2.42	2.85	0.95
Q96I99	SUCB2_HUMAN Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2	11.30		0.99		1.00	1.99	2.00		8.26 E-08		2.62 E-08	5.62 E-08	6.90 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O60884	DNJA2_HUMAN DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	6.10		1.00		1.00	2.00	2.00		1.41 E-07		3.93 E-08	7.32 E-08	1.43 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
H3BLZ8	H3BLZ8_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=2 SV=1	8.30	1.98			0.99	0.99	0.99	5.81 E-08			5.05 E-08	4.43 E-08	3.59 E-08	0.87	0.76	0.62
P01	HV303_HUMAN Ig heavy chain V-III region	18.80	4.00	7.00					2.53	6.94					Control	Control	Control1

764	VH26 OS=Homo sapiens PE=1 SV=1								E-06	E-06					1 Only	1 Only	Only
Q96PK6	RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	12.30		10.00						2.48 E-07							
F8W733	F8W733_HUMAN BRCA1-A complex subunit BRE (Fragment) OS=Homo sapiens GN=BRE PE=2 SV=1	16.50				6.00	4.00					1.10 E-06	4.56 E-07		Sample 1 Only	Sample 2 Only	
P08708	RS17_HUMAN 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	43.00		2.00				5.98		6.37 E-07				1.11 E-06			Sample 3 Only
F5H5Y3	F5H5Y3_HUMAN Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=2 SV=1	11.80	2.00	2.00				2.00	3.81 E-08	6.50 E-08				7.91 E-08	Control 1 Only	Control 1 Only	2.08
Q86X76	NIT1_HUMAN Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 PE=1 SV=2	9.30	1.98	1.99		1.98	0.99	0.99	1.99 E-07	6.54 E-07		4.10 E-07	1.38 E-07	6.41 E-08	2.06	0.69	0.32
B4DWW1	B4DWW1_HUMAN ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=2 SV=1	34.80		3.00		3.00				1.53 E-06		7.96 E-07			Sample 1 Only		
H0YM70	H0YM70_HUMAN Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=2 SV=1	26.30		2.00		4.00				3.09 E-07		1.07 E-06			Sample 1 Only		
B0UX83	B0UX83_HUMAN HLA-B associated transcript 3, isoform CRA_a OS=Homo sapiens GN=BAG6 PE=4 SV=1	5.80	1.00	2.00		2.00	2.00	1.00	2.13 E-08	3.15 E-08		4.16 E-08	3.33 E-08	1.50 E-08	1.95	1.56	0.70
E9PMA0	E9PMA0_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=2 SV=1	7.30	1.00	2.00		2.00	1.00	2.00	5.32 E-08	1.01 E-07		9.92 E-08	3.69 E-08	9.11 E-08	1.86	0.69	1.71
B4DJV2	B4DJV2_HUMAN Citrate synthase OS=Homo sapiens GN=CS PE=2 SV=1	6.20	0.99	1.00		1.98	1.98	0.99	6.32 E-08	3.45 E-08		2.43 E-07	1.68 E-07	4.04 E-08	3.84	2.65	0.64
P18077	RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	35.50		1.00		2.00		2.00		1.04 E-06		8.65 E-07		3.52 E-07	Sample 1 Only		Sample 3 Only
P61163	ACTZ_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	13.00		1.99		1.98	1.98	0.99		1.32 E-07		1.40 E-07	1.43 E-07	5.00 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P15927	RFA2_HUMAN Replication protein A 32 kDa subunit OS=Homo sapiens GN=RPA2 PE=1 SV=1	13.40		3.00			3.00			7.01 E-07			2.65 E-07			Sample 2 Only	
Q9UBV2	SE1L1_HUMAN Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3	3.80	1.00	2.00		2.00	2.00	1.00	1.04 E-08	5.59 E-08		6.25 E-08	4.96 E-08	1.94 E-08	6.02	4.77	1.87
C9K0U8	C9K0U8_HUMAN Single-stranded DNA-binding protein (Fragment) OS=Homo sapiens GN=SSBP1 PE=2 SV=1	19.00	1.00	1.00	1.00		1.00	1.00	4.07 E-07	3.96 E-07	1.05 E-07		1.96 E-07	3.02 E-07	Control 1 Only	0.48	0.74
E9PHA6	E9PHA6_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=2 SV=1	4.60	2.00	2.00		2.00	1.00		5.12 E-08	1.58 E-08		1.94 E-08	5.49 E-08		0.38	1.07	Control1 Only
P08123	CO1A2_HUMAN Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	3.40	3.00				2.00		5.74 E-08				3.07 E-08		Control 1 Only	0.54	Control1 Only
H3BTH6	H3BTH6_HUMAN F-box only protein 22 (Fragment) OS=Homo sapiens GN=FBXO22 PE=2 SV=1	10.00		2.00		1.00	1.00	2.00		3.00 E-07		9.29 E-08	1.54 E-07	8.78 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
I3L1P8	I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens GN=SLC25A11 PE=2 SV=1	18.20		1.00		2.00				6.34 E-08		1.44 E-07			Sample 1 Only		
P07951-2	TPM2_HUMAN Isoform 2 of Tropomyosin beta chain OS=Homo sapiens GN=TPM2	32.00		3.84	4.83					5.64 E-07	6.48 E-07						
P01876	IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	12.70	3.00			5.00			8.38 E-08			2.07 E-07			2.47	Control 1 Only	Control1 Only

P46783	RS10_HUMAN 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	18.20	1.00	1.99		1.99		1.99	6.91E-07	8.50E-07		1.17E-06		4.07E-07	1.69	Control 1 Only	0.59
Q08554	DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	5.50	1.00			2.00	1.00		4.10E-08			3.42E-08	1.72E-08		0.83	0.42	Control1 Only
H0YK49	H0YK49_HUMAN Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=2 SV=1	8.70		2.00		2.00	1.00	1.00		3.69E-07		1.84E-07	1.04E-07	9.70E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JTZ6	C9JTZ6_HUMAN 5'-nucleotidase domain-containing protein 2 OS=Homo sapiens GN=NT5DC2 PE=2 SV=1	4.30	0.99	0.99		1.98	0.99	0.99	1.56E-08	6.33E-08		6.65E-08	2.25E-08	1.38E-08	4.26	1.44	0.88
O75382	TRIM3_HUMAN Tripartite motif-containing protein 3 OS=Homo sapiens GN=TRIM3 PE=1 SV=2	4.50	0.99	1.99		0.99	0.99	0.99	6.79E-08	5.39E-08		3.91E-08	1.95E-08	3.75E-08	0.58	0.29	0.55
P49207	RL34_HUMAN 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	21.40			1.00			4.00			4.96E-08			6.74E-07			Sample 3 Only
Q8WXX5	DNJC9_HUMAN DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1	21.20						6.00						7.56E-07			Sample 3 Only
B4DJE5	B4DJE5_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1	19.80		2.97		0.99				2.97E-07		8.22E-08			Sample 1 Only		
Q9C075	K1C23_HUMAN Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2	10.20	2.00	1.00		2.00	1.00		4.26E-08	1.66E-08		3.09E-08	1.91E-08		0.73	0.45	Control1 Only
E7EMN3	E7EMN3_HUMAN Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=2 SV=1	27.70	3.00			4.00			8.10E-08			3.09E-07			3.81	Control 1 Only	Control1 Only
E7EP32	E7EP32_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=2 SV=1	9.10	0.99			1.00		1.98	4.49E-08			6.97E-08		8.18E-08	1.55	Control 1 Only	1.82
E9PJF0	E9PJF0_HUMAN Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3 PE=2 SV=1	9.80	1.00				1.00	1.00	7.84E-08				1.61E-07	6.81E-08	Control 1 Only	2.05	0.87
P62258	1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	20.00	0.99			1.98		1.98	7.91E-08			2.67E-07		9.96E-08	3.37	Control 1 Only	1.26
Q9BSJ8	ESYT1_HUMAN Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	3.60	1.00	2.00		2.00		1.00	1.91E-08	8.13E-08		3.30E-08		1.61E-08	1.73	Control 1 Only	0.85
E7ETK0	E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1	20.80	1.00	2.00				2.00	1.11E-07	2.08E-06				9.03E-07	Control 1 Only	Control 1 Only	8.14
Q9BVS5	TR61B_HUMAN tRNA (adenine(58)-N(1))-methyltransferase, mitochondrial OS=Homo sapiens GN=TRMT61B PE=1 SV=2	4.80	1.00	1.00			2.00	1.00	4.10E-08	3.88E-08			5.74E-08	2.21E-08	Control 1 Only	1.40	0.54
Q9HCM4	E41L5_HUMAN Band 4.1-like protein 5 OS=Homo sapiens GN=EPB41L5 PE=1 SV=3	15.60						7.00						2.27E-07			Sample 3 Only
Q9NYU2	UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	2.80	1.00			1.00	2.00	1.00	1.16E-08			6.49E-09	1.88E-08	1.34E-08	0.56	1.62	1.15
Q9Y2S7	PDIP2_HUMAN Polymerase delta-interacting protein 2 OS=Homo sapiens GN=POLDIP2 PE=1 SV=1	14.70		4.00		2.00				5.35E-07		1.89E-07			Sample 1 Only		
B0FLL2	B0FLL2_HUMAN 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 2 transcript variant 3 OS=Homo sapiens GN=PFKFB2 PE=2 SV=1	14.20				2.00	2.00					1.26E-07	1.34E-07		Sample 1 Only	Sample 2 Only	
B4DVB8	B4DVB8_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=2 SV=1	7.40	1.00	1.00		2.00	1.00		5.54E-08	1.35E-07		3.71E-07	1.52E-07		6.69	2.75	Control1 Only
F5GY37	F5GY37_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=2 SV=1	32.60				3.97						2.54E-07			Sample 1 Only		
P05	RLA1_HUMAN 60S acidic ribosomal protein P1	28.90	2.00	2.00		1.00		1.00	1.09	1.15		9.53		7.73	0.88	Control	0.71

386	OS=Homo sapiens GN=RPLP1 PE=1 SV=1								E-06	E-06		E-07		E-07		1 Only	
J3QRV5	J3QRV5_HUMAN Lethal(2) giant larvae protein homolog 2 OS=Homo sapiens GN=LLGL2 PE=2 SV=1	3.70	1.99	1.98			1.98	0.99	2.10 E-08	4.20 E-08			3.64 E-08	2.74 E-08	Control 1 Only	1.74	1.31
P53007	TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	12.90		2.00		2.00		1.00		1.67 E-07		1.56 E-07		7.64 E-08	Sample 1 Only		Sample 3 Only
Q14764	MVP_HUMAN Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	7.30				5.00	1.00					8.41 E-08	1.73 E-08		Sample 1 Only	Sample 2 Only	
P62829	RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	37.90		2.00				1.00		8.38 E-07				9.74 E-07			Sample 3 Only
P56537	IF6_HUMAN Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	9.80		1.00		1.00		2.00		8.79 E-08		1.32 E-07		2.36 E-07	Sample 1 Only		Sample 3 Only
P05109	S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	31.20		2.00			2.00	1.00		4.16 E-07			3.66 E-07	1.23 E-07		Sample 2 Only	Sample 3 Only
G3V1B3	G3V1B3_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=4 SV=1	29.90		3.00				1.00		2.43 E-06				3.22 E-07			Sample 3 Only
H3BVG0	H3BVG0_HUMAN Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=2 SV=1	3.80	1.00	0.99					3.11 E-08	1.43 E-08					Control 1 Only	Control 1 Only	Control1 Only
K7EKB2	K7EKB2_HUMAN TATA-binding protein-associated factor 2N (Fragment) OS=Homo sapiens GN=TAF15 PE=4 SV=1	21.50	0.99			0.99		1.99	4.09 E-07			1.80 E-07		3.98 E-07	0.44	Control 1 Only	0.97
P46109	CRKL_HUMAN Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1	14.20		2.00		2.00	1.00			4.04 E-07		3.53 E-07	9.66 E-08		Sample 1 Only	Sample 2 Only	
Q9NP72	RAB18_HUMAN Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1	15.50		0.99		1.98				2.07 E-07		3.05 E-07			Sample 1 Only		
Q12905	ILF2_HUMAN Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	14.60		2.00		2.00				3.06 E-07		1.10 E-07			Sample 1 Only		
H0Y566	H0Y566_HUMAN BTB/POZ domain-containing protein KCTD3 (Fragment) OS=Homo sapiens GN=KCTD3 PE=4 SV=1	16.90	1.00				2.00		2.02 E-08				5.33 E-08		Control 1 Only	2.64	Control1 Only
P22528	SPR1B_HUMAN Cornifin-B OS=Homo sapiens GN=SPRR1B PE=1 SV=2	27.00	1.99				1.00	1.00	2.67 E-07				9.30 E-08	1.04 E-07	Control 1 Only	0.35	0.39
Q9P225	DYH2_HUMAN Dynein heavy chain 2, axonemal OS=Homo sapiens GN=DNAH2 PE=2 SV=3	0.60					1.00	1.00					1.74 E-08	1.64 E-08		Sample 2 Only	Sample 3 Only
P47929	LEG7_HUMAN Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	18.40	1.00	1.00		1.00	1.00		1.30 E-07	1.22 E-07		1.06 E-07	8.08 E-08		0.82	0.62	Control1 Only
F8WCY5	F8WCY5_HUMAN Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=2 SV=1	13.60	0.99	0.99		1.98			6.27 E-08	2.97 E-07		5.26 E-07			8.39	Control 1 Only	Control1 Only
F5H423	F5H423_HUMAN ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=2 SV=1	32.60	0.99	0.99		1.98			1.12 E-07	6.40 E-07		4.86 E-07			4.34	Control 1 Only	Control1 Only
K7EIN2	K7EIN2_HUMAN Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=4 SV=1	27.30		1.98		2.97				3.95 E-07		3.97 E-07			Sample 1 Only		
Q3LXA3	DHAK_HUMAN Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2	8.90					1.00						3.08 E-08			Sample 2 Only	
Q5W0U4	BSPRY_HUMAN B box and SPRY domain-containing protein OS=Homo sapiens GN=BSPRY PE=2 SV=1	22.30				3.00		1.00				3.81 E-07		2.30 E-08	Sample 1 Only		Sample 3 Only

Q96NB2	SFXN2_HUMAN Sideroflexin-2 OS=Homo sapiens GN=SFXN2 PE=1 SV=2	6.80	1.00	1.00		1.00			1.10 E-07	1.14 E-07		1.19 E-07			1.08	Control 1 Only	Control1 Only
Q9Y6I8	PXMP4_HUMAN Peroxisomal membrane protein 4 OS=Homo sapiens GN=PXMP4 PE=1 SV=3	15.10		1.98		2.97				9.99 E-07		9.34 E-07			Sample 1 Only		
A1L0T0	ILVBL_HUMAN Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2	8.60						1.00						2.37 E-08			Sample 3 Only
E7EMS6	E7EMS6_HUMAN Catechol O-methyltransferase (Fragment) OS=Homo sapiens GN=COMT PE=2 SV=1	11.60		2.00			2.00	1.00		4.39 E-07			2.15 E-07	2.56 E-07		Sample 2 Only	Sample 3 Only
F5H2D9	F5H2D9_HUMAN mRNA cap guanine-N7 methyltransferase OS=Homo sapiens GN=RNMT PE=2 SV=1	11.50	1.00			2.00	2.00		1.11 E-07			3.34 E-07	2.20 E-07		3.01	1.98	Control1 Only
E9PKG1	E9PKG1_HUMAN Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=2 SV=1	8.30		1.00		1.00	1.00	1.00		4.35 E-07		1.02 E-07	8.66 E-08	6.16 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
F5GX77	F5GX77_HUMAN tRNA methyltransferase 112 homolog OS=Homo sapiens GN=TRMT112 PE=2 SV=1	19.80	1.99			0.99			5.01 E-07			3.26 E-07			0.65	Control 1 Only	Control1 Only
P40692	MLH1_HUMAN DNA mismatch repair protein Mlh1 OS=Homo sapiens GN=MLH1 PE=1 SV=1	4.00		0.99			1.98			4.44 E-08			3.68 E-08			Sample 2 Only	
G3V1R4	G3V1R4_HUMAN NOL1/NOP2/Sun domain family, member 2, isoform CRA_b OS=Homo sapiens GN=NSUN2 PE=2 SV=1	7.00		2.00		1.00	1.00			5.85 E-08		4.42 E-08	3.40 E-08		Sample 1 Only	Sample 2 Only	
C9JGT8	C9JGT8_HUMAN AP-2 complex subunit mu (Fragment) OS=Homo sapiens GN=AP2M1 PE=2 SV=1	14.40					2.98	0.99					4.68 E-07	7.95 E-08		Sample 2 Only	Sample 3 Only
A1A528	A1A528_HUMAN Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=2 SV=1	4.30	1.00	2.00		1.00	1.00		3.87 E-08	1.43 E-07		6.79 E-08	3.29 E-08		1.76	0.85	Control1 Only
B7Z3I9	B7Z3I9_HUMAN Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=2 SV=1	6.70		1.00		1.00	1.00			1.74 E-07		9.45 E-08	1.44 E-07		Sample 1 Only	Sample 2 Only	
Q15393	SF3B3_HUMAN Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	3.50		1.00		2.00		1.00		2.18 E-08		3.52 E-08		1.19 E-08	Sample 1 Only		Sample 3 Only
B1AHC3	B1AHC3_HUMAN Protein PRR5-ARHGAP8 OS=Homo sapiens GN=PRR5-ARHGAP8 PE=2 SV=1	5.40	1.00			1.00	2.00		2.04 E-08			7.34 E-08	7.56 E-08		3.59	3.70	Control1 Only
Q9Y3Y2	CHTOP_HUMAN Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2	12.90			1.00	1.00		2.00			1.72 E-08	6.81 E-09		1.48 E-07	Sample 1 Only		Sample 3 Only
B4DLN1	B4DLN1_HUMAN Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=2 SV=1	20.50				2.00						1.37 E-07			Sample 1 Only		
E7ERK9	E7ERK9_HUMAN Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=2 SV=1	7.10		1.00			1.00	2.00		9.25 E-08			5.05 E-08	9.70 E-08		Sample 2 Only	Sample 3 Only
E7EUI8	E7EUI8_HUMAN Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens GN=G6PD PE=2 SV=1	12.10				1.00	2.00	1.00				9.30 E-08	1.21 E-07	6.13 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7EW20	E7EW20_HUMAN Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=2 SV=1	2.40		1.00	2.00			1.00		7.23 E-09	1.51 E-08			2.09 E-08			Sample 3 Only
C9J1Z8	C9J1Z8_HUMAN ADP-ribosylation factor 5 (Fragment) OS=Homo sapiens GN=ARF5	27.30	1.00	1.00			1.00	1.00	6.06 E-08	2.05 E-07			4.12 E-08	9.47 E-08	Control 1 Only	0.68	1.56

	PE=2 SV=1																
P20700	LMNB1_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	7.20						1.00						1.26 E-08			Sample 3 Only
O43615	TIM44_HUMAN Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2	5.50		2.00						1.68 E-07							
P01857	IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	10.90				2.50	1.00					2.31 E-07	3.04 E-08		Sample 1 Only	Sample 2 Only	
P61981	1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	14.60		1.00		1.00		0.98		7.91 E-08		7.84 E-08		6.50 E-08	Sample 1 Only		Sample 3 Only
P62266	RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	15.40		2.00		1.00				5.48 E-07		1.24 E-07			Sample 1 Only		
Q14258	TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	3.70		1.00		1.00	1.00			3.16 E-08		8.83 E-09	8.17 E-09		Sample 1 Only	Sample 2 Only	
Q9NR30	DDX21_HUMAN Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	8.50	1.00	1.00			1.00	1.00	4.19 E-08	2.38 E-08			1.35 E-08	4.81 E-08	Control 1 Only	0.32	1.15
Q9UHD9	UBQL2_HUMAN Ubiquilin-2 OS=Homo sapiens GN=UBQLN2 PE=1 SV=2	10.30				1.00	0.98	0.98				1.13 E-08	3.30 E-08	4.33 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q12904	AIMP1_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	8.30		1.00		2.00	2.00			2.49 E-07		3.55 E-07	2.04 E-07		Sample 1 Only	Sample 2 Only	
M0QX M4	M0QXM4_HUMAN Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=2 SV=1	6.80		0.99		1.98				2.48 E-08		9.15 E-08			Sample 1 Only		
P33991	MCM4_HUMAN DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5	3.60	1.00	1.00			1.00	1.00	3.19 E-08	2.26 E-08			2.00 E-08	2.58 E-08	Control 1 Only	0.63	0.81
O00232	PSD12_HUMAN 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	5.00	1.00	2.00			1.00		4.19 E-08	2.82 E-07			7.52 E-08		Control 1 Only	1.80	Control1 Only
A0FGR8-2	ESYT2_HUMAN Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2	5.00		1.00			1.00			2.34 E-08			3.65 E-09			Sample 2 Only	
Q9BRZ2	TRI56_HUMAN E3 ubiquitin-protein ligase TRIM56 OS=Homo sapiens GN=TRIM56 PE=1 SV=3	3.30	1.00			1.00		1.99	1.05 E-08			7.69 E-09		3.21 E-08	0.74	Control 1 Only	3.07
E9PF10	E9PF10_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=2 SV=1	2.20		2.00			2.00			2.25 E-08			1.32 E-08			Sample 2 Only	
P40938	RFC3_HUMAN Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2	9.20		1.00			1.00	1.00		4.03 E-08			1.75 E-08	2.26 E-08		Sample 2 Only	Sample 3 Only
Q96S19	CP013_HUMAN UPF0585 protein C16orf13 OS=Homo sapiens GN=C16orf13 PE=1 SV=2	10.80		1.00		2.00				1.11 E-07		1.75 E-07			Sample 1 Only		
E5RFR9	E5RFR9_HUMAN Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform (Fragment) OS=Homo sapiens GN=PPP2R2A PE=2 SV=1	12.70		0.99		0.99				3.58 E-07		1.43 E-07			Sample 1 Only		
F5H2T0	F5H2T0_HUMAN Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=2 SV=1	4.50		1.00		1.00	1.00	1.00		1.24 E-08		1.57 E-08	1.06 E-08	9.66 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
O14929	HAT1_HUMAN Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1	6.00		1.00		1.00	2.00			7.40 E-08		7.53 E-08	9.05 E-08		Sample 1 Only	Sample 2 Only	
Q92820	GGH_HUMAN Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2	6.90				1.00	2.00					1.81 E-07	1.90 E-07		Sample 1 Only	Sample 2 Only	

F5GX23	F5GX23_HUMAN 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=2 SV=1	13.70		0.99		0.99		0.99		5.26 E-08		1.69 E-07		6.52 E-08	Sample 1 Only		Sample 3 Only
P02452	CO1A1_HUMAN Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	4.40	1.00						3.41 E-08						Control 1 Only	Control 1 Only	Control1 Only
O15260	SURF4_HUMAN Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3	21.40		1.00			1.00	1.00		7.49 E-07			8.45 E-08	8.42 E-08		Sample 2 Only	Sample 3 Only
Q08945	SSRP1_HUMAN FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1	3.50	2.00	1.00				1.00	4.33 E-08	2.43 E-08				1.63 E-08	Control 1 Only	Control 1 Only	0.38
B3KXD6	B3KXD6_HUMAN Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1	4.00		1.00				1.00		3.21 E-08				1.34 E-07			Sample 3 Only
P46939	UTRO_HUMAN Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2	0.40	1.00			2.00	1.00		2.37 E-08			2.45 E-08	5.37 E-09		1.03	0.23	Control1 Only
Q9BPX3	CND3_HUMAN Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1	2.90	1.00	2.00			1.00		5.71 E-09	2.23 E-08			6.06 E-09		Control 1 Only	1.06	Control1 Only
C9IZE4	C9IZE4_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=2 SV=1	11.80		1.98		1.98				2.40 E-07		8.68 E-08			Sample 1 Only		
Q14532	K1H2_HUMAN Keratin, type I cuticular Ha2 OS=Homo sapiens GN=KRT32 PE=1 SV=3	13.20	2.00				1.00		3.91 E-08				1.11 E-08		Control 1 Only	0.28	Control1 Only
B4DGU4	B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1	7.10	1.00			0.99			5.53 E-09			2.39 E-08			4.31	Control 1 Only	Control1 Only
P16152	CBR1_HUMAN Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	16.20				2.97						3.11 E-07			Sample 1 Only		
F8VQE1	F8VQE1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=2 SV=1	6.40	2.00	1.00	1.00				6.53 E-08	1.60 E-08	1.64 E-08				Control 1 Only	Control 1 Only	Control1 Only
J3QLS3	J3QLS3_HUMAN 28S ribosomal protein S7, mitochondrial OS=Homo sapiens GN=MRPS7 PE=2 SV=1	19.80				2.97						3.02 E-07			Sample 1 Only		
P61026	RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	20.50		1.00		1.00		0.66		6.90 E-07		2.80 E-08		4.72 E-08	Sample 1 Only		Sample 3 Only
P62263	RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	15.90		1.00				2.00		5.16 E-07				1.60 E-06			Sample 3 Only
Q8TEB1	DCA11_HUMAN DDB1- and CUL4-associated factor 11 OS=Homo sapiens GN=DCAF11 PE=1 SV=1	9.20						2.97						5.15 E-08			Sample 3 Only
Q86UY0	Q86UY0_HUMAN Protein BLOC1S5-TXNDC5 OS=Homo sapiens GN=TXNDC5 PE=2 SV=1	8.60		1.00			1.00	1.00		6.00 E-08			5.19 E-08	3.66 E-08		Sample 2 Only	Sample 3 Only
B7Z1R5	B7Z1R5_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=2 SV=1	5.50															
F5H897	F5H897_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=2 SV=1	7.20				1.00	1.00					2.58 E-08	3.45 E-08		Sample 1 Only	Sample 2 Only	
P04083	ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	8.70		1.00						2.06 E-08							
Q09666	AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	2.00	1.00				1.00		1.99 E-09				2.10 E-09		Control 1 Only	1.06	Control1 Only
Q96RQ1	ERGI2_HUMAN Endoplasmic reticulum-Golgi intermediate compartment protein 2 OS=Homo sapiens GN=ERGIC2 PE=1 SV=2	8.00		0.99		0.99	0.99			8.50 E-08		1.12 E-07	8.05 E-08		Sample 1 Only	Sample 2 Only	
J3KPF5	J3KPF5_HUMAN Prostamide/prostaglandin F synthase OS=Homo sapiens GN=FAM213B	19.50				1.00						1.98 E-07			Sample 1 Only		

	PE=2 SV=1																
Q8WUK0	PTPM1_HUMAN Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Homo sapiens GN=PTPMT1 PE=1 SV=1	9.50		1.00						9.23 E-08							
Q15427	SF3B4_HUMAN Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	5.20				1.00						1.10 E-07			Sample 1 Only		
P29508	SPB3_HUMAN Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	9.70	0.99			1.98			6.06 E-08			1.17 E-07			1.92	Control 1 Only	Control1 Only
H3BSW6	H3BSW6_HUMAN Cytoplasmic tRNA 2-thiolation protein 2 OS=Homo sapiens GN=CTU2 PE=2 SV=1	7.90					1.00	2.00					1.92 E-08	4.06 E-08		Sample 2 Only	Sample 3 Only
P10412	H14_HUMAN Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	9.70	1.00					2.00	3.85 E-08					1.33 E-07	Control 1 Only	Control 1 Only	3.44
K7EQ48	K7EQ48_HUMAN Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=2 SV=2	5.90				1.00						2.47 E-08			Sample 1 Only		
P12931	SRC_HUMAN Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens GN=SRC PE=1 SV=3	4.90					0.99	1.99					2.33 E-08	9.61 E-08		Sample 2 Only	Sample 3 Only
O60832	DKC1_HUMAN H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3	4.10						1.99						7.74 E-08			Sample 3 Only
Q15046	SYK_HUMAN Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3	5.00				1.99						1.05 E-07			Sample 1 Only		
B3KV55	B3KV55_HUMAN Glutamate dehydrogenase OS=Homo sapiens GN=GLUD1 PE=2 SV=1	4.90				1.00	1.00					5.49 E-08	7.26 E-08		Sample 1 Only	Sample 2 Only	
E9PKH5	E9PKH5_HUMAN Transcription factor p65 (Fragment) OS=Homo sapiens GN=RELA PE=2 SV=1	5.70		1.00			1.00			7.70 E-08			4.95 E-08			Sample 2 Only	
B4E3S0	B4E3S0_HUMAN Coronin OS=Homo sapiens GN=CORO1C PE=2 SV=1	4.30		1.00			1.00			1.59 E-07			3.68 E-08			Sample 2 Only	
Q9HCN8	SDF2L_HUMAN Stromal cell-derived factor 2-like protein 1 OS=Homo sapiens GN=SDF2L1 PE=1 SV=2	22.60		3.00						1.06 E-06							
Q9UER7	DAXX_HUMAN Death domain-associated protein 6 OS=Homo sapiens GN=DAXX PE=1 SV=2	4.80						3.00						1.94 E-07			Sample 3 Only
Q9BW19	KIFC1_HUMAN Kinesin-like protein KIFC1 OS=Homo sapiens GN=KIFC1 PE=1 SV=2	3.10		1.00			1.00			1.53 E-08			1.93 E-08			Sample 2 Only	
E7EN32	E7EN32_HUMAN Menin OS=Homo sapiens GN=MEN1 PE=2 SV=1	8.40	1.00	1.00		1.00			1.43 E-08	1.92 E-08		1.74 E-08			1.22	Control 1 Only	Control1 Only
O14980	XPO1_HUMAN Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	6.40		1.00		2.00				1.14 E-08		2.95 E-08			Sample 1 Only		
Q9BU23	LMF2_HUMAN Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 PE=1 SV=2	1.30					1.00	1.00					3.26 E-08	1.98 E-08		Sample 2 Only	Sample 3 Only
P25311	ZA2G_HUMAN Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	10.40	2.00			1.00			1.23 E-07			9.67 E-08			0.79	Control 1 Only	Control1 Only
P24844	MYL9_HUMAN Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4	48.30		1.00	1.00			1.00		3.75 E-07	1.44 E-07			1.01 E-07			Sample 3 Only
O15230	LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	1.00						3.00						1.72 E-08			Sample 3 Only
P51153	RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1	21.70		1.00				1.00		8.82 E-08				2.70 E-08			Sample 3 Only

Q9Y2T7	YBOX2_HUMAN Y-box-binding protein 2 OS=Homo sapiens GN=YBX2 PE=1 SV=2	11.80		1.00				1.00		3.79 E-08				2.95 E-08			Sample 3 Only
Q9ULE0	WWC3_HUMAN Protein WWC3 OS=Homo sapiens GN=WWC3 PE=1 SV=3	2.90	1.00			1.00	1.00		4.67 E-09			7.50 E-09	9.09 E-09		1.61	1.95	Control1 Only
Q12965	MYO1E_HUMAN Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2	3.50	1.00	2.00					1.63 E-08	2.45 E-08					Control 1 Only	Control 1 Only	Control1 Only
Q9NUP9	LIN7C_HUMAN Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1	19.80				3.00						5.17 E-07			Sample 1 Only		
F8W845	F8W845_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=2 SV=1	3.70		0.99			1.98			1.74 E-08			2.09 E-08			Sample 2 Only	
B1AK13	B1AK13_HUMAN 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (Hydroxymethylglutaricaciduria), isoform CRA_b OS=Homo sapiens GN=HMGCL PE=2 SV=1	8.30				2.00						2.07 E-07			Sample 1 Only		
B4DNL7	B4DNL7_HUMAN Cysteine desulfurase, mitochondrial OS=Homo sapiens GN=NFS1 PE=2 SV=1	13.30				1.00	0.99					5.07 E-08	5.87 E-08		Sample 1 Only	Sample 2 Only	
J3KSR8	J3KSR8_HUMAN Serine/arginine-rich-splicing factor 1 (Fragment) OS=Homo sapiens GN=SRSF1 PE=4 SV=1	13.30						1.99						2.47 E-07			Sample 3 Only
Q6PID8	KLD10_HUMAN Kelch domain-containing protein 10 OS=Homo sapiens GN=KLHDC10 PE=1 SV=1	7.40		1.00		1.00				8.79 E-08		1.72 E-07			Sample 1 Only		
P62140	PP1B_HUMAN Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	7.30				1.98						1.11 E-07			Sample 1 Only		
B4E1S6	B4E1S6_HUMAN Syndecan OS=Homo sapiens GN=SDC4 PE=2 SV=1	17.50						2.00						2.72 E-07			Sample 3 Only
B4DFJ5	B4DFJ5_HUMAN 28S ribosomal protein S25, mitochondrial OS=Homo sapiens GN=MRPS25 PE=2 SV=1	23.60						1.00						7.18 E-08			Sample 3 Only
B8ZZK2	B8ZZK2_HUMAN Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=2 SV=1	22.30				1.00	1.00					1.11 E-07	5.65 E-08		Sample 1 Only	Sample 2 Only	
B7Z8V7	B7Z8V7_HUMAN NAD kinase 2, mitochondrial OS=Homo sapiens GN=NADK2 PE=2 SV=1	10.00		1.00			1.00			1.12 E-07			5.33 E-08			Sample 2 Only	
Q8TAA9	VANG1_HUMAN Vang-like protein 1 OS=Homo sapiens GN=VANGL1 PE=1 SV=1	7.50					1.00						6.50 E-08			Sample 2 Only	
H0YJV2	H0YJV2_HUMAN Serine palmitoyltransferase 2 (Fragment) OS=Homo sapiens GN=SPTLC2 PE=3 SV=1	6.90						1.00						2.14 E-08			Sample 3 Only
B7Z5C0	B7Z5C0_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=2 SV=1	11.70		2.00						1.77 E-07							
B4DRF4	B4DRF4_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=2 SV=1	10.10				1.00						7.46 E-08			Sample 1 Only		
E9PKP7	E9PKP7_HUMAN Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=2 SV=1	3.90						2.00						9.00 E-08			Sample 3 Only
O00159-2	MYO1C_HUMAN Isoform 2 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	15.20			0.99			0.99			1.54 E-08			1.09 E-08			Sample 3 Only
P01621	KV303_HUMAN Ig kappa chain V-III region NG9 (Fragment) OS=Homo sapiens PE=1 SV=1	32.00		1.00						2.94 E-07							

P08729	K2C7_HUMAN Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	22.00						2.00					1.41 E-07			Sample 3 Only
Q13501	SQSTM_HUMAN Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1	11.50					1.00						3.18 E-08			Sample 2 Only	
Q8WXF1	PSPC1_HUMAN Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1	6.60															
P09382	LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	25.20				2.00						3.19 E-07			Sample 1 Only		
Q15633	TRBP2_HUMAN RISC-loading complex subunit TARBP2 OS=Homo sapiens GN=TARBP2 PE=1 SV=3	9.00				1.98						2.20 E-07			Sample 1 Only		
P30086	PEBP1_HUMAN Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	15.00															
B4DER1	B4DER1_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1	4.30		1.00						1.39 E-08							
E7ESI2	E7ESI2_HUMAN Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=2 SV=1	13.90				0.99						5.48 E-08			Sample 1 Only		
H0Y8Z9	H0Y8Z9_HUMAN Acyl-CoA dehydrogenase family member 9, mitochondrial (Fragment) OS=Homo sapiens GN=ACAD9 PE=2 SV=1	5.50						1.00					9.15 E-08			Sample 3 Only
P49721	PSB2_HUMAN Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	9.50				1.00						1.58 E-07			Sample 1 Only		
K7ENG2	K7ENG2_HUMAN Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=2 SV=1	12.10						1.00					9.36 E-08			Sample 3 Only
K7EJ81	K7EJ81_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=2 SV=1	2.70				1.00						9.24 E-09			Sample 1 Only		
O43865	SAHH2_HUMAN Putative adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 PE=1 SV=2	3.50				1.00						3.87 E-08			Sample 1 Only		
A7E2Y1	MYH7B_HUMAN Myosin-7B OS=Homo sapiens GN=MYH7B PE=1 SV=3	1.30	1.00						2.27 E-08						Control 1 Only	Control 1 Only	Control1 Only
Q14CN4	K2C72_HUMAN Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2	15.60															
H7BXY3	H7BXY3_HUMAN Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=2 SV=1	1.00						1.00					1.06 E-08			Sample 3 Only
E7END7	E7END7_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=2 SV=1	11.00															
Q9Y6K5	OAS3_HUMAN 2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3	0.90					1.00						9.82 E-09			Sample 2 Only	
P16989	YBOX3_HUMAN Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4	14.50						1.00					1.71 E-08			Sample 3 Only

Table A5. FLAG candidates from nuclear immunoprecipitations that had not been treated with RNase.

			SPECTRAL COUNTS				SPECTRAL INDEX (MIC SIn)				RATIOS	
Prot	Description	% Cover	C1	C2	S1	S2	C1	C2	S1	S2	S1/C1	S2/C2
P78527	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	46.50	89.95	123.91	189.41	459.18	1.09E-06	1.53E-06	4.74E-06	1.53E-05	4.34	14.02
Q15149	PLEC_HUMAN Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	34.20	122.81	73.90	68.86	136.82	1.11E-06	5.81E-07	6.90E-07	2.05E-06	0.62	1.84
A6NG51	A6NG51_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=2 SV=2	51.60	41.00	65.00	91.00	199.97	5.95E-07	1.34E-06	3.63E-06	1.29E-05	6.10	21.65
Q00610	CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	54.80	55.74	77.60	98.52	167.22	2.75E-06	3.50E-06	1.18E-05	1.87E-05	4.30	6.80
P04264	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	53.10	97.97	111.94	78.97	115.96	3.14E-05	4.48E-05	5.32E-05	5.17E-05	1.69	1.65
P58107	EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	53.50	42.50	39.50	56.00	88.50	4.46E-07	4.05E-07	9.66E-07	1.85E-06	2.17	4.14
P13645	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	62.70	83.56	108.45	63.70	92.45	2.43E-05	2.96E-05	3.01E-05	4.07E-05	1.24	1.68
P15924	DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	39.80	61.00	58.00	70.99	158.99	1.12E-06	8.59E-07	1.94E-06	7.24E-06	1.73	6.44
P21333	FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	34.50	45.60	52.12	46.13	112.14	8.09E-07	1.03E-06	1.67E-06	6.65E-06	2.07	8.21
E9PPU0	E9PPU0_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=4 SV=1	39.30	27.50	24.50	34.00	49.50	4.33E-07	3.90E-07	1.28E-06	2.36E-06	2.97	5.45
O15020	SPTN2_HUMAN Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	39.00	22.00	48.99	61.98	125.91	4.01E-07	9.42E-07	2.28E-06	9.99E-06	5.68	24.94
Q9UKV8	AGO2_HUMAN Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	67.40			104.95	154.96			2.55E-05	5.48E-05	Sample 1 Only	Sample 2 Only
P35527	K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	52.50	67.61	73.56	44.76	67.56	1.78E-05	1.91E-05	1.26E-05	3.11E-05	0.70	1.74
P53621	COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	52.10	24.99	32.98	59.97	129.96	6.81E-07	1.35E-06	8.16E-06	2.14E-05	11.98	31.43
P06310	KV206_HUMAN Ig kappa chain V-II region RPMI 6410 OS=Homo sapiens PE=4 SV=1	23.30	61.00	51.00	47.00	27.00	3.37E-03	2.22E-03	2.08E-03	2.34E-04	0.62	0.07
Q01082	SPTB2_HUMAN Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	35.70	14.96	35.95	51.89	108.73	1.47E-07	5.29E-07	1.84E-06	6.80E-06	12.53	46.29
P35908	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	73.90	45.00	57.00	44.00	59.00	1.28E-05	2.14E-05	1.13E-05	2.18E-05	0.88	1.70
P35579	MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	46.30	14.00	24.98	54.97	79.92	1.98E-07	3.95E-07	1.54E-06	4.87E-06	7.78	24.66
Q14980-2	NUMA1_HUMAN Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1	49.30	11.99	19.49	19.49	37.99	4.01E-07	1.01E-06	7.72E-07	3.42E-06	1.92	8.52
F5H335	F5H335_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1	38.50	23.00	29.00	26.00	83.00	5.19E-07	1.06E-06	1.56E-06	5.71E-06	3.01	11.00
M0QZM1	M0QZM1_HUMAN Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens GN=HNRNPM PE=4 SV=1	60.80	13.00	24.50	25.50	23.50	1.75E-06	7.56E-06	1.81E-05	3.64E-05	10.33	20.78
O75165	DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5	21.40	22.00	16.00	33.00	81.00	5.94E-07	9.32E-07	1.01E-06	1.74E-06	1.71	2.94
O75643	U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	25.40	16.00	27.99	31.00	69.99	2.24E-07	6.18E-07	7.67E-07	3.75E-06	3.42	16.71
P60709	ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	74.70	19.26	36.62	48.37	36.62	9.06E-06	4.99E-05	5.98E-05	4.15E-05	6.60	4.58

P52732	KIF11_HUMAN Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	32.40	22.00	28.00	48.00	47.00	1.27E-06	1.80E-06	9.57E-06	1.04E-05	7.52	8.15
P46940	IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	25.30	15.99	20.00	26.99	48.95	2.27E-07	5.29E-07	5.96E-07	2.49E-06	2.62	10.97
Q14204	DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	12.30		9.00	42.00	60.00		2.60E-08	3.09E-07	4.12E-07	Sample 1 Only	Sample 2 Only
Q8IX12	CCAR1_HUMAN Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	23.00	20.86	28.83	19.88	36.75	8.25E-07	2.84E-06	3.86E-06	7.31E-06	4.68	8.86
P05787	K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	70.20	69.44	8.93	9.92	21.85	3.50E-05	2.78E-06	6.24E-06	2.46E-05	0.18	0.70
Q9UPQ9-1	TNR6B_HUMAN Isoform 2 of Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B	25.50	0.50		23.37	29.98	8.54E-10		1.30E-06	3.60E-06	1522.25	4209.60
Q15393	SF3B3_HUMAN Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	30.70	15.98	29.95	19.95	35.95	3.05E-07	1.56E-06	2.03E-06	3.11E-06	6.65	10.19
P11388	TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	20.80	26.50	23.00	10.00	24.50	6.60E-07	5.88E-07	2.45E-07	1.93E-06	0.37	2.92
Q00341	VIGLN_HUMAN Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	34.50	4.93	13.73	20.64	56.07	2.78E-07	2.92E-07	1.09E-06	7.43E-06	3.93	26.75
Q9C0C2	TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	27.60	2.00	12.00	33.00	51.00	6.82E-09	1.82E-07	1.73E-06	4.76E-06	253.78	697.84
Q9ULV0	MYO5B_HUMAN Unconventional myosin-Vb OS=Homo sapiens GN=MYO5B PE=1 SV=3	25.70	35.94	8.97	16.98	29.91	1.60E-06	4.10E-07	6.51E-07	1.56E-06	0.41	0.98
O75533	SF3B1_HUMAN Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	24.70	11.00	15.99	17.00	50.99	5.22E-07	1.29E-06	2.47E-06	6.29E-06	4.73	12.04
O60264	SMCA5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1	24.70	7.00	24.00	16.00	39.99	1.77E-07	8.82E-07	2.45E-06	7.05E-06	13.88	39.86
F8VXC8	F8VXC8_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=2 SV=1	22.40	19.00	29.00	15.00	20.00	4.27E-07	7.30E-07	8.13E-07	1.17E-06	1.90	2.74
Q5UIP0	RIF1_HUMAN Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2	11.70	23.00	23.99	18.99	14.99	6.56E-07	5.72E-07	4.86E-07	3.13E-07	0.74	0.48
P52272	HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	53.00	5.48	13.43	13.90	23.24	2.32E-07	1.47E-06	3.83E-06	1.13E-05	16.48	48.77
Q08211	DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	22.30	9.00	8.00	15.00	43.00	1.38E-07	2.43E-07	1.19E-06	5.77E-06	8.62	41.86
Q9UH99	SUN2_HUMAN SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	38.20	17.94	21.87	21.91	14.96	2.70E-06	4.27E-06	1.47E-05	9.57E-06	5.45	3.55
P39023	RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	45.40	8.85	14.81	21.75	28.71	1.76E-06	1.16E-05	1.72E-05	1.69E-05	9.73	9.57
Q92616	GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	13.80	6.00	8.00	11.00	48.00	1.60E-08	4.05E-08	1.33E-07	4.77E-07	8.31	29.81
O00159-3	MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	30.70	2.02	12.19	7.12	15.75	5.27E-08	1.30E-06	3.66E-07	1.79E-06	6.95	33.99
Q7L014	DDX46_HUMAN Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2	23.70	9.00	13.00	22.00	27.98	1.63E-07	3.96E-07	1.38E-06	3.24E-06	8.47	19.83
P04843	RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	39.40	7.00	18.00	17.00	28.00	3.57E-07	2.88E-06	8.87E-06	1.19E-05	24.82	33.39
C9J9K3	C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	65.90	11.97	19.93	19.93	16.93	7.00E-06	4.93E-06	3.47E-05	3.74E-05	4.96	5.35
E7EX17	E7EX17_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=2 SV=1	35.80	15.95	16.43	10.46	10.47	1.82E-06	2.72E-06	3.00E-06	1.71E-06	1.64	0.94
Q96CW1	AP2M1_HUMAN AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2	45.00	5.88	11.75	22.51	24.44	1.90E-06	6.39E-06	2.57E-05	1.40E-05	13.52	7.35
Q8N3C0	ASCC3_HUMAN Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3	13.50	2.00	12.00	17.00	34.00	1.10E-08	7.85E-08	2.18E-07	1.13E-06	19.79	102.36

P23396	RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	76.10	11.71	17.59	25.44	9.74	9.44 E-06	4.23 E-05	5.88 E-05	3.24 E-05	6.22	3.43
P61978	HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	38.10	8.93	21.82	13.89	14.89	1.46 E-06	7.50 E-06	7.88 E-06	8.34 E-06	5.39	5.71
J3QRN6	J3QRN6_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=2 SV=1	33.30	0.99	13.90	11.93	33.81	3.03 E-08	1.00 E-06	1.40 E-06	6.01 E-06	46.02	198.35
A5YKK6	CNOT1_HUMAN CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	10.60		10.89	13.86	34.60		1.24 E-07	2.30 E-07	9.33 E-07	Sample 1 Only	Sample 2 Only
P13647	K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	43.20	18.93	13.95	14.92	12.95	1.62 E-06	1.25 E-06	2.89 E-06	1.72 E-06	1.78	1.06
P63244	GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	54.60	5.14	12.72	15.60	10.45	5.88 E-06	2.20 E-05	2.67 E-05	1.25 E-05	4.54	2.12
P36578	RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	40.70	3.99	11.96	18.91	23.88	2.56 E-07	6.62 E-06	8.59 E-06	1.45 E-05	33.55	56.66
Q14160	SCRIB_HUMAN Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4	16.60	8.91	10.89	10.89	22.77	9.00 E-08	1.98 E-07	2.10 E-07	8.53 E-07	2.34	9.48
E9PCY5	E9PCY5_HUMAN DNA topoisomerase 2 (Fragment) OS=Homo sapiens GN=TOP2B PE=2 SV=1	23.30	8.50	12.00	5.00	21.50	2.55 E-07	2.95 E-07	1.46 E-07	1.84 E-06	0.58	7.21
B4DZI8	B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	26.70	2.00	10.98	16.96	27.92	1.51 E-07	9.24 E-07	4.70 E-06	7.45 E-06	31.03	49.21
G3XAB8	G3XAB8_HUMAN Trinucleotide repeat containing 6C, isoform CRA_a OS=Homo sapiens GN=TNRC6C PE=2 SV=1	16.60			13.00	17.00			3.70 E-07	7.79 E-07	Sample 1 Only	Sample 2 Only
P08727	K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	71.00	41.86	3.00	5.99	5.00	3.46 E-05	1.76 E-06	1.27 E-06	7.31 E-06	0.04	0.21
Q07065	CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	44.50	7.00	18.00	16.00	12.00	6.85 E-07	2.13 E-06	2.87 E-06	6.58 E-06	4.20	9.61
F8W6L6	F8W6L6_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=2 SV=1	21.10	7.97	11.96	11.96	23.94	8.99 E-08	1.46 E-07	2.26 E-07	9.56 E-07	2.51	10.63
Q5JTH9	RRP12_HUMAN RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2	22.40	2.97	5.95	7.94	35.73	1.99 E-08	7.86 E-08	3.56 E-07	3.36 E-06	17.89	168.79
Q9HCJ0	TNR6C_HUMAN Trinucleotide repeat-containing gene 6C protein OS=Homo sapiens GN=TNRC6C PE=1 SV=3	16.60			12.00	14.00			5.33 E-07	7.51 E-07	Sample 1 Only	Sample 2 Only
F5GWX5	F5GWX5_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=2 SV=1	19.20	14.50	8.50	8.00	19.00	7.91 E-07	4.01 E-07	2.97 E-07	8.70 E-07	0.38	1.10
P22626	ROA2_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	33.40	16.00	14.00	9.00	11.00	1.46 E-05	3.65 E-06	5.64 E-06	5.44 E-06	0.39	0.37
Q6P2Q9	PRP8_HUMAN Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	15.50	2.00	5.00	4.00	39.00	6.48 E-09	3.00 E-08	5.39 E-08	1.50 E-06	8.31	230.60
Q10570	CPSF1_HUMAN Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2	15.20	6.00	8.00	8.00	28.00	9.54 E-08	1.47 E-07	2.35 E-07	2.14 E-06	2.46	22.42
P68104	EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	24.90	7.50	11.00	7.00	7.00	1.21 E-06	1.11 E-06	5.14 E-06	4.66 E-06	4.24	3.84
Q8N201	INT1_HUMAN Integrator complex subunit 1 OS=Homo sapiens GN=INTS1 PE=1 SV=2	8.80	4.00	8.00	7.98	29.98	2.64 E-08	5.73 E-08	6.92 E-08	4.59 E-07	2.62	17.40
P18583	SON_HUMAN Protein SON OS=Homo sapiens GN=SON PE=1 SV=4	7.60	12.89	10.89	7.94	17.85	8.76 E-08	7.05 E-08	9.54 E-08	2.38 E-07	1.09	2.71
Q09666	AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	8.10	9.00	12.00	9.00	16.00	3.69 E-08	1.00 E-07	3.68 E-08	1.34 E-07	1.00	3.63
P46977	STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	17.70	7.00	6.00	11.00	25.00	2.93 E-07	1.02 E-06	2.67 E-06	4.58 E-06	9.14	15.64
P05783	K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	46.30	37.99	1.00	3.00	6.00	1.38 E-05	3.54 E-09	1.55 E-06	4.24 E-06	0.11	0.31
P49327	FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	13.70		1.00	19.00	26.00		2.20 E-09	1.98 E-07	6.53 E-07	Sample 1 Only	Sample 2 Only
B4DF41	B4DF41_HUMAN DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=2 SV=1	20.60	3.00	3.75	8.75	31.00	4.77 E-08	2.70 E-08	2.31 E-07	1.35 E-06	4.84	28.28

O00571	DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	37.30	4.00	12.97	14.99	13.00	7.23 E-07	2.05 E-06	5.81 E-06	1.76 E-05	8.03	24.35
Q69YN4	VIR_HUMAN Protein virilizer homolog OS=Homo sapiens GN=KIAA1429 PE=1 SV=2	10.90	2.98	8.94	5.94	22.82	4.79 E-08	1.64 E-07	7.91 E-08	4.48 E-07	1.65	9.35
Q6P2E9	EDC4_HUMAN Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1	17.10	3.00	8.00	8.99	22.97	2.82 E-08	1.19 E-07	3.48 E-07	1.53 E-06	12.34	54.29
O15230	LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	6.70	6.00	7.00	10.00	20.00	5.21 E-08	6.24 E-08	5.63 E-08	5.23 E-07	1.08	10.05
Q05639	EF1A2_HUMAN Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	24.60	4.50	4.00	5.00	10.00	6.75 E-07	6.59 E-07	3.76 E-06	3.42 E-06	5.57	5.06
J3KNL6	J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=2 SV=1	8.40	8.00	6.00	9.00	19.00	1.01 E-07	5.61 E-08	2.10 E-07	1.54 E-06	2.07	15.25
E7EMW7	E7EMW7_HUMAN E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=2 SV=1	7.80	9.00	9.00	4.00	20.00	7.51 E-08	9.77 E-08	5.23 E-08	2.45 E-07	0.70	3.27
Q14789	GOGB1_HUMAN Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2	9.80	2.00	7.95	5.95	23.85	2.89 E-08	2.60 E-08	6.62 E-08	2.38 E-07	2.29	8.24
O00468-3	AGRIN_HUMAN Isoform 3 of Agrin OS=Homo sapiens GN=AGRN	9.00	4.95	10.90	8.92	15.85	4.08 E-08	1.31 E-07	1.73 E-07	7.22 E-07	4.25	17.70
Q86YZ3	HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	16.00	19.00	16.00	1.00	1.00	7.89 E-08	2.70 E-08	1.81 E-09	7.82 E-10	0.02	0.01
P62701	RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	42.20	8.99	13.97	10.97	5.00	1.11 E-05	2.90 E-05	1.90 E-05	5.30 E-06	1.71	0.48
P98175	RBM10_HUMAN RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3	22.50	7.00	18.97	6.99	7.99	3.38 E-07	1.76 E-06	1.92 E-06	1.85 E-06	5.67	5.48
F2Z2I2	F2Z2I2_HUMAN 6-phosphofructo-2-kinase OS=Homo sapiens GN=PFKFB3 PE=2 SV=1	37.80	7.95	13.89	14.89	2.99	2.78 E-06	3.59 E-06	9.77 E-06	2.92 E-06	3.51	1.05
Q12789	TF3C1_HUMAN General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4	8.00	1.00	7.00	10.00	21.00	4.38 E-07	7.68 E-07	2.76 E-07	4.44 E-07	0.63	1.01
O43143	DHX15_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	16.00	4.00	12.00	10.00	7.00	3.14 E-07	1.62 E-06	1.93 E-06	1.87 E-06	6.14	5.94
O14578-4	CTRO_HUMAN Isoform 4 of Citron Rho-interacting kinase OS=Homo sapiens GN=CIT	8.90	2.97	8.91	6.94	17.82	3.54 E-08	8.91 E-08	1.72 E-07	5.41 E-07	4.87	15.29
Q9Y6C9	MTCH2_HUMAN Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	28.70	3.00	9.00	12.00	10.00	3.21 E-07	1.57 E-06	1.12 E-05	2.28 E-06	34.95	7.11
Q08379	GOGA2_HUMAN Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3	15.50	3.99	6.98	6.97	14.92	3.84 E-08	3.32 E-07	9.27 E-07	1.98 E-06	24.17	51.58
H3BLZ8	H3BLZ8_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=2 SV=1	32.50	1.68	5.48	6.04	7.28	7.16 E-08	2.14 E-07	6.47 E-07	3.52 E-06	9.04	49.20
Q9UHX1	PUF60_HUMAN Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	42.70	2.99	9.93	10.92	9.93	7.21 E-07	1.78 E-06	6.27 E-06	1.01 E-05	8.70	14.04
P04844	RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	27.60	3.96	8.95	9.92	8.93	7.60 E-07	1.84 E-06	2.27 E-06	1.28 E-06	2.98	1.68
B4DGU4	B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1	20.80	1.00	4.00	9.00	15.00	1.87 E-08	4.58 E-08	9.55 E-07	3.70 E-06	51.20	198.02
P25705	ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	36.70	1.96	2.94	15.76	14.75	1.89 E-07	3.58 E-07	4.06 E-06	9.00 E-06	21.56	47.73
P61247	RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	51.50	4.86	14.51	10.73	3.87	5.17 E-07	4.00 E-05	6.75 E-06	4.57 E-06	13.06	8.84
O76024	WFS1_HUMAN Wolframin OS=Homo sapiens GN=WFS1 PE=1 SV=2	13.10	1.00	3.00	9.00	18.00	6.60 E-08	5.35 E-08	5.49 E-07	1.08 E-06	8.32	16.42
O95782	AP2A1_HUMAN AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	15.10	4.00	4.00	9.00	8.50	1.88 E-07	9.86 E-08	1.93 E-06	2.55 E-06	10.25	13.56
P02647	APOA1_HUMAN Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	47.60	14.00	13.00	2.00	3.00	1.56 E-06	1.50 E-06	1.37 E-07	1.28 E-07	0.09	0.08

Q9NTJ3	SMC4_HUMAN Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2	13.40	2.99	5.99	3.99	18.99	5.71E-06	7.25E-08	1.32E-07	7.86E-07	0.02	0.14
J3QK89	J3QK89_HUMAN Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=2 SV=1	10.20	5.00	14.00	3.00	7.00	1.47E-07	1.09E-06	2.31E-07	1.35E-06	1.57	9.20
K7ENG2	K7ENG2_HUMAN Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=2 SV=1	43.60	2.00	5.00	10.00	12.00	7.43E-07	1.40E-06	5.62E-06	1.42E-05	7.56	19.16
P05388	RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	47.90	4.82	9.66	9.69	1.92	2.42E-07	7.88E-06	1.11E-05	5.65E-07	45.84	2.34
P52597	HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	45.50	7.00	4.00	9.00	8.00	2.77E-06	1.98E-06	1.93E-05	6.21E-06	6.97	2.24
P53618	COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	18.20	1.00	5.99	5.00	15.98	1.70E-08	1.01E-07	3.72E-07	2.85E-06	21.84	167.67
F8VVM2	F8VVM2_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=2 SV=1	23.80	4.00	6.00	6.00	14.00	3.50E-07	1.39E-06	1.57E-06	7.72E-06	4.49	22.05
Q92878	RAD50_HUMAN DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1	8.80	4.95	4.95	5.94	14.85	3.90E-08	7.95E-08	3.12E-07	4.83E-07	8.00	12.40
Q96T23	RSF1_HUMAN Remodeling and spacing factor 1 OS=Homo sapiens GN=RSF1 PE=1 SV=2	12.80	1.98	6.93	5.94	14.85	2.58E-08	9.54E-08	1.15E-07	7.01E-07	4.44	27.14
A8MUD9	A8MUD9_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=2 SV=1	46.20	6.98	6.97	9.96	2.00	3.70E-06	2.35E-05	2.90E-05	1.72E-07	7.84	0.05
E7EUU4	E7EUU4_HUMAN Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=2 SV=1	8.60	0.99	1.98	3.96	16.47	1.09E-08	6.13E-08	7.93E-08	6.90E-07	7.26	63.22
Q8NDV7	TNR6A_HUMAN Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	11.80			6.77	9.89			1.46E-07	1.21E-06	Sample 1 Only	Sample 2 Only
P12830	CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	13.90	3.97	7.96	8.95	3.98	4.03E-07	3.83E-07	1.74E-06	1.87E-06	4.33	4.63
Q09028	RBBP4_HUMAN Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	16.30	6.89	6.90	6.88	4.91	2.71E-06	1.14E-06	2.33E-06	1.02E-06	0.86	0.38
F8VWC5	F8VWC5_HUMAN 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=2 SV=1	36.50	6.93	6.93	8.91	4.95	3.32E-06	1.04E-05	3.61E-05	6.22E-06	10.87	1.87
Q16531	DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	14.10	2.94	9.86	3.95	4.93	2.09E-08	7.30E-07	2.27E-07	2.33E-07	10.89	11.19
Q9P258	RCC2_HUMAN Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	19.00	3.00	7.00	5.00	9.00	3.44E-07	1.62E-06	2.82E-06	5.12E-06	8.18	14.86
F8W7C6	F8W7C6_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=2 SV=1	43.60	0.99	5.91	11.88	7.90	1.03E-06	2.19E-05	1.09E-05	1.56E-05	10.59	15.26
Q8WWY3	PRP31_HUMAN U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2	27.10	4.90	11.81	5.90	4.91	6.77E-07	3.08E-06	3.96E-07	3.35E-06	0.59	4.95
P42704	LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	10.90	2.00	2.00	4.00	19.00	1.35E-08	1.60E-08	2.01E-07	4.88E-07	14.86	36.03
P02533	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	46.60	4.50	5.50	5.00	8.00	1.04E-07	2.55E-07	2.49E-07	1.87E-06	2.40	18.06
A6NNK5	A6NNK5_HUMAN Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=2 SV=2	7.00	1.98	8.97	3.97	5.95	2.36E-08	4.41E-07	4.70E-08	4.08E-07	1.99	17.28
Q96PK6	RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	16.60	0.99	7.97	6.96	7.98	2.27E-08	1.03E-06	1.84E-06	4.42E-06	80.99	194.32
P62805	H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	38.80	6.00	6.00	9.00	3.00	1.60E-05	1.41E-05	3.66E-05	3.24E-06	2.29	0.20
B9A067	B9A067_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=2 SV=2	19.70	2.00	6.00	7.00	7.00	7.59E-08	6.61E-07	3.31E-06	1.40E-06	43.60	18.47
H0Y2W2	H0Y2W2_HUMAN ATPase family AAA domain-containing protein 3A (Fragment) OS=Homo sapiens GN=ATAD3A PE=4 SV=1	23.90		10.94	5.96	6.97		1.37E-06	2.28E-06	1.04E-06	Sample 1 Only	Sample 2 Only
Q15208	STK38_HUMAN Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1	18.10	5.00	7.98	6.98	3.00	1.66E-06	2.40E-06	3.95E-06	1.84E-07	2.37	0.11
P08621	RU17_HUMAN U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2	27.30	2.98	8.97	3.00	7.97	2.43E-07	2.49E-06	9.08E-07	1.01E-05	3.73	41.66

P11142	HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	30.20	2.91	5.84	2.92	9.73	3.58E-08	3.76E-07	2.07E-06	2.79E-06	57.84	78.08
P14923	PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	29.50	2.00	1.00	3.00	15.00	3.71E-08	6.43E-08	6.01E-07	1.63E-06	16.20	43.98
F2Z2U8	F2Z2U8_HUMAN Myosin-14 OS=Homo sapiens GN=MYH14 PE=2 SV=1	11.20	1.98	1.97	10.88	8.90	7.62E-08	1.03E-08	2.14E-07	2.32E-07	2.80	3.04
Q8TEQ6	GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	8.30	1.00	2.00	3.00	18.00	5.92E-09	2.04E-08	2.93E-08	2.79E-07	4.94	47.17
B3KXW5	B3KXW5_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=2 SV=1	10.20	2.00	4.00	6.51	8.00	1.93E-07	5.19E-07	3.18E-06	2.56E-06	16.50	13.27
B4DKM5	B4DKM5_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=2 SV=1	27.10	3.00	7.00	6.00	5.99	1.67E-07	7.67E-06	1.30E-05	1.80E-06	77.86	10.79
F8VSC5	F8VSC5_HUMAN SCY1-like protein 2 (Fragment) OS=Homo sapiens GN=SCYL2 PE=2 SV=1	22.50		5.00	13.00	4.00		1.39E-07	2.75E-06	2.04E-06	Sample 1 Only	Sample 2 Only
J3KNX9	J3KNX9_HUMAN Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=2 SV=1	4.00	1.98	0.99	0.99	6.94	9.20E-08	5.27E-07	6.52E-09	1.94E-07	0.07	2.11
Q7L576	CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	11.70	0.53	3.06	2.05	10.20	3.73E-09	3.38E-07	5.90E-08	6.22E-07	15.80	166.86
O94874	UFL1_HUMAN E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2	13.20	1.00	7.96	8.97	5.96	9.95E-08	1.34E-06	1.42E-06	2.51E-06	14.24	25.21
P46781	RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	46.90	5.00	7.99	8.00	1.00	8.85E-06	2.95E-05	2.14E-05	2.80E-07	2.42	0.03
G8JLB6	G8JLB6_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	51.90	2.90	4.77	5.76	8.68	4.31E-08	1.19E-06	2.69E-06	7.28E-06	62.46	169.18
Q6KC79	NIPBL_HUMAN Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2	3.70	1.00	4.00	4.00	13.00	4.49E-09	3.24E-08	4.48E-08	2.67E-07	9.98	59.42
P62424	RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	33.10	3.97	5.98	5.98	1.98	2.67E-06	5.30E-06	1.15E-05	5.17E-06	4.33	1.94
Q86U86	PB1_HUMAN Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1	7.90	4.93	9.88		4.93	8.48E-08	1.63E-07		9.12E-08	Control 1 Only	1.08
Q9UJS0	CMC2_HUMAN Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2	26.80	3.00	6.00	7.00	6.00	2.87E-07	3.77E-07	1.63E-06	5.17E-07	5.69	1.80
P22695	QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	22.10	2.96	2.96	8.90	3.96	7.89E-07	1.52E-06	2.44E-06	1.57E-06	3.09	1.99
P25205	MCM3_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	15.20	7.92	8.92	2.99	0.99	3.47E-07	4.35E-07	1.83E-07	1.29E-08	0.53	0.04
E7EPB3	E7EPB3_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=2 SV=1	54.00	4.00	4.00	7.00	3.00	1.28E-06	1.09E-05	2.33E-06	1.04E-05	1.83	8.14
P61313	RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	18.10	4.95	5.92	4.97	3.96	8.46E-06	1.68E-05	2.09E-05	7.04E-06	2.47	0.83
E1P5S2	E1P5S2_HUMAN RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=2 SV=1	25.50	0.99	2.98	6.94	9.90	1.38E-07	3.23E-07	6.20E-06	2.63E-06	44.91	19.06
G3V1L9	G3V1L9_HUMAN Tight junction protein 1 (Zona occludens 1), isoform CRA_a OS=Homo sapiens GN=TJP1 PE=2 SV=1	7.90	2.00	3.00	5.00	10.00	7.88E-09	2.37E-08	7.33E-08	4.42E-07	9.30	56.11
H0Y465	H0Y465_HUMAN Neurofibromin truncated (Fragment) OS=Homo sapiens GN=NF1 PE=2 SV=1	4.10	1.99	4.98	2.99	6.97	2.91E-08	5.08E-08	3.26E-08	7.14E-08	1.12	2.46
O95218	ZRAB2_HUMAN Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2 PE=1 SV=2	26.60	9.00	6.00	2.00	3.00	8.63E-06	8.59E-06	7.51E-07	1.51E-06	0.09	0.17
P62917	RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	24.10	3.95	6.91	0.99	3.95	3.48E-06	9.27E-06	1.70E-06	8.06E-07	0.49	0.23
Q14573	ITPR3_HUMAN Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2	7.70		1.00	2.00	17.00		2.61E-09	9.21E-09	1.01E-07	Sample 1 Only	Sample 2 Only
H0YEN5	H0YEN5_HUMAN 40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=2 SV=1	40.00	3.96	6.93	5.94	1.98	1.99E-06	1.04E-05	1.81E-05	1.28E-06	9.11	0.64
P48668	K2C6C_HUMAN Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	37.20	3.97	5.94	3.97	4.95	8.65E-08	4.55E-07	1.58E-07	6.05E-07	1.83	7.00

Q9H6S0	YTDC2_HUMAN Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=1 SV=2	8.60	2.00	3.00	3.99	9.99	1.57 E-08	4.76 E-08	2.44 E-08	2.85 E-07	1.55	18.13
Q9UHB9	SRP68_HUMAN Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2	25.50		3.95	5.92	8.87		3.18 E-07	7.89 E-07	2.84 E-06	Sample 1 Only	Sample 2 Only
F8WE88	F8WE88_HUMAN Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=2 SV=1	9.50	1.00	3.00	3.00	9.98	4.04 E-09	4.10 E-08	2.90 E-08	4.11 E-07	7.18	101.63
Q9UQ35	SRRM2_HUMAN Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	4.90	3.00	6.00	4.00	4.00	2.11 E-08	6.42 E-08	3.58 E-08	3.47 E-08	1.70	1.64
Q9Y285	SYFA_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3	16.70	2.96	4.92	4.93	4.94	2.48 E-07	4.57 E-07	7.40 E-07	2.57 E-06	2.98	10.35
P26641	EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	18.30	3.00	2.00	4.00	9.00	3.37 E-07	5.77 E-07	1.24 E-06	5.33 E-06	3.67	15.81
H7BXY3	H7BXY3_HUMAN Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=2 SV=1	10.10		1.00	6.00	12.00		1.14 E-08	3.45 E-07	8.09 E-07	Sample 1 Only	Sample 2 Only
Q08945	SSRP1_HUMAN FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1	13.50	2.00	5.00	10.00	2.00	6.90 E-08	2.88 E-07	1.74 E-06	1.67 E-07	25.15	2.41
H0YGW7	H0YGW7_HUMAN ATP-binding cassette sub-family F member 1 (Fragment) OS=Homo sapiens GN=ABCF1 PE=4 SV=1	13.10	2.00	7.00	6.00	3.00	6.11 E-07	2.11 E-06	2.11 E-06	1.17 E-06	3.44	1.92
P17844	DDX5_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	28.70	0.98	5.91	3.95	8.86	8.85 E-09	9.61 E-07	1.83 E-06	3.61 E-06	206.71	407.32
Q9UHF7	TRPS1_HUMAN Zinc finger transcription factor Trps1 OS=Homo sapiens GN=TRPS1 PE=1 SV=2	11.60	1.96	2.94	3.92	7.87	2.45 E-08	8.37 E-08	1.18 E-07	5.35 E-07	4.80	21.84
P05141	ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	46.00	3.00	6.50	4.00	5.00	1.30 E-07	6.46 E-06	1.00 E-05	1.36 E-06	77.26	10.50
Q9UPY3	DICER_HUMAN Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	7.10			7.00	11.48			1.16 E-07	4.42 E-07	Sample 1 Only	Sample 2 Only
H3BQZ7	H3BQZ7_HUMAN HCG2044799 OS=Homo sapiens GN=hCG_2044799 PE=4 SV=1	14.60	3.00	2.00	1.00	6.00	3.90 E-08	9.43 E-08	1.85 E-08	1.16 E-06	0.47	29.74
P51659	DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	17.50	2.99	4.97	3.98	1.00	5.61 E-07	8.02 E-07	2.19 E-06	2.59 E-08	3.90	0.05
E7EUE1	E7EUE1_HUMAN ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=2 SV=1	16.00	3.00	1.99	5.99	5.00	5.94 E-08	1.08 E-07	3.21 E-06	1.22 E-06	54.14	20.60
Q9NRL2	BAZ1A_HUMAN Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens GN=BAZ1A PE=1 SV=2	7.10	2.00	4.00	3.00	9.00	2.89 E-08	4.08 E-08	8.69 E-08	3.85 E-07	3.01	13.33
P55884	EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	10.70	2.99	3.99	5.00	4.99	2.35 E-07	7.98 E-07	1.22 E-06	1.95 E-06	5.20	8.30
P62913	RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	43.80	1.00	2.96	3.97	3.97	2.62 E-07	2.26 E-05	9.15 E-06	1.10 E-06	34.94	4.20
D6RGG3	D6RGG3_HUMAN Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=2 SV=1	2.80	2.99	1.99	5.99	5.96	1.79 E-08	3.62 E-08	6.63 E-08	4.55 E-08	3.71	2.54
Q13315	ATM_HUMAN Serine-protein kinase ATM OS=Homo sapiens GN=ATM PE=1 SV=3	3.20		1.00	1.00	12.00		4.56 E-09	7.56 E-09	8.49 E-08	Sample 1 Only	Sample 2 Only
Q92673	SORL_HUMAN Sortilin-related receptor OS=Homo sapiens GN=SORL1 PE=1 SV=2	5.20			4.00	12.00			3.86 E-08	1.34 E-07	Sample 1 Only	Sample 2 Only
Q9BZE4	NOG1_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3	22.40	0.99	0.99	5.95	7.92	3.30 E-08	6.98 E-08	6.39 E-07	3.51 E-06	19.34	106.33
Q9Y3I0	RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	13.10		6.00	4.00	7.00		5.99 E-07	2.08 E-06	3.26 E-06	Sample 1 Only	Sample 2 Only
P49454	CENPF_HUMAN Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2	3.40	3.00	5.00	1.00	9.00	2.55 E-08	4.25 E-08	8.64 E-09	5.66 E-08	0.34	2.22
Q8TCJ2	STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1	7.50	3.00	4.00	2.00	7.00	4.98 E-08	1.33 E-07	2.17 E-07	2.35 E-07	4.36	4.73
A8MXP9	A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	16.40	1.98	2.97	4.93	3.94	1.22 E-07	5.18 E-07	1.39 E-06	1.39 E-06	11.37	11.35
Q13435	SF3B2_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	8.40	1.96	7.86	2.95	1.96	2.35 E-08	1.66 E-06	7.21 E-07	3.09 E-06	30.64	131.38

Q6PKG0	LARP1_HUMAN La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	8.60	0.99	2.98	4.97	6.96	1.34E-08	6.46E-08	3.11E-07	5.65E-07	23.33	42.31
O95714	HERC2_HUMAN E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2	2.70		1.00	2.00	12.00		9.13E-10	7.00E-09	5.62E-08	Sample 1 Only	Sample 2 Only
Q9HD45	TM9S3_HUMAN Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2	8.50		1.00	2.00	10.00		2.06E-08	4.43E-07	1.02E-06	Sample 1 Only	Sample 2 Only
P11021	GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	22.90	1.00	4.00	2.00	7.00	3.80E-09	1.83E-07	3.24E-07	1.37E-06	85.46	360.38
P26373	RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	41.20	7.98	3.00	3.98		4.25E-06	4.37E-06	9.99E-06		2.35	Control 1 Only
P30050	RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	50.30		5.00	8.00	3.00		9.68E-06	1.91E-05	5.60E-07	Sample 1 Only	Sample 2 Only
P33992	MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	13.10	5.99	6.98	1.00	2.00	3.34E-07	5.69E-07	1.15E-08	5.03E-07	0.03	1.51
P46777	RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	29.00		6.00	6.00	4.00		9.46E-06	1.59E-05	6.21E-06	Sample 1 Only	Sample 2 Only
P50416	CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	14.20		1.00	5.00	10.00		2.90E-08	5.21E-07	4.57E-06	Sample 1 Only	Sample 2 Only
P62269	RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	36.20	3.00	6.00	7.00		3.30E-06	3.31E-05	1.64E-05		4.97	Control 1 Only
Q92804	RBP56_HUMAN TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1	23.30	0.99	4.95	3.96	4.95	1.66E-07	1.34E-06	9.39E-07	3.54E-06	5.67	21.36
P08779	K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	39.70	2.50	4.00	0.50	2.50	1.31E-07	2.77E-07	4.57E-08	1.06E-06	0.35	8.14
P39656	OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	14.90	0.99	1.99	5.99	5.99	2.99E-09	1.12E-07	1.63E-06	1.46E-06	543.66	487.79
P40429	RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	29.10	4.00	3.00	5.00	4.00	1.84E-06	4.62E-06	1.04E-05	9.43E-07	5.63	0.51
P46779	RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	43.10	2.94	5.91	2.95	2.94	5.34E-06	1.86E-05	1.13E-05	1.98E-06	2.12	0.37
F2Z2E2	F2Z2E2_HUMAN Ras GTPase-activating-like protein IQGAP3 OS=Homo sapiens GN=IQGAP3 PE=2 SV=1	8.60	1.00	3.00		9.00	7.40E-09	1.80E-08		1.36E-07	Control 1 Only	18.36
P62906	RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	35.50	2.00	5.00	4.00	2.00	2.71E-07	7.84E-06	9.80E-06	8.26E-07	36.15	3.05
P62753	RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	23.70	2.00	2.99	5.99	3.00	1.25E-05	2.91E-05	3.92E-05	2.21E-06	3.14	0.18
F5H4R9	F5H4R9_HUMAN Dynamin-2 OS=Homo sapiens GN=DNM2 PE=2 SV=1	9.60	1.00	2.99	1.99	4.98	2.48E-08	1.00E-07	2.55E-07	8.94E-07	10.27	36.03
F5H6B1	F5H6B1_HUMAN Transferrin receptor protein 1, serum form OS=Homo sapiens GN=TFRC PE=2 SV=1	15.30	3.00		3.00	5.00	9.14E-08		2.32E-07	7.96E-07	2.54	8.70
Q14571	ITPR2_HUMAN Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2	5.40		2.00	1.00	10.00		1.47E-08	5.53E-09	1.31E-07	Sample 1 Only	Sample 2 Only
Q8WWQ0	PHIP_HUMAN PH-interacting protein OS=Homo sapiens GN=PHIP PE=1 SV=2	3.90	2.00	3.98	1.99	4.95	1.03E-08	5.75E-08	1.52E-08	8.89E-08	1.47	8.60
Q9BQA1	MEP50_HUMAN Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	14.90	3.00	1.99	4.99	2.99	2.31E-06	2.17E-06	4.63E-06	9.24E-06	2.00	3.99
P07814	SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	4.40	2.00	2.00	2.00	9.00	4.38E-08	3.12E-08	3.90E-08	5.89E-07	0.89	13.43
P53007	TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	15.10			4.00	8.00			4.64E-06	3.70E-06	Sample 1 Only	Sample 2 Only
P62241	RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	47.10		2.00	7.00	5.00		3.96E-06	2.72E-06	8.06E-06	Sample 1 Only	Sample 2 Only
B4DEB1	B4DEB1_HUMAN Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1	29.30	3.00	4.00	2.00	1.00	5.62E-06	5.14E-05	3.77E-05	8.11E-07	6.71	0.14
Q02878	RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	25.30	2.00	3.98	4.00	1.00	1.63E-07	1.39E-05	3.46E-06	4.83E-08	21.24	0.30

Q10567	AP1B1_HUMAN AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2	8.70	1.34	2.01	5.34	1.67	1.52 E-08	9.48 E-08	5.90 E-07	1.07 E-07	38.91	7.05
F8VU39	F8VU39_HUMAN Bromodomain adjacent to zinc finger domain protein 2A OS=Homo sapiens GN=BAZ2A PE=2 SV=1	3.80	1.00	3.00	3.00	6.00	2.48 E-08	9.63 E-08	1.01 E-07	3.72 E-07	4.06	15.02
G3XAI2	G3XAI2_HUMAN Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1	4.30	2.00	3.00	4.00	5.00	6.10 E-09	1.67 E-08	3.79 E-08	8.69 E-08	6.21	14.25
J3KP15	J3KP15_HUMAN Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens GN=SRSF2 PE=2 SV=1	29.10	1.98	3.97	2.97	2.98	1.07 E-06	4.31 E-06	9.73 E-06	8.64 E-06	9.12	8.10
M0R117	M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=2 SV=1	32.60	2.00	3.00	7.00	1.00	7.82 E-06	1.44 E-05	4.40 E-05	3.81 E-07	5.63	0.05
Q86UP2	KTN1_HUMAN Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1	4.30	2.00	1.00	1.98	2.98	8.63 E-09	1.48 E-09	5.06 E-08	4.10 E-08	5.86	4.75
O94973	AP2A2_HUMAN AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2	11.10	1.00	2.00	2.00	3.48	1.16 E-07	3.63 E-08	1.29 E-06	4.19 E-07	11.09	3.62
Q9NQX4	MYO5C_HUMAN Unconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	5.70	2.97	3.97	1.98	3.96	3.01 E-08	7.93 E-08	1.98 E-08	7.59 E-08	0.66	2.52
Q9Y383	LC7L2_HUMAN Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2	16.10		1.98	4.97	5.97		1.90 E-07	8.69 E-07	1.65 E-06	Sample 1 Only	Sample 2 Only
Q9Y4B6	VPRBP_HUMAN Protein VPRBP OS=Homo sapiens GN=VPRBP PE=1 SV=3	6.00	1.98	0.99	2.97	4.95	2.04 E-08	3.58 E-09	3.71 E-08	1.77 E-07	1.82	8.68
P31930	QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	11.70	1.00	3.00	3.00	5.00	1.14 E-06	1.99 E-06	3.57 E-07	1.25 E-06	0.31	1.09
P46778	RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	30.00	3.00	3.00	5.00		1.38 E-05	4.04 E-06	6.95 E-05		5.05	Control 1 Only
P46939	UTRO_HUMAN Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2	2.90		3.00	2.00	8.99		7.55 E-09	6.10 E-09	7.43 E-08	Sample 1 Only	Sample 2 Only
Q5VY93	Q5VY93_HUMAN Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=2 SV=1	6.90		3.00	3.00	3.00		3.04 E-07	6.29 E-07	4.35 E-07	Sample 1 Only	Sample 2 Only
Q8WX92	NELFB_HUMAN Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1	12.80	2.00	4.00	5.00	2.00	6.96 E-08	1.05 E-06	2.58 E-06	7.63 E-07	37.11	10.96
Q92499	DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	16.20	1.00	2.00	6.00	3.00	1.61 E-07	3.17 E-07	1.11 E-06	4.00 E-07	6.89	2.48
Q12873	CHD3_HUMAN Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3	9.90	3.50	3.50	1.00	3.00	3.52 E-08	4.15 E-08	2.43 E-08	1.18 E-07	0.69	3.36
Q13247	SRSF6_HUMAN Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2	9.60	1.98	2.98	0.99	4.96	1.17 E-06	4.39 E-06	4.34 E-07	1.66 E-06	0.37	1.42
Q14247	SRC8_HUMAN Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	14.00	0.99	2.99	1.00	2.98	5.02 E-09	6.40 E-07	1.91 E-07	1.91 E-06	38.06	380.80
G3V1A9	G3V1A9_HUMAN Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=2 SV=1	10.10			1.00	7.28			1.80 E-08	1.99 E-07	Sample 1 Only	Sample 2 Only
H0Y7P1	H0Y7P1_HUMAN Mediator of RNA polymerase II transcription subunit 12 (Fragment) OS=Homo sapiens GN=MED12 PE=2 SV=1	3.50	2.00	4.00	1.00	6.00	1.94 E-08	4.79 E-08	2.95 E-08	9.94 E-08	1.52	5.12
H0YH81	H0YH81_HUMAN ATP synthase subunit beta (Fragment) OS=Homo sapiens GN=ATP5B PE=3 SV=1	22.40	1.99	1.99	2.98	5.95	1.56 E-07	9.06 E-08	2.82 E-07	6.27 E-06	1.81	40.32
H3BTW3	H3BTW3_HUMAN Chromodomain-helicase-DNA-binding protein 9 (Fragment) OS=Homo sapiens GN=CHD9 PE=2 SV=1	4.70	1.96	0.99	1.97	5.93	4.31 E-08	1.88 E-08	6.58 E-08	1.80 E-07	1.53	4.18
O00148	DX39A_HUMAN ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2	16.40	0.99	1.98	1.95	4.91	2.65 E-08	4.36 E-08	9.50 E-07	1.93 E-06	35.82	72.82
Q8WXH0	SYNE2_HUMAN Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3	2.90		1.98	1.97	4.95		6.53 E-09	5.39 E-08	1.67 E-08	Sample 1 Only	Sample 2 Only
Q9UHB6	LIMA1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	14.80		0.99	3.96	5.94		6.35 E-08	1.04 E-06	8.54 E-07	Sample 1 Only	Sample 2 Only
P12236	ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	31.50	1.00	2.00	3.00	5.00	2.21 E-08	3.50 E-08	2.30 E-07	5.42 E-07	10.41	24.56
P01625	KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	14.00	4.00	2.00	2.00	3.00	1.13 E-05	5.96 E-07	5.94 E-07	5.49 E-07	0.05	0.05

P51531	SMCA2_HUMAN Probable global transcription activator SNF2L2 OS=Homo sapiens GN=SMARCA2 PE=1 SV=2	7.30		3.50	1.50	2.50		2.62 E-08	1.40 E-08	6.67 E-08	Sample 1 Only	Sample 2 Only
P51532	SMCA4_HUMAN Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2	7.70	1.00	4.50	1.50	2.50	4.27 E-09	2.04 E-08	8.87 E-09	4.36 E-08	2.08	10.21
O75146	HIP1R_HUMAN Huntingtin-interacting protein 1-related protein OS=Homo sapiens GN=HIP1R PE=1 SV=2	8.80		2.00	4.00	5.00		6.49 E-08	2.90 E-07	1.88 E-07	Sample 1 Only	Sample 2 Only
E7EW20	E7EW20_HUMAN Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=2 SV=1	11.60				11.00				4.44 E-07		Sample 2 Only
E7EW34	E7EW34_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=2 SV=1	8.00		2.00	4.99	2.00		2.71 E-07	8.33 E-07	1.79 E-07	Sample 1 Only	Sample 2 Only
F5GX68	F5GX68_HUMAN Cytosine-specific methyltransferase OS=Homo sapiens GN=DNMT1 PE=2 SV=1	7.40	2.00	3.00		4.00	1.17 E-08	2.31 E-08		8.84 E-08	Control 1 Only	7.57
J3KTE4	J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=2 SV=1	31.60	2.00	4.00	4.00		1.80 E-06	7.14 E-06	1.47 E-05		8.17	Control 1 Only
J3KTL2	J3KTL2_HUMAN Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=2 SV=1	29.00	1.98	1.98	2.97	1.98	3.53 E-07	1.14 E-06	1.03 E-05	1.62 E-07	29.15	0.46
M0R210	M0R210_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=2 SV=1	45.70		2.98	4.96	1.98		6.38 E-06	1.39 E-05	4.58 E-07	Sample 1 Only	Sample 2 Only
O15031	PLXB2_HUMAN Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3	5.90		0.99	1.99	6.99		3.11 E-08	2.37 E-08	1.53 E-07	Sample 1 Only	Sample 2 Only
P01024	CO3_HUMAN Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	5.20	7.00	3.00			1.75 E-07	2.88 E-08			Control 1 Only	Control 1 Only
Q96I24	FUBP3_HUMAN Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2	13.30	1.00	3.98	2.99	3.98	6.19 E-08	2.84 E-07	1.24 E-06	8.24 E-07	20.05	13.30
Q9Y230	RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	12.30	0.99	3.97	2.97	1.98	9.19 E-08	3.40 E-07	1.92 E-06	4.47 E-07	20.86	4.86
Q9Y265	RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	16.70	0.98	2.97	1.97	3.95	7.58 E-08	9.39 E-08	3.68 E-07	7.80 E-07	4.86	10.29
Q9Y678	COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	10.10	1.00	1.00	5.00	3.50	6.08 E-08	8.07 E-08	1.99 E-06	3.96 E-07	32.73	6.51
P23458	JAK1_HUMAN Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2	5.80	2.00	2.00	3.00	3.00	6.35 E-08	7.43 E-08	1.12 E-07	5.70 E-07	1.77	8.98
Q9NR30	DDX21_HUMAN Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	12.00		2.00	4.00	5.00		2.10 E-07	2.18 E-06	8.84 E-07	Sample 1 Only	Sample 2 Only
C9JJN9	C9JJN9_HUMAN Vacuolar protein sorting-associated protein 8 homolog OS=Homo sapiens GN=VPS8 PE=2 SV=1	5.20		2.00	1.00	7.00		2.46 E-08	1.71 E-08	1.12 E-07	Sample 1 Only	Sample 2 Only
E9PK09	E9PK09_HUMAN Bcl-2-associated transcription factor 1 (Fragment) OS=Homo sapiens GN=BCLAF1 PE=2 SV=1	6.10	4.95	0.99	0.99	0.99	3.98 E-07	1.35 E-07	3.54 E-07	6.03 E-08	0.89	0.15
F5H740	F5H740_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=2 SV=1	26.50		3.00	2.00	3.00		2.58 E-06	1.08 E-06	9.64 E-07	Sample 1 Only	Sample 2 Only
Q14739	LBR_HUMAN Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2	7.30		1.00	3.00	3.00		3.01 E-08	1.32 E-06	1.96 E-06	Sample 1 Only	Sample 2 Only
G5E933	G5E933_HUMAN Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=2 SV=1	4.10		3.00	1.00	3.64		2.58 E-08	4.47 E-09	9.27 E-08	Sample 1 Only	Sample 2 Only
Q16643	DREB_HUMAN Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4	6.50	1.00	1.99	2.99	2.99	3.07 E-07	7.97 E-07	2.08 E-06	6.25 E-07	6.77	2.04
O43390	HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	10.50		1.49	2.48	2.98		7.44 E-09	5.36 E-07	1.10 E-06	Sample 1 Only	Sample 2 Only
O60244	MED14_HUMAN Mediator of RNA polymerase II transcription subunit 14 OS=Homo sapiens GN=MED14 PE=1 SV=2	3.90		1.00	2.00	5.00		8.88 E-09	9.76 E-09	9.61 E-08	Sample 1 Only	Sample 2 Only
Q96A33	CCD47_HUMAN Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1	14.10		2.00	2.00	6.00		3.01 E-07	2.02 E-07	3.23 E-06	Sample 1 Only	Sample 2 Only
Q9Y446	PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	8.80	1.00	4.00	3.00	3.00	9.06 E-08	1.21 E-06	8.31 E-07	1.38 E-07	9.17	1.53
Q9Y5B9	SP16H_HUMAN FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1	6.90	1.00	1.00	2.00	2.00	1.31 E-08	4.87 E-08	3.79 E-07	5.71 E-07	28.94	43.67

P46100	ATRX_HUMAN Transcriptional regulator ATRX OS=Homo sapiens GN=ATRX PE=1 SV=5	4.20		3.00	3.00	3.00		8.90E-08	3.34E-08	1.45E-08	Sample 1 Only	Sample 2 Only
Q96QK1	VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	7.40		3.00	2.00	4.00		7.80E-08	5.93E-07	6.44E-07	Sample 1 Only	Sample 2 Only
P55036	PSMD4_HUMAN 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	8.80	1.98	1.98	3.96	0.99	3.75E-07	8.40E-07	2.57E-06	2.80E-08	6.85	0.07
B0QY89	B0QY89_HUMAN Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=2 SV=1	8.70		3.96	3.96	1.98		8.72E-07	1.13E-06	1.81E-07	Sample 1 Only	Sample 2 Only
D6RAF8	D6RAF8_HUMAN Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=2 SV=1	18.10	1.99	1.99	2.96	1.98	3.73E-08	4.57E-07	1.30E-06	2.61E-06	34.91	69.95
Q00839	HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	3.10	1.98	1.99	2.97	1.98	4.35E-08	3.85E-07	5.15E-07	2.05E-07	11.86	4.71
Q8WXA9	SREK1_HUMAN Splicing regulatory glutamine/lysine-rich protein 1 OS=Homo sapiens GN=SREK1 PE=1 SV=1	6.10	1.00	4.00	1.00	4.00	1.12E-08	1.70E-07	1.83E-08	7.78E-07	1.64	69.45
Q8TDI0	CHD5_HUMAN Chromodomain-helicase-DNA-binding protein 5 OS=Homo sapiens GN=CHD5 PE=2 SV=1	11.00	3.97			1.99	3.31E-05			5.51E-09	Control 1 Only	0.00
Q14151	SAFB2_HUMAN Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	3.30		1.98	2.97	1.98		2.16E-08	8.22E-08	4.42E-08	Sample 1 Only	Sample 2 Only
P02545	LMNA_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	13.60	4.00	2.00	1.00	2.00	7.80E-07	5.76E-08	2.08E-07	8.67E-08	0.27	0.11
Q9NTI5	PDS5B_HUMAN Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B PE=1 SV=1	4.30			2.00	7.00			2.14E-08	9.84E-08	Sample 1 Only	Sample 2 Only
P07437	TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	39.40		1.97	4.93	1.98		3.46E-08	6.37E-07	4.36E-06	Sample 1 Only	Sample 2 Only
Q9BTC0	DIDO1_HUMAN Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5	1.20	1.00	3.00	2.00	2.00	1.80E-08	3.64E-08	4.84E-08	6.54E-08	2.70	3.64
Q71F56	MD13L_HUMAN Mediator of RNA polymerase II transcription subunit 13-like OS=Homo sapiens GN=MED13L PE=1 SV=1	1.20	2.00	3.00	1.00	2.00	1.74E-08	4.71E-08	6.23E-08	1.90E-07	3.59	10.93
F5H3I5	F5H3I5_HUMAN CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=2 SV=1	9.30		1.98	2.97	3.96		9.10E-08	9.55E-07	2.53E-07	Sample 1 Only	Sample 2 Only
F5H5N0	F5H5N0_HUMAN Serine/threonine-protein kinase MRCK alpha OS=Homo sapiens GN=CDC42BPA PE=2 SV=1	3.80	0.99	0.99		3.98	4.36E-09	5.19E-09		8.29E-08	Control 1 Only	19.01
Q14683	SMC1A_HUMAN Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2	3.10	1.00	1.00		4.99	2.42E-08	1.52E-08		6.17E-07	Control 1 Only	25.52
I3L1L3	I3L1L3_HUMAN Myb-binding protein 1A (Fragment) OS=Homo sapiens GN=MYBBP1A PE=4 SV=1	5.80				8.00				1.69E-07		Sample 2 Only
J3KPZ3	J3KPZ3_HUMAN Probable E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens GN=MYCBP2 PE=2 SV=1	1.20	1.00	2.00		3.00	2.86E-09	6.67E-09		3.06E-08	Control 1 Only	10.71
M0R0F0	M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=2 SV=1	31.50		5.00	2.00	1.00		1.50E-05	1.88E-05	6.70E-06	Sample 1 Only	Sample 2 Only
O00139	KIF2A_HUMAN Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=1 SV=3	8.20	1.00	4.00	1.00	3.00	3.06E-08	4.30E-07	1.75E-07	1.26E-07	5.73	4.11
Q8NI35	INADL_HUMAN InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3	4.20		1.00	2.00	3.00		1.18E-08	5.60E-08	1.77E-07	Sample 1 Only	Sample 2 Only
Q8TB61	S35B2_HUMAN Adenosine 3'-phospho 5'-phosphosulfate transporter 1 OS=Homo sapiens GN=SLC35B2 PE=1 SV=1	10.70		1.00	2.00	5.00		1.86E-07	1.20E-07	6.12E-07	Sample 1 Only	Sample 2 Only
Q7Z794	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	19.00		5.00	3.00	1.00		2.02E-07	6.77E-08	2.50E-08	Sample 1 Only	Sample 2 Only
Q9Y4W6	AFG32_HUMAN AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2	4.50		1.00	3.00	1.00		6.55E-08	4.47E-07	1.02E-08	Sample 1 Only	Sample 2 Only
P11047	LAMC1_HUMAN Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	2.10	2.00	2.00	2.00	2.00	2.15E-08	3.07E-08	2.94E-08	4.87E-08	1.37	2.27
P23246	SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	7.60	1.00	1.96	2.98	3.00	5.31E-08	5.01E-07	1.38E-06	7.45E-07	25.96	14.04
P42345	MTOR_HUMAN Serine/threonine-protein kinase mTOR OS=Homo sapiens GN=MTOR PE=1 SV=1	4.10		1.00		6.00		4.07E-08		4.77E-08		Sample 2 Only

P51116	FXR2_HUMAN Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2	5.90		1.96	1.96	1.98		1.19E-06	1.89E-06	1.60E-07	Sample 1 Only	Sample 2 Only
H7C5E4	H7C5E4_HUMAN 5'-3' exoribonuclease 1 (Fragment) OS=Homo sapiens GN=XRN1 PE=4 SV=1	3.40	1.00	3.00	1.00	2.00	5.64E-09	3.95E-08	2.33E-08	7.03E-08	4.12	12.47
Q6ZRS2	SRCAP_HUMAN Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3	1.70	2.00	2.00	2.00	1.00	9.87E-09	1.27E-08	5.48E-09	5.68E-09	0.56	0.58
E5RHU3	E5RHU3_HUMAN Syndecan-2 (Fragment) OS=Homo sapiens GN=SDC2 PE=2 SV=2	21.90		1.00	3.00	3.00		1.72E-07	1.27E-06	2.69E-06	Sample 1 Only	Sample 2 Only
E7ER77	E7ER77_HUMAN Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=2 SV=1	6.80		1.00	3.00	4.00		6.43E-08	2.93E-07	5.55E-07	Sample 1 Only	Sample 2 Only
E7EUV3	E7EUV3_HUMAN Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 PE=2 SV=1	2.00			1.98	5.94			1.31E-08	3.63E-08	Sample 1 Only	Sample 2 Only
Q03519	TAP2_HUMAN Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1	5.40	0.99	0.99	1.98	1.98	9.91E-08	1.25E-07	6.92E-07	7.30E-08	6.98	0.74
Q14669	TRIPC_HUMAN E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1	2.00		1.00	2.00	5.00		2.92E-09	3.63E-08	1.15E-07	Sample 1 Only	Sample 2 Only
F8W7S5	F8W7S5_HUMAN Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=2 SV=1	7.60	1.00	2.00	4.00	1.00	1.55E-07	4.75E-07	4.99E-07	2.02E-07	3.22	1.30
H9KV75	H9KV75_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=2 SV=1	8.20		0.97	1.96	4.92		1.76E-08	2.24E-07	3.69E-06	Sample 1 Only	Sample 2 Only
Q8IUE6	H2A2B_HUMAN Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3	23.10	0.99	3.93	1.96		6.19E-07	1.32E-05	1.04E-05		16.80	Control 1 Only
O43242	PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	8.10	1.00	3.00	1.00	2.00	1.43E-08	3.14E-07	6.04E-07	1.69E-07	42.30	11.85
Q96I25	SPF45_HUMAN Splicing factor 45 OS=Homo sapiens GN=RBM17 PE=1 SV=1	10.70	1.00	3.00	2.00	2.00	5.36E-07	1.75E-06	1.31E-06	1.00E-06	2.44	1.87
Q9BUQ8	DDX23_HUMAN Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens GN=DDX23 PE=1 SV=3	7.30		2.00	1.00	3.00		1.08E-07	1.97E-07	3.85E-07	Sample 1 Only	Sample 2 Only
Q9NSD9	SYFB_HUMAN Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3	9.00		1.00	1.00	3.00		9.43E-08	4.90E-08	2.14E-07	Sample 1 Only	Sample 2 Only
Q9NZB2	F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	6.50		2.00	1.00	3.00		8.39E-08	2.57E-08	5.12E-07	Sample 1 Only	Sample 2 Only
Q9UBM7	DHCR7_HUMAN 7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	9.50				5.97				4.73E-07		Sample 2 Only
P08237	K6PF_HUMAN 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	10.50		1.98	2.96	0.99		3.63E-07	4.98E-07	4.35E-07	Sample 1 Only	Sample 2 Only
P11182	ODB2_HUMAN Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3	3.70	3.00	3.00	1.00		7.42E-07	5.77E-07	6.25E-07		0.84	Control 1 Only
Q9Y512	SAM50_HUMAN Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3	10.70		1.00	1.00	3.00		7.13E-08	1.75E-07	1.15E-06	Sample 1 Only	Sample 2 Only
A2A2F0	A2A2F0_HUMAN Ral GTPase-activating protein subunit beta (Fragment) OS=Homo sapiens GN=RALGAPB PE=2 SV=1	3.50			1.99	1.99			1.01E-08	2.76E-08	Sample 1 Only	Sample 2 Only
P24928	RPB1_HUMAN DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2	2.20	1.00	1.00	1.00	3.00	4.67E-09	7.20E-09	8.99E-09	1.12E-07	1.93	23.97
A8MUS3	A8MUS3_HUMAN 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=2 SV=1	34.30	2.00	1.00	2.00		6.06E-07	2.14E-06	2.37E-06		3.91	Control 1 Only
E9PF10	E9PF10_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=2 SV=1	3.80		1.00		6.00		9.00E-09		7.79E-08		Sample 2 Only
G3V3A0	G3V3A0_HUMAN Alpha-1-antichymotrypsin OS=Homo sapiens GN=SERPINA3 PE=2 SV=1	14.10	3.00	2.00	1.00		8.67E-07	4.39E-07	1.16E-07		0.13	Control 1 Only
P02652	APOA2_HUMAN Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	21.00	3.00	3.00			2.02E-06	1.24E-06			Control 1 Only	Control 1 Only
P81605	DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	22.70	1.00	3.00		1.00	3.01E-06	3.49E-06		2.06E-07	Control 1 Only	0.07
A3KMH1	VWA8_HUMAN von Willebrand factor A domain-containing protein 8 OS=Homo sapiens GN=VWA8 PE=1 SV=2	2.80		0.99	0.99	4.96		5.47E-09	1.08E-08	6.81E-08	Sample 1 Only	Sample 2 Only

P63092	GNAS2_HUMAN Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1	12.70		1.00	2.00	1.00		2.75E-08	1.80E-07	1.23E-07	Sample 1 Only	Sample 2 Only
E5RI99	E5RI99_HUMAN 60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=2 SV=1	41.20		2.00	3.00	2.00		1.08E-05	2.20E-05	8.29E-06	Sample 1 Only	Sample 2 Only
E7EWK3	E7EWK3_HUMAN Probable ATP-dependent RNA helicase DHX36 (Fragment) OS=Homo sapiens GN=DHX36 PE=2 SV=1	5.50		2.00	2.00	1.00		1.02E-07	1.59E-07	1.83E-07	Sample 1 Only	Sample 2 Only
E9PF19	E9PF19_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=2 SV=1	14.10		1.00	1.99	3.00		1.72E-07	4.44E-07	1.51E-06	Sample 1 Only	Sample 2 Only
Q13263	TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	8.20		3.00	2.00			2.59E-07	1.24E-07		Sample 1 Only	
Q14694	UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2	7.80			2.97	3.96			2.32E-07	1.93E-06	Sample 1 Only	Sample 2 Only
F8WJN3	F8WJN3_HUMAN Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=2 SV=1	7.50		3.00	2.00	1.00		7.84E-07	2.73E-06	2.69E-07	Sample 1 Only	Sample 2 Only
J3KTL7	J3KTL7_HUMAN Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=2 SV=1	7.80		1.00	2.00	3.00		1.02E-07	2.43E-07	2.67E-06	Sample 1 Only	Sample 2 Only
Q7KZ85	SPT6H_HUMAN Transcription elongation factor SPT6 OS=Homo sapiens GN=SUPT6H PE=1 SV=2	4.20			1.00	5.00			1.68E-08	1.89E-07	Sample 1 Only	Sample 2 Only
H3BPE7	H3BPE7_HUMAN RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=2 SV=1	13.00		1.00	1.00	2.00		9.96E-08	1.45E-06	1.38E-06	Sample 1 Only	Sample 2 Only
Q9P035	HACD3_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1 SV=2	11.90			0.99	3.96			1.67E-07	8.16E-07	Sample 1 Only	Sample 2 Only
P08238	HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	10.50			0.99	3.98			5.88E-09	1.84E-06	Sample 1 Only	Sample 2 Only
B4DJ96	B4DJ96_HUMAN Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=2 SV=1	9.60			1.00	2.98			8.25E-07	2.05E-06	Sample 1 Only	Sample 2 Only
E7ENU4	E7ENU4_HUMAN Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=2 SV=1	6.00		1.99	0.99	1.99		2.17E-08	9.95E-08	2.96E-07	Sample 1 Only	Sample 2 Only
B0QYA3	B0QYA3_HUMAN Eukaryotic translation initiation factor 3 subunit D (Fragment) OS=Homo sapiens GN=EIF3D PE=2 SV=1	19.40		1.00	2.00	1.00		5.75E-08	1.24E-06	6.89E-07	Sample 1 Only	Sample 2 Only
D3YTB1	D3YTB1_HUMAN 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=2 SV=1	10.50	1.00	1.00	2.00		7.06E-07	3.58E-07	3.68E-06		5.21	Control 1 Only
E9PMA0	E9PMA0_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=2 SV=1	9.60	1.00	1.00	1.00	2.00	1.51E-07	6.55E-07	1.71E-07	7.40E-07	1.14	4.91
P55795	HNRH2_HUMAN Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	40.50		1.00	2.00	2.00		2.89E-08	1.37E-06	1.09E-06	Sample 1 Only	Sample 2 Only
P61254	RL26_HUMAN 60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	17.90		1.00	4.00			2.57E-06	1.11E-05		Sample 1 Only	
P62277	RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	19.20	0.99	2.99	2.00		1.57E-06	6.95E-06	9.36E-06		5.98	Control 1 Only
B3KSQ1	B3KSQ1_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=2 SV=1	9.10				6.00				1.23E-06		Sample 2 Only
B3KTC7	B3KTC7_HUMAN Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=2 SV=1	10.40	1.00	1.00	3.00	1.00	2.30E-09	6.69E-09	7.05E-07	1.74E-08	306.97	7.58
D6RAN4	D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1	35.20		0.99	4.95			1.00E-06	9.09E-06		Sample 1 Only	
E5RJX2	E5RJX2_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=2 SV=1	29.50	1.00	3.00	2.00		5.34E-06	3.67E-05	3.54E-06		0.66	Control 1 Only
Q13547	HDAC1_HUMAN Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1	9.50		1.98	1.52	0.99		1.02E-07	5.44E-07	9.18E-08	Sample 1 Only	Sample 2 Only
Q14980	NUMA1_HUMAN Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2	49.10	0.99	0.99	1.98	1.98	5.40E-09	3.56E-09	1.44E-08	3.00E-08	2.67	5.57
O94776	MTA2_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1	10.20	1.00	2.00	1.99		7.89E-08	2.64E-07	1.17E-06		14.80	Control 1 Only
Q969V3	NCLN_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2	7.30		1.98	1.98	1.99		4.40E-07	1.89E-06	5.52E-07	Sample 1 Only	Sample 2 Only

Q9BYK8	HELZ2_HUMAN Helicase with zinc finger domain 2 OS=Homo sapiens GN=HELZ2 PE=1 SV=6	3.20			1.00	5.00			7.39E-09	8.09E-08	Sample 1 Only	Sample 2 Only
Q9H267	VP33B_HUMAN Vacuolar protein sorting-associated protein 33B OS=Homo sapiens GN=VPS33B PE=1 SV=2	7.60			1.00	4.00			1.86E-07	1.07E-06	Sample 1 Only	Sample 2 Only
Q9H9G7	AGO3_HUMAN Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	14.50			3.00	3.00			1.64E-06	4.58E-07	Sample 1 Only	Sample 2 Only
P05386	RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	28.90		3.00	2.00			9.29E-06	3.13E-06		Sample 1 Only	
E9PGR2	E9PGR2_HUMAN Cyclin-G-associated kinase OS=Homo sapiens GN=GAK PE=2 SV=1	1.60		0.99	0.99	2.99		2.18E-08	2.40E-08	8.53E-08	Sample 1 Only	Sample 2 Only
Q07666	KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	2.60		2.00	2.00	2.00		2.03E-07	5.97E-07	5.94E-07	Sample 1 Only	Sample 2 Only
A6NIF9	A6NIF9_HUMAN Protein transport protein Sec61 subunit alpha isoform 2 OS=Homo sapiens GN=SEC61A2 PE=2 SV=1	15.80		1.00	1.00	2.00		7.95E-07	1.68E-06	2.40E-06	Sample 1 Only	Sample 2 Only
Q8TEM1	PO210_HUMAN Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3	1.30	2.00	1.00		3.00	2.74E-08	5.00E-09		7.71E-08	Control 1 Only	2.82
O60306	AQR_HUMAN Intron-binding protein aquarius OS=Homo sapiens GN=AQR PE=1 SV=4	3.10		1.00		2.00		2.91E-09		1.08E-08		Sample 2 Only
P35251	RFC1_HUMAN Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4	4.00			1.00	5.00			1.51E-08	3.27E-07	Sample 1 Only	Sample 2 Only
P38646	GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	9.10		1.00		5.00		3.77E-09		1.53E-06		Sample 2 Only
P39019	RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	31.70		1.00	5.00			2.78E-06	9.05E-06		Sample 1 Only	
P42166	LAP2A_HUMAN Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	9.20		1.00	1.00	3.00		4.82E-07	7.89E-08	4.70E-07	Sample 1 Only	Sample 2 Only
P06748	NPM_HUMAN Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	24.30	0.99	1.00		0.99	1.60E-07	9.03E-08		1.65E-07	Control 1 Only	1.03
G3V2D8	G3V2D8_HUMAN Zinc finger FYVE domain-containing protein 26 OS=Homo sapiens GN=ZFYVE26 PE=2 SV=1	2.00				1.99				1.33E-08		Sample 2 Only
Q9NU22	MDN1_HUMAN Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2	0.60			1.00	2.99			1.02E-09	5.83E-09	Sample 1 Only	Sample 2 Only
P52292	IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	8.30		2.00	2.00			2.48E-07	3.20E-07		Sample 1 Only	
O60841	IF2P_HUMAN Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4	1.60	1.00	1.00			1.38E-08	6.16E-09			Control 1 Only	Control 1 Only
P55268	LAMB2_HUMAN Laminin subunit beta-2 OS=Homo sapiens GN=LAMB2 PE=1 SV=2	1.20		1.00		2.00		8.55E-09		5.74E-08		Sample 2 Only
Q14692	BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	2.20		1.00	1.00	3.00		4.48E-09	1.03E-08	1.26E-07	Sample 1 Only	Sample 2 Only
Q8N3X1	FNBP4_HUMAN Formin-binding protein 4 OS=Homo sapiens GN=FNBP4 PE=1 SV=3	1.70			1.00	2.00			3.26E-08	9.96E-08	Sample 1 Only	Sample 2 Only
Q9BRX2	PELO_HUMAN Protein pelota homolog OS=Homo sapiens GN=PELO PE=1 SV=2	7.80	2.00	1.00	1.00		2.83E-07	4.84E-07	4.58E-08		0.16	Control 1 Only
Q9Y6Q5	AP1M2_HUMAN AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2 PE=1 SV=4	29.80	0.99	0.99	0.99	1.98	2.76E-08	2.69E-07	8.76E-07	2.88E-06	31.74	104.42
B7Z4B8	B7Z4B8_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=2 SV=1	8.60		0.99	1.98	0.99		5.75E-08	7.45E-07	1.13E-06	Sample 1 Only	Sample 2 Only
C9JW96	C9JW96_HUMAN Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=2 SV=2	20.70	0.99	2.00	2.00		2.20E-07	2.34E-07	4.17E-06		18.91	Control 1 Only
Q05519	SRS11_HUMAN Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1	13.60		1.00	1.00	2.00		7.81E-08	7.85E-08	1.47E-06	Sample 1 Only	Sample 2 Only
Q12906	ILF3_HUMAN Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	5.90		0.99	1.00	1.99		3.19E-08	1.10E-07	5.98E-07	Sample 1 Only	Sample 2 Only
F8VU51	F8VU51_HUMAN YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=2 SV=1	3.60			0.99	3.95			1.71E-08	2.41E-07	Sample 1 Only	Sample 2 Only

Q8IY17	PLPL6_HUMAN Neuropathy target esterase OS=Homo sapiens GN=PNPLA6 PE=1 SV=2	2.90		1.00		4.00		3.21 E-09		2.42 E-07		Sample 2 Only
Q8N163	CCAR2_HUMAN Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2	4.10		1.98	1.98			9.90 E-08	1.18 E-07		Sample 1 Only	
Q92615	LAR4B_HUMAN La-related protein 4B OS=Homo sapiens GN=LARP4B PE=1 SV=3	3.40		1.00	1.00	2.00		2.56 E-07	1.44 E-07	1.72 E-07	Sample 1 Only	Sample 2 Only
P08729	K2C7_HUMAN Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	24.30	5.00				2.49 E-07				Control 1 Only	Control 1 Only
Q9C0J8	WDR33_HUMAN pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2	3.70		2.00		2.00		2.90 E-08		2.45 E-07		Sample 2 Only
Q29RF7	PDS5A_HUMAN Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	3.40				4.00				1.48 E-07		Sample 2 Only
O75746	CMC1_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2	11.90		1.00	1.00	3.00		1.54 E-07	5.41 E-07	8.99 E-07	Sample 1 Only	Sample 2 Only
Q9Y6K5	OAS3_HUMAN 2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3	4.90		3.00				1.19 E-07				
Q12905	ILF2_HUMAN Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	8.50		2.00	1.00	1.00		3.78 E-07	7.39 E-08	1.19 E-08	Sample 1 Only	Sample 2 Only
F5GWP8	F5GWP8_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=2 SV=1	31.00	0.99	1.98		1.98	5.71 E-09	3.10 E-08		2.68 E-08	Control 1 Only	4.70
F5H2S7	F5H2S7_HUMAN Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=2 SV=1	7.60		1.98	1.98			2.00 E-07	3.50 E-07		Sample 1 Only	
Q5JUA9	Q5JUA9_HUMAN Vacuolar protein sorting-associated protein 16 homolog (Fragment) OS=Homo sapiens GN=VPS16 PE=2 SV=1	12.80	0.99	0.99	1.98		2.46 E-07	4.16 E-07	1.66 E-06		6.75	Control 1 Only
J3KRX5	J3KRX5_HUMAN 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=2 SV=1	25.40	1.00	1.00	1.00		5.63 E-07	5.49 E-06	1.86 E-07		0.33	Control 1 Only
E9PK59	E9PK59_HUMAN N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1 PE=2 SV=1	8.90			1.99	1.99			3.21 E-07	7.81 E-08	Sample 1 Only	Sample 2 Only
F5H7E2	F5H7E2_HUMAN Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=2 SV=1	3.80		0.99		2.99		1.08 E-07		7.79 E-08		Sample 2 Only
Q9UQE7	SMC3_HUMAN Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2	3.00		2.00	1.00			2.80 E-08	4.70 E-08		Sample 1 Only	
B7ZAV6	B7ZAV6_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=2 SV=1	2.60	1.00	1.00	2.00		7.05 E-08	5.96 E-08	4.47 E-07		6.33	Control 1 Only
P33993	MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	10.30		0.99	0.99	1.99		9.33 E-08	1.35 E-07	6.90 E-08	Sample 1 Only	Sample 2 Only
E7ENR4	E7ENR4_HUMAN Hexokinase-1 OS=Homo sapiens GN=HK1 PE=2 SV=1	4.80		1.98	1.98			1.77 E-08	2.90 E-07		Sample 1 Only	
P62851	RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	20.80		1.00	1.00	1.00		1.34 E-07	2.83 E-05	3.00 E-07	Sample 1 Only	Sample 2 Only
M0QXS5	M0QXS5_HUMAN Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=4 SV=1	7.00			1.98	1.00			1.95 E-07	3.01 E-07	Sample 1 Only	Sample 2 Only
P16989	YBOX3_HUMAN Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4	13.20	2.97	0.99			1.39 E-06	1.69 E-07			Control 1 Only	Control 1 Only
B7Z2F4	B7Z2F4_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1	9.30		1.00	1.00	1.00		1.61 E-07	7.55 E-08	2.69 E-08	Sample 1 Only	Sample 2 Only
C9JNW5	C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1	23.10			3.00				7.26 E-06		Sample 1 Only	
F8W726	F8W726_HUMAN Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=2 SV=1	3.40		2.00	1.00	1.00		3.68 E-07	7.13 E-08	4.86 E-07	Sample 1 Only	Sample 2 Only
G3V4I1	G3V4I1_HUMAN Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=2 SV=1	37.30		0.99		1.98		4.17 E-07		2.55 E-06		Sample 2 Only
M0QXB4	M0QXB4_HUMAN Coatomer protein complex, subunit epsilon, isoform CRA_g OS=Homo sapiens GN=COPE PE=2 SV=1	14.40		2.00	2.00			1.06 E-06	5.51 E-07		Sample 1 Only	
Q9P219	DAPLE_HUMAN Protein Daple OS=Homo sapiens GN=CCDC88C PE=1 SV=3	1.00	2.00	1.00			8.63 E-09	3.42 E-09			Control 1 Only	Control 1 Only

E7ETK0	E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1	13.80	1.00	1.00	2.00		8.75E-07	2.23E-06	1.77E-06		2.03	Control 1 Only
Q9Y2A7	NCKP1_HUMAN Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	4.60		2.00	1.00	1.00		7.33E-08	7.54E-08	3.33E-08	Sample 1 Only	Sample 2 Only
Q9Y2W1	TR150_HUMAN Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	3.90	2.00			2.00	8.37E-08			6.04E-08	Control 1 Only	0.72
A0FGR8-2	ESYT2_HUMAN Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2	4.40		1.00	1.00	1.99		1.70E-08	9.75E-08	2.16E-07	Sample 1 Only	Sample 2 Only
B0QZ43	B0QZ43_HUMAN Erlin-1 (Fragment) OS=Homo sapiens GN=ERLIN1 PE=2 SV=1	11.60		1.00		2.00		8.88E-07		2.59E-06		Sample 2 Only
P62280	RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	27.20		2.00	1.00	0.99		4.73E-07	5.52E-06	1.74E-07	Sample 1 Only	Sample 2 Only
Q9Y6Q5-2	AP1M2_HUMAN Isoform 2 of AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2	30.60		0.50	0.50	1.50		6.90E-08	2.57E-08	8.58E-07	Sample 1 Only	Sample 2 Only
E5RIU6	E5RIU6_HUMAN Cyclin-dependent kinase 1 (Fragment) OS=Homo sapiens GN=CDK1 PE=2 SV=2	14.30		0.99	0.99			3.79E-07	1.73E-06		Sample 1 Only	
E7EQD7	E7EQD7_HUMAN Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=2 SV=1	5.20		1.00	1.00	1.00		9.83E-08	2.81E-07	2.00E-07	Sample 1 Only	Sample 2 Only
E9PH82	E9PH82_HUMAN Protein FAM98A OS=Homo sapiens GN=FAM98A PE=2 SV=1	7.10			0.99	1.98			1.41E-08	6.57E-07	Sample 1 Only	Sample 2 Only
B0FLL2	B0FLL2_HUMAN 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 2 transcript variant 3 OS=Homo sapiens GN=PFKFB2 PE=2 SV=1	12.50		1.98	1.99			3.42E-07	2.27E-07		Sample 1 Only	
F5GZS6	F5GZS6_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=2 SV=1	7.40				3.96				3.93E-06		Sample 2 Only
H7BXZ6	H7BXZ6_HUMAN Mitochondrial Rho GTPase OS=Homo sapiens GN=RHOT1 PE=2 SV=2	5.70			0.99	2.97			8.89E-08	4.59E-07	Sample 1 Only	Sample 2 Only
K7EJ81	K7EJ81_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=2 SV=1	5.00	1.00	0.78	0.99	1.00	7.46E-08	3.10E-08	5.71E-08	3.34E-08	0.77	0.45
Q8WVX9	FACR1_HUMAN Fatty acyl-CoA reductase 1 OS=Homo sapiens GN=FAR1 PE=1 SV=1	8.30				3.00				1.14E-06		Sample 2 Only
O75367	H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	15.70		1.00	1.00	1.99		6.55E-08	4.66E-06	6.99E-07	Sample 1 Only	Sample 2 Only
J3QST3	J3QST3_HUMAN Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=2 SV=1	15.40				3.00				3.72E-07		Sample 2 Only
P01009	A1AT_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	5.60	2.00	2.00			1.25E-07	8.15E-08			Control 1 Only	Control 1 Only
B9EK38	B9EK38_HUMAN GARNL1 protein OS=Homo sapiens GN=GARNL1 PE=2 SV=1	2.20				3.00				2.14E-08		Sample 2 Only
O96019	ACL6A_HUMAN Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1	4.70	0.99	0.99			1.55E-07	2.16E-07			Control 1 Only	Control 1 Only
Q96NB2	SFXN2_HUMAN Sideroflexin-2 OS=Homo sapiens GN=SFXN2 PE=1 SV=2	13.00				3.00				1.18E-06		Sample 2 Only
P19338	NUCL_HUMAN Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	5.40		2.00	1.00	1.00		7.53E-08	1.75E-07	3.50E-08	Sample 1 Only	Sample 2 Only
C9JDM9	C9JDM9_HUMAN Cadherin EGF LAG seven-pass G-type receptor 1 OS=Homo sapiens GN=CELSR1 PE=2 SV=1	3.20		1.00	1.00	2.00		1.40E-08	8.13E-09	2.56E-08	Sample 1 Only	Sample 2 Only
Q96T88	UHRF1_HUMAN E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1	3.40	1.00	1.00	1.00	1.00	6.25E-08	9.88E-08	1.68E-07	1.67E-08	2.69	0.27
B3KVR1	B3KVR1_HUMAN Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPN PE=2 SV=1	8.90				1.98				6.53E-07		Sample 2 Only
O15156	ZBT7B_HUMAN Zinc finger and BTB domain-containing protein 7B OS=Homo sapiens GN=ZBTB7B PE=1 SV=2	4.10			1.00	2.00			1.28E-07	1.28E-06	Sample 1 Only	Sample 2 Only
P01615	KV202_HUMAN Ig kappa chain V-II region FR OS=Homo sapiens PE=1 SV=1	17.70	1.00				4.20E-07				Control 1 Only	Control 1 Only

P04207	KV308_HUMAN Ig kappa chain V-III region CLL OS=Homo sapiens PE=1 SV=2	19.40	1.00		0.99		3.99 E-07		1.30 E-06		3.25	Control 1 Only
Q8TD43	TRPM4_HUMAN Transient receptor potential cation channel subfamily M member 4 OS=Homo sapiens GN=TRPM4 PE=1 SV=1	1.80		0.99		2.99		1.33 E-08		7.05 E-08		Sample 2 Only
J3QR68	J3QR68_HUMAN Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=3 SV=1	9.70	0.99			0.99	2.64 E-08			2.38 E-08	Control 1 Only	0.90
Q9Y4K1	AIM1_HUMAN Absent in melanoma 1 protein OS=Homo sapiens GN=AIM1 PE=1 SV=3	1.40		1.00	2.00	1.00		4.55 E-09	1.92 E-08	1.54 E-08	Sample 1 Only	Sample 2 Only
P26599	PTBP1_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	9.40		2.97		0.99		3.59 E-07		4.13 E-07		Sample 2 Only
P31431	SDC4_HUMAN Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2	32.00		3.00		1.00		4.57 E-07		1.89 E-07		Sample 2 Only
B5MCP9	B5MCP9_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=2 SV=1	13.40		2.00	1.00			9.68 E-06	1.57 E-05		Sample 1 Only	
D6RB59	D6RB59_HUMAN Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=2 SV=1	4.30		1.00	1.00	1.00		1.32 E-07	1.44 E-07	1.56 E-07	Sample 1 Only	Sample 2 Only
F5H8H4	F5H8H4_HUMAN Pogo transposable element with ZNF domain OS=Homo sapiens GN=POGZ PE=2 SV=1	2.20				2.00				1.95 E-07		Sample 2 Only
H3BN98	H3BN98_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2	22.00		1.00	2.00			1.49 E-07	1.43 E-05		Sample 1 Only	
Q13523	PRP4B_HUMAN Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens GN=PRPF4B PE=1 SV=3	3.80			1.00	0.99			2.78 E-08	9.95 E-09	Sample 1 Only	Sample 2 Only
H0UI80	H0UI80_HUMAN Negative elongation factor C/D OS=Homo sapiens GN=TH1L PE=2 SV=1	6.70		1.00				3.33 E-08				
B7ZM62	B7ZM62_HUMAN Protein kinase C-binding protein 1 OS=Homo sapiens GN=ZMYND8 PE=2 SV=1	2.00		0.99		0.99		2.68 E-08		1.73 E-08		Sample 2 Only
P08240	SRPR_HUMAN Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2	3.80		2.00	1.00			1.96 E-07	3.83 E-07		Sample 1 Only	
O00443	P3C2A_HUMAN Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Homo sapiens GN=PIK3C2A PE=1 SV=2	1.60				1.98				8.14 E-08		Sample 2 Only
P54886	P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	3.50		2.00	1.00			1.69 E-07	7.55 E-08		Sample 1 Only	
F5H1D6	F5H1D6_HUMAN DNA polymerase OS=Homo sapiens GN=POLE PE=2 SV=1	1.00		1.00		1.00		5.32 E-09		1.83 E-08		Sample 2 Only
Q9UMS4	PRP19_HUMAN Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	4.60			1.99				3.49 E-07		Sample 1 Only	
Q9BQ39	DDX50_HUMAN ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1	7.20				3.00				1.42 E-06		Sample 2 Only
Q9NZT1	CALL5_HUMAN Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	34.20		3.00				7.42 E-07				
Q9UGP8	SEC63_HUMAN Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2	3.40			1.00	2.00			7.40 E-08	6.57 E-07	Sample 1 Only	Sample 2 Only
H3BSK9	H3BSK9_HUMAN Ataxin-2-like protein (Fragment) OS=Homo sapiens GN=ATXN2L PE=2 SV=1	5.40		1.00	1.00			1.48 E-07	2.68 E-07		Sample 1 Only	
B4DXM1	B4DXM1_HUMAN FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=2 SV=1	6.90	1.00	1.00		1.00	1.02 E-07	5.14 E-08		5.51 E-08	Control 1 Only	0.54
Q13127	REST_HUMAN RE1-silencing transcription factor OS=Homo sapiens GN=REST PE=1 SV=3	1.60	1.00	1.00			2.91 E-09	2.03 E-09			Control 1 Only	Control 1 Only
B4DDG7	B4DDG7_HUMAN AP-1 complex subunit mu-1 OS=Homo sapiens GN=AP1M1 PE=2 SV=1	14.00	0.99			1.98	2.34 E-07			9.66 E-07	Control 1 Only	4.13
Q6P158	DHX57_HUMAN Putative ATP-dependent RNA helicase DHX57 OS=Homo sapiens GN=DHX57 PE=1 SV=2	3.50			1.00	2.00			1.38 E-08	5.22 E-08	Sample 1 Only	Sample 2 Only
O60506	HNRPQ_HUMAN Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	5.90			0.99	0.99			8.70 E-09	2.02 E-07	Sample 1 Only	Sample 2 Only
E7ESY4	E7ESY4_HUMAN Metastasis-associated protein MTA1 OS=Homo sapiens GN=MTA1 PE=2 SV=1	12.30		0.99	0.99	0.99		3.39 E-08	1.22 E-07	9.04 E-08	Sample 1 Only	Sample 2 Only

Q8N1N4	K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	11.30		1.00	1.00	1.00		2.69 E-08	3.23 E-08	2.24 E-08	Sample 1 Only	Sample 2 Only
Q9BR76	COR1B_HUMAN Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	4.30			1.00	1.00			6.33 E-07	6.10 E-07	Sample 1 Only	Sample 2 Only
Q9BZH6	WDR11_HUMAN WD repeat-containing protein 11 OS=Homo sapiens GN=WDR11 PE=1 SV=1	2.00				2.00				2.03 E-07		Sample 2 Only
Q9H4M9	EHD1_HUMAN EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2	9.00				2.98				9.64 E-07		Sample 2 Only
B4DL14	B4DL14_HUMAN ATP synthase subunit gamma OS=Homo sapiens GN=ATP5C1 PE=2 SV=1	8.80	1.00		2.00		1.06 E-07		8.31 E-07		7.82	Control 1 Only
F5H1Z7	F5H1Z7_HUMAN Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=2 SV=1	3.90				3.00				1.73 E-07		Sample 2 Only
F5H4J2	F5H4J2_HUMAN Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14 PE=2 SV=1	11.50		1.00		2.00		1.37 E-08		1.40 E-06		Sample 2 Only
F5GWA7	F5GWA7_HUMAN Prohibitin-2 (Fragment) OS=Homo sapiens GN=PHB2 PE=2 SV=1	13.60		1.00	2.00			1.66 E-08	4.39 E-07		Sample 1 Only	
O76094	SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3	5.10				2.97				9.48 E-07		Sample 2 Only
Q5T2T1	MPP7_HUMAN MAGUK p55 subfamily member 7 OS=Homo sapiens GN=MPP7 PE=1 SV=1	4.70		1.00		2.00		3.98 E-08		1.50 E-07		Sample 2 Only
O43719	HTSF1_HUMAN HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1	10.80	1.00	2.00			7.43 E-08	3.00 E-07			Control 1 Only	Control 1 Only
E9PD56	E9PD56_HUMAN PX domain-containing protein kinase-like protein OS=Homo sapiens GN=PXK PE=2 SV=1	4.60		1.00	1.00			4.27 E-08	3.87 E-07		Sample 1 Only	
P62266	RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	15.40			2.00	1.00			4.20 E-07	1.72 E-07	Sample 1 Only	Sample 2 Only
A6NFQ9	A6NFQ9_HUMAN Septin-8 OS=Homo sapiens GN=SEPT8 PE=2 SV=1	4.30	0.99			0.99	8.24 E-08			3.49 E-07	Control 1 Only	4.24
P09874	PARP1_HUMAN Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	2.80	1.00	1.00			7.83 E-09	3.83 E-08			Control 1 Only	Control 1 Only
F5H3T8	F5H3T8_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=2 SV=1	4.60				2.00				2.28 E-07		Sample 2 Only
Q96ST3	SIN3A_HUMAN Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2	2.30	1.00	2.00			3.84 E-08	1.08 E-08			Control 1 Only	Control 1 Only
F5GWF6	F5GWF6_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=2 SV=2	11.30		1.00				1.94 E-07				
B3KXD6	B3KXD6_HUMAN Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1	3.60		0.99		1.00		6.19 E-08		5.08 E-07		Sample 2 Only
F2Z388	F2Z388_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=2 SV=1	24.00		1.00	1.00			1.10 E-06	1.22 E-06		Sample 1 Only	
Q92544	TM9S4_HUMAN Transmembrane 9 superfamily member 4 OS=Homo sapiens GN=TM9SF4 PE=1 SV=2	3.90				2.00				1.57 E-07		Sample 2 Only
Q6PL18	ATAD2_HUMAN ATPase family AAA domain-containing protein 2 OS=Homo sapiens GN=ATAD2 PE=1 SV=1	1.40	1.00	2.00			2.72 E-08	3.25 E-08			Control 1 Only	Control 1 Only
F8VWW8	F8VWW8_HUMAN Acid sphingomyelinase-like phosphodiesterase 3b OS=Homo sapiens GN=SMPDL3B PE=2 SV=1	5.40		1.00		0.99		9.52 E-08		4.56 E-07		Sample 2 Only
Q9P253	VPS18_HUMAN Vacuolar protein sorting-associated protein 18 homolog OS=Homo sapiens GN=VPS18 PE=1 SV=2	1.50	1.00	1.00	1.00		3.13 E-08	8.04 E-08	2.43 E-07		7.76	Control 1 Only
B4DT77	B4DT77_HUMAN Annexin OS=Homo sapiens GN=ANXA7 PE=2 SV=1	6.00	1.00			1.00	3.84 E-08			5.23 E-08	control	1.36
B4DYD8	B4DYD8_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	4.00		2.00				3.92 E-07				
Q14008	CKAP5_HUMAN Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	1.20		1.00		1.00		3.53 E-08		1.49 E-08		Sample 2 Only

K7EKI8	K7EKI8_HUMAN Periplakin OS=Homo sapiens GN=PPL PE=2 SV=1	3.00			1.00	1.00			7.31E-09	8.83E-09	Sample 1 Only	Sample 2 Only
K7EIS0	K7EIS0_HUMAN Tubulin gamma chain (Fragment) OS=Homo sapiens GN=TUBG1 PE=2 SV=1	15.60			1.00	1.00			5.85E-07	3.05E-06	Sample 1 Only	Sample 2 Only
Q6NZY4	ZCHC8_HUMAN Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 PE=1 SV=2	10.60				1.00				9.05E-08		Sample 2 Only
B4DR63	B4DR63_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=2 SV=1	2.70		1.00		1.00		2.97E-08		5.93E-08		Sample 2 Only
Q13185	CBX3_HUMAN Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4	10.40		1.00				3.04E-07				
H0YFD6	H0YFD6_HUMAN Trifunctional enzyme subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=HADHA PE=2 SV=1	6.80			1.00				1.96E-07		Sample 1 Only	
Q99569	PKP4_HUMAN Plakophilin-4 OS=Homo sapiens GN=PKP4 PE=1 SV=2	1.50			1.00	1.00			1.04E-07	3.88E-08	Sample 1 Only	Sample 2 Only
Q86UK0	ABCAC_HUMAN ATP-binding cassette sub-family A member 12 OS=Homo sapiens GN=ABCA12 PE=1 SV=3	0.90				2.00				9.57E-09		Sample 2 Only
F5H7B0	F5H7B0_HUMAN Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=2 SV=1	1.70				2.00				3.57E-08		Sample 2 Only
B4DDM6	B4DDM6_HUMAN Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=2 SV=1	6.90			1.00				6.35E-08		Sample 1 Only	
Q99959	PKP2_HUMAN Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2	1.90		1.00	1.00			4.20E-08	4.78E-08		Sample 1 Only	
E5KLJ5	E5KLJ5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1	2.00		1.00				5.83E-08				
F8VXG7	F8VXG7_HUMAN Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=2 SV=1	2.00		1.00	1.00			2.07E-08	1.04E-08		Sample 1 Only	
J3QTP8	J3QTP8_HUMAN E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=2 SV=1	1.40			1.00	1.00			1.05E-08	8.99E-09	Sample 1 Only	Sample 2 Only
O75843	AP1G2_HUMAN AP-1 complex subunit gamma-like 2 OS=Homo sapiens GN=AP1G2 PE=1 SV=1	1.10			0.99	0.99			1.27E-07	3.81E-08	Sample 1 Only	Sample 2 Only
H3BQN7	H3BQN7_HUMAN Serine/threonine-protein kinase SMG1 (Fragment) OS=Homo sapiens GN=SMG1 PE=2 SV=2	4.00				2.00				2.57E-08		Sample 2 Only
F5H564	F5H564_HUMAN Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=2 SV=1	0.70			0.99				7.15E-08		Sample 1 Only	
E9PLA9	E9PLA9_HUMAN Caprin-1 (Fragment) OS=Homo sapiens GN=CAPRIN1 PE=2 SV=1	12.40				2.00				2.36E-06		Sample 2 Only
O00567	NOP56_HUMAN Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4	3.90				2.00				1.08E-06		Sample 2 Only
Q15437	SC23B_HUMAN Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	5.30				2.00				7.19E-07		Sample 2 Only
Q92841-2	DDX17_HUMAN Isoform 3 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17	34.70			1.00				3.24E-07		Sample 1 Only	
Q5XKE5	K2C79_HUMAN Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	15.90		1.00		1.00		1.60E-08		9.50E-08		Sample 2 Only
Q9H223	EHD4_HUMAN EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1	4.10		1.00		1.00		8.59E-08		1.14E-06		Sample 2 Only
P68371	TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	32.10			0.99	1.00			1.29E-07	2.35E-06	Sample 1 Only	Sample 2 Only
Q9Y2X3	NOP58_HUMAN Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1	4.30				2.00				1.62E-06		Sample 2 Only
Q9UBF2	COPG2_HUMAN Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1	5.50			1.00	1.00			2.14E-07	2.56E-08	Sample 1 Only	Sample 2 Only
F5H493	F5H493_HUMAN DNA excision repair protein ERCC-6 OS=Homo sapiens GN=ERCC6 PE=2 SV=1	2.40				2.00				1.34E-07		Sample 2 Only

Q9HCU4	CELR2_HUMAN Cadherin EGF LAG seven-pass G-type receptor 2 OS=Homo sapiens GN=CELSR2 PE=1 SV=1	0.90		2.00				1.30E-08				
A6NEM5	A6NEM5_HUMAN GPI-anchor transamidase OS=Homo sapiens GN=PIGK PE=2 SV=1	9.00			1.00	1.00			5.01E-07	7.64E-07	Sample 1 Only	Sample 2 Only
P49756	RBM25_HUMAN RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3	3.60			2.00				3.69E-07		Sample 1 Only	
P56182	RRP1_HUMAN Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens GN=RRP1 PE=1 SV=1	4.60				2.00				1.74E-06		Sample 2 Only
Q13045	FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	1.70				2.00				4.39E-08		Sample 2 Only
B4DKZ7	B4DKZ7_HUMAN Transcriptional repressor p66-alpha OS=Homo sapiens GN=GATAD2A PE=2 SV=1	3.90		2.00				3.21E-07				
E7EP00	E7EP00_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=2 SV=2	3.20		1.00	1.00			3.86E-08	3.48E-07		Sample 1 Only	
Q8WUA4	TF3C2_HUMAN General transcription factor 3C polypeptide 2 OS=Homo sapiens GN=GTF3C2 PE=1 SV=2	3.20		1.00		1.00		4.85E-08		3.51E-07		Sample 2 Only
B3KPU1	B3KPU1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=2 SV=1	9.20				1.98				1.15E-06		Sample 2 Only
B4DLC0	B4DLC0_HUMAN Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1	15.20				1.99				4.83E-07		Sample 2 Only
P43246	MSH2_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	3.00			1.00	1.00			1.24E-07	1.47E-07	Sample 1 Only	Sample 2 Only
H7C5K0	H7C5K0_HUMAN Helicase-like transcription factor (Fragment) OS=Homo sapiens GN=HLTF PE=2 SV=1	4.90		1.00		1.00		1.87E-07		4.75E-08		Sample 2 Only
O95365	ZBT7A_HUMAN Zinc finger and BTB domain-containing protein 7A OS=Homo sapiens GN=ZBTB7A PE=1 SV=1	6.50			1.00	1.00			1.41E-07	5.21E-07	Sample 1 Only	Sample 2 Only
Q86TG7	PEG10_HUMAN Retrotransposon-derived protein PEG10 OS=Homo sapiens GN=PEG10 PE=1 SV=2	3.00				2.00				1.03E-06		Sample 2 Only
F5H2X0	F5H2X0_HUMAN Tight junction protein ZO-3 OS=Homo sapiens GN=TJP3 PE=2 SV=1	2.30			0.50	1.00			5.81E-08	6.10E-07	Sample 1 Only	Sample 2 Only
P12270	TPR_HUMAN Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3	0.80	1.00	1.00			4.85E-09	2.95E-09			Control 1 Only	Control 1 Only
E7EMM2	E7EMM2_HUMAN AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=2 SV=1	3.20			1.00	1.00			2.27E-08	1.18E-07	Sample 1 Only	Sample 2 Only
B4DJ81	B4DJ81_HUMAN NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=2 SV=1	4.90			2.00				9.81E-08		Sample 1 Only	
Q8TDD1	DDX54_HUMAN ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2	1.60			0.99	1.00			2.30E-07	7.81E-08	Sample 1 Only	Sample 2 Only
P31151	S10A7_HUMAN Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	23.80		2.00				9.38E-08				
Q9P2M7	CING_HUMAN Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	1.60				2.00				5.59E-08		Sample 2 Only
Q9UHD8	SEPT9_HUMAN Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	6.00		0.99	0.99			5.21E-08	1.49E-07		Sample 1 Only	
D6R904	D6R904_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=2 SV=1	22.10		1.98				1.63E-06				
Q9Y4D1	DAAM1_HUMAN Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens GN=DAAM1 PE=1 SV=2	2.00		1.00	1.00			6.14E-08	1.70E-07		Sample 1 Only	
Q08378	GOGA3_HUMAN Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2	1.90		1.00		1.00		1.16E-08		1.88E-08		Sample 2 Only
P07996	TSP1_HUMAN Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	1.90				2.00				3.83E-08		Sample 2 Only
I3L1P8	I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens GN=SLC25A11 PE=2 SV=1	7.10			1.00				1.66E-07		Sample 1 Only	
E9PIF8	E9PIF8_HUMAN Ribosome biogenesis protein BOP1 (Fragment) OS=Homo sapiens GN=BOP1 PE=2 SV=1	20.70			1.00				4.33E-07		Sample 1 Only	

B7Z888	B7Z888_HUMAN Protein SCAF8 OS=Homo sapiens GN=SCAF8 PE=2 SV=1	1.70				1.00				1.23E-08		Sample 2 Only
H3BPU4	H3BPU4_HUMAN Gamma-tubulin complex component 4 (Fragment) OS=Homo sapiens GN=TUBGCP4 PE=4 SV=1	7.60				1.00				4.00E-07		Sample 2 Only
A8MWU4	A8MWU4_HUMAN Synergin gamma OS=Homo sapiens GN=SYNRG PE=2 SV=2	1.80			1.00				1.70E-08		Sample 1 Only	
F5H658	F5H658_HUMAN ATP-dependent RNA helicase DHX8 OS=Homo sapiens GN=DHX8 PE=2 SV=1	2.00				1.00				1.76E-08		Sample 2 Only
O94906	PRP6_HUMAN Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1	2.20				1.00				1.79E-07		Sample 2 Only
B9ZVN9	B9ZVN9_HUMAN DNA-directed RNA polymerase OS=Homo sapiens GN=POLR1A PE=2 SV=1	1.10				1.00				5.81E-09		Sample 2 Only
Q9UG01	IF172_HUMAN Intraflagellar transport protein 172 homolog OS=Homo sapiens GN=IFT172 PE=1 SV=2	1.30				1.00				5.65E-09		Sample 2 Only
O60216	RAD21_HUMAN Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2	3.60		1.00				5.52E-08				
E7EUT5	E7EUT5_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=2 SV=1	9.60		1.00				3.57E-08				
H0YG10	H0YG10_HUMAN Nucleolar GTP-binding protein 2 (Fragment) OS=Homo sapiens GN=GNL2 PE=4 SV=1	9.40										
P18077	RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	21.80										
Q562R1	ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	19.70			1.00				5.15E-07		Sample 1 Only	
D6REE5	D6REE5_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 (Fragment) OS=Homo sapiens GN=GNB2L1 PE=2 SV=1	32.70				0.99				1.71E-08		Sample 2 Only
P20585	MSH3_HUMAN DNA mismatch repair protein Msh3 OS=Homo sapiens GN=MSH3 PE=1 SV=4	1.10				1.00				8.77E-08		Sample 2 Only
F8VSC7	F8VSC7_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=2 SV=1	27.30			1.00				7.32E-08		Sample 1 Only	
K7EJT8	K7EJT8_HUMAN AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=2 SV=1	6.90				1.00				6.47E-09		Sample 2 Only
B3KRS5	B3KRS5_HUMAN Histone deacetylase OS=Homo sapiens GN=HDAC2 PE=2 SV=1	8.10			1.00				1.13E-07		Sample 1 Only	
F5H019	F5H019_HUMAN GPI transamidase component PIG-S OS=Homo sapiens GN=PIGS PE=2 SV=1	3.00			1.00				2.71E-07		Sample 1 Only	
F8W9B8	F8W9B8_HUMAN Exocyst complex component 5 OS=Homo sapiens GN=EXOC5 PE=2 SV=1	2.60			1.00				2.42E-08		Sample 1 Only	
E9PDF6	E9PDF6_HUMAN Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=2 SV=1	4.30				0.99				2.10E-08		Sample 2 Only
F5H6E2	F5H6E2_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=2 SV=1	30.60	1.00				1.51E-08				Control 1 Only	Control 1 Only
P13639	EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	2.10		1.00				4.50E-08				
E7EVF4	E7EVF4_HUMAN Cytoplasmic FMR1-interacting protein 2 OS=Homo sapiens GN=CYFIP2 PE=2 SV=1	6.50				0.99				5.00E-09		Sample 2 Only
H7C269	H7C269_HUMAN Trinucleotide repeat-containing gene 6A protein (Fragment) OS=Homo sapiens GN=TNRC6A PE=2 SV=1	18.50			1.00				8.98E-10		Sample 1 Only	
Q9UPQ9	TNR6B_HUMAN Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	24.30			0.99				7.65E-08		Sample 1 Only	
P08107	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	8.40		0.99				3.47E-08				
Q9H089	LSG1_HUMAN Large subunit GTPase 1 homolog OS=Homo sapiens GN=LSG1 PE=1 SV=2	1.40			1.00				6.06E-07		Sample 1 Only	
Q96N66	MBOA7_HUMAN Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2	7.00				1.00				5.55E-08		Sample 2 Only

B4DKG8	B4DKG8_HUMAN Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=2 SV=1	3.50				1.00				5.64E-07		Sample 2 Only
F8WE98	F8WE98_HUMAN Filamin-A (Fragment) OS=Homo sapiens GN=FLNA PE=2 SV=2	26.30			1.00				6.86E-08		Sample 1 Only	

Table A6. Endogenous candidates from nuclear immunoprecipitations that had not been treated with RNase.

			SPECTRAL COUNTS						SPECTRAL INDEX (MIC SIn)						RATIOS		
Prot	Description	% Cover	C1	C2	C3	S1	S2	S3	C1	C2	C3	S1	S2	S3	S1/C1	S2/C1	S3/C1
P01614	KV201_HUMAN Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	14.20	5.00	7.00	4.00	1.00	1.00		1.73 E-05	1.01 E-06	1.37 E-05	1.16 E-08	1.50 E-08		0.00	0.00	Control 1 Only
P62805	H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	54.40	41.00	6.00	23.00	4.00	2.00	6.00	7.77 E-05	1.27 E-05	6.16 E-05	3.59 E-06	3.06 E-06	4.29 E-06	0.05	0.04	0.06
Q8NDV7-6	TNR6A_HUMAN Isoform 6 of Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A	44.30	0.99		0.99	108.52	68.12	52.33	1.13 E-09		5.58 E-10	6.59 E-06	4.49 E-06	2.32 E-06	5817.30	3958.52	2047.66
J3KT73	J3KT73_HUMAN 60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=2 SV=1	39.10	4.00	2.00	6.00	1.00			3.04 E-06	2.84 E-06	7.46 E-06	1.06 E-07			0.03	Control 1 Only	Control 1 Only
Q9Y305	ACOT9_HUMAN Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2	51.00	22.84	0.99	0.99	1.98	0.99		7.88 E-06	8.92 E-08	3.64 E-08	5.15 E-08	3.83 E-08		0.01	0.00	Control 1 Only
B4DEB1	B4DEB1_HUMAN Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1	29.30	13.00	2.00	7.00	5.00	1.00	2.00	2.91 E-05	2.83 E-06	5.87 E-06	3.70 E-06	1.60 E-07	4.25 E-07	0.13	0.01	0.01
P05783	K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	65.80	9.99	17.00	27.00	9.00	1.00	3.00	1.21 E-06	3.34 E-06	9.53 E-06	8.02 E-07	8.27 E-08	1.35 E-07	0.67	0.07	0.11
P22392	NDKB_HUMAN Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	42.80		0.99		1.98	2.97	1.98		5.75 E-09		3.68 E-08	8.28 E-07	1.14 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P20930	FILA_HUMAN Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	7.80	14.00	8.00	11.00	2.00	10.00	6.00	8.71 E-07	1.26 E-06	3.63 E-08	2.18 E-09	5.85 E-09	6.30 E-09	0.00	0.01	0.01
P05109	S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	62.40	5.00	4.00	8.00	15.00	5.00	1.00	2.81 E-07	9.07 E-08	1.15 E-06	1.36 E-05	7.47 E-07	1.31 E-08	48.17	2.66	0.05
Q99459	CDC5L_HUMAN Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2	5.40	3.00	4.00	2.00	1.00			2.09 E-07	6.57 E-07	6.32 E-07	2.64 E-09			0.01	Control 1 Only	Control 1 Only
P08727	K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	76.80	16.97	13.99	28.91	20.96	6.99	6.99	3.12 E-06	4.99 E-06	2.13 E-05	3.42 E-06	6.29 E-07	3.40 E-07	1.09	0.20	0.11
P05787	K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	77.20	29.77	25.81	44.65	25.81	4.96	5.96	5.26 E-06	7.45 E-06	1.81 E-05	4.31 E-06	2.14 E-07	1.69 E-07	0.82	0.04	0.03
P24539	AT5F1_HUMAN ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2	39.00		1.00		1.00	9.00	2.00		1.42 E-07		1.06 E-07	2.89 E-06	1.31 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9NXS2	QPCTL_HUMAN Glutaminyl-peptide cyclotransferase-like protein OS=Homo sapiens GN=QPCTL PE=1 SV=2	17.00	4.00	3.00	3.00	2.00	1.00		2.53 E-06	4.83 E-07	1.22 E-06	2.01 E-07	5.56 E-08		0.08	0.02	Control 1 Only
P12035	K2C3_HUMAN Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3	32.80	4.00	7.00		2.00	1.00		6.11 E-08	2.24 E-07		4.08 E-06	2.83 E-08		66.75	0.46	Control 1 Only
P09382	LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	64.40	3.00	2.00	1.00	8.00	7.00	6.00	3.80 E-07	2.21 E-07	1.59 E-08	2.44 E-06	2.14 E-06	1.75 E-06	6.43	5.64	4.61
P06702	S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	51.80	1.00	2.00	2.00	11.00	1.00	1.00	3.56 E-07	3.15 E-07	3.87 E-07	8.43 E-06	8.86 E-08	4.90 E-08	23.69	0.25	0.14
P05549	AP2A_HUMAN Transcription factor AP-2-alpha OS=Homo sapiens GN=TFAP2A PE=1 SV=1	23.20	7.97	1.00	1.00	1.00			6.90 E-07	1.03 E-08	2.63 E-08	6.86 E-09			0.01	Control 1 Only	Control 1 Only
P42766	RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	42.30	6.00	3.00	13.00	5.00	6.00	2.00	3.37 E-06	1.08 E-05	2.32 E-05	1.21 E-06	4.38 E-06	1.91 E-06	0.36	1.30	0.57
Q04695	K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	73.60	12.94	4.97	2.98	41.84	18.87	6.96	1.17 E-06	1.85 E-07	3.76 E-08	8.09 E-06	1.20 E-06	7.17 E-07	6.91	1.03	0.61
Q15459	SF3A1_HUMAN Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	4.20	2.00	3.00	2.00	1.00			2.87 E-07	5.25 E-07	2.86 E-07	4.11 E-08			0.14	Control 1 Only	Control 1 Only

Q14247	SRC8_HUMAN Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	39.50		4.92	6.84	9.83	14.75	11.84		8.73E-08	1.80E-07	4.77E-07	1.32E-06	1.01E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P26373	RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	42.70	24.82	18.92	20.91	21.87	15.92	18.90	1.92E-05	1.54E-05	4.24E-05	9.27E-06	4.93E-06	6.17E-06	0.48	0.26	0.32
O94906	PRP6_HUMAN Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1	13.50	1.00	1.00	9.00	1.00			1.30E-08	2.66E-08	2.89E-07	1.27E-09			0.10	Control 1 Only	Control 1 Only
P23771	GATA3_HUMAN Trans-acting T-cell-specific transcription factor GATA-3 OS=Homo sapiens GN=GATA3 PE=1 SV=1	5.60	3.00	2.00	1.00			1.00	2.56E-07	1.35E-08	3.61E-08			4.71E-09	Control 1 Only	Control 1 Only	0.02
P62854	RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	50.40	10.00	8.00	15.00	10.00	3.00	3.00	2.10E-05	1.07E-05	3.19E-05	1.12E-05	4.54E-06	1.82E-06	0.53	0.22	0.09
P51116	FXR2_HUMAN Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2	21.70	3.90	3.90	5.92	4.94	0.97	1.96	1.72E-06	3.08E-06	5.77E-06	1.84E-06	7.56E-08	9.36E-08	1.07	0.04	0.05
P15924	DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	31.50	58.98	24.00	69.99	6.00	13.00	14.00	8.61E-07	7.93E-08	3.90E-07	1.24E-08	3.24E-08	7.38E-08	0.01	0.04	0.09
P50914	RL14_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	38.10	17.00	10.00	18.00	20.00	9.00	10.00	6.23E-06	3.47E-06	1.75E-05	3.03E-06	1.45E-06	2.08E-06	0.49	0.23	0.33
G5E9Q2	G5E9Q2_HUMAN Cold shock domain containing E1, RNA-binding, isoform CRA_d OS=Homo sapiens GN=CSDE1 PE=2 SV=1	11.20	0.99	0.99		0.99	7.93	0.99	2.85E-09	7.13E-09		4.47E-09	3.30E-07	4.85E-09	1.57	115.86	1.70
P62277	RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	62.30	23.89	15.93	23.90	21.93	14.94	18.95	2.74E-05	2.24E-05	6.24E-05	2.00E-05	4.64E-06	1.14E-05	0.73	0.17	0.42
Q14527	HLTF_HUMAN Helicase-like transcription factor OS=Homo sapiens GN=HLTF PE=1 SV=2	16.10	5.97	4.98	10.99		1.99	1.00	8.19E-08	9.54E-08	6.00E-08		2.98E-09	3.07E-09	Control 1 Only	0.04	0.04
Q13247	SRSF6_HUMAN Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2	42.70	9.04	3.02	17.54	9.55	1.02	1.53	3.63E-06	5.82E-07	4.33E-06	1.62E-06	3.97E-08	7.74E-08	0.45	0.01	0.02
Q99442	SEC62_HUMAN Translocation protein SEC62 OS=Homo sapiens GN=SEC62 PE=1 SV=1	16.50	1.00	2.00	3.00	6.00	5.00	2.00	6.40E-08	3.04E-08	2.46E-08	9.11E-07	1.66E-07	3.26E-09	14.24	2.59	0.05
P26599	PTBP1_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	49.70	7.92	9.89	14.85	20.79	14.85	9.90	1.08E-07	3.54E-07	3.36E-07	2.49E-06	1.05E-06	8.65E-07	23.00	9.70	8.00
Q15149	PLEC_HUMAN Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	33.00	38.59	49.46	108.76	15.81	2.98	0.99	1.34E-07	1.77E-07	5.01E-07	6.92E-08	1.01E-08	9.34E-10	0.52	0.08	0.01
P62851	RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	35.20	11.00	6.00	6.00	7.00	3.00	5.00	1.42E-05	1.09E-05	8.66E-06	8.10E-06	8.90E-07	5.78E-07	0.57	0.06	0.04
P40938	RFC3_HUMAN Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2	25.00	2.00	3.00	4.00	4.00	1.00		5.87E-07	6.58E-07	1.03E-06	2.70E-07	7.91E-08		0.46	0.13	Control 1 Only
F8VP71	F8VP71_HUMAN LETM1 domain-containing protein 1 OS=Homo sapiens GN=LETMD1 PE=2 SV=1	23.60	3.95	0.98	2.97	0.98			4.93E-07	1.10E-07	7.31E-07	1.71E-07			0.35	Control 1 Only	Control 1 Only
P58107	EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	30.10	26.00	4.00	8.00	2.00	3.00		1.40E-07	1.47E-08	2.87E-08	9.91E-10	4.78E-09		0.01	0.03	Control 1 Only
B4E2V5	B4E2V5_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=2 SV=1	28.30		3.00	1.00	2.00	3.00	7.00		1.65E-07	5.35E-08	5.02E-07	5.64E-07	4.53E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q00059	TFAM_HUMAN Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1	8.40	3.00	1.00	1.00	1.00			4.59E-07	1.57E-07	7.56E-08	7.17E-08			0.16	Control 1 Only	Control 1 Only
C9JAB2	C9JAB2_HUMAN Serine/arginine-rich-splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=2 SV=1	43.40	2.99	4.00	16.92	12.97	3.99	4.00	3.50E-06	5.16E-07	1.23E-05	2.04E-06	2.54E-07	1.96E-06	0.58	0.07	0.56
B3KTC7	B3KTC7_HUMAN Double-strand break repair protein MRE11A OS=Homo sapiens	17.10	1.99	2.99	1.00	6.99	3.99	3.99	1.68E-08	3.11E-08	3.93E-08	3.51E-07	2.51E-07	1.58E-07	20.82	14.89	9.37

	GN=MRE11A PE=2 SV=1																
C9IZQ1	C9IZQ1_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=2 SV=1	8.90	3.00	3.00	2.00	3.00	3.00	4.00	2.20 E-06	7.74 E-06	2.01 E-06	8.39 E-07	2.29 E-07	1.91 E-06	0.38	0.10	0.87
P62269	RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	67.80	32.99	23.99	39.98	21.99	19.99	15.99	8.01 E-05	9.87 E-05	1.69 E-04	6.62 E-05	4.69 E-05	2.89 E-05	0.83	0.58	0.36
Q14974	IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	12.40	1.00	5.96	2.99	8.96	6.98	4.98	2.42 E-08	6.88 E-08	3.59 E-08	2.76 E-07	2.01 E-07	5.06 E-07	11.43	8.29	20.93
Q96QK1	VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	14.70		8.00	2.00		15.00	6.00		1.35 E-07	6.99 E-10		8.15 E-07	1.98 E-07		Sample 2 Only	Sample 3 Only
Q96AG4	LRC59_HUMAN Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	32.90	2.00	5.00	6.00	5.00	7.00	2.00	5.77 E-08	6.70 E-07	2.57 E-06	1.47 E-07	4.80 E-07	6.93 E-09	2.54	8.32	0.12
Q13242	SRSF9_HUMAN Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	61.50	3.98	3.48	20.39	7.98	1.99	1.49	1.32 E-06	1.06 E-06	4.56 E-06	1.00 E-06	2.87 E-07	3.11 E-07	0.76	0.22	0.24
O75607	NPM3_HUMAN Nucleoplasmin-3 OS=Homo sapiens GN=NPM3 PE=1 SV=3	29.20	1.00		6.00	1.00		1.00	3.29 E-07		9.29 E-06	6.81 E-07		1.77 E-06	2.07	Control 1 Only	5.37
P08107	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	31.20	4.94	5.94	0.99	6.91	12.86	8.88	5.16 E-07	1.17 E-06	3.69 E-08	1.47 E-06	3.75 E-06	1.86 E-06	2.85	7.26	3.61
P11388	TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	43.80	24.00	16.00	64.00	21.00	5.00	5.00	9.07 E-07	4.64 E-07	1.91 E-06	6.02 E-07	3.52 E-08	3.36 E-08	0.66	0.04	0.04
K7EQJ5	K7EQJ5_HUMAN 40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=2 SV=2	41.80	7.92	0.99	15.84	4.95	3.96	1.98	1.25 E-06	4.14 E-08	4.89 E-06	7.14 E-07	1.37 E-07	6.14 E-07	0.57	0.11	0.49
P25705	ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	63.30	6.87	17.65	13.74	12.78	31.47	15.75	8.65 E-08	2.64 E-06	1.40 E-06	1.43 E-06	1.16 E-05	1.58 E-06	16.52	134.45	18.30
Q6IAN0	DRS7B_HUMAN Dehydrogenase/reductase SDR family member 7B OS=Homo sapiens GN=DHRS7B PE=1 SV=2	6.50	4.00	4.00	2.00	3.00	2.00	2.00	2.33 E-07	3.18 E-07	1.54 E-07	2.94 E-08	1.67 E-08	4.77 E-08	0.13	0.07	0.20
E9PLL6	E9PLL6_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1	50.90	3.97	1.98	8.97	5.95	2.98	2.99	8.74 E-06	1.27 E-05	6.09 E-06	6.31 E-06	4.61 E-07	1.86 E-06	0.72	0.05	0.21
Q96CU9	FXRD1_HUMAN FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=1 SV=2	19.10	2.97	1.98	1.98	4.95	2.97	1.98	6.37 E-08	5.83 E-08	6.30 E-08	4.73 E-07	5.42 E-07	1.41 E-07	7.44	8.51	2.22
Q9H9Z2	LN28A_HUMAN Protein lin-28 homolog A OS=Homo sapiens GN=LIN28A PE=1 SV=1	13.90		3.00		2.00	3.00	1.00		8.76 E-07		1.02 E-06	2.67 E-06	2.46 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
J3KP33	J3KP33_HUMAN Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=2 SV=1	14.70	0.99	1.98	3.96		0.99		1.34 E-08	7.20 E-08	2.72 E-07		3.68 E-08		Control 1 Only	2.74	Control 1 Only
Q9UKD2	MRT4_HUMAN mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2	33.90	5.00	1.00	4.00	2.00	1.00	1.00	1.16 E-06	6.03 E-08	1.88 E-07	1.63 E-07	5.45 E-08	2.87 E-08	0.14	0.05	0.02
P35268	RL22_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	62.50	6.91	6.93	15.85	6.94	5.94	4.93	1.11 E-05	2.15 E-06	2.11 E-06	1.70 E-06	1.80 E-06	9.96 E-07	0.15	0.16	0.09
J3QLS3	J3QLS3_HUMAN 28S ribosomal protein S7, mitochondrial OS=Homo sapiens GN=MRPS7 PE=2 SV=1	34.30	16.83	5.94	9.90	6.93	4.95	3.96	6.16 E-06	1.19 E-06	2.49 E-06	1.52 E-06	8.68 E-07	2.98 E-07	0.25	0.14	0.05
Q69YN4	VIR_HUMAN Protein virilizer homolog OS=Homo sapiens GN=KIAA1429 PE=1 SV=2	8.30			0.99	10.92	2.97	1.98			3.11 E-09	7.52 E-08	2.64 E-09	6.29 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
F5GX29	F5GX29_HUMAN Calcineurin B homologous protein 1 OS=Homo sapiens GN=CHP1 PE=2 SV=1	30.80		1.00		1.00	2.00	3.00		1.77 E-07		1.84 E-07	3.78 E-07	5.03 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P32969	RL9_HUMAN 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	74.00	18.76	15.79	25.66	19.73	9.87	8.88	3.24 E-06	1.36 E-05	1.92 E-05	8.96 E-06	2.20 E-06	9.36 E-07	2.76	0.68	0.29

Q8WXF1	PSPC1_HUMAN Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1	48.40	14.98	18.00	15.99	37.99	39.96	32.97	4.34E-06	3.48E-06	2.84E-06	7.29E-06	1.30E-05	1.17E-05	1.68	3.01	2.70
Q8NC51	PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	22.00	2.00	2.00	1.00	4.00	1.00	2.00	3.06E-08	1.09E-08	2.41E-09	3.23E-07	4.72E-09	4.71E-08	10.56	0.15	1.54
Q99714	HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	63.60		4.96	0.99	2.99	10.94	8.94		4.44E-07	1.89E-09	5.59E-08	1.65E-06	4.75E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y6K5	OAS3_HUMAN 2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3	25.30	10.96	10.97	6.96	20.93	12.99	17.95	2.58E-07	2.21E-07	7.14E-08	1.01E-06	1.06E-06	5.05E-07	3.91	4.09	1.96
P01620	KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	39.40	1.98	2.98	0.99	1.98	0.99	0.99	2.41E-07	2.15E-06	1.99E-07	7.17E-08	2.85E-07	1.91E-07	0.30	1.18	0.79
J3KTL2	J3KTL2_HUMAN Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=2 SV=1	58.10	22.77	19.80	33.66	30.69	13.86	8.91	3.78E-06	6.36E-06	2.53E-05	8.11E-06	2.85E-06	1.09E-06	2.15	0.75	0.29
P61353	RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	58.80	13.93	12.94	19.90	12.94	16.90	10.95	2.69E-05	3.76E-05	5.93E-05	6.35E-06	3.67E-05	6.16E-06	0.24	1.36	0.23
O43148	MCES_HUMAN mRNA cap guanine-N7 methyltransferase OS=Homo sapiens GN=RNMT PE=1 SV=1	19.70	1.99	1.99		2.98	1.98	2.97	8.91E-08	1.42E-08		1.89E-07	1.73E-07	3.22E-07	2.13	1.94	3.62
Q6P2E9	EDC4_HUMAN Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1	2.70		1.99		2.00	2.99	1.00		4.82E-09		4.30E-08	3.53E-08	1.42E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y3C6	PPIL1_HUMAN Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens GN=PPIL1 PE=1 SV=1	38.00	2.00	2.00	1.00	2.00	6.00	4.00	1.71E-07	9.85E-07	5.27E-08	1.23E-06	2.10E-06	1.48E-06	7.19	12.24	8.64
F5GYQ1	F5GYQ1_HUMAN V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=2 SV=1	16.40		1.00		3.00	2.00	3.00		6.39E-08		2.41E-07	3.60E-08	1.93E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
G3V4F7	G3V4F7_HUMAN Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=2 SV=1	15.50	2.00	3.00	2.00	3.00	4.00		2.74E-08	1.66E-07	9.45E-08	3.69E-07	1.11E-06		13.47	40.48	Control 1 Only
Q08188	TGM3_HUMAN Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	12.00	6.00	1.00	1.00			1.00	1.09E-07	1.04E-08	2.37E-09			8.08E-09	Control 1 Only	Control 1 Only	0.07
F5GWY0	F5GWY0_HUMAN GPI transamidase component PIG-T OS=Homo sapiens GN=PIGT PE=2 SV=1	22.00		7.91	2.96	1.98	0.99			9.44E-07	2.00E-07	1.64E-07	4.41E-08		Sample 1 Only	Sample 2 Only	
P15880	RS2_HUMAN 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	54.90	37.42	16.74	21.68	29.56	14.79	16.78	8.65E-06	3.19E-06	1.46E-05	4.88E-06	1.72E-06	2.25E-06	0.56	0.20	0.26
P62241	RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	58.20	23.00	9.00	23.00	19.00	6.00	11.00	1.06E-05	5.28E-06	7.48E-06	3.94E-06	2.03E-06	1.73E-06	0.37	0.19	0.16
Q9P2E9	RRBP1_HUMAN Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	58.70	15.85	17.83	60.62	10.92	4.96	17.86	2.69E-07	5.69E-07	1.64E-06	1.22E-07	1.02E-07	3.26E-07	0.45	0.38	1.21
Q9P0L0	VAPA_HUMAN Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3	15.70	0.99	0.99	0.99	1.99	1.99	2.98	3.58E-08	2.52E-08	1.66E-08	1.86E-07	6.86E-08	2.64E-07	5.21	1.92	7.39
Q9Y3U8	RL36_HUMAN 60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	48.60	2.98	0.99	4.96	1.99		0.99	7.42E-07	2.69E-07	2.06E-06	2.74E-07		4.49E-07	0.37	Control 1 Only	0.61
P13646	K1C13_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	53.50	10.84	7.46	9.84	0.56	10.84		1.98E-06	1.94E-06	4.65E-07	2.94E-08	1.08E-06		0.01	0.55	Control 1 Only
J3QRN6	J3QRN6_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=2 SV=1	26.60	1.99	1.98	17.90	3.98		0.99	8.74E-09	1.38E-08	2.67E-07	2.86E-08		5.96E-09	3.27	Control 1 Only	0.68
P01857	IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	23.90	1.00	4.00	4.00	8.00	1.00	3.00	3.92E-09	4.78E-08	1.25E-08	3.79E-07	3.31E-08	2.88E-08	96.81	8.44	7.35
P08	HS90B_HUMAN Heat shock protein HSP 90-	16.20	0.50	3.49	0.50	1.50	5.99	2.00	9.63	6.97	5.33	8.31	3.67	5.94	8.63	38.13	6.17

238	beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4								E-09	E-08	E-10	E-08	E-07	E-08			
P05089	ARGI1_HUMAN Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	27.00	10.00	2.00	7.00	1.00	1.00	1.00	4.96 E-07	8.78 E-08	1.80 E-07	4.95 E-08	4.13 E-08	4.74 E-08	0.10	0.08	0.10
P46781	RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	66.00	33.93	31.92	39.92	31.91	25.94	21.92	5.11 E-05	4.21 E-05	3.57 E-05	2.17 E-05	1.74 E-05	1.56 E-05	0.42	0.34	0.31
D6RA37	D6RA37_HUMAN Tumor suppressor candidate 3 OS=Homo sapiens GN=TUSC3 PE=2 SV=1	9.40		2.00	1.50	3.00	2.00			1.14 E-07	1.51 E-07	7.59 E-07	4.92 E-07		Sample 1 Only	Sample 2 Only	
Q6UXN9	WDR82_HUMAN WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1	14.70	1.00	3.00	3.00	7.00	5.00	1.00	1.15 E-08	1.67 E-07	8.92 E-08	8.48 E-07	3.45 E-07	6.47 E-08	73.56	29.90	5.61
Q96T37	RBM15_HUMAN Putative RNA-binding protein 15 OS=Homo sapiens GN=RBM15 PE=1 SV=2	6.90	1.00	1.00	5.00	2.00			2.54 E-09	3.26 E-08	3.07 E-08	4.34 E-09			1.71	Control 1 Only	Control 1 Only
P39656	OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	53.70	8.97	8.96	8.97	18.92	16.95	12.96	9.33 E-07	9.25 E-07	2.03 E-06	4.78 E-06	3.82 E-06	3.28 E-06	5.12	4.10	3.52
P05388	RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	66.20	40.75	27.20	32.95	38.87	29.17	26.24	1.68 E-05	1.17 E-05	2.49 E-05	7.50 E-06	8.50 E-06	5.07 E-06	0.45	0.51	0.30
Q01082	SPTB2_HUMAN Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	28.20	3.06	2.04	8.65	9.67	13.24	17.32	1.39 E-08	6.83 E-09	5.61 E-08	6.17 E-08	1.57 E-07	2.31 E-07	4.43	11.32	16.64
E7EQ69	E7EQ69_HUMAN N-alpha-acetyltransferase 50 OS=Homo sapiens GN=NAA50 PE=2 SV=1	62.50	9.89	19.76	20.74	17.79	28.65	11.85	2.00 E-06	9.36 E-06	5.75 E-06	8.27 E-06	3.24 E-05	3.08 E-06	4.14	16.22	1.54
Q96HY6	DDRGK_HUMAN DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1 PE=1 SV=2	45.90	1.00	5.00	5.00	12.00	9.00	4.00	2.18 E-07	1.20 E-06	8.97 E-07	3.21 E-06	2.78 E-06	1.48 E-06	14.77	12.76	6.80
P31930	QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	42.50	8.00	9.00	10.00	15.00	18.00	16.00	6.14 E-07	3.55 E-06	3.46 E-06	4.72 E-06	1.03 E-05	6.14 E-06	7.68	16.81	10.01
P11021	GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	56.00	24.00	25.00	22.00	35.00	39.00	31.00	1.15 E-06	1.97 E-06	1.69 E-06	3.62 E-06	6.22 E-06	4.19 E-06	3.14	5.39	3.64
J3KN66	J3KN66_HUMAN Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=2 SV=1	10.50		1.98	0.99	0.99	6.93	0.99		2.85 E-08	6.62 E-10	7.53 E-10	1.70 E-07	3.79 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P68371	TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	40.70	1.02	1.51			2.51	2.49	2.35 E-08	1.96 E-08			9.79 E-08	1.77 E-07	Control 1 Only	4.18	7.54
Q9Y3B4	PM14_HUMAN Pre-mRNA branch site protein p14 OS=Homo sapiens GN=SF3B14 PE=1 SV=1	29.60	2.00	2.00	3.00	1.00		2.00	1.41 E-07	2.28 E-07	2.05 E-07	7.16 E-09		1.03 E-07	0.05	Control 1 Only	0.73
P49756	RBM25_HUMAN RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3	17.00	3.98	4.99	6.96	5.96		1.00	1.82 E-07	1.55 E-07	3.04 E-07	1.20 E-07		6.82 E-09	0.66	Control 1 Only	0.04
O75306	NDUS2_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=1 SV=2	35.70	1.00	11.00	2.00	7.00	12.00	11.00	4.12 E-07	1.48 E-06	2.13 E-07	1.01 E-06	2.95 E-06	2.71 E-06	2.46	7.16	6.59
P14868	SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	27.70	4.98	7.94	4.95	6.96	2.98	0.99	2.35 E-07	1.11 E-06	1.84 E-07	2.30 E-07	9.57 E-08	4.72 E-08	0.98	0.41	0.20
Q6KB66	K2C80_HUMAN Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	20.10	7.00	1.00	1.00			1.00	6.86 E-08	3.22 E-08	2.47 E-09			1.11 E-08	Control 1 Only	Control 1 Only	0.16
P40937	RFC5_HUMAN Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=1 SV=1	40.10	5.93	1.98	8.90	5.93	4.95	1.98	5.02 E-07	5.49 E-07	1.17 E-06	2.81 E-07	2.58 E-07	4.62 E-08	0.56	0.51	0.09
E7ENU4	E7ENU4_HUMAN Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=2 SV=1	23.10	2.00	3.00	15.00	5.00		1.00	6.08 E-08	5.32 E-08	2.73 E-07	5.42 E-08		1.50 E-08	0.89	Control 1 Only	0.25

Q9BRJ7	SDOS_HUMAN Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1	66.40	3.98	12.91	3.97	5.96	25.81	12.92	2.19E-07	2.70E-06	2.90E-07	1.18E-06	4.61E-06	3.73E-06	5.38	21.09	17.02
Q13813	SPTN1_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	58.50	40.60	33.68	75.27	78.23	104.95	95.06	7.81E-07	3.69E-07	1.12E-06	2.12E-06	1.83E-06	3.03E-06	2.71	2.34	3.88
Q5HYI8	RABL3_HUMAN Rab-like protein 3 OS=Homo sapiens GN=RABL3 PE=1 SV=1	21.60		2.98	2.99	4.97	3.99	0.99		2.73E-07	2.18E-07	1.00E-06	7.28E-07	1.37E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
O15371	EIF3D_HUMAN Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1	28.60	1.99	1.99	4.96	7.93	6.93	2.97	2.81E-07	1.27E-07	1.19E-07	4.13E-07	1.39E-06	1.61E-07	1.47	4.96	0.57
Q969Q0	RL36L_HUMAN 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3	17.90	2.00	1.00	4.50	2.00	1.00	1.00	1.05E-06	1.00E-06	2.07E-06	5.31E-07	6.48E-07	6.96E-08	0.51	0.62	0.07
B7Z6A4	B7Z6A4_HUMAN Surfeit 4, isoform CRA_c OS=Homo sapiens GN=SURF4 PE=2 SV=1	30.50		3.00	2.00	1.00	6.00	2.00		1.45E-07	5.63E-08	8.37E-09	8.40E-07	2.17E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7EW34	E7EW34_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=2 SV=1	11.40	4.00	6.99	2.00	6.00	7.00	2.00	5.85E-08	2.88E-07	4.37E-08	4.75E-07	8.07E-07	2.16E-07	8.12	13.78	3.70
P62266	RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	49.00	8.96	0.99	8.97	7.95	1.00	2.99	1.86E-05	6.19E-07	8.41E-06	9.35E-06	1.01E-08	1.58E-06	0.50	0.00	0.08
P62995	TRA2B_HUMAN Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1	51.70	8.95	13.90	22.88	25.85	5.97	10.92	1.65E-06	3.15E-06	1.87E-05	7.01E-06	5.72E-07	1.57E-06	4.24	0.35	0.95
Q9BUB7	TMM70_HUMAN Transmembrane protein 70, mitochondrial OS=Homo sapiens GN=TMEM70 PE=1 SV=2	15.80		1.00	3.00	2.00	2.00	1.00		4.88E-08	1.13E-07	4.51E-08	6.09E-07	5.79E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O43684	BUB3_HUMAN Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1	42.90	5.94	9.90	7.92	11.88	14.85	10.89	1.72E-07	1.14E-06	9.42E-07	2.17E-06	2.43E-06	2.10E-06	12.59	14.12	12.20
Q08554	DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	7.90	3.00	2.00	3.00	1.00		2.00	7.91E-08	6.64E-08	1.79E-08	8.16E-09		1.71E-08	0.10	Control 1 Only	0.22
B0QY89	B0QY89_HUMAN Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=2 SV=1	41.10	5.97	7.97	1.00	6.98	10.97	4.98	6.88E-07	5.38E-07	6.97E-08	1.24E-06	2.11E-06	7.26E-07	1.80	3.06	1.06
Q7Z794	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	21.80	4.00	5.00	7.00	3.00	3.00	2.00	1.74E-07	2.09E-07	1.04E-07	4.00E-08	3.93E-08	2.46E-08	0.23	0.23	0.14
B0QYK0	B0QYK0_HUMAN RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=2 SV=1	11.20	2.97	1.98	3.96	9.90	1.98	4.95	4.99E-07	5.47E-07	3.40E-07	3.67E-06	3.06E-07	3.45E-07	7.34	0.61	0.69
B4E241	B4E241_HUMAN Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SFRS3 PE=2 SV=1	59.70	13.00	5.00	12.00	6.00	3.00	3.50	3.60E-06	9.98E-07	6.80E-06	2.06E-06	5.46E-07	1.55E-06	0.57	0.15	0.43
O43172	PRP4_HUMAN U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens GN=PRPF4 PE=1 SV=2	21.90	1.00	3.00	2.00	3.00	3.00	4.00	1.66E-08	4.33E-08	1.87E-07	8.24E-08	7.73E-07	1.24E-07	4.97	46.64	7.50
Q12906	ILF3_HUMAN Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	27.10	5.98	5.97	17.91	12.90		7.97	1.90E-07	2.52E-07	1.19E-06	2.31E-07		2.19E-07	1.21	Control 1 Only	1.15
P12830	CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	15.90	6.96	4.96	1.98	6.94	8.94	7.95	1.44E-07	1.37E-07	2.42E-08	5.81E-07	1.32E-07	4.52E-07	4.03	0.92	3.13
Q8N5M9	JAGN1_HUMAN Protein jagunal homolog 1 OS=Homo sapiens GN=JAGN1 PE=1 SV=1	13.10		3.00	1.00		2.00	4.00		1.11E-07	9.53E-09		1.56E-07	3.81E-07		Sample 2 Only	Sample 3 Only
P62316	SMD2_HUMAN Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1	50.80	1.99	1.00	3.97	0.99	0.99	3.98	7.42E-07	2.61E-07	4.15E-07	6.55E-07	1.31E-07	3.54E-06	0.88	0.18	4.77
Q96EY1	DNJA3_HUMAN DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens	12.60	1.00	2.00	2.00	6.00	1.00	1.00	3.34E-08	8.68E-08	5.19E-08	4.48E-07	1.55E-07	1.09E-07	13.40	4.62	3.26

	GN=DNAJA3 PE=1 SV=2																
B4DE93	B4DE93_HUMAN NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Homo sapiens GN=NDUFV1 PE=2 SV=1	36.40	1.99	2.97	2.99	7.96	4.97	3.98	1.65 E-07	3.87 E-07	7.66 E-09	7.74 E-07	5.55 E-07	5.83 E-07	4.70	3.37	3.54
P62273	RS29_HUMAN 40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2	39.30	1.00		6.00	2.00	1.00	1.00	1.33 E-06		1.52 E-06	2.23 E-07	1.79 E-07	4.90 E-07	0.17	0.13	0.37
P08493	MGP_HUMAN Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2	38.80	3.00	4.00	7.00	6.00	2.00	1.00	1.42 E-06	4.33 E-06	8.41 E-06	5.00 E-06	2.38 E-07	2.66 E-07	3.53	0.17	0.19
P09874	PARP1_HUMAN Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	33.40	14.00	22.00	31.00	17.00	12.00	6.00	5.10 E-07	1.04 E-06	1.09 E-06	4.45 E-07	2.26 E-07	1.56 E-07	0.87	0.44	0.31
Q8NC69	KCTD6_HUMAN BTB/POZ domain-containing protein KCTD6 OS=Homo sapiens GN=KCTD6 PE=2 SV=2	43.00	0.50	15.00		11.50	21.50	10.00	2.82 E-09	1.61 E-06		6.20 E-07	3.39 E-06	6.81 E-07	220.32	1203.91	241.74
P62280	RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	67.10	28.82	15.91	32.81	17.92	13.93	13.93	2.10 E-05	1.27 E-05	3.20 E-05	1.51 E-05	7.34 E-06	7.68 E-06	0.72	0.35	0.37
Q8WXI9	P66B_HUMAN Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1	10.50	1.00	1.00	1.00	5.00			1.98 E-08	7.96 E-09	4.26 E-08	3.24 E-07			16.40	Control 1 Only	Control 1 Only
O95104	SFR15_HUMAN Splicing factor, arginine/serine-rich 15 OS=Homo sapiens GN=SCAF4 PE=1 SV=3	4.70		0.99	0.99	2.98	2.97	1.98		7.80 E-09	4.20 E-08	1.16 E-07	5.83 E-08	7.13 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O00231	PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	25.80	1.00	4.00	3.00	5.00	4.00	2.00	3.89 E-08	1.15 E-07	7.58 E-08	4.20 E-07	2.26 E-07	2.10 E-07	10.78	5.81	5.40
P42704	LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	38.70	3.00	28.00	26.00	22.00	41.00	33.00	2.11 E-08	3.78 E-07	4.16 E-07	8.13 E-07	1.00 E-06	7.27 E-07	38.55	47.58	34.45
F8WJN3	F8WJN3_HUMAN Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=2 SV=1	13.60	5.00	4.00	2.00	3.00	2.00	1.00	2.73 E-07	2.18 E-07	7.94 E-08	5.80 E-08	7.66 E-08	6.86 E-09	0.21	0.28	0.03
Q9P2M7	CING_HUMAN Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	7.00		2.99	6.00	1.00	1.00			4.96 E-08	6.82 E-08	1.93 E-08	1.17 E-09		Sample 1 Only	Sample 2 Only	
O76062	ERG24_HUMAN Delta(14)-sterol reductase OS=Homo sapiens GN=TM7SF2 PE=2 SV=3	9.60		0.98	0.98	2.95	3.92	1.97		4.45 E-08	6.66 E-08	9.11 E-08	3.10 E-07	5.43 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7ESZ7	E7ESZ7_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=2 SV=1	23.90	3.98	6.97	5.98	7.96	7.98	5.97	1.31 E-07	1.36 E-06	7.05 E-07	2.10 E-07	3.67 E-07	1.22 E-07	1.60	2.81	0.93
P0DI83	NARR_HUMAN Ras-related protein Rab-34, isoform NARR OS=Homo sapiens GN=RAB34 PE=1 SV=1	27.30	2.00	1.00	2.00	5.00	3.00	1.00	7.23 E-09	2.81 E-07	2.05 E-08	8.09 E-07	3.57 E-08	2.30 E-07	111.81	4.94	31.74
P35251	RFC1_HUMAN Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4	8.50	3.00	3.00	7.00	1.00	1.00		2.29 E-08	3.19 E-08	9.73 E-08	2.23 E-08	6.58 E-09		0.97	0.29	Control 1 Only
Q9BY77	PDIP3_HUMAN Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=1 SV=2	15.90	3.97	0.99		3.96	0.99	5.95	2.13 E-07	1.03 E-07		3.34 E-07	1.92 E-07	5.60 E-07	1.57	0.91	2.64
Q96CS3	FAF2_HUMAN FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2	28.80		4.00	5.00	4.00	9.00	8.00		6.04 E-07	5.29 E-07	8.57 E-07	1.56 E-06	8.71 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
O14949	QCR8_HUMAN Cytochrome b-c1 complex subunit 8 OS=Homo sapiens GN=UQCRQ PE=1 SV=4	58.50	1.00	4.00	6.00	4.00	5.00	4.00	1.63 E-08	1.51 E-06	2.50 E-06	5.73 E-07	7.90 E-06	1.66 E-06	35.18	484.84	101.60
Q7Z5K2	WAPL_HUMAN Wings apart-like protein homolog OS=Homo sapiens GN=WAPAL PE=1 SV=1	7.70		2.00	4.00	1.00	2.00	1.00		7.25 E-09	4.48 E-09	3.70 E-09	3.20 E-08	3.69 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P39023	RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	57.60	39.56	33.59	48.52	43.49	18.84	19.77	1.70 E-05	1.61 E-05	2.34 E-05	1.55 E-05	5.99 E-06	5.19 E-06	0.91	0.35	0.31

P62829	RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	72.90	15.84	14.86	19.77	18.80	8.90	13.87	1.65E-05	1.37E-05	8.56E-06	8.51E-06	3.42E-06	5.79E-06	0.52	0.21	0.35
B3KXW5	B3KXW5_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=2 SV=1	15.70	3.00	6.98	5.00	7.98	10.96	7.98	2.21E-08	1.65E-07	1.08E-07	1.20E-07	6.35E-07	2.46E-07	5.45	28.72	11.12
Q15437	SC23B_HUMAN Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	17.20		2.00	1.00		7.00	2.00		1.40E-07	2.11E-08		5.80E-07	1.70E-08		Sample 2 Only	Sample 3 Only
B4DJ96	B4DJ96_HUMAN Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=2 SV=1	12.60	3.98		2.97	3.96		1.98	1.17E-06		4.21E-07	3.15E-07		1.90E-07	0.27	Control 1 Only	0.16
Q9HAV0	GBB4_HUMAN Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3	15.30	1.96	1.97	0.98	2.94	2.94	2.94	1.74E-07	2.84E-07	7.07E-09	3.43E-07	8.61E-07	2.66E-07	1.98	4.96	1.53
Q9Y5X2	SNX8_HUMAN Sorting nexin-8 OS=Homo sapiens GN=SNX8 PE=1 SV=1	14.60	2.99	2.98	2.99	2.98		1.00	2.77E-07	1.83E-07	2.72E-07	1.77E-07		3.07E-08	0.64	Control 1 Only	0.11
O95782	AP2A1_HUMAN AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	45.40	7.00	21.00	17.00	33.00	23.00	23.00	6.34E-08	4.56E-07	4.18E-07	9.96E-07	9.32E-07	7.41E-07	15.71	14.70	11.70
J3KP15	J3KP15_HUMAN Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens GN=SRSF2 PE=2 SV=1	57.50	10.99	9.96	16.95	10.97	0.99	4.96	4.20E-06	2.30E-06	6.70E-06	3.47E-06	1.01E-07	2.00E-06	0.83	0.02	0.48
F5H157	F5H157_HUMAN Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=2 SV=1	45.90	1.00	4.99	2.00	5.99	7.99	3.00	1.61E-08	9.06E-07	4.96E-08	6.84E-07	1.53E-06	5.24E-07	42.46	94.79	32.53
J3KR12	J3KR12_HUMAN Uncharacterized protein OS=Homo sapiens PE=4 SV=1	8.80	1.99	4.96	0.99	2.97	1.99	5.96	2.52E-07	6.13E-07	3.40E-08	6.31E-07	3.04E-07	1.61E-06	2.51	1.21	6.40
Q00325-2	MPCP_HUMAN Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3	46.30	12.84	23.73	31.62	18.76	30.66	31.64	1.87E-06	3.97E-06	5.33E-06	2.28E-06	1.33E-05	9.03E-06	1.22	7.08	4.82
Q13011	ECH1_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	34.50	5.99	10.98	6.99	8.00	11.97	13.97	6.19E-07	1.51E-06	3.86E-07	1.62E-06	1.44E-06	3.28E-06	2.61	2.32	5.30
Q9Y678	COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	23.10	5.00	11.50	1.00	7.00	15.50	9.00	7.44E-08	2.92E-07	1.18E-08	5.62E-08	8.83E-07	2.42E-07	0.76	11.86	3.25
P62244	RS15A_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	80.00	18.82	11.89	29.75	16.83	9.90	7.93	2.69E-05	4.70E-05	3.55E-05	3.23E-05	1.63E-05	7.76E-06	1.20	0.60	0.29
M0QZM1	M0QZM1_HUMAN Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens GN=HNRNPM PE=4 SV=1	73.40	7.00	6.50	9.00	7.00	3.00	7.00	1.36E-06	3.77E-07	2.66E-06	7.19E-07	4.09E-07	5.44E-07	0.53	0.30	0.40
Q3SY84	K2C71_HUMAN Keratin, type II cytoskeletal 71 OS=Homo sapiens GN=KRT71 PE=1 SV=3	12.20	6.86	5.88	10.81	1.96	5.88	11.79	2.55E-06	9.88E-07	1.04E-06	4.93E-08	7.21E-07	9.79E-07	0.02	0.28	0.38
Q02878	RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	51.70	18.96	14.96	28.90	29.88	10.97	9.97	1.30E-05	4.91E-06	2.58E-05	1.25E-05	4.18E-06	4.27E-06	0.96	0.32	0.33
P62249	RS16_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	81.50	26.74	19.77	38.58	19.76	19.76	16.81	3.47E-05	2.33E-05	4.17E-05	2.31E-05	1.44E-05	1.36E-05	0.67	0.42	0.39
P53396	ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	7.50		5.97	1.00		1.99	0.99		1.54E-07	1.72E-08		3.05E-08	8.43E-09		Sample 2 Only	Sample 3 Only
F8W6I7	F8W6I7_HUMAN Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=4 SV=2	66.30	12.78	21.63	13.75	27.55	27.54	17.71	2.73E-06	7.02E-06	4.00E-06	1.30E-05	1.04E-05	5.98E-06	4.77	3.82	2.19
F6TQG2	F6TQG2_HUMAN Probable global transcription activator SNF2L1 (Fragment) OS=Homo sapiens GN=SMARCA1 PE=2 SV=1	20.70	8.50	5.00	7.50	6.00	3.50	3.50	5.76E-07	7.93E-08	1.29E-07	1.35E-07	5.36E-08	5.06E-08	0.23	0.09	0.09
P62701	RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	61.20	49.88	40.89	60.88	40.87	41.90	39.88	4.06E-05	3.36E-05	6.80E-05	2.11E-05	3.57E-05	1.86E-05	0.52	0.88	0.46
Q96I	FUBP3_HUMAN Far upstream element-binding	21.50		2.00	2.00	1.00	0.99	4.97		9.84	7.34	1.17	8.28	3.83	Sample	Sample	Sample

24	protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2									E-08	E-08	E-07	E-08	E-07	1 Only	2 Only	3 Only
P82930	RT34_HUMAN 28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=1 SV=2	17.00	5.00	3.00	3.00	2.00	2.00	2.00	6.18 E-07	1.28 E-06	1.20 E-08	8.73 E-08	3.59 E-08	5.44 E-07	0.14	0.06	0.88
B7ZAB3	B7ZAB3_HUMAN Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3 OS=Homo sapiens GN=B3GAT3 PE=2 SV=1	13.00		2.99		1.98	0.99	0.99		1.93 E-07		4.56 E-07	1.51 E-07	2.68 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
O00139	KIF2A_HUMAN Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=1 SV=3	7.00	2.00	2.00	1.00	3.00	1.00		1.26 E-09	2.29 E-09	6.87 E-09	5.45 E-08	6.85 E-10		43.09	0.54	Control 1 Only
P62913	RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	63.50	4.50	2.00	7.00	8.00	5.00	3.50	1.16 E-05	3.10 E-06	1.40 E-05	6.94 E-06	4.94 E-06	1.73 E-06	0.60	0.43	0.15
K7EJT8	K7EJT8_HUMAN AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=2 SV=1	20.90	5.96	8.93	8.93	17.90	8.96	14.91	6.80 E-08	2.54 E-07	1.08 E-07	4.04 E-07	5.54 E-07	3.08 E-07	5.93	8.15	4.53
F5GYL3	F5GYL3_HUMAN ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=2 SV=1	7.20	1.00	2.00	4.00	1.00	1.00		5.44 E-09	5.13 E-08	2.27 E-07	5.73 E-08	1.89 E-08		10.53	3.47	Control 1 Only
Q6YN16	HSDL2_HUMAN Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	19.60		3.99	1.99		3.99	0.99		4.15 E-07	1.07 E-07		1.15 E-06	3.44 E-07		Sample 2 Only	Sample 3 Only
P62906	RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	67.70	38.00	34.00	49.00	43.00	28.00	25.00	1.60 E-05	2.85 E-05	5.69 E-05	3.16 E-05	1.56 E-05	6.33 E-06	1.97	0.97	0.39
Q4VXZ8	Q4VXZ8_HUMAN Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=2 SV=1	32.90	2.96	4.95	1.98	4.94	5.94	8.91	2.86 E-07	3.51 E-07	2.08 E-07	6.68 E-07	5.97 E-07	9.83 E-07	2.34	2.09	3.44
Q15029	U5S1_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1	24.50	5.50	9.47	19.45	8.97			5.12 E-08	1.86 E-07	4.57 E-07	2.23 E-07			4.36	Control 1 Only	Control 1 Only
Q15007	FL2D_HUMAN Pre-mRNA-splicing regulator WTAP OS=Homo sapiens GN=WTAP PE=1 SV=2	24.50	2.00		4.00	6.00		1.00	8.32 E-08		1.71 E-07	6.15 E-07		1.58 E-07	7.39	Control 1 Only	1.90
P60866	RS20_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	39.50	14.85	11.88	15.84	15.84	12.87	12.87	4.21 E-05	2.73 E-05	2.86 E-05	2.53 E-05	2.08 E-05	6.21 E-06	0.60	0.49	0.15
Q14258	TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	22.90	3.00	8.00	3.00	13.00	9.00	8.00	6.85 E-08	7.15 E-07	4.64 E-08	1.56 E-06	3.62 E-07	2.62 E-07	22.79	5.28	3.82
Q07065	CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	69.90	32.00	24.00	42.00	46.00	46.00	31.00	5.42 E-06	3.81 E-06	5.44 E-06	9.19 E-06	1.27 E-05	7.90 E-06	1.69	2.35	1.46
O94776	MTA2_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1	20.80	5.00	2.00	2.00	7.00	2.00	4.00	1.61 E-07	9.04 E-08	1.35 E-07	4.67 E-07	2.54 E-07	3.81 E-07	2.89	1.57	2.36
P62917	RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	59.10	17.77	15.79	23.69	21.73	17.77	12.83	9.92 E-06	1.08 E-05	1.26 E-05	4.15 E-05	1.60 E-05	6.17 E-06	4.19	1.61	0.62
P49755	TMEDA_HUMAN Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2	50.70	5.00	6.00	23.00	5.00	6.00	7.00	4.10 E-07	5.15 E-07	3.73 E-06	8.95 E-07	3.75 E-07	6.57 E-07	2.18	0.91	1.60
P46783	RS10_HUMAN 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	55.80	13.99	13.99	19.97	7.99	10.99	10.99	4.13 E-06	5.31 E-06	7.30 E-06	1.48 E-06	3.15 E-06	3.22 E-06	0.36	0.76	0.78
F5GX55	F5GX55_HUMAN Williams-Beuren syndrome chromosomal region 16 protein OS=Homo sapiens GN=WBSCR16 PE=2 SV=1	19.60		2.00		3.00	3.00	1.00		3.60 E-07		5.75 E-07	3.76 E-07	7.95 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P38646	GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	72.60	41.96	52.96	28.95	72.95	59.95	52.96	8.69 E-06	1.06 E-05	3.78 E-06	1.60 E-05	1.62 E-05	1.28 E-05	1.83	1.86	1.48

E9PD56	E9PD56_HUMAN PX domain-containing protein kinase-like protein OS=Homo sapiens GN=PXK PE=2 SV=1	13.30	0.99	2.97	1.98		1.98	0.99	9.82E-10	4.16E-08	1.31E-09		2.20E-08	1.43E-07	Control 1 Only	22.40	145.48
Q02880	TOP2B_HUMAN DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3	26.20	13.00	4.00	30.00	10.00	3.00	3.00	7.74E-08	4.79E-08	4.55E-07	1.59E-07	8.65E-09	2.18E-08	2.05	0.11	0.28
P46940	IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	52.60	84.95	63.96	65.95	38.97	47.97	30.98	3.30E-06	1.95E-06	1.06E-06	7.86E-07	1.34E-06	6.10E-07	0.24	0.40	0.18
Q9Y230	RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	28.30	2.97	4.95	1.99	3.96	3.98	3.96	2.36E-07	2.57E-07	2.10E-09	3.58E-07	5.81E-07	4.10E-07	1.52	2.46	1.74
Q00610	CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	57.80	63.52	71.59	90.42	97.39	87.42	101.35	2.84E-06	2.25E-06	2.74E-06	7.10E-06	3.22E-06	6.14E-06	2.50	1.13	2.17
F5GX39	F5GX39_HUMAN Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=2 SV=1	26.70	3.00	4.00	7.00	5.00	3.00	2.00	1.01E-07	1.28E-06	7.22E-07	5.08E-07	2.07E-07	1.00E-07	5.03	2.05	0.99
P09012	SNRPA_HUMAN U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=1 SV=3	27.70	1.98	2.98	0.99	2.96	6.96	6.92	1.07E-07	2.28E-06	1.71E-07	5.85E-07	2.90E-06	2.40E-06	5.47	27.14	22.44
P08574	CY1_HUMAN Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3	47.10	8.00	21.00	11.00	17.00	23.00	29.00	3.79E-07	2.57E-06	1.65E-06	1.57E-06	5.29E-06	3.17E-06	4.15	13.98	8.38
H0Y8Z9	H0Y8Z9_HUMAN Acyl-CoA dehydrogenase family member 9, mitochondrial (Fragment) OS=Homo sapiens GN=ACAD9 PE=2 SV=1	20.80		2.00	1.00	1.00		3.00		6.77E-08	1.05E-09	1.26E-09		2.36E-07	Sample 1 Only		Sample 3 Only
P23396	RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	81.90	51.88	38.21	51.89	48.00	39.18	41.15	7.08E-05	5.64E-05	7.84E-05	5.09E-05	3.86E-05	2.87E-05	0.72	0.55	0.41
F5H335	F5H335_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1	30.50	16.00	24.00	25.00	26.00	28.00	23.00	3.64E-07	5.41E-07	2.97E-07	9.02E-07	1.31E-06	7.36E-07	2.48	3.59	2.02
P62753	RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	49.00	29.97	18.96	30.96	34.96	19.97	18.95	2.03E-05	1.04E-05	2.07E-05	1.38E-05	7.08E-06	6.06E-06	0.68	0.35	0.30
P04792	HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	21.00		2.00		3.00	2.00	2.00		3.87E-07		3.27E-07	6.57E-07	8.10E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q12959	DLG1_HUMAN Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2	23.70	2.96	6.88	0.99	7.86	5.90	4.94	6.44E-08	9.05E-08	6.93E-10	2.26E-07	1.48E-07	1.02E-07	3.52	2.29	1.59
C9J1V9	C9J1V9_HUMAN HCG2043275 OS=Homo sapiens GN=hCG_2043275 PE=4 SV=2	20.60		1.00	3.00	2.00		2.00		6.35E-08	4.22E-08	1.95E-07		1.45E-07	Sample 1 Only		Sample 3 Only
P35249	RFC4_HUMAN Replication factor C subunit 4 OS=Homo sapiens GN=RFC4 PE=1 SV=2	32.20	1.99	1.99	4.95	1.99	1.99		6.49E-08	3.97E-07	1.31E-07	5.22E-08	1.48E-07		0.80	2.28	Control 1 Only
Q9Y5B9	SP16H_HUMAN FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1	30.00	23.00	14.00	10.00	8.00	9.00	5.00	9.17E-07	4.64E-07	1.81E-07	2.03E-07	2.08E-07	1.87E-07	0.22	0.23	0.20
F5H7B0	F5H7B0_HUMAN Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=2 SV=1	11.30		4.00	4.00	4.00	7.00	6.00		4.31E-08	5.73E-08	9.06E-08	1.23E-07	1.08E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q00341	VIGLN_HUMAN Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	37.90	27.63	12.76	34.45	12.80	15.78	5.88	6.01E-07	1.56E-07	7.25E-07	2.16E-07	2.77E-07	7.49E-08	0.36	0.46	0.12
O95793	STAU1_HUMAN Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2	32.00	8.99	8.00	5.00	10.00	1.00	2.00	3.35E-07	6.20E-07	5.02E-07	3.06E-07	1.48E-07	1.04E-07	0.91	0.44	0.31
Q13151	ROA0_HUMAN Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1	37.00	5.00	12.00	7.00	17.00	17.00	13.00	9.50E-07	2.33E-06	2.49E-06	3.97E-06	7.24E-06	9.34E-07	4.18	7.62	0.98
P33992	MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	49.90	23.94	31.92	5.99	33.87	35.87	17.93	1.56E-06	1.41E-06	2.34E-07	2.90E-06	3.45E-06	7.18E-07	1.86	2.21	0.46
I3L1P8	I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment)	49.00	9.00	9.00	8.00	9.00	9.00	8.00	5.87E-07	4.43E-06	2.71E-06	8.70E-07	1.74E-06	9.24E-07	1.48	2.96	1.57

	OS=Homo sapiens GN=SLC25A11 PE=2 SV=1																
O14646	CHD1_HUMAN Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens GN=CHD1 PE=1 SV=2	4.60	2.00		3.99	1.00	1.00		9.03E-09		2.30E-08	5.49E-09	9.47E-10		0.61	0.10	Control 1 Only
Q969Z3	MOSC2_HUMAN MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1	22.40		1.99	3.98	4.98	2.98	0.99		1.31E-07	4.11E-07	6.44E-08	1.08E-07	1.30E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P60228	EIF3E_HUMAN Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	33.00	4.96	5.93	2.97	6.93	4.95	1.97	3.54E-07	5.34E-07	1.39E-07	1.28E-06	1.02E-06	1.86E-07	3.63	2.88	0.53
P62888	RL30_HUMAN 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	67.00	13.97	15.98	23.95	18.95	12.98	13.96	2.14E-05	1.61E-05	1.58E-05	1.70E-05	4.96E-06	6.65E-06	0.80	0.23	0.31
P52272	HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	64.00	19.82	13.38	41.53	19.81	15.84	20.84	1.47E-06	1.03E-06	4.54E-06	1.44E-06	7.83E-07	9.94E-07	0.98	0.53	0.68
Q08945	SSRP1_HUMAN FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1	19.90	9.00	8.00	7.00	7.00	1.00		4.97E-07	1.05E-07	1.17E-07	2.55E-07	2.89E-09		0.51	0.01	Control 1 Only
P26368	U2AF2_HUMAN Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	45.00	14.00	10.00	7.00	11.00	5.00	7.00	2.71E-06	8.27E-07	9.08E-07	9.34E-07	5.90E-07	4.38E-07	0.34	0.22	0.16
Q92878	RAD50_HUMAN DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1	27.70		12.89	14.88	22.87	16.91	17.89		2.29E-07	2.12E-07	5.07E-07	3.82E-07	2.60E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P50416	CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	11.10	4.00	5.00	6.00		6.00	2.00	2.11E-07	5.01E-07	3.71E-07		2.11E-07	2.01E-07	Control 1 Only	1.00	0.95
P62081	RS7_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	71.60	25.00	22.00	41.00	29.00	30.00	17.00	1.97E-05	1.27E-05	1.56E-05	8.54E-06	7.55E-06	9.84E-06	0.43	0.38	0.50
A6NEM5	A6NEM5_HUMAN GPI-anchor transamidase OS=Homo sapiens GN=PIGK PE=2 SV=1	13.30	2.00	3.00	1.00	1.00	1.00	2.00	1.36E-07	8.98E-07	6.88E-08	3.66E-08	1.30E-07	2.58E-07	0.27	0.96	1.90
B7Z7A3	B7Z7A3_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=2 SV=1	19.30	4.95	0.99	5.94	1.98	0.99		5.06E-08	2.58E-08	2.86E-07	9.55E-08	2.57E-08		1.89	0.51	Control 1 Only
F8VXC8	F8VXC8_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=2 SV=1	19.10	7.00	8.00	4.00	10.00	12.00	8.00	1.58E-07	1.18E-07	1.65E-08	2.58E-07	3.00E-07	2.26E-07	1.63	1.89	1.43
Q6UWP8	SBSN_HUMAN Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2	15.30	4.00	2.00	1.00		2.00	1.00	2.30E-07	2.04E-07	8.15E-09		1.08E-07	4.53E-08	Control 1 Only	0.47	0.20
P04844	RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	59.00	22.86	37.75	32.75	45.70	34.79	27.78	1.58E-06	1.03E-05	4.99E-06	8.22E-06	1.46E-05	9.05E-06	5.20	9.25	5.73
Q9Y3I0	RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	56.60	14.00	16.00	18.00	28.00	16.00	16.00	1.43E-06	1.82E-06	2.26E-06	3.47E-06	4.70E-06	3.07E-06	2.42	3.28	2.15
J3KR24	J3KR24_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=2 SV=1	15.20	2.00	4.99	6.00	8.00	4.00	5.00	1.18E-08	5.01E-08	5.50E-08	2.25E-07	4.81E-08	7.06E-08	18.99	4.06	5.97
O00148	DX39A_HUMAN ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2	60.20	12.57	19.37	19.49	29.16	21.34	17.35	1.41E-06	7.24E-06	1.90E-06	6.55E-06	6.88E-06	7.01E-06	4.66	4.89	4.99
Q9UHX1-2	PUF60_HUMAN Isoform 2 of Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60	59.30	27.51	15.69	14.78	19.67	11.79	10.80	4.96E-06	2.12E-06	1.33E-06	1.80E-06	1.37E-06	8.81E-07	0.36	0.28	0.18
E7ENR4	E7ENR4_HUMAN Hexokinase-1 OS=Homo sapiens GN=HK1 PE=2 SV=1	44.50	17.95	46.91	39.92	28.95	14.95	25.94	3.35E-07	1.97E-06	1.13E-06	5.22E-07	2.61E-07	7.58E-07	1.56	0.78	2.26

P62424	RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	48.10	27.93	21.96	31.93	26.93	13.94	18.93	7.54E-06	7.21E-06	2.03E-05	8.60E-06	6.70E-06	3.68E-06	1.14	0.89	0.49
Q9UGP8	SEC63_HUMAN Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2	10.50	1.00	5.00	1.00		1.00	1.00	6.41E-09	7.35E-08	4.09E-08		2.00E-08	1.59E-08	Control 1 Only	3.11	2.48
E7ESA8	E7ESA8_HUMAN U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=2 SV=1	26.60		2.97	2.97	4.95	1.98			1.11E-07	2.20E-07	6.33E-07	2.13E-07		Sample 1 Only	Sample 2 Only	
Q02413	DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	13.30	15.00	4.00	9.00	2.00	3.00	9.00	3.75E-07	6.11E-08	1.62E-07	5.73E-09	4.98E-08	1.69E-07	0.02	0.13	0.45
Q9NZ01	TECR_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1	33.10	9.92	8.93	11.88	8.92	5.94	5.95	8.67E-07	6.04E-07	1.93E-06	1.11E-06	2.64E-07	1.65E-07	1.28	0.30	0.19
O95168	NDUB4_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=Homo sapiens GN=NDUFB4 PE=1 SV=3	44.20	5.00	6.00	7.00	6.00	3.00	4.00	1.51E-06	1.80E-06	1.83E-06	1.18E-06	9.21E-07	3.14E-07	0.78	0.61	0.21
P28331	NDUS1_HUMAN NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3	42.00	8.92	10.90	9.91	9.90	13.86	8.91	2.16E-07	4.78E-07	3.36E-07	8.01E-07	9.77E-07	5.69E-07	3.71	4.53	2.63
B8ZZ50	B8ZZ50_HUMAN Eukaryotic translation initiation factor 4E type 2 OS=Homo sapiens GN=EIF4E2 PE=2 SV=1	13.10	0.99	0.99			2.98	0.99	1.40E-08	9.29E-08			2.55E-07	5.10E-08	Control 1 Only	18.15	3.64
P53618	COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	27.60	9.00	17.00	7.00	14.98	21.95	15.98	9.44E-08	4.20E-07	6.37E-08	2.90E-07	6.78E-07	4.14E-07	3.08	7.18	4.38
D3YTB1	D3YTB1_HUMAN 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=2 SV=1	51.90	10.00	3.00	13.00	9.00	3.00	4.00	3.55E-06	6.90E-07	6.64E-06	3.94E-06	7.80E-07	7.66E-07	1.11	0.22	0.22
P55795	HNRH2_HUMAN Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	39.40	6.00	4.00	8.00	11.00	7.00	5.00	2.16E-07	4.06E-07	3.07E-07	1.23E-06	6.08E-07	2.71E-07	5.69	2.81	1.25
Q9HD45	TM9S3_HUMAN Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2	23.30	4.00	11.00	9.00	16.00	15.00	10.00	1.70E-07	1.48E-06	7.49E-07	2.38E-06	1.92E-06	7.28E-07	14.05	11.33	4.30
P18077	RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	57.30	20.93	19.95	27.90	17.94	17.93	17.95	4.16E-05	4.47E-05	2.37E-05	3.42E-05	1.42E-05	1.67E-05	0.82	0.34	0.40
O75643	U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	20.40	9.00	9.00	34.00	11.00	6.00	4.00	4.92E-08	5.71E-08	3.09E-07	1.27E-07	1.65E-08	1.03E-08	2.58	0.34	0.21
P62857	RS28_HUMAN 40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	46.40	4.00	2.00	5.00	5.00	2.00	2.00	1.93E-06	5.17E-07	4.71E-06	2.05E-06	5.77E-07	9.02E-07	1.06	0.30	0.47
Q8N1N4	K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	23.10	16.46	3.49	7.98	1.50	4.49	7.49	8.93E-07	3.35E-07	2.14E-07	7.17E-08	1.80E-07	3.64E-07	0.08	0.20	0.41
P02786	TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	19.10	2.00	5.98	2.99	0.99	10.96	9.95	1.75E-08	2.18E-07	3.69E-08	1.46E-08	4.66E-07	2.01E-07	0.84	26.65	11.53
P51991	ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	43.10	4.50	2.00	11.50	5.50	4.50	4.50	7.86E-07	5.25E-07	3.34E-06	6.52E-07	7.48E-07	8.35E-07	0.83	0.95	1.06
Q86YZ3	HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	38.60	88.00	60.00	77.00	37.00	54.00	33.00	8.49E-07	4.53E-07	5.60E-07	1.26E-07	3.65E-07	3.35E-07	0.15	0.43	0.39
Q05639	EF1A2_HUMAN Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	42.80	3.50	10.00	6.00	7.50	12.50	15.50	5.49E-07	6.26E-06	2.99E-06	4.75E-06	8.46E-06	5.06E-06	8.65	15.41	9.22
J3KNW4	J3KNW4_HUMAN Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=2 SV=1	36.90	4.00	1.00	6.00	8.00	1.00	5.00	1.20E-07	2.01E-07	9.80E-07	5.59E-07	1.23E-07	2.13E-06	4.66	1.03	17.74
Q8N3E9	PLCD3_HUMAN 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-3	4.20	2.00	1.00	1.00	3.00			1.19E-07	2.91E-08	3.75E-09	5.03E-08			0.42	Control 1 Only	Control 1 Only

	OS=Homo sapiens GN=PLCD3 PE=1 SV=3																
Q9Y2A7	NCKP1_HUMAN Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	4.70		3.00	2.00	1.00	2.00	1.00		4.35 E-08	1.51 E-08	8.67 E-09	4.95 E-09	3.53 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P23284	PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	21.30	1.00	1.00	3.00	3.00	4.00	5.00	9.80 E-08	6.11 E-07	2.46 E-07	6.86 E-07	8.08 E-07	5.99 E-07	7.00	8.25	6.11
P27635	RL10_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	51.40	31.73	23.81	44.63	40.63	22.81	21.80	3.51 E-05	1.04 E-05	3.15 E-05	3.31 E-05	8.30 E-06	4.23 E-06	0.94	0.24	0.12
Q5TDF0	Q5TDF0_HUMAN Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=2 SV=1	35.80	3.00	2.00	5.00	3.00	5.00	2.00	8.10 E-08	5.67 E-07	9.03 E-08	5.17 E-07	6.78 E-07	4.55 E-07	6.39	8.37	5.62
E7EMN3	E7EMN3_HUMAN Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=2 SV=1	10.00	3.00	1.00	1.00	1.00	1.00	1.00	1.64 E-07	3.00 E-08	7.02 E-09	4.03 E-08	6.52 E-09	2.47 E-08	0.25	0.04	0.15
O95831	AIFM1_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	9.70		1.98	2.97	2.97	3.96	0.99		6.36 E-07	2.12 E-07	1.04 E-07	2.38 E-07	1.48 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
G5E9L8	G5E9L8_HUMAN Epithelial cell transforming sequence 2 oncogene, isoform CRA_b OS=Homo sapiens GN=ECT2 PE=2 SV=1	4.60	4.00	2.00	3.00	3.63			6.97 E-08	6.82 E-08	1.37 E-07	1.02 E-07			1.46	Control 1 Only	Control 1 Only
E9PK25	E9PK25_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=2 SV=1	16.80	1.00	2.00	4.00	2.00	1.00	1.00	5.21 E-08	1.75 E-07	7.16 E-07	2.13 E-07	1.88 E-07	2.35 E-09	4.08	3.60	0.05
A6NES3	A6NES3_HUMAN Etoposide-induced protein 2.4 homolog OS=Homo sapiens GN=EI24 PE=2 SV=1	47.30	1.00	4.00	3.99		6.00	4.00	2.38 E-08	3.84 E-07	6.66 E-07		3.03 E-07	1.62 E-07	Control 1 Only	12.75	6.83
P51571	SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1	36.40	6.00	8.00	10.00	9.00	13.00	13.00	6.53 E-07	1.27 E-06	2.58 E-06	2.68 E-06	2.73 E-06	3.21 E-06	4.10	4.17	4.91
P42677	RS27_HUMAN 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3	40.50	2.50	3.50	6.50	3.00	1.50	1.50	2.81 E-06	2.21 E-06	4.69 E-06	2.64 E-06	1.38 E-06	1.10 E-06	0.94	0.49	0.39
Q68E01	INT3_HUMAN Integrator complex subunit 3 OS=Homo sapiens GN=INTS3 PE=1 SV=1	10.60		2.00	2.99	4.00		1.99		2.23 E-08	2.49 E-08	1.04 E-07		3.17 E-08	Sample 1 Only		Sample 3 Only
Q5T749	KPRP_HUMAN Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	14.00	7.00	3.00	10.00	4.00	1.00	5.00	3.98 E-07	6.43 E-09	3.43 E-07	3.80 E-08	5.91 E-08	2.20 E-07	0.10	0.15	0.55
Q96HS1	PGAM5_HUMAN Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	40.80	12.99	10.00	16.95	14.98	7.00	2.00	4.01 E-06	4.70 E-06	6.56 E-06	7.03 E-06	1.17 E-06	1.62 E-07	1.75	0.29	0.04
Q16531	DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	40.70	15.78	25.65	11.83	31.55	32.54	19.72	5.02 E-07	1.31 E-06	1.41 E-07	1.68 E-06	1.32 E-06	9.30 E-07	3.35	2.64	1.85
Q93009	UBP7_HUMAN Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2	14.40	1.00	3.98	3.96	8.89	6.94	1.98	1.17 E-09	4.00 E-08	5.84 E-08	1.39 E-07	8.79 E-08	3.27 E-08	118.53	75.02	27.89
Q12905	ILF2_HUMAN Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	51.30	16.00	15.00	16.00	18.00	7.00	12.00	1.70 E-06	1.49 E-06	1.58 E-06	1.09 E-06	2.73 E-07	1.06 E-06	0.64	0.16	0.62
Q08379	GOGA2_HUMAN Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3	46.30	7.97	27.91	24.91	44.83	29.92	20.93	3.56 E-07	8.98 E-07	6.07 E-07	2.28 E-06	1.10 E-06	3.46 E-07	6.41	3.09	0.97
P84090	ERH_HUMAN Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	21.20	1.00	1.00	3.00	1.00		1.00	5.20 E-07	8.69 E-07	7.07 E-07	7.27 E-07		2.73 E-07	1.40	Control 1 Only	0.53
Q6Y1H2	HACD2_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 2 OS=Homo sapiens GN=PTPLB PE=1 SV=1	17.30	5.00	4.00	7.00	5.00	4.00	4.00	2.30 E-07	1.61 E-07	9.99 E-07	2.03 E-07	1.83 E-07	2.56 E-07	0.88	0.80	1.12
P05386	RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	66.70	3.00	3.00	4.00	8.00	3.00	2.00	1.11 E-06	2.18 E-06	1.36 E-06	3.36 E-06	5.22 E-06	9.69 E-08	3.03	4.70	0.09

P25205	MCM3_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	24.40	1.00	16.86	2.99	13.88	17.85	6.94	5.63E-09	5.15E-07	2.15E-08	1.43E-07	8.33E-07	2.08E-07	25.44	148.03	36.98
H0YK61	H0YK61_HUMAN ER membrane protein complex subunit 4 OS=Homo sapiens GN=EMC4 PE=2 SV=1	37.20		1.98	3.96	0.99	0.99	2.97		6.45E-07	1.12E-06	1.99E-07	1.34E-07	5.03E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P04264	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	72.50	278.97	233.97	272.97	177.97	212.97	209.98	1.26E-04	1.12E-04	1.06E-04	4.34E-05	8.59E-05	9.80E-05	0.34	0.68	0.78
B4DWJ2	B4DWJ2_HUMAN Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=2 SV=1	4.80	0.99	2.98	2.97	1.98	1.98	1.98	6.34E-08	3.71E-08	9.38E-08	1.83E-08	4.17E-09	5.18E-08	0.29	0.07	0.82
P35908	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	91.10	69.50	61.50	78.00	60.00	61.00	59.50	5.69E-05	3.77E-05	3.12E-05	2.33E-05	2.87E-05	2.77E-05	0.41	0.50	0.49
Q9Y4W6	AFG32_HUMAN AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2	13.80	2.00	7.00	3.00	9.00	7.00	4.00	5.43E-08	6.63E-07	1.66E-07	8.09E-07	6.67E-07	3.57E-07	14.90	12.28	6.57
E1P5S2	E1P5S2_HUMAN RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=2 SV=1	36.20	10.89	5.93	6.93	4.94	2.96	2.97	1.41E-06	4.00E-07	3.53E-07	4.43E-07	2.92E-07	3.22E-07	0.31	0.21	0.23
P62263	RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	41.10	18.00	13.00	21.00	13.00	10.00	6.00	9.17E-06	9.46E-06	1.01E-05	9.04E-06	5.17E-06	2.65E-06	0.99	0.56	0.29
P47985	UCRI_HUMAN Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 PE=1 SV=2	39.80	1.00	5.00	1.00	3.00	3.00	8.00	2.36E-08	1.06E-06	2.22E-07	6.60E-07	3.79E-07	1.57E-06	28.04	16.09	66.62
P08754	GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	41.50	1.00	6.00	2.00	9.00	3.00	4.00	4.89E-07	1.79E-06	5.01E-07	1.63E-06	2.89E-06	7.46E-07	3.33	5.91	1.53
O00159-3	MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	30.70	14.96	14.91	20.95	15.91	6.00	8.96	4.62E-07	3.51E-07	5.05E-07	4.39E-07	7.02E-08	1.13E-07	0.95	0.15	0.24
P00403	COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1	26.40	2.62	12.81	9.81	10.62	19.62	7.81	6.57E-07	2.33E-05	4.34E-06	2.32E-06	8.22E-06	6.14E-06	3.53	12.52	9.35
J3KPX7	J3KPX7_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=2 SV=1	56.90	11.78	18.66	7.85	15.72	13.77	7.87	1.55E-06	4.60E-06	1.37E-06	1.44E-06	1.74E-06	9.00E-07	0.93	1.12	0.58
P61313	RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	53.40	19.72	10.87	25.66	16.78	10.87	10.87	9.85E-06	4.19E-06	1.63E-05	9.93E-06	4.10E-06	3.95E-06	1.01	0.42	0.40
P48047	ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	42.30		4.99	1.00	2.00	9.97	6.00		5.32E-07	8.49E-08	1.21E-07	6.87E-07	4.90E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q15526	SURF1_HUMAN Surfeit locus protein 1 OS=Homo sapiens GN=SURF1 PE=1 SV=1	23.60		4.00		2.00	3.00	4.00		3.55E-07		1.38E-07	4.36E-07	2.06E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P04843	RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	68.70	36.00	46.00	66.00	67.00	51.00	44.00	4.85E-06	1.18E-05	1.21E-05	2.08E-05	1.49E-05	1.13E-05	4.29	3.08	2.33
P12273	PIP_HUMAN Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	43.80	3.00	4.00	6.00	1.00	5.00	5.00	1.70E-07	6.44E-07	2.02E-07	5.63E-08	9.75E-07	1.01E-06	0.33	5.75	5.96
B4DGU4	B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1	11.40	1.50	2.50	0.50	1.00	2.50	1.50	1.23E-07	1.17E-07	2.91E-09	4.75E-10	7.33E-08	2.53E-08	0.00	0.60	0.21
Q9UKS6	PACN3_HUMAN Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens GN=PACSIN3 PE=1 SV=2	20.80	2.00	2.99	1.99	4.97	1.99	1.98	6.54E-08	3.52E-07	3.61E-08	5.84E-07	1.89E-07	1.94E-07	8.93	2.89	2.97
E7EP00	E7EP00_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=2 SV=2	7.10		3.00	1.00	1.00	1.00	2.00		1.33E-07	2.41E-09	6.17E-09	4.13E-08	4.57E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7ERS3	E7ERS3_HUMAN Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=2 SV=1	13.50	3.00	5.00	4.00	6.00	3.00	4.00	3.38E-08	9.30E-08	6.08E-08	2.95E-07	8.34E-08	5.04E-08	8.74	2.47	1.49

Q96N66	MBOA7_HUMAN Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2	21.40	1.97	2.96	3.95	2.97	3.96	3.97	5.92E-08	5.14E-08	2.40E-07	4.23E-07	2.12E-07	1.22E-07	7.14	3.58	2.05
Q09472	EP300_HUMAN Histone acetyltransferase p300 OS=Homo sapiens GN=EP300 PE=1 SV=2	5.30	1.69	4.38	1.00	3.07	4.38	3.38	2.65E-09	1.06E-08	1.96E-10	5.49E-09	3.10E-08	3.54E-09	2.08	11.71	1.34
P08779	K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	70.40	27.00	16.00	19.00	14.00	39.00	15.00	1.70E-06	1.63E-06	1.00E-06	1.02E-06	5.76E-06	9.77E-07	0.60	3.38	0.57
Q7L014	DDX46_HUMAN Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2	23.50	18.00	10.99	9.99	11.00	10.00	4.99	5.19E-07	3.60E-07	2.95E-07	3.40E-07	1.78E-07	5.28E-08	0.66	0.34	0.10
Q1KMD3	HNRL2_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1	54.20	32.00	57.99	39.00	75.98	52.98	38.00	1.44E-06	5.25E-06	2.39E-06	6.46E-06	4.60E-06	4.49E-06	4.47	3.19	3.11
E5RJ68	E5RJ68_HUMAN AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=2 SV=1	4.90		2.00	1.00	3.00	1.00	1.00		1.76E-08	1.90E-09	2.92E-08	2.16E-08	4.50E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9P032	NDUF4_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4 OS=Homo sapiens GN=NDUFAF4 PE=1 SV=1	10.90		1.00		2.00	3.00	1.00		1.63E-07		1.76E-07	1.04E-07	8.97E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q29RF7	PDS5A_HUMAN Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	23.60		2.00	16.98	5.99	1.00	2.00		3.95E-09	2.14E-07	6.31E-08	1.82E-08	1.02E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P36578	RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	53.60	27.86	19.88	38.79	34.83	14.92	17.92	4.78E-06	2.17E-06	1.40E-05	6.32E-06	3.36E-06	2.84E-06	1.32	0.70	0.59
O76094	SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3	15.40	0.99		2.99	2.99	2.98	1.98	4.16E-08		1.66E-07	1.56E-07	2.39E-07	6.32E-08	3.74	5.75	1.52
Q9UH99	SUN2_HUMAN SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	18.00	6.99	4.99	5.99	5.99	5.99	2.98	3.08E-07	5.58E-07	2.71E-07	2.37E-07	6.97E-08	2.51E-07	0.77	0.23	0.82
P67809	YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	58.30	8.93	9.93	6.94	20.90	11.93	4.96	7.98E-06	8.37E-06	4.27E-06	2.44E-05	5.29E-06	3.77E-06	3.06	0.66	0.47
Q9NR30	DDX21_HUMAN Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	24.20	9.00	5.00	10.50	7.00	2.00	1.00	1.18E-07	5.11E-08	2.63E-07	1.91E-07	3.42E-09	1.53E-09	1.61	0.03	0.01
A6NFQ9	A6NFQ9_HUMAN Septin-8 OS=Homo sapiens GN=SEPT8 PE=2 SV=1	14.20	1.00		2.00	1.00	0.99	2.99	1.35E-07		6.85E-07	6.89E-08	3.21E-08	2.93E-07	0.51	0.24	2.17
Q9NVI7-2	ATD3A_HUMAN Isoform 2 of ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A	42.20	15.71	9.82	15.74	13.71	2.96	2.96	5.72E-07	6.37E-07	1.41E-06	9.77E-07	2.62E-07	1.40E-07	1.71	0.46	0.24
Q8TD43	TRPM4_HUMAN Transient receptor potential cation channel subfamily M member 4 OS=Homo sapiens GN=TRPM4 PE=1 SV=1	7.80		1.00	5.00	2.00	1.00	1.00		3.71E-09	2.69E-08	6.20E-08	8.14E-09	1.02E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
M0R117	M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=2 SV=1	68.20	18.84	11.91	27.81	16.87	10.92	15.88	1.39E-05	1.22E-05	5.09E-05	2.68E-05	6.96E-06	1.59E-05	1.92	0.50	1.14
O94905	ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1	71.70	21.85	22.88	28.84	49.74	31.80	29.84	1.16E-05	1.03E-05	8.81E-06	7.21E-06	5.21E-06	6.50E-06	0.62	0.45	0.56
Q5D862	FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	9.10	15.00	11.00	12.00	5.00	7.00	11.00	3.43E-07	5.81E-08	8.07E-08	1.26E-07	5.22E-08	4.56E-08	0.37	0.15	0.13
Q9UN86	G3BP2_HUMAN Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens GN=G3BP2 PE=1 SV=2	18.70	4.00	1.00	2.99	3.00	1.00		2.22E-07	3.63E-07	4.02E-07	2.87E-07	2.02E-07		1.29	0.91	Control 1 Only
Q6P1M0	S27A4_HUMAN Long-chain fatty acid transport protein 4 OS=Homo sapiens GN=SLC27A4 PE=1 SV=1	10.70	3.00	1.00		3.00		1.00	1.33E-07	4.51E-09		2.09E-07		9.67E-08	1.58	Control 1 Only	0.73
P19	NUCL_HUMAN Nucleolin OS=Homo sapiens	15.60	11.0	3.00	7.00	3.00	7.00	2.00	2.25	1.49	4.33	8.52	1.11	6.86	0.04	0.49	0.03

338	GN=NCL PE=1 SV=3		0						E-07	E-08	E-08	E-09	E-07	E-09			
B3KRI2	B3KRI2_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens GN=NDUFS7 PE=2 SV=1	22.00		4.00	5.00	3.00	4.00	5.00		3.20 E-06	3.30 E-07	1.25 E-07	5.16 E-07	1.29 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P02538	K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	65.10	3.99	6.98	1.98	8.97	5.99	3.99	1.09 E-06	1.87 E-06	4.69 E-07	3.23 E-06	2.56 E-06	2.55 E-07	2.96	2.34	0.23
F8WAK8	F8WAK8_HUMAN Cohesin subunit SA-2 OS=Homo sapiens GN=STAG2 PE=2 SV=1	15.30	1.98	5.93	1.97	7.90	4.95	1.97	2.67 E-09	5.98 E-08	1.08 E-08	9.40 E-08	2.93 E-08	4.80 E-08	35.25	10.97	18.01
Q92616	GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	8.50		4.00	12.00		3.00	1.00		1.28 E-08	3.91 E-08		1.68 E-08	2.53 E-09		Sample 2 Only	Sample 3 Only
P06493	CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	43.40	1.00	7.99	1.99	5.47	10.45	2.00	1.51 E-07	1.48 E-06	8.44 E-08	1.09 E-06	1.77 E-06	2.84 E-07	7.19	11.72	1.88
P11142	HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	63.00	38.91	43.82	24.33	49.63	48.59	33.06	6.41 E-06	6.06 E-06	4.49 E-06	9.17 E-06	1.10 E-05	7.13 E-06	1.43	1.71	1.11
E9PG39	E9PG39_HUMAN Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=2 SV=1	16.80	0.99	2.97	1.98	2.97	1.98	1.98	1.04 E-08	4.44 E-07	2.58 E-07	5.52 E-07	5.42 E-07	2.89 E-07	52.90	51.98	27.67
P22695	QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	54.70	17.82	35.60	21.76	34.65	41.57	34.65	3.49 E-06	1.02 E-05	3.58 E-06	6.62 E-06	1.34 E-05	7.69 E-06	1.90	3.84	2.20
P63244	GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	76.70	39.24	32.56	28.74	43.04	22.98	26.84	2.76 E-05	2.08 E-05	3.12 E-05	2.71 E-05	1.64 E-05	8.75 E-06	0.98	0.59	0.32
O14684	PTGES_HUMAN Prostaglandin E synthase OS=Homo sapiens GN=PTGES PE=1 SV=2	26.30	1.00	1.00	6.00	2.00	2.00		3.12 E-09	8.27 E-08	7.83 E-07	2.29 E-07	2.05 E-07		73.24	65.69	Control 1 Only
Q12873	CHD3_HUMAN Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3	8.40	2.50	1.00	1.00	1.50			2.54 E-08	1.19 E-08	7.43 E-09	1.64 E-08			0.64	Control 1 Only	Control 1 Only
P07355	ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	53.40	7.69	6.73	12.55	4.80	11.54	4.85	1.13 E-06	2.52 E-06	3.32 E-06	8.78 E-07	2.52 E-06	6.55 E-07	0.78	2.24	0.58
Q96PK6	RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	25.40	9.98	4.99	10.95	10.97	5.99	10.97	2.07 E-06	5.45 E-07	2.71 E-06	1.63 E-06	2.97 E-07	1.12 E-06	0.79	0.14	0.54
B4DVB8	B4DVB8_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=2 SV=1	53.10	14.98	18.96	16.96	33.91	32.94	22.96	1.84 E-06	2.25 E-06	6.39 E-06	7.09 E-06	5.63 E-06	4.31 E-06	3.86	3.07	2.35
Q9UBS4	DJB11_HUMAN DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1	27.90	1.00	2.00	2.00	3.00	5.00	4.00	2.81 E-07	4.43 E-07	5.52 E-07	1.03 E-06	4.12 E-07	8.93 E-07	3.65	1.47	3.18
Q69YL0	YC029_HUMAN Uncharacterized protein DKFZp762I1415 OS=Homo sapiens PE=4 SV=1	38.40		1.00	1.00		1.00	3.00		1.12 E-08	2.71 E-07		2.10 E-08	5.52 E-07		Sample 2 Only	Sample 3 Only
P52597	HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	58.80	17.00	21.00	21.00	34.00	34.00	19.00	6.86 E-06	9.89 E-06	3.66 E-06	1.57 E-05	1.36 E-05	2.73 E-06	2.28	1.98	0.40
P16615	AT2A2_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	45.20	12.86	37.61	48.50	54.45	45.57	48.52	4.30 E-07	2.26 E-06	2.33 E-06	3.08 E-06	2.61 E-06	2.76 E-06	7.17	6.08	6.42
O60264	SMCA5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1	31.80	20.50	11.00	12.50	13.00	10.50	9.50	8.95 E-07	1.78 E-07	2.73 E-07	2.84 E-07	2.84 E-07	1.42 E-07	0.32	0.32	0.16
O95758	PTBP3_HUMAN Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 PE=1 SV=2	21.70		1.98	0.99	1.98	3.96	0.99		2.52 E-08	7.22 E-08	3.03 E-08	1.83 E-07	1.22 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q09666	AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens	7.00	2.00	11.00	2.00	2.00	14.00	7.00	2.31 E-09	1.85 E-08	3.73 E-09	8.62 E-10	4.54 E-08	1.49 E-08	0.37	19.66	6.46

	GN=AHNAK PE=1 SV=2																
O43143	DHX15_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	14.50	6.00	5.00	12.00	5.00	1.00	4.00	2.00E-07	6.45E-08	3.24E-07	5.90E-08	7.58E-08	1.57E-07	0.29	0.38	0.78
O76024	WFS1_HUMAN Wolframin OS=Homo sapiens GN=WFS1 PE=1 SV=2	10.00	1.00	3.00	3.00	2.00	4.00	3.00	3.06E-09	3.94E-08	1.02E-07	1.12E-07	1.30E-07	6.47E-08	36.47	42.28	21.13
O94973	AP2A2_HUMAN AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2	29.80	3.00	5.99	1.98	11.99	3.98	6.94	5.31E-08	1.05E-07	6.68E-08	1.88E-07	1.20E-07	1.53E-07	3.54	2.26	2.88
P62195	PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	24.90	1.98	2.97	0.99	4.96	2.97	2.97	1.48E-07	2.56E-07	4.36E-08	6.31E-07	8.75E-08	1.53E-07	4.26	0.59	1.03
J3KTE4	J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=2 SV=1	45.60	13.00	9.00	17.00	18.00	15.00	8.00	6.45E-06	3.17E-06	9.42E-06	6.19E-06	4.61E-06	1.10E-06	0.96	0.71	0.17
P63220	RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	35.80	3.00	4.00	7.00	3.00	1.00	3.00	4.97E-07	2.34E-06	2.82E-06	3.26E-06	2.31E-06	3.82E-06	6.56	4.65	7.67
Q9H269	VPS16_HUMAN Vacuolar protein sorting-associated protein 16 homolog OS=Homo sapiens GN=VPS16 PE=1 SV=2	8.30		2.96	1.97		5.93	1.97		4.47E-08	3.50E-08		1.61E-07	1.33E-08		Sample 2 Only	Sample 3 Only
Q9P0I2	EMC3_HUMAN ER membrane protein complex subunit 3 OS=Homo sapiens GN=EMC3 PE=1 SV=3	19.60	1.00	4.99	1.00	1.99	2.00	1.99	3.52E-08	1.38E-06	2.27E-08	5.48E-07	8.11E-08	1.52E-07	15.59	2.31	4.33
P36542	ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	30.50	2.00	7.00	1.00	6.00	11.00	8.00	2.40E-07	7.76E-07	9.42E-07	1.66E-07	2.34E-06	8.96E-07	0.69	9.75	3.74
Q86UP2	KTN1_HUMAN Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1	51.50	14.79	34.53	36.51	48.34	34.50	33.57	2.09E-07	1.19E-06	8.53E-07	1.94E-06	7.98E-07	1.14E-06	9.28	3.82	5.45
E7EUE1	E7EUE1_HUMAN ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=2 SV=1	32.90	4.99	4.00	9.00	17.99	9.99	7.00	1.28E-07	3.63E-07	3.60E-07	1.04E-06	3.35E-07	1.61E-07	8.10	2.62	1.26
E9PPM8	E9PPM8_HUMAN Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=2 SV=1	36.70	2.97	9.88	3.93	5.90	11.85	10.85	3.34E-07	1.28E-06	1.18E-06	6.94E-07	2.31E-06	1.70E-06	2.08	6.92	5.07
P31327	CPSM_HUMAN Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2	2.30	3.00	3.00	2.00		1.00	2.00	2.15E-08	4.32E-08	5.67E-09		7.34E-09	2.30E-08	Control 1 Only	0.34	1.07
P40429	RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	53.20	22.94	20.94	25.91	22.94	18.96	13.96	2.20E-05	2.53E-05	4.29E-05	3.39E-05	1.53E-05	1.28E-05	1.54	0.69	0.58
C9JNW5	C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1	55.30	16.00	14.00	28.00	18.00	14.00	7.00	4.36E-06	3.96E-06	6.78E-06	6.60E-06	1.73E-06	1.25E-06	1.51	0.40	0.29
Q9Y512	SAM50_HUMAN Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3	25.20	1.00	5.00	5.00	6.00	1.00	1.00	7.70E-08	3.96E-07	3.61E-07	3.74E-07	7.01E-08	2.14E-09	4.85	0.91	0.03
P51659	DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	59.20	25.73	34.63	33.58	36.56	41.51	41.53	1.97E-06	3.50E-06	4.91E-06	3.01E-06	7.79E-06	5.46E-06	1.53	3.95	2.77
P60842	IF4A1_HUMAN Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	46.10	0.98	13.69	2.96	3.93	7.88	6.85	4.00E-08	2.29E-06	6.75E-07	1.16E-07	8.28E-07	8.06E-07	2.91	20.71	20.17
H7BXY3	H7BXY3_HUMAN Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=2 SV=1	25.50	9.00	8.00	20.00	10.00	9.00	1.00	8.25E-08	7.76E-08	1.33E-07	1.07E-07	3.28E-08	5.64E-09	1.30	0.40	0.07
Q8IX12	CCAR1_HUMAN Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	10.70	4.95	1.99	2.98	7.94	2.98	4.96	6.90E-08	1.08E-08	1.85E-08	1.17E-07	2.66E-08	5.93E-08	1.70	0.39	0.86
Q14444	CAPR1_HUMAN Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	17.70	7.89	7.89	17.77	17.79	8.88	9.87	1.09E-07	1.66E-07	5.64E-07	1.05E-06	2.78E-07	1.66E-07	9.66	2.55	1.52

O75396	SC22B_HUMAN Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4	12.10		1.00	2.00	1.00	2.00	3.00		1.40E-07	5.67E-08	6.36E-08	2.18E-07	1.02E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4DKG8	B4DKG8_HUMAN Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=2 SV=1	12.40	2.00	5.00	5.00	3.00	1.00	1.00	3.32E-08	1.02E-07	1.82E-07	6.07E-08	3.31E-08	4.98E-07	1.83	1.00	14.99
O95298	NDUC2_HUMAN NADH dehydrogenase [ubiquinone] 1 subunit C2 OS=Homo sapiens GN=NDUFC2 PE=1 SV=1	36.10		2.98	2.98	0.98	1.98	2.97		9.89E-07	1.00E-06	7.73E-08	1.66E-06	1.59E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y6C9	MTCH2_HUMAN Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	48.50	12.50	12.50	14.50	21.00	16.00	17.00	1.73E-06	5.72E-06	4.33E-06	7.36E-06	7.80E-06	2.86E-06	4.25	4.50	1.65
P18124	RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	56.50	31.88	28.90	23.91	26.92	20.88	18.92	1.50E-05	1.35E-05	1.72E-05	9.31E-06	1.16E-05	1.02E-05	0.62	0.78	0.68
P06576	ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	38.40	1.98	6.93	1.98		12.87	3.97	3.98E-08	5.45E-07	3.03E-08		1.02E-06	7.60E-08	Control 1 Only	25.52	1.91
P60709	ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	75.70	31.21	34.11	31.22	52.64	55.43	40.99	2.39E-05	2.54E-05	3.29E-05	4.22E-05	5.80E-05	1.61E-05	1.76	2.42	0.67
Q9UQE7	SMC3_HUMAN Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2	24.00	5.00	13.00	6.00	10.00	16.00	10.00	1.05E-07	1.96E-07	3.67E-08	1.63E-07	2.40E-07	2.21E-07	1.56	2.30	2.11
P05387	RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	92.20	7.00	8.00	9.00	2.00	5.00	6.00	6.46E-06	5.05E-06	3.49E-06	1.22E-06	3.31E-06	5.21E-06	0.19	0.51	0.81
P04259	K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	63.30	0.99	0.99			2.98	0.99	1.26E-07	3.48E-08			2.48E-08	2.87E-07	Control 1 Only	0.20	2.27
P13645	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	71.10	216.76	153.64	194.33	151.33	162.21	156.22	1.28E-04	8.39E-05	8.88E-05	5.41E-05	7.72E-05	8.89E-05	0.42	0.60	0.69
B4DZI8	B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	36.00	3.00	23.96	6.99	15.98	27.95	12.99	8.83E-08	1.35E-06	1.38E-07	5.64E-07	1.58E-06	5.01E-07	6.39	17.87	5.67
Q7L576	CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	12.10	1.99	5.96	2.99	1.96	7.90	2.99	1.21E-08	2.62E-07	2.78E-08	2.69E-08	6.73E-08	6.18E-08	2.22	5.57	5.11
O94874	UFL1_HUMAN E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2	42.30	9.93	21.87	24.82	27.83	26.82	14.90	2.75E-07	1.41E-06	9.35E-07	1.64E-06	2.01E-06	6.02E-07	5.95	7.30	2.19
Q9BWF3	RBM4_HUMAN RNA-binding protein 4 OS=Homo sapiens GN=RBM4 PE=1 SV=1	41.20		7.93	2.98	6.96	7.94	2.98		1.79E-06	6.30E-07	1.16E-06	2.22E-06	5.63E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P12236	ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	62.40	2.56	3.56	4.12	9.12	5.56	2.12	2.12E-07	2.01E-06	7.90E-07	7.63E-07	1.04E-06	1.85E-08	3.60	4.92	0.09
P07437	TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	46.00	0.99	3.96		0.99	0.99	4.95	1.77E-07	1.97E-07		4.76E-08	4.15E-09	6.24E-07	0.27	0.02	3.52
B7Z596	B7Z596_HUMAN Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=2 SV=1	22.40	5.72	4.78	1.87	4.68	4.68	5.67	6.61E-07	6.29E-07	4.97E-08	3.08E-07	9.09E-07	1.02E-06	0.47	1.37	1.54
F8W726	F8W726_HUMAN Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=2 SV=1	16.30		6.96	4.99	10.95	3.99	5.97		3.28E-07	4.84E-08	4.62E-07	1.11E-07	1.02E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
H3BLZ8	H3BLZ8_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=2 SV=1	49.90	17.81	15.81	17.80	28.67	17.79	20.75	1.32E-06	1.68E-06	1.90E-06	3.58E-06	1.37E-06	2.69E-06	2.72	1.04	2.04
O14965	AURKA_HUMAN Aurora kinase A OS=Homo sapiens GN=AURKA PE=1 SV=2	16.60	1.99	3.00	1.00	0.99	2.00		9.31E-08	1.76E-07	1.39E-07	2.84E-08	1.93E-07		0.30	2.08	Control 1 Only
Q00839-2	HNRPU_HUMAN Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU	50.70		5.00	3.00	4.00	2.00	2.00		4.37E-08	1.53E-07	6.72E-08	8.37E-09	2.66E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
A6NGW1	A6NGW1_HUMAN Protein YIF1A OS=Homo sapiens GN=YIF1A PE=2 SV=1	16.20	1.98	1.98		0.99	3.96	1.98	2.08E-07	1.90E-07		1.68E-07	3.35E-07	1.99E-07	0.81	1.61	0.95
P62	RL23A_HUMAN 60S ribosomal protein L23a	59.00	19.8	13.8	24.7	20.8	9.91	9.90	9.90	8.61	5.33	1.03	3.66	2.26	1.04	0.37	0.23

750	OS=Homo sapiens GN=RPL23A PE=1 SV=1		1	7	6	2			E-06	E-06	E-06	E-05	E-06	E-06			
P19013	K2C4_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	32.00	1.11	1.67	4.91		4.23		2.60 E-08	2.85 E-08	1.25 E-07		9.25 E-08		Control 1 Only	3.56	Control 1 Only
P61513	RL37A_HUMAN 60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2	73.90	9.87	7.92	18.77	7.88	5.92	2.97	8.85 E-06	8.03 E-06	1.70 E-05	9.35 E-06	8.69 E-06	5.43 E-06	1.06	0.98	0.61
Q9UHQ9	NB5R1_HUMAN NADH-cytochrome b5 reductase 1 OS=Homo sapiens GN=CYB5R1 PE=1 SV=1	30.50		3.00	2.00	2.00	10.00	2.00		2.98 E-07	7.52 E-07	5.62 E-08	1.66 E-06	2.37 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P49207	RL34_HUMAN 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	43.60	5.00	7.00	16.00	10.00	5.00	4.00	3.06 E-06	6.88 E-06	1.54 E-05	5.81 E-06	4.09 E-06	7.51 E-06	1.89	1.34	2.45
P50402	EMD_HUMAN Emerin OS=Homo sapiens GN=EMD PE=1 SV=1	39.80	3.00	6.00	7.00	8.99	5.00	4.00	1.43 E-07	2.80 E-06	1.87 E-06	1.28 E-06	9.01 E-07	8.90 E-07	8.95	6.29	6.22
I1E4Y6	I1E4Y6_HUMAN PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=2 SV=1	7.50		1.97	5.93	4.95	1.97			4.42 E-08	4.45 E-08	3.61 E-08	8.15 E-09		Sample 1 Only	Sample 2 Only	
Q15024	EXOS7_HUMAN Exosome complex component RRP42 OS=Homo sapiens GN=EXOSC7 PE=1 SV=3	20.60	1.00	1.00	3.00	3.00	1.00	1.00	5.66 E-09	2.65 E-07	2.79 E-07	4.74 E-08	4.23 E-08	2.23 E-07	8.38	7.48	39.48
Q5JTH9	RRP12_HUMAN RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2	9.60	3.00	1.00	9.00	4.00	4.00		1.01 E-07	1.05 E-08	1.16 E-07	9.32 E-08	2.88 E-08		0.92	0.29	Control 1 Only
P62873	GBB1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3	25.30		1.97	2.00	5.94	2.94	2.97		9.91 E-07	7.63 E-09	6.84 E-07	4.75 E-07	4.84 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
O75494	SRS10_HUMAN Serine/arginine-rich splicing factor 10 OS=Homo sapiens GN=SRSF10 PE=1 SV=1	42.40	6.00	3.00	6.00	7.00		4.00	5.07 E-07	1.80 E-07	7.73 E-07	1.98 E-06		3.73 E-07	3.90	Control 1 Only	0.74
F6S0T5	F6S0T5_HUMAN Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=2 SV=1	7.00	2.00	4.99	1.00	1.00	2.00		5.52 E-08	3.92 E-08	7.83 E-09	1.06 E-09	5.07 E-08		0.02	0.92	Control 1 Only
A8MWD9	RUXGL_HUMAN Small nuclear ribonucleoprotein G-like protein OS=Homo sapiens PE=3 SV=2	31.20	3.00	3.00	4.00	4.00	2.00	4.00	2.27 E-06	1.39 E-06	1.37 E-06	2.62 E-06	6.65 E-07	4.36 E-06	1.15	0.29	1.92
Q8N766	EMC1_HUMAN ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1	23.50	2.99	16.95	10.96	12.97	9.97	2.99	5.01 E-09	4.75 E-07	4.73 E-08	2.25 E-07	6.44 E-08	1.16 E-08	44.91	12.84	2.32
Q9UMS4	PRP19_HUMAN Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	59.90	6.99	6.99	14.98	15.96	6.99	8.98	2.68 E-06	1.32 E-06	2.93 E-06	2.33 E-06	5.75 E-07	1.64 E-06	0.87	0.21	0.61
P14923	PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	32.60	33.44	17.46	13.46	9.97	18.44	9.49	1.84 E-06	4.59 E-07	3.95 E-07	5.32 E-07	8.25 E-07	3.36 E-07	0.29	0.45	0.18
B5ME97	B5ME97_HUMAN Septin 10, isoform CRA_c OS=Homo sapiens GN=SEPT10 PE=2 SV=2	13.10	2.00	2.00	3.00	2.00	2.00	1.00	3.47 E-08	2.25 E-07	1.05 E-07	1.79 E-08	1.92 E-08	1.68 E-07	0.51	0.55	4.82
B4E1G1	B4E1G1_HUMAN Derlin-1 OS=Homo sapiens GN=DERL1 PE=2 SV=1	23.80	1.00	3.00	2.00	1.00	2.00	2.00	1.54 E-07	1.96 E-07	7.84 E-08	1.63 E-07	1.85 E-07	3.79 E-07	1.06	1.20	2.47
P62314	SMD1_HUMAN Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	37.80	4.00	3.00	5.00	5.00	4.00	4.00	1.18 E-06	1.37 E-06	1.78 E-06	7.58 E-07	1.06 E-06	9.87 E-07	0.64	0.90	0.84
P51153	RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1	38.40		3.50	1.00		3.50	3.00		7.13 E-07	6.71 E-09		1.06 E-06	1.25 E-07		Sample 2 Only	Sample 3 Only
P46777	RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	64.30	46.00	39.00	38.00	59.00	44.00	30.00	1.48 E-05	1.13 E-05	1.58 E-05	1.69 E-05	7.12 E-06	5.85 E-06	1.14	0.48	0.40
O60306	AQR_HUMAN Intron-binding protein aquarius OS=Homo sapiens GN=AQR PE=1 SV=4	4.40	1.00	1.00	5.00	2.00	3.00	3.00	1.42 E-09	5.80 E-10	2.42 E-08	2.51 E-08	2.08 E-08	6.90 E-09	17.70	14.64	4.87
P04899	GNAI2_HUMAN Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	35.20		0.99	0.99	3.96	3.96	1.98		4.59 E-07	4.93 E-07	5.30 E-07	4.51 E-07	5.54 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only

B3KVR1	B3KVR1_HUMAN Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPN PE=2 SV=1	26.00	3.00	5.00	6.00	5.00	3.00	5.00	8.69E-07	3.91E-07	6.31E-07	1.08E-06	1.34E-07	1.73E-06	1.24	0.15	2.00
P49750	YLPM1_HUMAN YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=3	15.50	2.00	6.97	8.97	19.91	2.00	9.96	7.81E-09	6.11E-07	1.37E-07	3.20E-07	2.81E-09	1.29E-07	40.97	0.36	16.49
P05141	ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	72.50	7.00	10.12	13.00	7.00	10.06	10.50	9.30E-07	4.46E-06	1.23E-05	6.08E-06	8.94E-06	1.01E-05	6.54	9.61	10.90
P46779	RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	64.20	24.82	19.86	29.80	19.87	19.86	13.91	2.17E-05	2.17E-05	2.18E-05	2.34E-05	9.40E-06	1.47E-05	1.08	0.43	0.68
Q9Y5M8	SRPRB_HUMAN Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3	45.80	4.00	8.00	7.00	6.00	8.00	6.00	4.17E-07	7.36E-07	1.80E-06	1.36E-06	2.17E-06	9.67E-07	3.27	5.21	2.32
P13010	XRCC5_HUMAN X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	9.40	1.00	1.00	3.00		1.00	1.00	3.72E-08	7.02E-08	1.74E-07		1.28E-07	3.08E-08	Control 1 Only	3.45	0.83
Q9ULV4	COR1C_HUMAN Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	23.40	2.97	2.96	1.98	6.93	3.95	2.97	3.67E-07	8.58E-07	5.03E-08	6.08E-07	4.17E-07	9.91E-07	1.66	1.14	2.70
E9PPJ0	E9PPJ0_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=2 SV=1	17.90	2.99	7.99	5.00	9.98	5.98	3.99	5.48E-08	1.69E-07	8.46E-08	3.07E-07	1.30E-07	8.73E-08	5.61	2.37	1.59
Q15233	NONO_HUMAN Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	67.70	64.44	54.51	67.39	85.27	81.24	65.42	2.40E-05	1.85E-05	2.18E-05	3.42E-05	2.57E-05	2.73E-05	1.42	1.07	1.14
Q9UHF7	TRPS1_HUMAN Zinc finger transcription factor Trps1 OS=Homo sapiens GN=TRPS1 PE=1 SV=2	28.60	24.78	13.87	25.76	22.80	9.90	8.93	8.30E-07	2.72E-07	6.23E-07	8.95E-07	7.39E-08	1.14E-07	1.08	0.09	0.14
B7Z6Z4	B7Z6Z4_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	49.20	1.98	2.96	3.96	0.98	0.98	0.98	8.77E-08	1.06E-06	1.79E-07	2.54E-07	2.90E-07	2.78E-07	2.89	3.31	3.17
P51798	CLCN7_HUMAN H(+)/Cl(-) exchange transporter 7 OS=Homo sapiens GN=CLCN7 PE=1 SV=2	5.60	1.00	4.00		5.00	3.00	2.00	1.71E-07	8.28E-07		7.01E-07	8.07E-07	8.48E-08	4.11	4.73	0.50
Q8WVX9	FACR1_HUMAN Fatty acyl-CoA reductase 1 OS=Homo sapiens GN=FAR1 PE=1 SV=1	18.30	7.00	8.00	5.00	5.00	2.00	4.00	5.20E-07	7.49E-07	1.31E-07	1.97E-07	2.25E-07	4.51E-07	0.38	0.43	0.87
Q9BRX2	PELO_HUMAN Protein pelota homolog OS=Homo sapiens GN=PELO PE=1 SV=2	16.90		2.00	2.00	3.00	3.00			2.11E-07	7.99E-08	4.32E-08	1.23E-07		Sample 1 Only	Sample 2 Only	
Q10570	CPSF1_HUMAN Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2	6.40	4.00	3.00	5.00	4.00	4.00	3.00	1.86E-07	6.02E-08	9.22E-08	8.02E-08	3.15E-08	8.37E-08	0.43	0.17	0.45
B5ME19	EIFCL_HUMAN Eukaryotic translation initiation factor 3 subunit C-like protein OS=Homo sapiens GN=EIF3CL PE=2 SV=1	9.90	3.00	8.00	2.00	7.00	7.00		9.09E-08	1.74E-07	1.55E-08	2.04E-07	2.68E-07		2.24	2.95	Control 1 Only
P30050	RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	69.10	19.00	17.00	27.00	19.00	18.00	16.00	8.06E-06	2.14E-05	2.34E-05	1.33E-05	1.37E-05	1.17E-05	1.65	1.70	1.45
Q53EP0	FND3B_HUMAN Fibronectin type III domain-containing protein 3B OS=Homo sapiens GN=FNDC3B PE=1 SV=2	10.00	4.00	5.00	5.00	5.00	3.00	2.00	4.96E-08	4.25E-08	4.88E-08	1.75E-07	3.95E-08	3.13E-08	3.52	0.80	0.63
O14880	MGST3_HUMAN Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1	38.20	4.00	5.00	7.00	8.00	6.00	5.00	2.37E-07	7.17E-06	1.42E-06	2.57E-06	6.74E-06	3.34E-06	10.80	28.40	14.08
P54886	P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	29.40	1.00	16.00	1.00	3.00	22.00	2.00	3.63E-10	1.10E-06	1.46E-07	1.27E-07	1.76E-06	4.98E-08	350.14	4851.24	137.19
P23258	TBG1_HUMAN Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	21.10	2.98	4.99	1.99	1.98	3.99	2.99	2.71E-07	3.79E-07	5.38E-08	1.72E-07	1.75E-07	8.29E-08	0.63	0.64	0.31
P42285	SK2L2_HUMAN Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3	22.10	7.98	12.98	11.98	13.98	12.97	10.98	1.26E-07	4.38E-07	1.19E-07	3.72E-07	4.65E-07	2.54E-07	2.95	3.68	2.01

Q13555	KCC2G_HUMAN Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Homo sapiens GN=CAMK2G PE=1 SV=3	9.10	0.99	1.98	2.97	2.97	1.98		1.57E-08	2.70E-08	5.00E-08	1.22E-07	4.24E-08		7.78	2.70	Control 1 Only
Q13263	TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	19.40	2.00	6.00		2.00	11.00	3.00	1.24E-08	3.35E-07		1.99E-07	2.55E-07	1.18E-07	16.08	20.61	9.56
P01834	IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	54.70	2.00	4.00	7.00	16.00	7.00	9.00	1.69E-06	1.67E-06	3.09E-06	6.12E-06	1.63E-06	1.56E-06	3.62	0.96	0.92
P17844	DDX5_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	49.50	15.77	17.75	36.49	26.60	12.82	18.72	2.92E-06	2.82E-06	1.00E-05	6.76E-06	1.88E-06	2.50E-06	2.32	0.65	0.86
Q14683	SMC1A_HUMAN Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2	16.50	1.00	12.46	3.00	7.97	13.47	5.97	4.50E-09	2.85E-07	1.15E-08	1.82E-07	1.99E-07	1.16E-07	40.52	44.22	25.77
Q9UBM7	DHCR7_HUMAN 7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	16.60	2.99	3.98	4.98	6.98	4.97	3.99	4.17E-07	1.31E-06	4.76E-07	8.80E-07	5.30E-07	1.90E-06	2.11	1.27	4.54
Q9C0C2	TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	21.20	4.00	9.00	8.00	4.00	12.00	10.00	1.42E-08	9.03E-08	1.20E-07	1.89E-08	1.40E-07	2.17E-07	1.33	9.88	15.33
G3V2S6	G3V2S6_HUMAN V-type proton ATPase subunit D OS=Homo sapiens GN=ATP6V1D PE=2 SV=1	14.60	0.99	1.98	0.99	2.97	1.98	0.99	9.55E-08	6.29E-07	2.24E-07	8.05E-07	4.91E-07	1.82E-07	8.43	5.14	1.91
Q6PKG0	LARP1_HUMAN La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	17.70	8.92	5.93	6.95	14.85	4.95	3.98	6.16E-08	1.31E-07	4.29E-08	2.42E-07	8.68E-08	6.33E-08	3.92	1.41	1.03
Q14980	NUMA1_HUMAN Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2	45.10	38.63	38.62	24.72	61.28	35.60	42.56	8.16E-07	7.94E-07	2.26E-07	1.32E-06	4.70E-07	9.73E-07	1.62	0.58	1.19
M0QYZ2	M0QYZ2_HUMAN AP-2 complex subunit sigma OS=Homo sapiens GN=AP2S1 PE=2 SV=1	35.20	4.93	1.97	3.95	0.99	2.96	3.94	8.18E-07	6.19E-07	7.20E-07	1.87E-08	1.07E-06	2.13E-06	0.02	1.30	2.60
P04406	G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	34.80	6.99	2.00	5.00	5.00	4.00	3.00	4.65E-07	1.59E-07	3.10E-07	8.69E-08	3.08E-07	1.96E-07	0.19	0.66	0.42
P61247	RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	75.80	50.41	36.79	41.69	48.50	34.85	30.99	2.76E-05	1.81E-05	2.19E-05	3.04E-05	1.19E-05	8.36E-06	1.10	0.43	0.30
P52292	IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	24.00	5.00	8.00	9.00	12.00	8.00	9.00	4.31E-07	5.90E-07	1.49E-06	2.21E-06	9.81E-07	5.29E-07	5.12	2.28	1.23
Q96NB2	SFXN2_HUMAN Sideroflexin-2 OS=Homo sapiens GN=SFXN2 PE=1 SV=2	27.00		6.98	1.99	2.00	7.97	8.98		5.78E-07	3.59E-07	9.84E-08	8.45E-07	5.05E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P53007	TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	26.40	8.00	12.00	14.00	13.00	13.00	14.00	1.23E-06	2.25E-06	2.11E-06	1.73E-06	4.43E-06	1.85E-06	1.41	3.59	1.50
Q8WY22	BRI3B_HUMAN BRI3-binding protein OS=Homo sapiens GN=BRI3BP PE=1 SV=1	14.30		3.00	2.00	4.00	1.00			3.36E-07	1.63E-08	1.93E-07	1.94E-08		Sample 1 Only	Sample 2 Only	
Q14160	SCRIB_HUMAN Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4	13.80	1.00	4.49	1.00	9.97	2.99	0.99	3.69E-09	7.45E-08	3.19E-09	1.16E-07	1.91E-08	6.93E-09	31.43	5.17	1.88
B7ZAQ6	GPHRA_HUMAN Golgi pH regulator A OS=Homo sapiens GN=GPR89A PE=1 SV=2	10.50	2.00	2.00	1.00	3.00	3.00	3.00	1.14E-07	5.11E-08	1.63E-07	1.14E-07	2.19E-07	1.98E-07	1.00	1.92	1.74
Q15006	EMC2_HUMAN ER membrane protein complex subunit 2 OS=Homo sapiens GN=EMC2 PE=1 SV=1	18.20		2.00	1.00	3.00	2.00	3.00		2.62E-07	2.61E-08	2.18E-08	4.54E-08	1.05E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P21333	FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	26.40	3.98	33.77	35.74	11.92	26.84	23.85	3.56E-08	6.15E-07	2.98E-07	1.26E-07	2.11E-07	2.69E-07	3.55	5.93	7.55
Q13	NNTM_HUMAN NAD(P) transhydrogenase,	29.00		15.9	1.99	3.97	20.8	17.8		5.77	4.07	2.47	5.08	4.33	Sample	Sample	Sample

423	mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3			1			5	8		E-07	E-08	E-08	E-07	E-07	1 Only	2 Only	3 Only
P35527	K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	75.90	164.88	138.05	155.91	116.16	129.05	137.05	6.60E-05	7.34E-05	5.10E-05	2.88E-05	5.16E-05	6.74E-05	0.44	0.78	1.02
P08240	SRPR_HUMAN Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2	26.80	1.00	11.00	9.00	15.00	11.00	6.00	8.00E-08	8.95E-07	2.78E-07	9.87E-07	5.65E-07	3.42E-07	12.33	7.06	4.27
P08621	RU17_HUMAN U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2	32.20	12.97	4.00	2.00	10.97	5.99	10.97	1.70E-06	1.76E-07	2.75E-08	9.83E-07	6.19E-07	1.22E-06	0.58	0.36	0.72
Q9BQ39	DDX50_HUMAN ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1	11.10	2.00	1.00	2.50	2.00	1.00		1.66E-08	3.38E-09	6.82E-09	4.16E-08	7.71E-09		2.50	0.46	Control 1 Only
G3V1L9	G3V1L9_HUMAN Tight junction protein 1 (Zona occludens 1), isoform CRA_a OS=Homo sapiens GN=TJP1 PE=2 SV=1	10.30	2.99	3.99	4.00	7.98	3.00	2.00	9.06E-09	3.35E-08	2.27E-08	6.94E-08	2.39E-08	2.05E-08	7.65	2.64	2.26
Q9BR76	COR1B_HUMAN Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	20.70	2.98	3.97	2.98	6.97	5.98	0.99	4.41E-07	5.29E-07	7.57E-07	9.55E-07	6.26E-07	9.83E-07	2.17	1.42	2.23
O75477	ERLN1_HUMAN Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1	54.00	5.50	5.00	7.50	13.00	6.50	3.00	6.91E-07	1.05E-06	2.56E-06	3.04E-06	2.05E-06	1.07E-06	4.40	2.96	1.55
Q5QPL9	Q5QPL9_HUMAN RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1	50.20	8.89	7.89	10.83	8.89	7.88	7.87	4.38E-06	4.48E-06	3.28E-06	4.19E-06	1.60E-06	2.91E-06	0.96	0.37	0.66
P35637	FUS_HUMAN RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1	30.10	9.49	12.50	14.50	28.50	14.00	16.00	1.08E-06	2.03E-06	8.50E-06	9.97E-06	3.98E-06	2.07E-06	9.20	3.67	1.91
Q8WXA9	SREK1_HUMAN Splicing regulatory glutamine/lysine-rich protein 1 OS=Homo sapiens GN=SREK1 PE=1 SV=1	10.40	3.00	1.00		1.00	1.00	2.00	4.54E-08	2.60E-08		1.31E-08	1.87E-08	8.27E-09	0.29	0.41	0.18
P50570	DYN2_HUMAN Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2	22.10	1.97	14.72	6.86	5.90	17.65	7.86	1.84E-08	4.90E-07	8.77E-08	5.74E-08	5.94E-07	2.70E-07	3.12	32.32	14.68
P10620	MGST1_HUMAN Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1	41.30	9.92	18.88	22.86	18.89	16.89	16.91	1.67E-06	1.03E-05	6.68E-06	4.17E-06	5.34E-06	4.11E-06	2.50	3.20	2.46
Q05048	CSTF1_HUMAN Cleavage stimulation factor subunit 1 OS=Homo sapiens GN=CSTF1 PE=1 SV=1	16.20	2.00	3.00	2.00	2.00	3.00	2.00	4.18E-07	3.82E-07	1.77E-07	1.42E-07	4.20E-07	9.10E-07	0.34	1.00	2.18
Q9Y383	LC7L2_HUMAN Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2	21.90	8.96	1.99	2.98	3.98	2.98	3.99	9.35E-07	2.62E-08	9.53E-07	9.11E-07	2.29E-07	1.50E-07	0.97	0.24	0.16
O96008	TOM40_HUMAN Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1	50.40	2.97	7.93	11.89	9.91	12.88	4.95	4.36E-07	2.91E-06	2.46E-06	1.52E-06	2.37E-06	2.24E-07	3.48	5.43	0.51
O15020	SPTN2_HUMAN Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	43.10	24.99	17.00	63.95	47.97	66.94	54.96	2.74E-07	1.89E-06	1.04E-06	1.14E-06	1.77E-06	1.65E-06	4.17	6.46	6.03
P14866	HNRPL_HUMAN Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2	56.50	12.85	17.75	25.64	28.62	16.79	24.73	1.35E-06	1.86E-06	4.59E-06	4.92E-06	1.22E-06	4.61E-06	3.64	0.91	3.41
P46063	RECQ1_HUMAN ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3	14.90	2.00	4.00	1.00	3.00	3.00	3.00	4.18E-09	1.02E-07	7.81E-09	1.29E-07	4.34E-08	1.48E-08	30.78	10.36	3.53
Q96S52	PIGS_HUMAN GPI transamidase component PIG-S OS=Homo sapiens GN=PIGS PE=1 SV=3	21.10	2.99	12.92	3.00	3.00	5.98	4.97	1.33E-07	1.35E-06	3.38E-07	2.09E-07	5.88E-07	4.42E-07	1.57	4.42	3.32
B4DWR7	B4DWR7_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens	8.80	11.00	10.00	11.00	7.00	8.00	8.00	2.36E-05	2.82E-05	1.23E-05	1.16E-05	1.25E-05	2.52E-05	0.49	0.53	1.07

	GN=TGM1 PE=2 SV=1																
P26640	SYVC_HUMAN Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4	7.50		3.00	4.00	1.00	3.00	2.00		1.22E-07	6.34E-08	7.97E-09	6.39E-08	4.21E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
E7ETY4	E7ETY4_HUMAN Serine/threonine-protein kinase MARK2 OS=Homo sapiens GN=MARK2 PE=2 SV=1	9.80	2.00	1.99	3.99	2.99	5.98	1.00	6.01E-08	9.33E-08	9.66E-08	8.66E-08	3.01E-07	3.79E-09	1.44	5.02	0.06
Q99460	PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	11.50		6.99		7.98	1.00	2.00		9.11E-08		1.27E-07	6.00E-09	1.64E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q15365	PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	31.20	5.95	3.96	6.93	3.97	4.94	2.97	1.10E-07	1.71E-07	5.03E-07	9.10E-08	3.54E-07	7.67E-08	0.83	3.22	0.70
Q9NZB2	F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	40.80	25.86	23.85	36.74	28.82	12.93	26.84	1.00E-06	8.51E-07	1.20E-06	1.05E-06	2.68E-07	8.30E-07	1.05	0.27	0.83
P53350	PLK1_HUMAN Serine/threonine-protein kinase PLK1 OS=Homo sapiens GN=PLK1 PE=1 SV=1	15.40	2.00	2.99	4.00	5.99		2.00	2.99E-07	1.61E-07	1.41E-07	2.36E-07		1.60E-07	0.79	Control 1 Only	0.54
J3KN00	J3KN00_HUMAN NADH dehydrogenase (Ubiquinone) 1 alpha subcomplex, 13 OS=Homo sapiens GN=NDUFA13 PE=4 SV=1	42.40	2.00	5.97	9.94	1.00	3.99	7.96	2.92E-07	3.34E-06	1.41E-06	1.01E-06	1.37E-06	1.24E-06	3.46	4.70	4.26
P08708	RS17_HUMAN 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	65.90	20.94	15.95	23.91	19.93	15.94	12.96	1.23E-05	1.51E-05	8.48E-06	1.56E-05	8.49E-06	3.35E-06	1.27	0.69	0.27
P09669	COX6C_HUMAN Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2	76.00	3.00	7.00	15.00	7.00	10.00	9.00	4.70E-06	6.91E-06	1.03E-05	8.72E-06	1.08E-05	9.21E-06	1.86	2.29	1.96
M0R0F0	M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=2 SV=1	59.50	19.88	18.89	25.86	21.90	11.94	15.91	7.00E-06	6.05E-06	8.61E-06	8.35E-06	3.43E-06	4.61E-06	1.19	0.49	0.66
C9JRZ6	C9JRZ6_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=2 SV=1	52.40	5.95	9.93	11.92	15.91	8.94	10.91	8.14E-07	2.69E-06	3.33E-06	2.67E-06	9.77E-07	1.34E-06	3.28	1.20	1.64
E9PIK4	E9PIK4_HUMAN Tumor protein p53-inducible protein 11 OS=Homo sapiens GN=TP53I11 PE=2 SV=1	47.90		4.00	4.00	2.00	3.00	2.00		1.53E-06	1.70E-06	1.05E-06	2.01E-06	1.43E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P41091	IF2G_HUMAN Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	46.20	4.96	11.91	6.96	8.94	10.93	6.96	1.31E-06	2.26E-06	1.88E-06	1.28E-06	3.82E-06	2.33E-06	0.98	2.91	1.77
E7ETK0	E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1	41.50	9.00	7.00	8.00	11.00	3.00	3.00	4.84E-06	1.85E-06	3.90E-06	4.16E-06	2.15E-06	1.56E-06	0.86	0.44	0.32
P38159	RBMX_HUMAN RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3	11.10	2.97		2.97	2.97	0.99	1.98	2.81E-07		4.52E-07	5.71E-07	1.22E-07	3.74E-07	2.03	0.43	1.33
B4E2P2	B4E2P2_HUMAN Translocon-associated protein subunit gamma OS=Homo sapiens GN=SSR3 PE=2 SV=1	19.50	5.00	12.00	15.00	11.00	9.00	5.00	6.07E-07	4.11E-06	3.07E-06	2.02E-06	2.93E-06	8.08E-07	3.32	4.83	1.33
E5RJR5	E5RJR5_HUMAN S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=2 SV=1	25.80	0.99	1.99	1.99	1.00	2.98	1.00	1.47E-07	2.85E-08	1.43E-07	2.33E-08	4.47E-07	7.62E-09	0.16	3.05	0.05
B4DF41	B4DF41_HUMAN DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=2 SV=1	18.00	1.00	9.00	5.00	5.00	9.00	4.00	2.75E-09	4.78E-08	2.12E-08	6.11E-08	4.66E-08	6.44E-09	22.23	16.95	2.34
Q9UL03	INT6_HUMAN Integrator complex subunit 6 OS=Homo sapiens GN=INTS6 PE=1 SV=1	11.90	7.88	4.93		3.94		0.98	2.25E-07	4.89E-08		1.11E-07		6.91E-08	0.49	Control 1 Only	0.31
Q9H0U3	MAGT1_HUMAN Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1	19.70	3.00	6.00	5.50	6.00	3.00	3.00	1.69E-07	1.32E-06	5.97E-07	1.78E-06	8.86E-07	2.13E-07	10.49	5.23	1.26

	PE=1 SV=1																	
Q9Y6A4	CP080_HUMAN UPF0468 protein C16orf80 OS=Homo sapiens GN=C16orf80 PE=1 SV=1	17.10	2.00	1.00	3.00	1.00	1.00	2.00	8.29E-08	1.10E-07	1.28E-07	1.66E-07	7.23E-08	2.36E-07	2.00	0.87	2.85
Q9Y4P3	TBL2_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1	51.90	11.96	6.97	10.95	14.92	8.97	2.98	1.70E-06	1.40E-06	3.96E-06	2.38E-06	1.66E-06	1.23E-06	1.40	0.97	0.72
Q92804	RBP56_HUMAN TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1	44.10	10.89	9.90	16.83	28.71	13.86	12.87	4.94E-06	3.02E-06	2.23E-06	5.72E-06	3.27E-06	4.39E-06	1.16	0.66	0.89
A8MXZ4	A8MXZ4_HUMAN G-protein-coupled receptor family C group 5 member C (Fragment) OS=Homo sapiens GN=GPRC5C PE=4 SV=2	23.00		2.00	1.00	3.00	1.00	1.00		1.98E-07	4.89E-08	1.54E-07	1.31E-07	8.37E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
F5H564	F5H564_HUMAN Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=2 SV=1	6.00	1.97	3.91	5.82	3.91	1.94	1.94	1.47E-08	9.57E-08	6.60E-08	5.79E-08	4.84E-08	8.09E-09	3.95	3.30	0.55
P24752	THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	36.80	2.99	6.97	4.98		6.97	1.99	5.23E-07	1.17E-06	1.73E-06		4.52E-06	1.17E-07	Control 1 Only	8.65	0.22
P35250	RFC2_HUMAN Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3	21.80	0.99	3.98	2.98	3.99		0.99	1.15E-07	2.31E-07	6.26E-07	5.99E-07		7.99E-08	5.20	Control 1 Only	0.69
E9PC52	E9PC52_HUMAN Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=2 SV=1	28.40	2.00	3.98	1.00	4.96	2.98	2.99	1.93E-07	8.63E-07	2.47E-08	6.11E-07	4.51E-07	4.54E-07	3.17	2.34	2.36
Q9UHB6	LIMA1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	21.30	0.99	0.99	5.93	9.90	3.95	3.96	6.39E-08	9.72E-09	2.26E-07	1.35E-07	1.30E-07	1.72E-07	2.11	2.03	2.70
P42166	LAP2A_HUMAN Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	30.30		1.00	7.00	5.00	2.00	3.00		1.31E-07	1.76E-07	1.05E-07	2.75E-07	6.69E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JZR2	C9JZR2_HUMAN Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=2 SV=2	39.20	10.76	21.51	23.45	43.04	21.49	17.58	3.11E-07	9.51E-07	1.09E-06	1.76E-06	8.17E-07	6.04E-07	5.67	2.63	1.94
I3L1L3	I3L1L3_HUMAN Myb-binding protein 1A (Fragment) OS=Homo sapiens GN=MYBBP1A PE=4 SV=1	6.70	2.00	1.00	2.00	4.00		2.00	1.51E-08	8.43E-09	5.86E-09	3.16E-08		1.54E-08	2.09	Control 1 Only	1.02
A8MXP9	A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	48.10	20.60	19.67	49.13	45.25	17.65	23.55	6.56E-07	1.20E-06	2.70E-06	3.40E-06	7.20E-07	1.91E-06	5.18	1.10	2.91
O60231	DHX16_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 OS=Homo sapiens GN=DHX16 PE=1 SV=2	4.90		3.00		2.00	1.00	1.00		5.19E-08		1.34E-08	1.14E-08	7.98E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
O14980	XPO1_HUMAN Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	7.60		4.00	1.00	2.00	3.99	1.00		5.38E-08	5.86E-09	6.46E-08	1.91E-08	9.05E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q92499	DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	48.00	17.00	12.00	21.00	22.00	17.00	21.00	8.87E-07	9.97E-07	2.00E-06	1.47E-06	1.79E-06	1.90E-06	1.66	2.01	2.14
Q9H4H8	FA83D_HUMAN Protein FAM83D OS=Homo sapiens GN=FAM83D PE=1 SV=3	9.20	1.00	1.00			3.00	1.00	4.14E-08	9.55E-08			1.74E-07	3.06E-08	Control 1 Only	4.19	0.74
P63000	RAC1_HUMAN Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1	29.20	4.94	2.97	7.92	7.89	3.95	3.93	9.92E-07	1.46E-06	3.61E-06	3.62E-06	2.11E-06	2.21E-06	3.65	2.13	2.23
Q9UHB9	SRP68_HUMAN Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2	51.60	12.82	8.88	24.65	10.85	8.87	8.89	6.18E-07	8.29E-07	1.69E-06	5.50E-07	1.23E-06	5.56E-07	0.89	1.98	0.90
Q96TC7	RMD3_HUMAN Regulator of microtubule dynamics protein 3 OS=Homo sapiens GN=RMDN3 PE=1 SV=2	24.70	4.99	6.98	2.99	6.97	2.98	5.98	2.79E-07	2.83E-07	3.39E-08	3.77E-07	3.48E-07	1.11E-07	1.35	1.24	0.40
B4E2W0	B4E2W0_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1	36.30	5.93	1.98	1.98	4.95	3.96	4.94	3.69E-07	9.12E-08	4.06E-07	2.39E-07	5.98E-07	3.59E-07	0.65	1.62	0.97

P98175	RBM10_HUMAN RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3	13.90	4.00	7.00	4.00	8.00	4.00	1.00	9.51E-08	8.12E-08	3.55E-08	2.52E-07	4.19E-08	1.30E-08	2.65	0.44	0.14
E7EWP0	E7EWP0_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial OS=Homo sapiens GN=NDUFB5 PE=2 SV=1	22.60		1.50	2.00	2.00	2.50			7.78E-07	2.04E-07	7.86E-07	5.56E-07		Sample 1 Only	Sample 2 Only	
Q9P035	HACD3_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=1 SV=2	26.80	6.93	6.93	11.86	17.80	10.89	6.96	1.87E-06	1.44E-06	2.18E-06	3.44E-06	2.91E-06	7.76E-07	1.84	1.56	0.42
O75340	PDCD6_HUMAN Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	46.60	6.00	5.00	3.00	4.99	5.00	6.00	4.22E-07	8.06E-07	1.59E-07	2.10E-07	1.26E-06	4.02E-07	0.50	2.98	0.95
P78347	GTF2I_HUMAN General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	55.10	40.99	52.95	66.88	51.93	41.00	69.90	2.04E-06	4.38E-06	2.66E-06	4.07E-06	2.23E-06	5.30E-06	2.00	1.09	2.60
Q9Y277	VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	61.80	16.74	29.57	21.67	46.36	34.53	37.44	2.36E-06	1.54E-05	4.80E-06	8.99E-06	1.07E-05	8.44E-06	3.81	4.53	3.58
P53621	COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	58.30	22.98	31.99	50.98	33.98	46.98	44.98	6.65E-07	1.85E-06	1.53E-06	1.47E-06	1.52E-06	2.27E-06	2.20	2.29	3.41
M0R1Y2	M0R1Y2_HUMAN ER lumen protein retaining receptor (Fragment) OS=Homo sapiens GN=KDELR1 PE=2 SV=1	14.60	1.50	2.50	2.00	1.00	1.00	0.50	5.74E-08	2.30E-07	7.33E-08	2.76E-07	8.52E-08	1.42E-07	4.81	1.48	2.47
P20042	IF2B_HUMAN Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2	15.00	1.00	1.00	3.00	3.00	1.00	1.00	5.48E-08	2.11E-07	4.33E-07	3.56E-07	8.99E-09	1.43E-07	6.50	0.16	2.61
E9PKH6	E9PKH6_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial (Fragment) OS=Homo sapiens GN=NDUFS8 PE=2 SV=1	27.30	1.00	3.00	4.00	1.00	2.00	2.00	7.47E-08	4.49E-07	5.84E-07	8.87E-08	6.42E-07	7.56E-07	1.19	8.59	10.12
Q9NSD9	SYFB_HUMAN Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3	25.60	8.00	4.00	10.00	8.00	5.00	4.00	4.42E-07	1.61E-07	1.06E-06	7.51E-07	3.85E-07	1.11E-07	1.70	0.87	0.25
F5GWX5	F5GWX5_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=2 SV=1	18.60	7.48	9.98	5.99	12.48	11.98	12.98	9.90E-08	2.07E-07	4.43E-08	2.58E-07	9.86E-08	1.29E-07	2.60	1.00	1.30
P05198	IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	60.30	10.00	11.00	6.00	13.00	14.00	6.00	9.24E-07	1.55E-06	9.03E-07	1.29E-06	2.09E-06	9.89E-07	1.39	2.27	1.07
Q9Y2K7	KDM2A_HUMAN Lysine-specific demethylase 2A OS=Homo sapiens GN=KDM2A PE=1 SV=3	3.30	1.98	0.99	2.97	1.98		1.98	4.61E-08	9.70E-09	7.84E-08	8.24E-08		1.02E-08	1.79	Control 1 Only	0.22
P61978	HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	50.20	18.66	26.53	33.37	36.39	33.43	28.49	3.53E-06	7.68E-06	2.32E-05	1.61E-05	1.17E-05	1.42E-05	4.55	3.32	4.03
Q8TCJ2	STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1	21.80	8.00	14.00	22.00	20.00	14.00	13.00	6.75E-08	4.28E-07	4.25E-07	7.25E-07	2.49E-07	2.56E-07	10.74	3.69	3.79
P21796	VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	58.30	11.50	14.00	10.00	17.50	24.50	15.00	1.25E-06	3.16E-06	2.80E-06	2.78E-06	4.14E-06	2.19E-06	2.22	3.31	1.75
F5H3I5	F5H3I5_HUMAN CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=2 SV=1	34.40	0.99	6.92	5.93	5.93	9.89	4.94	7.69E-08	8.74E-07	3.79E-07	6.64E-07	8.54E-07	2.36E-07	8.64	11.12	3.08
Q13283	G3BP1_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens	23.80	6.00	8.97	4.99	9.97	6.99	4.00	3.61E-07	6.16E-07	1.34E-07	3.36E-07	6.16E-07	5.17E-07	0.93	1.71	1.43

	GN=G3BP1 PE=1 SV=1																
Q7KZF4	SND1_HUMAN Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1	6.90	1.00	2.00	1.00	1.00	4.00	1.00	2.24E-08	2.81E-08	1.97E-08	3.78E-08	5.45E-08	9.14E-09	1.69	2.43	0.41
P81605	DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	30.00	7.00	4.00	5.00	1.00	8.00	4.00	1.41E-05	6.25E-06	3.92E-06	1.45E-07	1.93E-05	3.59E-07	0.01	1.37	0.03
O60841	IF2P_HUMAN Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4	8.60	2.00	3.00	7.00	3.00	3.00	1.00	1.93E-08	2.03E-08	5.23E-08	4.92E-08	1.11E-08	3.45E-09	2.55	0.57	0.18
Q92544	TM9S4_HUMAN Transmembrane 9 superfamily member 4 OS=Homo sapiens GN=TM9SF4 PE=1 SV=2	13.20	3.00		2.00	7.00	4.00	1.00	3.21E-07		7.68E-09	1.85E-07	2.41E-07	2.09E-08	0.58	0.75	0.07
C9JCN0	C9JCN0_HUMAN Myoferlin OS=Homo sapiens GN=MYOF PE=2 SV=2	10.90	1.98	4.95	7.92	2.97	9.89	4.95	3.30E-09	4.94E-08	4.82E-08	2.11E-08	9.13E-08	3.00E-08	6.39	27.69	9.10
Q15005	SPCS2_HUMAN Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3	47.80		4.96	10.87	6.92	9.89	8.89		1.35E-06	1.36E-06	9.77E-07	1.73E-06	7.49E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
P39019	RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	72.40	20.00	16.00	23.00	12.00	12.00	12.00	6.71E-06	1.57E-05	8.33E-06	1.55E-05	2.61E-06	7.27E-06	2.31	0.39	1.08
P12532	KCRU_HUMAN Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1	17.00	2.98	3.96	3.97	5.93	5.95	4.93	1.93E-07	3.27E-07	1.65E-07	4.57E-07	2.76E-07	1.71E-07	2.36	1.43	0.89
B4DZC3	B4DZC3_HUMAN 5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=2 SV=1	13.00	6.00	4.00	2.00	2.00	1.00	3.00	1.68E-07	7.08E-08	4.78E-08	9.64E-08	2.94E-09	1.11E-07	0.57	0.02	0.66
P13647	K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	59.70	60.80	46.80	57.82	45.83	51.76	47.80	1.06E-05	4.47E-06	3.46E-06	3.65E-06	5.65E-06	5.90E-06	0.35	0.54	0.56
B0YIW6	B0YIW6_HUMAN Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=2 SV=1	6.80		1.00	1.00		3.00	1.00		5.61E-08	2.20E-08		7.12E-08	3.87E-08		Sample 2 Only	Sample 3 Only
G3V1R4	G3V1R4_HUMAN NOL1/NOP2/Sun domain family, member 2, isoform CRA_b OS=Homo sapiens GN=NSUN2 PE=2 SV=1	11.90	2.00	4.00	3.00	5.00	1.00	1.00	3.03E-08	7.21E-08	8.05E-08	7.50E-08	5.49E-08	3.02E-09	2.48	1.81	0.10
P54136	SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	18.60	2.97	5.95	5.95	12.90	1.98	3.96	1.01E-07	2.93E-07	2.55E-07	6.61E-07	4.77E-08	1.42E-07	6.52	0.47	1.40
Q9P258	RCC2_HUMAN Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	22.40	4.00	6.00	8.00	4.00	9.00	6.00	1.25E-07	4.92E-07	6.17E-07	2.54E-07	8.72E-07	4.63E-07	2.03	6.98	3.71
Q14244	MAP7_HUMAN Ensconsin OS=Homo sapiens GN=MAP7 PE=1 SV=1	19.50	2.95	14.74	2.94	12.78	2.95	7.87	8.90E-08	7.65E-07	1.95E-08	5.37E-07	9.30E-08	5.00E-07	6.03	1.05	5.62
B4DR03	B4DR03_HUMAN N-alpha-acetyltransferase 40 OS=Homo sapiens GN=NAA40 PE=2 SV=1	16.70		2.97	2.97	1.98	1.98			1.44E-07	1.65E-07	2.39E-07	1.72E-07		Sample 1 Only	Sample 2 Only	
Q9NTI5	PDS5B_HUMAN Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B PE=1 SV=1	11.30	1.00	2.00	5.00	4.00	2.00		5.97E-09	1.58E-08	4.51E-08	7.36E-08	1.94E-08		12.34	3.25	Control 1 Only
O43809	CPSF5_HUMAN Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens GN=NUDT21 PE=1 SV=1	39.20	8.00	6.00	8.00	8.00	7.00	9.00	1.22E-06	1.70E-06	1.21E-06	1.19E-06	9.43E-07	1.18E-06	0.97	0.77	0.97
Q9BU61	NDUF3_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Homo sapiens GN=NDUFAF3 PE=1 SV=1	19.00		3.00	1.00	2.00	2.00	3.00		8.34E-07	1.69E-07	1.95E-07	6.00E-07	4.92E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y446	PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	14.70	7.00	6.00	6.00	13.98	2.00	5.00	1.79E-07	2.81E-07	7.40E-07	6.84E-07	1.22E-07	1.29E-07	3.83	0.68	0.72
P35579	MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	22.10	2.99	3.96	14.93	1.99	18.94	4.96	1.12E-08	4.46E-08	7.81E-08	2.87E-08	1.28E-07	2.49E-08	2.56	11.39	2.23
Q9NPD3	EXOS4_HUMAN Exosome complex component RRP41 OS=Homo sapiens	26.10	2.00	6.00	4.00	2.00	5.00	3.00	6.32E-08	1.11E-06	3.42E-07	5.33E-07	1.26E-06	1.27E-07	8.42	19.90	2.00

	GN=EXOSC4 PE=1 SV=3																
Q00839	HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	51.80	17.00	19.50	28.50	33.50	13.00	22.00	2.04E-06	2.14E-06	2.56E-06	3.39E-06	6.25E-07	1.48E-06	1.66	0.31	0.72
P63092	GNAS2_HUMAN Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1	32.50	2.00	8.99	6.00	10.99	4.00	4.00	2.53E-07	7.46E-07	5.35E-07	1.10E-06	2.86E-07	5.46E-07	4.34	1.13	2.16
P33991	MCM4_HUMAN DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5	22.20	1.00	14.99	1.00	5.00	8.98	1.00	2.75E-08	3.05E-07	5.41E-08	9.57E-08	3.88E-07	1.95E-08	3.48	14.14	0.71
Q13185	CBX3_HUMAN Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4	27.30	11.00	7.00	8.00	8.00	6.00	6.00	8.38E-07	6.35E-07	4.85E-07	1.25E-06	7.51E-07	4.45E-07	1.49	0.90	0.53
P55884	EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	29.40	6.00	12.98	4.99	15.97	7.98	8.97	2.61E-07	8.45E-07	1.35E-07	1.17E-06	1.27E-07	2.68E-07	4.47	0.49	1.03
Q8N163	CCAR2_HUMAN Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2	56.00	27.60	23.66	17.77	47.35	31.59	18.73	2.14E-06	4.95E-06	4.63E-07	5.90E-06	2.32E-06	9.07E-07	2.76	1.09	0.42
Q92615	LAR4B_HUMAN La-related protein 4B OS=Homo sapiens GN=LARP4B PE=1 SV=3	14.60	3.00	7.53	7.53	5.00	5.00	1.00	4.75E-08	2.09E-07	2.29E-07	2.54E-07	1.19E-07	2.29E-09	5.36	2.52	0.05
Q8TEQ6	GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	11.20		10.00	3.00	9.00	6.00	1.00		1.47E-07	2.29E-08	1.49E-07	7.18E-08	3.84E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
F5H047	F5H047_HUMAN Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) OS=Homo sapiens GN=CPSF7 PE=2 SV=1	24.90	1.99	2.98	1.99	3.98	1.99	1.99	2.64E-07	7.14E-07	2.85E-07	5.44E-07	1.63E-07	3.01E-07	2.06	0.62	1.14
Q9Y6Q5-2	AP1M2_HUMAN Isoform 2 of AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2	42.40	0.50	2.50		2.00	1.00	1.50	4.79E-09	4.08E-07		1.21E-07	1.47E-07	5.26E-08	25.20	30.71	10.99
P62899	RL31_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	57.60	15.92	11.94	17.89	11.93	7.95	7.95	1.07E-05	2.97E-05	9.58E-06	3.16E-05	1.88E-05	7.64E-06	2.96	1.76	0.72
P40939	ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	35.50	13.00	12.00	7.00	12.00	9.00	8.00	9.74E-07	9.00E-07	5.67E-07	9.21E-07	8.20E-07	2.47E-07	0.94	0.84	0.25
P33993	MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	45.50	10.94	28.89	9.94	27.88	15.91	8.94	9.14E-07	1.95E-06	4.66E-07	1.71E-06	1.81E-06	5.21E-07	1.87	1.98	0.57
F5GX68	F5GX68_HUMAN Cytosine-specific methyltransferase OS=Homo sapiens GN=DNMT1 PE=2 SV=1	9.10	1.00	6.00	3.00		7.00	2.00	2.17E-09	6.62E-08	1.02E-08		7.92E-08	2.50E-08	Control 1 Only	36.53	11.52
P62304	RUXE_HUMAN Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1	38.00	6.00	4.00	5.00	5.00	2.00	7.00	8.34E-07	9.61E-07	7.26E-07	1.19E-06	3.82E-07	1.50E-06	1.43	0.46	1.80
Q16891	IMMT_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1	45.50	17.66	28.48	26.49	36.31	22.58	9.81	1.53E-06	1.95E-06	3.69E-06	4.71E-06	2.23E-06	1.62E-06	3.08	1.46	1.06
Q9NRZ9	HELLS_HUMAN Lymphoid-specific helicase OS=Homo sapiens GN=HELLS PE=1 SV=1	5.00	1.00	5.00	2.00	2.00			7.05E-08	1.22E-07	7.05E-08	3.37E-07			4.78	Control 1 Only	Control 1 Only
P02533	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	72.00	33.00	25.00	27.50	21.50	35.00	30.50	6.33E-06	1.81E-06	2.02E-06	3.38E-06	5.22E-06	3.43E-06	0.53	0.82	0.54
J3KTL7	J3KTL7_HUMAN Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=2 SV=1	15.00	1.98	2.97	1.98	3.96	1.98	2.97	2.92E-08	3.35E-08	9.47E-08	5.20E-08	7.71E-08	7.49E-08	1.78	2.64	2.56
P25398	RS12_HUMAN 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	40.20	1.00	2.00	7.00	4.00	4.00	2.00	2.68E-07	8.83E-07	1.30E-05	3.70E-06	2.39E-06	5.93E-06	13.80	8.91	22.15
Q08211	DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	34.20	17.00	17.00	38.00	19.00	19.00	18.00	4.08E-07	4.12E-07	8.67E-07	5.74E-07	3.93E-07	4.16E-07	1.41	0.96	1.02

B4DR61	B4DR61_HUMAN Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=2 SV=1	12.40		4.00	5.99	3.98	3.00	5.00		1.78 E-06	9.18 E-07	4.67 E-07	1.68 E-07	1.60 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P06748	NPM_HUMAN Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	67.00	22.81	20.79	40.64	41.64	37.65	22.77	1.23 E-05	8.93 E-06	2.60 E-05	1.51 E-05	1.29 E-05	1.31 E-05	1.23	1.05	1.07
O00767	ACOD_HUMAN Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2	7.00		1.00	4.00	1.00	3.00	3.00		5.81 E-08	2.34 E-07	2.06 E-09	1.03 E-07	2.62 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6ZXV5	TMTC3_HUMAN Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2	6.80		1.00	3.97	1.97	2.00			2.28 E-08	4.04 E-08	2.87 E-08	1.97 E-08		Sample 1 Only	Sample 2 Only	
C9J9K3	C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	72.00	26.88	23.90	24.91	27.88	21.92	17.92	2.50 E-05	7.67 E-06	1.64 E-05	2.37 E-05	1.56 E-05	3.72 E-06	0.95	0.62	0.15
Q9Y295	DRG1_HUMAN Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1	38.40	4.00	7.00	2.00	11.00	7.00	9.00	3.19 E-07	1.40 E-06	2.43 E-08	7.38 E-07	2.15 E-07	1.14 E-06	2.31	0.67	3.56
K7ER00	K7ER00_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=2 SV=1	49.60	23.61	19.67	22.64	25.59	23.59	11.80	2.49 E-06	1.72 E-06	4.25 E-06	5.69 E-06	2.42 E-06	1.76 E-06	2.28	0.97	0.70
Q9NTJ3	SMC4_HUMAN Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2	25.00	3.95	14.82	11.85	4.93	10.87	2.97	4.72 E-08	3.77 E-07	9.35 E-08	2.23 E-07	3.80 E-07	3.03 E-08	4.72	8.05	0.64
Q96TA2	YMEL1_HUMAN ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1 PE=1 SV=2	18.70	2.99	6.98	2.99	5.96	2.99	3.99	9.22 E-08	2.76 E-07	1.50 E-07	2.94 E-08	5.02 E-08	7.90 E-08	3.19	0.54	0.86
P48651	PTSS1_HUMAN Phosphatidylserine synthase 1 OS=Homo sapiens GN=PTDSS1 PE=1 SV=1	10.10	3.98	3.97	5.99	3.99	3.97	1.98	3.61 E-08	6.75 E-08	3.67 E-07	1.89 E-07	2.13 E-07	1.72 E-07	5.25	5.91	4.77
Q96T88	UHRF1_HUMAN E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1	12.20	1.00	3.00	2.00	11.00	1.00		1.02 E-07	1.44 E-07	8.34 E-08	3.62 E-07	4.22 E-08		3.56	0.42	Control 1 Only
P46778	RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	55.00	18.88	13.91	20.86	18.88	14.89	11.90	1.59 E-05	1.78 E-05	1.61 E-05	1.97 E-05	1.23 E-05	1.21 E-05	1.24	0.77	0.76
O43390	HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	17.20	4.91	2.95	2.94	8.82		3.90	1.02 E-07	3.64 E-08	1.05 E-07	2.23 E-07		7.66 E-08	2.19	Control 1 Only	0.75
K7ENA8	K7ENA8_HUMAN Eukaryotic translation initiation factor 3 subunit G (Fragment) OS=Homo sapiens GN=EIF3G PE=2 SV=1	18.00	2.97	0.99	0.99	2.97	1.98	1.98	7.90 E-07	3.27 E-07	1.28 E-07	1.76 E-07	4.17 E-07	4.54 E-07	0.22	0.53	0.57
O95347	SMC2_HUMAN Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	33.50	3.00	13.98	29.95	14.99	13.99	4.99	3.07 E-08	3.34 E-07	3.15 E-07	2.42 E-07	2.67 E-07	5.70 E-08	7.89	8.70	1.86
Q13547	HDAC1_HUMAN Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1	18.90	2.00	2.00	2.00	5.00	1.00	1.00	3.54 E-07	5.07 E-07	3.21 E-07	8.02 E-07	5.46 E-07	5.26 E-08	2.27	1.54	0.15
Q9H2P0	ADNP_HUMAN Activity-dependent neuroprotector homeobox protein OS=Homo sapiens GN=ADNP PE=1 SV=1	13.30	3.00	6.00		7.00	3.00	2.00	1.86 E-08	1.78 E-07		1.31 E-07	6.49 E-08	4.52 E-08	7.08	3.50	2.43
Q92797	SYMPK_HUMAN Symplekin OS=Homo sapiens GN=SYMPK PE=1 SV=2	7.80	1.99	1.99	3.99	3.99	1.00	1.99	5.92 E-09	1.97 E-08	6.91 E-08	8.73 E-08	5.05 E-09	2.54 E-08	14.73	0.85	4.30
Q01081	U2AF1_HUMAN Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3	39.20	11.90	3.97	9.92	12.88	6.94	5.96	1.24 E-06	1.26 E-06	3.41 E-06	3.00 E-06	2.45 E-06	1.35 E-06	2.43	1.98	1.09
O75533	SF3B1_HUMAN Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	25.80	17.00	14.00	19.00	24.00	16.00	14.00	5.35 E-07	3.55 E-07	4.19 E-07	5.80 E-07	3.40 E-07	6.19 E-07	1.08	0.64	1.16
P07814	SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	21.00	3.00	8.00	15.00	16.00	4.00	12.00	4.80 E-08	2.43 E-07	1.92 E-07	3.38 E-07	3.14 E-08	2.07 E-07	7.05	0.66	4.31

Q14011	CIRBP_HUMAN Cold-inducible RNA-binding protein OS=Homo sapiens GN=CIRBP PE=1 SV=1	30.20	1.99	1.99	1.99	3.97	2.98	3.98	3.49 E-07	2.88 E-07	9.86 E-08	1.34 E-07	2.46 E-07	4.91 E-07	0.38	0.70	1.41
Q8NFW8	NEUA_HUMAN N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2	33.90	5.97	3.99	4.97	7.96	3.98	4.97	6.94 E-07	5.81 E-07	7.09 E-07	1.66 E-06	2.86 E-07	3.64 E-07	2.39	0.41	0.53
P61254	RL26_HUMAN 60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	66.20	5.44	4.48	11.42	5.46	3.98	1.00	6.90 E-06	3.34 E-06	1.09 E-05	1.23 E-05	5.47 E-06	9.82 E-07	1.78	0.79	0.14
E9PH82	E9PH82_HUMAN Protein FAM98A OS=Homo sapiens GN=FAM98A PE=2 SV=1	23.70	1.00	1.00	7.00	6.00	3.00	1.00	2.99 E-07	4.25 E-08	1.00 E-06	8.90 E-07	6.24 E-07	5.65 E-08	2.97	2.09	0.19
Q96AX1	VP33A_HUMAN Vacuolar protein sorting-associated protein 33A OS=Homo sapiens GN=VPS33A PE=1 SV=1	10.70		1.00	1.00		3.00	1.00		4.82 E-07	4.31 E-08		2.95 E-07	1.46 E-07		Sample 2 Only	Sample 3 Only
Q9Y265	RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	29.40	1.99	6.92	1.99	7.91	5.94	3.96	9.88 E-09	7.36 E-07	6.99 E-08	5.09 E-07	3.82 E-07	6.62 E-08	51.50	38.65	6.70
P51991-2	ROA3_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3	40.40	1.00	1.00	2.00	2.00	3.00	1.00	7.43 E-07	9.40 E-07	1.79 E-06	3.95 E-07	1.33 E-06	1.30 E-06	0.53	1.79	1.75
P62136	PP1A_HUMAN Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	32.50			1.99	2.98	0.99	0.99			1.47 E-07	1.65 E-07	3.45 E-09	9.21 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8NBU5	ATAD1_HUMAN ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1	19.50		1.00	3.00	3.00	3.00	3.00		7.32 E-07	1.11 E-06	1.12 E-06	5.78 E-07	4.26 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q96KR1	ZFR_HUMAN Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2	12.50	1.00	3.00	6.00	3.00		5.00	2.11 E-08	4.07 E-08	1.17 E-07	8.67 E-08		6.24 E-08	4.11	Control 1 Only	2.96
Q14739	LBR_HUMAN Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2	13.70	6.00	7.00	7.00	10.00	5.00	4.00	2.18 E-07	4.09 E-07	1.83 E-07	6.90 E-07	5.75 E-08	1.93 E-07	3.16	0.26	0.88
Q9BPW8	NIPS1_HUMAN Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1	16.90	3.97	4.96		2.97	4.96	0.99	2.12 E-07	3.39 E-07		2.42 E-07	3.76 E-07	2.49 E-08	1.14	1.77	0.12
A5YKK6	CNOT1_HUMAN CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	6.00		3.95	3.94	4.95	2.95	0.98		1.84 E-08	1.70 E-08	1.40 E-08	1.05 E-08	4.42 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P26641	EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	46.90	13.00	34.00	25.00	28.00	35.00	23.00	2.19 E-06	1.60 E-05	8.24 E-06	4.96 E-06	1.21 E-05	6.84 E-06	2.26	5.52	3.12
Q9Y4D1	DAAM1_HUMAN Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens GN=DAAM1 PE=1 SV=2	8.50	3.00	4.00	2.00	5.00	2.00	1.00	7.87 E-08	1.02 E-07	6.96 E-09	1.69 E-07	4.22 E-08	1.05 E-08	2.14	0.54	0.13
P45880	VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	62.90	18.75	26.68	24.73	26.70	26.69	26.68	6.86 E-06	2.82 E-05	2.30 E-05	1.44 E-05	2.87 E-05	9.83 E-06	2.10	4.18	1.43
P56556	NDUA6_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 OS=Homo sapiens GN=NDUFA6 PE=1 SV=3	39.60	1.00	3.00	4.00	3.00	5.00	2.00	6.92 E-08	1.34 E-06	1.21 E-06	5.42 E-07	1.79 E-06	6.35 E-07	7.84	25.90	9.17
Q9UJS0	CMC2_HUMAN Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2	42.40	8.00	12.00	14.00	15.00	14.00	11.00	3.04 E-07	5.49 E-07	9.95 E-07	3.59 E-07	8.60 E-07	4.03 E-07	1.18	2.83	1.33
P38919	IF4A3_HUMAN Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	28.20	1.00	8.00	5.00	1.00	2.00	1.00	7.04 E-08	3.63 E-07	1.13 E-06	5.11 E-07	1.20 E-06	7.14 E-08	7.26	17.03	1.01
H0YGW7	H0YGW7_HUMAN ATP-binding cassette sub-family F member 1 (Fragment) OS=Homo sapiens GN=ABCF1 PE=4 SV=1	30.40	2.00	11.00	12.00	10.00	8.00	3.00	1.19 E-07	9.33 E-07	4.76 E-07	1.19 E-06	2.84 E-07	2.66 E-07	9.99	2.38	2.23
H7BYN4	H7BYN4_HUMAN Kinesin-like protein KIF23 OS=Homo sapiens GN=KIF23 PE=2 SV=1	10.40	1.98	2.96	6.92	7.91	2.97	1.98	4.46 E-08	3.17 E-08	5.22 E-08	7.27 E-08	3.84 E-08	4.01 E-08	1.63	0.86	0.90
Q04	SSBP_HUMAN Single-stranded DNA-binding	58.10	1.98	3.97	7.93	1.98	5.97	2.98	1.46	6.30	2.40	1.40	5.79	1.97	0.96	3.98	1.36

837	protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1								E-06	E-06	E-06	E-06	E-06	E-06			
G3V325	G3V325_HUMAN Pentatricopeptide repeat-containing protein 1, mitochondrial OS=Homo sapiens GN=ATP5J2-PTCD1 PE=4 SV=1	4.90	2.00	3.00	2.00	1.00	2.00	2.00	1.93 E-08	6.38 E-08	2.20 E-08	8.95 E-10	6.74 E-08	2.08 E-08	0.05	3.48	1.07
Q16795	NDUA9_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens GN=NDUFA9 PE=1 SV=2	23.10	4.99	4.99	3.00	4.00	8.00	3.00	2.39 E-07	1.22 E-07	2.11 E-07	1.17 E-07	2.67 E-07	1.15 E-07	0.49	1.12	0.48
E7EPX0	E7EPX0_HUMAN Double-stranded RNA-binding protein Staufen homolog 2 OS=Homo sapiens GN=STAU2 PE=2 SV=1	17.70	0.99	0.99	4.95	1.98	0.99	1.98	4.65 E-09	4.35 E-09	9.39 E-08	3.81 E-08	8.77 E-09	7.40 E-08	8.19	1.89	15.90
Q10469	MGAT2_HUMAN Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT2 PE=1 SV=1	9.20	2.00		1.00	4.00	1.00	2.00	2.83 E-07		9.60 E-08	1.93 E-07	7.46 E-08	6.17 E-08	0.68	0.26	0.22
Q969V3	NCLN_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2	23.50	1.99	5.95	4.94	5.95	2.99	3.97	5.90 E-08	1.37 E-06	1.46 E-07	6.15 E-07	4.46 E-07	3.34 E-07	10.42	7.57	5.67
O95994	AGR2_HUMAN Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1	33.10	1.98	7.95	3.96	2.97	6.95	5.96	1.60 E-07	1.60 E-06	4.56 E-07	6.32 E-07	1.13 E-06	7.27 E-07	3.94	7.07	4.53
B4DER1	B4DER1_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1	9.90	4.00	4.00	5.00	5.00	6.00	5.00	4.04 E-08	4.87 E-08	1.86 E-08	6.72 E-08	2.46 E-08	3.44 E-08	1.66	0.61	0.85
P51532	SMCA4_HUMAN Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2	6.10	4.96	3.98	2.99	1.00	1.99	2.98	4.04 E-08	2.88 E-08	3.91 E-08	4.50 E-09	4.10 E-08	4.70 E-08	0.11	1.01	1.16
P22626	ROA2_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	54.30	51.00	51.00	41.00	51.00	46.00	48.00	7.15 E-05	1.25 E-04	5.66 E-05	5.34 E-05	1.02 E-04	1.16 E-04	0.75	1.43	1.63
Q15125	EBP_HUMAN 3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase OS=Homo sapiens GN=EBP PE=1 SV=3	16.50	2.00	4.00	4.00	7.00	6.00	4.00	5.04 E-07	4.80 E-07	1.32 E-06	7.72 E-07	6.19 E-07	1.19 E-06	1.53	1.23	2.36
Q14008	CKAP5_HUMAN Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	8.60	2.00	7.00	4.00	5.00	5.00	1.00	4.07 E-09	4.29 E-08	1.75 E-08	2.01 E-08	3.01 E-08	4.70 E-09	4.94	7.39	1.15
Q7Z2W4	ZCCHV_HUMAN Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3	9.20	0.99	5.96	1.99	2.99	1.00	1.98	4.63 E-08	1.64 E-07	7.80 E-08	1.36 E-07	6.01 E-08	5.61 E-08	2.93	1.30	1.21
Q09161	NCBP1_HUMAN Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1	2.90	1.00	2.00	2.00	1.00	3.00	2.00	2.94 E-08	9.53 E-08	7.42 E-08	3.23 E-08	4.56 E-08	1.50 E-07	1.10	1.55	5.10
O43242	PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	34.10	4.00	8.00	9.99	7.99	6.00	5.00	1.37 E-07	5.12 E-07	4.91 E-07	4.80 E-07	2.82 E-07	2.57 E-07	3.51	2.06	1.88
P35232	PHB_HUMAN Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	62.10	7.96	13.93	8.94	10.94	8.96	9.95	5.19 E-07	2.75 E-06	1.01 E-06	1.79 E-06	1.09 E-06	1.83 E-06	3.45	2.10	3.53
Q9Y2T7	YBOX2_HUMAN Y-box-binding protein 2 OS=Homo sapiens GN=YBX2 PE=1 SV=2	29.90	4.00	2.00	3.00	4.00	3.00	1.00	1.06 E-06	7.00 E-08	2.32 E-07	1.02 E-06	2.21 E-07	2.76 E-07	0.96	0.21	0.26
H0UI80	H0UI80_HUMAN Negative elongation factor C/D OS=Homo sapiens GN=TH1L PE=2 SV=1	11.20		3.00	2.00	1.00	4.00			1.97 E-07	5.97 E-08	1.75 E-08	2.73 E-07		Sample 1 Only	Sample 2 Only	
F8WCY5	F8WCY5_HUMAN Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=2 SV=1	11.00	3.00	4.00	1.00	6.00	3.00		5.93 E-08	1.24 E-07	1.80 E-08	1.00 E-07	7.71 E-08		1.69	1.30	Control 1 Only
Q14694	UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2	26.90	11.97	12.99	12.98	16.97	9.98	10.98	3.36 E-07	6.84 E-07	2.67 E-07	7.61 E-07	2.14 E-07	1.89 E-07	2.27	0.64	0.56
G8J	G8JLB6_HUMAN Heterogeneous nuclear	49.70	16.4	10.6	10.6	16.5	16.5	13.6	1.46	1.55	2.12	1.95	1.25	2.39	1.34	0.86	1.64

LB6	ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1		7	9	5	6	2	0	E-06	E-06	E-06	E-06	E-06	E-06			
O75165	DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5	14.70	3.00	10.00	14.00	9.00	9.00	9.00	1.07 E-08	6.22 E-08	5.62 E-08	9.63 E-08	1.38 E-08	3.56 E-08	8.96	1.29	3.31
Q9H0H5	RGAP1_HUMAN Rac GTPase-activating protein 1 OS=Homo sapiens GN=RACGAP1 PE=1 SV=1	16.80	2.00	2.96	3.97	4.96	0.99	1.99	1.68 E-08	8.63 E-08	3.73 E-07	3.95 E-07	2.21 E-08	1.19 E-08	23.51	1.31	0.70
Q96A33	CCD47_HUMAN Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1	38.50	6.00	20.00	11.00	18.99	12.00	13.99	9.02 E-07	3.67 E-06	1.49 E-06	2.98 E-06	1.45 E-06	2.12 E-06	3.30	1.61	2.35
P47914	RL29_HUMAN 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	14.50	3.00	1.00	2.00	2.00	1.00		4.89 E-07	1.24 E-07	7.61 E-07	1.13 E-06	1.25 E-07		2.31	0.25	Control 1 Only
O95239	KIF4A_HUMAN Chromosome-associated kinesin KIF4A OS=Homo sapiens GN=KIF4A PE=1 SV=3	10.30		4.00	4.00	3.00	2.00	1.00		7.75 E-08	6.99 E-09	5.39 E-08	1.44 E-08	6.79 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P31942	HNRH3_HUMAN Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2	31.40	2.95	9.82	6.88	12.76	15.71	14.76	4.58 E-07	2.23 E-06	1.79 E-07	9.63 E-07	6.48 E-07	1.03 E-06	2.10	1.42	2.26
P56192	SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	13.30	1.97	4.94	4.94	5.94	0.99	1.98	2.76 E-08	7.43 E-08	7.74 E-08	1.23 E-07	9.61 E-09	2.85 E-08	4.46	0.35	1.03
P78527	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	49.60	73.96	110.90	223.87	154.91	97.95	107.92	5.46 E-07	1.39 E-06	2.46 E-06	2.10 E-06	8.79 E-07	1.10 E-06	3.85	1.61	2.02
M0QXB4	M0QXB4_HUMAN Coatomer protein complex, subunit epsilon, isoform CRA_g OS=Homo sapiens GN=COPE PE=2 SV=1	51.90	5.88	12.78	8.85	15.73	19.65	5.89	5.27 E-07	1.14 E-06	9.03 E-07	7.03 E-07	1.38 E-06	2.95 E-07	1.33	2.63	0.56
J9JIE6	J9JIE6_HUMAN Transmembrane and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=TMCO1 PE=2 SV=1	32.50	0.99	5.94	6.93	4.95	3.96	2.97	9.23 E-08	4.25 E-07	4.13 E-07	6.44 E-07	2.79 E-07	9.00 E-08	6.98	3.03	0.98
F5H2F4	F5H2F4_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1	32.80	4.00	21.98	6.00	8.00	24.00	4.00	2.81 E-08	1.04 E-06	4.78 E-08	1.92 E-07	9.52 E-07	6.91 E-08	6.84	33.90	2.46
P26196	DDX6_HUMAN Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2	32.90	3.00	7.00	8.00	5.00	4.00	4.00	1.80 E-07	4.21 E-07	6.56 E-07	3.63 E-07	3.29 E-07	4.67 E-07	2.02	1.83	2.60
Q9NXV6	CARF_HUMAN CDKN2A-interacting protein OS=Homo sapiens GN=CDKN2AIP PE=1 SV=3	9.50		2.00	2.00	3.00		1.00		3.87 E-08	4.79 E-08	3.72 E-08		4.08 E-08	Sample 1 Only		Sample 3 Only
O75146	HIP1R_HUMAN Huntingtin-interacting protein 1-related protein OS=Homo sapiens GN=HIP1R PE=1 SV=2	14.00	2.00	7.00	10.00	4.00	5.00	3.00	1.86 E-09	7.01 E-08	8.83 E-08	2.75 E-08	9.07 E-08	2.76 E-08	14.80	48.82	14.85
Q92900	RENT1_HUMAN Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	28.40	2.00	16.00	11.00	14.00	15.00	11.00	4.70 E-08	6.04 E-07	2.25 E-07	3.72 E-07	4.34 E-07	1.33 E-07	7.90	9.23	2.82
O15258	RER1_HUMAN Protein RER1 OS=Homo sapiens GN=RER1 PE=1 SV=1	36.70	5.00	7.00	7.00	7.00	5.00	5.00	4.17 E-07	1.11 E-06	8.28 E-07	7.42 E-07	1.27 E-06	4.81 E-07	1.78	3.04	1.15
P46977	STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	26.70	12.99	16.00	20.00	16.00	20.00	12.98	1.25 E-06	4.34 E-06	3.12 E-06	3.01 E-06	3.61 E-06	2.53 E-06	2.41	2.89	2.02
Q9Y5A9	YTHD2_HUMAN YTH domain family protein 2 OS=Homo sapiens GN=YTHDF2 PE=1 SV=2	7.40	1.00	2.00	3.00	3.00	3.00	1.00	2.54 E-08	2.54 E-07	4.24 E-07	4.30 E-07	8.87 E-08	1.43 E-07	16.97	3.50	5.65
Q9HD20	AT131_HUMAN Probable cation-transporting ATPase 13A1 OS=Homo sapiens	13.70	1.00	9.00	6.00	7.00	6.00	6.00	3.79 E-09	1.48 E-07	1.77 E-07	1.26 E-07	4.70 E-08	1.35 E-07	33.34	12.40	35.64

	GN=ATP13A1 PE=1 SV=2																
O00291	HIP1_HUMAN Huntingtin-interacting protein 1 OS=Homo sapiens GN=HIP1 PE=1 SV=5	9.30	1.00	5.00	1.00	5.00	4.00	3.00	6.00 E-09	6.74 E-08	6.80 E-08	5.27 E-08	6.01 E-08	1.90 E-08	8.78	10.03	3.17
Q15424	SAFB1_HUMAN Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4	26.80	0.99	0.99	4.94	3.95		2.96	8.11 E-10	2.86 E-08	1.67 E-07	5.72 E-08		1.27 E-07	70.51	Control 1 Only	156.08
Q9H061	T126A_HUMAN Transmembrane protein 126A OS=Homo sapiens GN=TMEM126A PE=1 SV=1	28.70	3.99	3.99	4.99	5.99	4.99	5.98	1.86 E-07	2.22 E-06	3.22 E-07	3.75 E-07	1.90 E-06	5.82 E-07	2.01	10.18	3.12
Q9NS69	TOM22_HUMAN Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3	77.50	9.00	12.00	15.00	15.00	16.00	14.00	2.47 E-06	5.49 E-06	4.19 E-06	3.98 E-06	3.91 E-06	3.85 E-06	1.61	1.58	1.56
Q14789	GOGB1_HUMAN Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2	7.90		5.98		1.00	8.96	1.00		3.01 E-08		2.77 E-10	3.02 E-08	2.04 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q7Z417	NUFP2_HUMAN Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1	3.90		1.00	3.00	1.00		1.00		4.31 E-08	8.94 E-08	4.78 E-08		7.77 E-08	Sample 1 Only		Sample 3 Only
P49916	DNLI3_HUMAN DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2	5.60	1.00	2.00	4.00	3.00	1.00		1.26 E-09	1.97 E-08	5.94 E-08	7.43 E-08	1.04 E-08		59.03	8.24	Control 1 Only
P23246	SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	48.40	63.65	50.74	64.67	97.43	70.60	64.65	1.38 E-05	1.03 E-05	1.73 E-05	1.46 E-05	1.37 E-05	1.43 E-05	1.06	0.99	1.04
H3BNF1	H3BNF1_HUMAN Ceroid-lipofuscinosis neuronal protein 6 OS=Homo sapiens GN=CLN6 PE=2 SV=1	30.50	1.98	2.97	1.98	1.98	2.97	1.98	2.71 E-07	1.00 E-06	6.66 E-07	6.06 E-07	7.46 E-07	6.62 E-07	2.24	2.75	2.44
P68104	EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	44.60	11.50	23.00	22.00	18.50	27.50	29.50	1.29 E-06	1.90 E-05	7.45 E-06	6.48 E-06	1.35 E-05	8.54 E-06	5.03	10.50	6.63
Q15393	SF3B3_HUMAN Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	34.40	29.95	23.96	26.94	29.96	13.99	25.97	1.02 E-06	5.25 E-07	7.67 E-07	1.32 E-06	2.67 E-07	8.02 E-07	1.29	0.26	0.79
Q13148	TADBP_HUMAN TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1	15.20	2.98	4.96	3.97	2.98	3.97	1.98	2.20 E-07	9.28 E-07	9.32 E-07	4.31 E-07	1.25 E-06	3.33 E-07	1.96	5.70	1.52
Q9BW19	KIFC1_HUMAN Kinesin-like protein KIFC1 OS=Homo sapiens GN=KIFC1 PE=1 SV=2	15.00	5.00	2.00	4.00	6.00	2.00	1.00	3.98 E-07	2.77 E-08	2.33 E-07	4.62 E-07	1.50 E-07	2.35 E-08	1.16	0.38	0.06
Q9H223	EHD4_HUMAN EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1	19.40	2.00	4.00	1.00		6.99	3.00	1.63 E-08	2.66 E-07	2.28 E-07		3.24 E-07	2.05 E-07	Control 1 Only	19.90	12.61
H0YK72	H0YK72_HUMAN SEC11-like 1 (S. cerevisiae), isoform CRA_a OS=Homo sapiens GN=SEC11A PE=2 SV=1	47.90	2.95	8.87	7.88	3.93	2.96	5.90	4.77 E-07	3.57 E-06	7.52 E-07	2.46 E-06	1.42 E-06	1.05 E-06	5.17	2.97	2.20
P61009	SPCS3_HUMAN Signal peptidase complex subunit 3 OS=Homo sapiens GN=SPCS3 PE=1 SV=1	26.70	3.00	4.00	3.00	3.00	5.00	3.00	3.77 E-07	9.19 E-07	8.21 E-07	3.99 E-07	1.17 E-06	6.10 E-07	1.06	3.10	1.62
Q8TAA9	VANG1_HUMAN Vang-like protein 1 OS=Homo sapiens GN=VANGL1 PE=1 SV=1	22.00	8.00	6.00	5.00	10.00	8.00	9.00	1.10 E-06	1.74 E-06	5.32 E-07	1.73 E-06	7.93 E-07	9.40 E-07	1.58	0.72	0.86
E9PF10	E9PF10_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=2 SV=1	10.20	1.00	6.98	4.00	1.00	5.99	3.99	3.12 E-09	7.74 E-08	2.17 E-08	4.76 E-09	7.93 E-08	2.21 E-08	1.53	25.46	7.08
Q5VTR2	BRE1A_HUMAN E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2	7.60	1.00	4.00			3.00	1.00	4.09 E-09	4.68 E-08			4.64 E-08	2.88 E-09	Control 1 Only	11.35	0.70
P37108	SRP14_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2	41.20	4.00	5.00	4.00	5.00	3.00	4.00	1.51 E-06	2.43 E-06	4.91 E-07	1.98 E-06	1.45 E-06	1.09 E-06	1.32	0.96	0.73
Q13347	EIF3I_HUMAN Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	15.70	3.00	3.00	5.00	2.00	6.00	4.00	8.85 E-07	2.17 E-06	5.11 E-07	1.15 E-06	1.78 E-06	5.71 E-07	1.30	2.01	0.65

Q09028	RBBP4_HUMAN Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	26.80	1.98	0.99	1.97	3.94	0.99	0.99	1.10E-06	4.68E-07	6.66E-07	1.04E-06	7.83E-07	4.52E-07	0.94	0.71	0.41
Q96A65	EXOC4_HUMAN Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=1 SV=1	11.30		4.96	1.99	0.99	1.99			6.33E-08	7.07E-09	2.92E-08	3.97E-08		Sample 1 Only	Sample 2 Only	
Q9Y224	CN166_HUMAN UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	52.90	7.97	10.93	9.93	12.94	6.96	10.92	3.94E-07	3.20E-06	2.81E-06	1.83E-06	1.07E-06	3.44E-06	4.64	2.71	8.74
O00571	DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	55.30	25.72	25.71	30.68	40.62	24.71	22.75	2.86E-06	2.38E-06	5.26E-06	5.06E-06	2.96E-06	2.56E-06	1.77	1.03	0.89
Q07666	KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	24.80	5.93	4.95	13.85	17.85	6.93	5.94	4.53E-07	5.30E-07	3.23E-06	3.62E-06	4.71E-07	1.55E-07	8.00	1.04	0.34
O75489	NDUS3_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1	46.20	8.00	14.98	11.97	10.99	10.98	10.98	4.36E-07	1.78E-06	1.36E-06	1.01E-06	1.65E-06	9.37E-07	2.31	3.78	2.15
B0AZV0	B0AZV0_HUMAN Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=2 SV=1	19.50		2.00		1.00	7.00	1.00		1.02E-06		1.23E-08	7.78E-07	2.35E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q5T2T1	MPP7_HUMAN MAGUK p55 subfamily member 7 OS=Homo sapiens GN=MPP7 PE=1 SV=1	18.80	1.99	3.98	2.98	5.94	4.96	2.99	1.18E-07	4.87E-07	1.05E-07	2.42E-07	3.06E-07	1.64E-07	2.06	2.60	1.40
A4D212	A4D212_HUMAN DKFZP586J0619 protein OS=Homo sapiens GN=DKFZP586J0619 PE=2 SV=1	1.10			2.00						8.05E-09						
B4DR63	B4DR63_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=2 SV=1	7.40				1.00		1.00				2.50E-08		2.21E-07	Sample 1 Only		Sample 3 Only
B4E0K2	B4E0K2_HUMAN Translocating chain-associated membrane protein 1 OS=Homo sapiens GN=TRAM1 PE=2 SV=1	11.50		1.00	2.00	1.00				4.72E-08	1.34E-07	1.23E-07			Sample 1 Only		
Q9H6Y2	WDR55_HUMAN WD repeat-containing protein 55 OS=Homo sapiens GN=WDR55 PE=1 SV=2	18.30		3.00		3.00	3.00			7.05E-07		3.95E-07	7.63E-07		Sample 1 Only	Sample 2 Only	
Q9HCD5	NCOA5_HUMAN Nuclear receptor coactivator 5 OS=Homo sapiens GN=NCOA5 PE=1 SV=2	12.10			1.00	3.00		1.00			8.13E-09	7.58E-08		3.97E-09	Sample 1 Only		Sample 3 Only
C9IYT0	C9IYT0_HUMAN H/ACA ribonucleoprotein complex subunit 4 (Fragment) OS=Homo sapiens GN=DKC1 PE=2 SV=1	43.40	2.00		1.00	1.00			1.09E-07		4.48E-08	5.03E-08			0.46	Control 1 Only	Control 1 Only
C9JQV0	C9JQV0_HUMAN Uncharacterized protein C7orf50 (Fragment) OS=Homo sapiens GN=C7orf50 PE=2 SV=1	14.80				2.00						1.39E-07			Sample 1 Only		
E7ERY0	E7ERY0_HUMAN Nuclear valosin-containing protein-like OS=Homo sapiens GN=NVL PE=2 SV=1	5.00			1.00	1.00					2.81E-08	6.09E-08			Sample 1 Only		
E7ESL0	E7ESL0_HUMAN 39S ribosomal protein L22, mitochondrial OS=Homo sapiens GN=MRPL22 PE=2 SV=1	30.80	3.00		1.00				4.63E-07		1.78E-07				Control 1 Only	Control 1 Only	Control 1 Only
P48594	SPB4_HUMAN Serpin B4 OS=Homo sapiens GN=SERPINB4 PE=1 SV=2	23.80				3.98	0.99					6.57E-07	1.65E-08		Sample 1 Only	Sample 2 Only	
P29508	SPB3_HUMAN Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	26.70				3.00						6.20E-08			Sample 1 Only		
E7ETY7	E7ETY7_HUMAN Glutathione peroxidase OS=Homo sapiens GN=GPX8 PE=2 SV=1	17.10			2.00						1.51E-07						
E7E	E7EXA6_HUMAN Chromosome transmission	5.60		1.00	1.00	2.00	1.00			1.66	1.14	2.72	4.19		Sample	Sample	

XA6	fidelity protein 18 homolog OS=Homo sapiens GN=CHTF18 PE=2 SV=1									E-08	E-08	E-08	E-09		1 Only	2 Only	
E9PN11	E9PN11_HUMAN Rho-related GTP-binding protein RhoC (Fragment) OS=Homo sapiens GN=RHOC PE=2 SV=1	17.20			1.00		2.00				2.23 E-08		1.43 E-07			Sample 2 Only	
E9PSG0	E9PSG0_HUMAN Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein OS=Homo sapiens GN=NOS1AP PE=2 SV=1	8.60		2.00	1.00	1.00	1.00	1.00		1.90 E-07	7.16 E-09	1.04 E-08	6.32 E-09	4.82 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
E9PP21	E9PP21_HUMAN Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=2 SV=1	40.00		2.00			3.00	1.00		1.30 E-07			1.49 E-07	7.66 E-08		Sample 2 Only	Sample 3 Only
F5H2X0	F5H2X0_HUMAN Tight junction protein ZO-3 OS=Homo sapiens GN=TJP3 PE=2 SV=1	4.60	1.00	1.00		4.00			1.84 E-08	2.96 E-09		1.52 E-07			8.24	Control 1 Only	Control 1 Only
P49368	TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	13.60	0.99	1.98	0.99		0.99	1.98	4.26 E-09	9.19 E-08	2.81 E-08		6.92 E-09	2.13 E-08	Control 1 Only	1.62	4.99
F5H8H4	F5H8H4_HUMAN Pogo transposable element with ZNF domain OS=Homo sapiens GN=POGZ PE=2 SV=1	7.90	2.00	1.00	1.00	1.00			3.15 E-08	4.76 E-09	1.98 E-08	5.08 E-09			0.16	Control 1 Only	Control 1 Only
F8VQX7	F8VQX7_HUMAN Oxysterol-binding protein (Fragment) OS=Homo sapiens GN=OSBPL8 PE=2 SV=1	7.10		1.00	1.00	2.00	2.00			2.01 E-08	6.19 E-09	2.95 E-08	1.24 E-08		Sample 1 Only	Sample 2 Only	
F8VU11	F8VU11_HUMAN PRP40 pre-mRNA processing factor 40 homolog B (Yeast), isoform CRA_a OS=Homo sapiens GN=PRPF40B PE=2 SV=2	5.80	1.00	1.00	1.00	2.00			3.89 E-08	1.39 E-08	3.23 E-08	6.60 E-08			1.70	Control 1 Only	Control 1 Only
P49458	SRP09_HUMAN Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	45.30	2.00	2.00	4.00				3.89 E-07	3.02 E-07	6.57 E-07				Control 1 Only	Control 1 Only	Control 1 Only
F8VXG7	F8VXG7_HUMAN Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=2 SV=1	3.10	1.00	2.00	1.00	2.00			2.07 E-08	1.07 E-08	1.01 E-08	5.84 E-08			2.82	Control 1 Only	Control 1 Only
G3V1D4	G3V1D4_HUMAN Lin-7 homolog C (C. elegans), isoform CRA_b OS=Homo sapiens GN=LIN7C PE=2 SV=1	20.20		2.00		2.00	2.00	1.00		2.25 E-07		2.46 E-07	2.41 E-07	3.27 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
G3V5V3	G3V5V3_HUMAN Nuclear export mediator factor NEMF (Fragment) OS=Homo sapiens GN=NEMF PE=2 SV=1	4.50		2.00	2.00	1.00				4.89 E-08	4.80 E-09	8.72 E-10			Sample 1 Only		
H0YHS6	H0YHS6_HUMAN Tyrosine--tRNA ligase, mitochondrial (Fragment) OS=Homo sapiens GN=YARS2 PE=2 SV=1	11.30		1.00			1.00			1.11 E-07			5.01 E-07			Sample 2 Only	
H7BYJ3	H7BYJ3_HUMAN Citron Rho-interacting kinase (Fragment) OS=Homo sapiens GN=CIT PE=4 SV=1	3.20	1.00		5.00		1.00		5.68 E-09		1.94 E-08		1.71 E-09		Control 1 Only	0.30	Control 1 Only
J3QRS3	J3QRS3_HUMAN Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=2 SV=1	12.30			2.00		1.00				9.39 E-08		1.10 E-07			Sample 2 Only	
O00232	PSD12_HUMAN 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	4.40				2.00		1.00				1.61 E-07		7.84 E-09	Sample 1 Only		Sample 3 Only
O00483	NDUA4_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1	37.00		1.00	3.00		2.00			4.85 E-07	2.25 E-07		9.56 E-06			Sample 2 Only	
O43920	NDUS5_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Homo sapiens GN=NDUFS5 PE=1 SV=3	17.90		2.00	2.00		2.00	2.00		9.77 E-07	2.35 E-08		8.23 E-07	6.38 E-07		Sample 2 Only	Sample 3 Only
O60	MED14_HUMAN Mediator of RNA polymerase	2.80		1.00	3.00		1.00			1.70	1.11		3.65			Sample	

244	II transcription subunit 14 OS=Homo sapiens GN=MED14 PE=1 SV=2									E-08	E-08		E-09			2 Only	
O60830	TI17B_HUMAN Mitochondrial import inner membrane translocase subunit Tim17-B OS=Homo sapiens GN=TIMM17B PE=1 SV=1	21.50	1.00	2.00	2.00	2.00	2.00	2.00	3.27 E-07	7.46 E-07	8.21 E-07	5.67 E-07	1.53 E-06	5.56 E-08	1.74	4.68	0.17
P02452	CO1A1_HUMAN Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	5.50					6.00						6.01 E-08			Sample 2 Only	
P08123	CO1A2_HUMAN Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7	2.00					3.00						8.55 E-08			Sample 2 Only	
F5GYR8	F5GYR8_HUMAN General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=2 SV=1	8.70		2.00		2.00	5.00			4.77 E-08		9.11 E-09	1.27 E-07		Sample 1 Only	Sample 2 Only	
P61006	RAB8A_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1	27.50				1.00	3.00	1.00				1.17 E-08	3.14 E-08	1.11 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P61026	RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	31.00		1.00			3.00			6.48 E-09			4.15 E-07			Sample 2 Only	
P12259	FA5_HUMAN Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=4	1.00	1.00				1.00		1.40 E-08				5.07 E-08		Control 1 Only	3.63	Control 1 Only
P19388	RPAB1_HUMAN DNA-directed RNA polymerases I, II, and III subunit RPABC1 OS=Homo sapiens GN=POLR2E PE=1 SV=4	23.30		1.00		1.00	1.00	1.00		1.35 E-07		1.12 E-07	4.91 E-09	6.03 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P19525	E2AK2_HUMAN Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens GN=EIF2AK2 PE=1 SV=2	7.30		2.00	1.00	2.00	1.00			1.10 E-07	1.48 E-09	4.05 E-08	2.63 E-08		Sample 1 Only	Sample 2 Only	
C9J6W2	C9J6W2_HUMAN Kinesin-like protein KIF20B OS=Homo sapiens GN=KIF20B PE=2 SV=1	2.60		1.00	1.00	2.00	2.00			2.30 E-09	1.69 E-09	3.16 E-08	8.60 E-10		Sample 1 Only	Sample 2 Only	
P49454	CENPF_HUMAN Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2	1.70	1.00	1.00		1.00			6.85 E-10	5.17 E-09		3.71 E-09			5.41	Control 1 Only	Control 1 Only
P51398	RT29_HUMAN 28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3 PE=1 SV=1	10.60	3.00						4.28 E-07						Control 1 Only	Control 1 Only	Control 1 Only
P52907	CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	15.70	1.00	2.00	2.00	2.00	1.00	1.00	1.24 E-07	4.74 E-07	3.76 E-07	4.55 E-07	1.56 E-07	5.32 E-09	3.67	1.26	0.04
Q00577	PURA_HUMAN Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2	18.00			1.00	2.00	3.00				9.63 E-08	2.75 E-07	2.96 E-07		Sample 1 Only	Sample 2 Only	
Q9P253	VPS18_HUMAN Vacuolar protein sorting-associated protein 18 homolog OS=Homo sapiens GN=VPS18 PE=1 SV=2	12.30		3.00		1.00	8.00			2.95 E-08		6.78 E-09	1.33 E-07		Sample 1 Only	Sample 2 Only	
Q13835	PKP1_HUMAN Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	5.90	3.00						1.41 E-07						Control 1 Only	Control 1 Only	Control 1 Only
Q14566	MCM6_HUMAN DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	11.10		4.00		2.00	3.00			1.27 E-07		2.71 E-08	1.36 E-07		Sample 1 Only	Sample 2 Only	
Q15388	TOM20_HUMAN Mitochondrial import receptor subunit TOM20 homolog OS=Homo sapiens GN=TOMM20 PE=1 SV=1	17.20	1.00	2.00		2.00	2.00	1.00	6.72 E-08	2.64 E-07		2.54 E-07	1.86 E-07	8.95 E-08	3.78	2.77	1.33
Q52LJ0	FA98B_HUMAN Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1	14.20	2.00	1.00			2.00	2.00	5.86 E-08	1.32 E-07			3.89 E-07	2.24 E-08	Control 1 Only	6.63	0.38
Q5JY65	Q5JY65_HUMAN Crooked neck-like protein 1 OS=Homo sapiens GN=CRNKL1 PE=2 SV=1	3.30	1.00	1.00			1.00	1.00	7.88 E-09	5.17 E-08			1.70 E-08	1.47 E-08	Control 1 Only	2.15	1.86
P51665	PSMD7_HUMAN 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	16.40			0.99	1.98	1.99				1.98 E-08	1.05 E-07	2.38 E-07		Sample 1 Only	Sample 2 Only	
Q5V	Q5VY93_HUMAN Rho guanine nucleotide	3.80	1.00	1.00		2.00			6.12	8.42		1.38			0.23	Control	Control

Y93	exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=2 SV=1								E-08	E-09		E-08				1 Only	1 Only
Q7KZN9	COX15_HUMAN Cytochrome c oxidase assembly protein COX15 homolog OS=Homo sapiens GN=COX15 PE=1 SV=1	8.00	1.00	1.00		1.00	1.00		2.62 E-07	9.55 E-08		3.06 E-08	7.95 E-08		0.12	0.30	Control 1 Only
Q96LL9	DJC30_HUMAN DnaJ homolog subfamily C member 30 OS=Homo sapiens GN=DNAJC30 PE=1 SV=3	17.30	1.00	1.00	1.00	1.00	2.00	2.00	3.54 E-08	1.45 E-08	1.24 E-08	3.22 E-08	3.73 E-08	1.11 E-07	0.91	1.06	3.14
Q9BUQ8	DDX23_HUMAN Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens GN=DDX23 PE=1 SV=3	3.90	1.00		2.00	2.00			6.10 E-08		5.17 E-08	1.12 E-07			1.84	Control 1 Only	Control 1 Only
Q9Y4C8	RBM19_HUMAN Probable RNA-binding protein 19 OS=Homo sapiens GN=RBM19 PE=1 SV=3	3.00	1.00	1.00		1.00			3.11 E-08	1.65 E-08		8.32 E-08			2.68	Control 1 Only	Control 1 Only
A2A2E9	A2A2E9_HUMAN Ral GTPase-activating protein subunit beta OS=Homo sapiens GN=RALGAPB PE=2 SV=1	4.00		0.99		0.99				1.14 E-08		1.46 E-08			Sample 1 Only		
F8W0J4	F8W0J4_HUMAN YEATS domain-containing protein 4 OS=Homo sapiens GN=YEATS4 PE=2 SV=1	13.30		3.00			1.00	1.00		2.52 E-07			2.04 E-09	6.74 E-08		Sample 2 Only	Sample 3 Only
F8W840	F8W840_HUMAN YTH domain family protein 1 OS=Homo sapiens GN=YTHDF1 PE=2 SV=1	9.00		0.99	0.99	1.99	0.99	0.99		8.23 E-08	5.32 E-08	1.85 E-07	6.44 E-08	9.99 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
A6NEM2	A6NEM2_HUMAN HCF N-terminal chain 5 OS=Homo sapiens GN=HCFC1 PE=2 SV=2	2.00		4.00		1.00				4.58 E-08		6.70 E-09			Sample 1 Only		
D6RER5	D6RER5_HUMAN Septin-11 OS=Homo sapiens GN=SEPT11 PE=2 SV=1	17.40	1.99	1.50	1.50		1.00	2.00	2.89 E-07	8.34 E-09	6.36 E-08		1.00 E-08	9.71 E-08	Control 1 Only	0.03	0.34
B1AMS2	B1AMS2_HUMAN Septin 6, isoform CRA_b OS=Homo sapiens GN=SEPT6 PE=2 SV=1	11.00			0.99	0.99		0.99			3.72 E-08	4.24 E-08		5.32 E-08	Sample 1 Only		Sample 3 Only
G3V1C3	G3V1C3_HUMAN Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=2 SV=1	8.30	0.99		1.98				6.14 E-08		5.00 E-07				Control 1 Only	Control 1 Only	Control 1 Only
Q9UI09	NDUAC_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Homo sapiens GN=NDUFA12 PE=1 SV=1	20.70		2.00	2.00	2.00	1.00	1.00		4.77 E-07	4.70 E-07	5.79 E-07	4.27 E-07	3.67 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
O75746	CMC1_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2	19.30	1.00	2.00	2.00	2.00	2.00	2.00	3.06 E-08	1.70 E-07	3.75 E-08	5.82 E-08	1.13 E-07	1.95 E-08	1.90	3.71	0.64
G3V2S9	G3V2S9_HUMAN SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=2 SV=1	37.50	0.99		1.98	0.99	0.99	1.98	6.74 E-09		9.86 E-08	3.56 E-07	7.56 E-07	2.77 E-07	52.86	112.26	41.05
A6NHR9	SMHD1_HUMAN Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2	2.10			3.00						7.63 E-09						
Q9UJX3	APC7_HUMAN Anaphase-promoting complex subunit 7 OS=Homo sapiens GN=ANAPC7 PE=1 SV=4	6.70		2.00		1.00				1.15 E-07		4.04 E-09			Sample 1 Only		
G3XAB8	G3XAB8_HUMAN Trinucleotide repeat containing 6C, isoform CRA_a OS=Homo sapiens GN=TNRC6C PE=2 SV=1	49.90				78.97	80.97	68.95				3.24 E-06	2.63 E-06	2.10 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
A8MW61	A8MW61_HUMAN Pleiotropic regulator 1 OS=Homo sapiens GN=PLRG1 PE=2 SV=1	15.40	1.00		2.00			1.00	3.15 E-07		3.22 E-07			1.30 E-07	Control 1 Only	Control 1 Only	0.41
Q9UKV8	AGO2_HUMAN Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	83.00				273.94	270.44	229.45				1.32 E-04	1.49 E-04	9.00 E-05	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9UL18	AGO1_HUMAN Protein argonaute-1 OS=Homo sapiens GN=AGO1 PE=1 SV=3	79.00				71.50	58.00	56.00				8.59 E-06	9.38 E-06	6.97 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9H9G7	AGO3_HUMAN Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	72.30				80.00	75.00	55.00				6.77 E-06	1.27 E-05	6.22 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only

Q9HCK5	AGO4_HUMAN Protein argonaute-4 OS=Homo sapiens GN=AGO4 PE=1 SV=2	32.90				7.00	2.00	1.00				1.11 E-07	9.21 E-08	3.58 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
G5E9V5	G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1	13.50	1.98			0.99	0.99	0.99	1.53 E-07			4.47 E-08	6.82 E-08	5.82 E-08	0.29	0.45	0.38
H0Y8C3	H0Y8C3_HUMAN Mitochondrial carrier homolog 1 (Fragment) OS=Homo sapiens GN=MTCH1 PE=2 SV=1	11.00	0.99		1.00		1.00		4.66 E-08		3.11 E-07		5.23 E-09		Control 1 Only	0.11	Control 1 Only
H0YFA4	H0YFA4_HUMAN Cysteine-rich protein 2 (Fragment) OS=Homo sapiens GN=CRIP2 PE=4 SV=1	34.90		1.00			5.00	3.00		1.42 E-07			1.48 E-06	3.03 E-07		Sample 2 Only	Sample 3 Only
P54803	GALC_HUMAN Galactocerebrosidase OS=Homo sapiens GN=GALC PE=1 SV=2	7.90		1.00		1.98	0.99	1.99		2.00 E-09		1.57 E-07	1.42 E-07	1.67 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
B0QYD3	B0QYD3_HUMAN DNA dC->dU-editing enzyme APOBEC-3B OS=Homo sapiens GN=APOBEC3B PE=2 SV=1	14.10	3.96		0.99				1.45 E-07		2.11 E-08				Control 1 Only	Control 1 Only	Control 1 Only
H0YME5	H0YME5_HUMAN Eukaryotic translation initiation factor 2-alpha kinase 4 (Fragment) OS=Homo sapiens GN=EIF2AK4 PE=4 SV=1	1.80		2.00		1.00	2.00			8.32 E-09		1.45 E-08	2.97 E-09		Sample 1 Only	Sample 2 Only	
B1AHC9	B1AHC9_HUMAN X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=2 SV=1	11.80			1.00		2.00				1.48 E-08		1.35 E-07			Sample 2 Only	
H7C0X4	H7C0X4_HUMAN Dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase (Fragment) OS=Homo sapiens GN=ALG3 PE=4 SV=1	6.80			0.99			0.99			1.20 E-07			2.67 E-08			Sample 3 Only
I3L0X9	I3L0X9_HUMAN Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens GN=PAM16 PE=2 SV=1	37.60	2.00	1.00	1.00	1.00		1.00	9.02 E-08	4.50 E-08	2.83 E-08	6.77 E-08		1.48 E-07	0.75	Control 1 Only	1.63
P61160	ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	11.40		1.00	1.00			2.00		2.82 E-07	1.27 E-07			3.41 E-07			Sample 3 Only
Q562R1	ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	19.70				1.00	1.00	3.00				1.88 E-08	1.70 E-06	6.13 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6S8J3	POTEE_HUMAN POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	11.80		0.99	0.99		1.98			8.05 E-09	3.21 E-08		5.54 E-08			Sample 2 Only	
I3L2C7	I3L2C7_HUMAN Gem-associated protein 4 OS=Homo sapiens GN=GEMIN4 PE=2 SV=1	1.20		1.00				1.98		2.94 E-08				4.04 E-07			Sample 3 Only
J3KNN5	J3KNN5_HUMAN Probable ATP-dependent RNA helicase DDX41 (Fragment) OS=Homo sapiens GN=DDX41 PE=2 SV=1	9.00	1.00			2.00			8.42 E-08			3.26 E-08			0.39	Control 1 Only	Control 1 Only
B3KQ95	B3KQ95_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1	10.50		1.98		0.99				7.81 E-08		9.04 E-08			Sample 1 Only		
B3KSH1	B3KSH1_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1	9.80	1.98				1.98	0.99	2.51 E-08				7.53 E-08	2.88 E-08	Control 1 Only	3.01	1.15
Q14573	ITPR3_HUMAN Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2	1.10		1.52	1.04	0.52	0.52	0.52		2.54 E-09	3.75 E-10	3.21 E-10	7.66 E-10	3.04 E-10	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q14571	ITPR2_HUMAN Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2	0.90		1.00		1.00	1.00			2.98 E-09		2.26 E-09	3.75 E-09		Sample 1 Only	Sample 2 Only	
Q9UPQ9	TNR6B_HUMAN Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	56.50				115.87	94.06	105.97				5.93 E-06	4.49 E-06	7.08 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
B4D	B4DEM7_HUMAN T-complex protein 1 subunit	8.40						2.00						7.66			Sample

EM7	theta OS=Homo sapiens GN=CCT8 PE=2 SV=1													E-08			3 Only
B4D FA2	B4DFA2_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1	16.30					8.00	5.00					2.29 E-07	2.77 E-07		Sample 2 Only	Sample 3 Only
B4D FG0	B4DFG0_HUMAN Protein DEK OS=Homo sapiens GN=DEK PE=2 SV=1	15.80	3.95		1.97	4.94			6.13 E-07		7.67 E-08	4.27 E-07			0.70	Control 1 Only	Control 1 Only
J3Q RV5	J3QRV5_HUMAN Lethal(2) giant larvae protein homolog 2 OS=Homo sapiens GN=LLGL2 PE=2 SV=1	4.20		1.00		2.00				3.84 E-08		1.87 E-08			Sample 1 Only		
P61 158	ARP3_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	21.10	0.99	1.98	4.97				9.91 E-08	9.02 E-08	3.95 E-07				Control 1 Only	Control 1 Only	Control 1 Only
B4D JP7	B4DJP7_HUMAN Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=2 SV=1	33.30	2.00		2.00		2.00	1.00	5.63 E-07		5.29 E-07		9.62 E-07	3.77 E-06	Control 1 Only	1.71	6.69
B4D P17	B4DP17_HUMAN Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=2 SV=1	25.00				1.00	4.00					1.02 E-08	1.19 E-07		Sample 1 Only	Sample 2 Only	
Q9U PY3	DICER_HUMAN Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	2.10		1.00	1.00					5.76 E-09	7.56 E-09						
Q9U Q35	SRRM2_HUMAN Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	1.70	3.00			2.00			2.79 E-08			1.66 E-08			0.60	Control 1 Only	Control 1 Only
B4D TC3	B4DTC3_HUMAN Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=2 SV=1	32.40	2.92			4.89		2.92	5.62 E-08			4.38 E-07		1.32 E-07	7.79	Control 1 Only	2.35
O14 979	HNRDL_HUMAN Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3	18.00			1.00	1.00		1.00			1.83 E-07	2.66 E-07		1.26 E-08	Sample 1 Only		Sample 3 Only
D6R 9P3	D6R9P3_HUMAN Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=2 SV=1	9.60		1.00		1.00	1.00	1.00		1.03 E-08		2.48 E-08	2.88 E-07	1.19 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y 2X3	NOP58_HUMAN Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1	4.30		1.00	2.00	1.00				2.74 E-08	7.38 E-08	8.34 E-08			Sample 1 Only		
B4D WZ5	B4DWZ5_HUMAN Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=2 SV=1	13.50			1.00	1.00	1.00	2.00			3.87 E-08	8.78 E-08	1.61 E-07	1.41 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
E5RI T6	E5RIT6_HUMAN 60S ribosomal protein L26-like 1 (Fragment) OS=Homo sapiens GN=RPL26L1 PE=2 SV=1	64.10			1.98						8.91 E-07						
B4E 1K7	B4E1K7_HUMAN Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=2 SV=1	18.60		1.00		1.00	1.00	1.00		5.77 E-08		2.59 E-08	8.35 E-08	3.49 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y 3Q3	TMED3_HUMAN Transmembrane emp24 domain-containing protein 3 OS=Homo sapiens GN=TMED3 PE=1 SV=1	20.70		2.00	3.00	1.00				9.12 E-07	2.00 E-07	2.74 E-08			Sample 1 Only		
P33 947	ERD22_HUMAN ER lumen protein retaining receptor 2 OS=Homo sapiens GN=KDELR2 PE=1 SV=1	10.20			0.99						2.95 E-07						
Q9U BF2	COPG2_HUMAN Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1	10.40		3.00		1.00	1.00			1.54 E-08		5.32 E-09	1.57 E-08		Sample 1 Only	Sample 2 Only	
P62 140	PP1B_HUMAN Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	34.30		1.00	1.98			2.98		3.04 E-08	3.32 E-08			7.44 E-08			Sample 3 Only
F8V YE8	F8VYE8_HUMAN Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CC PE=2 SV=1	24.70	0.99	1.98	0.99			0.99	2.88 E-07	3.38 E-07	6.68 E-07			2.95 E-08	Control 1 Only	Control 1 Only	0.10

Q9Y6I8	PXMP4_HUMAN Peroxisomal membrane protein 4 OS=Homo sapiens GN=PXMP4 PE=1 SV=3	8.50	2.00	1.00	1.00	2.00	2.00	1.00	4.17 E-07	1.05 E-06	4.32 E-07	7.85 E-07	5.24 E-07	2.60 E-07	1.88	1.26	0.62
B7Z817	B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1	6.70		2.00	2.00		3.00			4.83 E-07	2.25 E-07		4.67 E-07			Sample 2 Only	
B7Z9L0	B7Z9L0_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1	9.50		1.00	1.00	1.00		1.00		1.35 E-07	2.44 E-09	8.18 E-09		4.88 E-09	Sample 1 Only		Sample 3 Only
B8ZZU8	B8ZZU8_HUMAN Transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), isoform CRA_b OS=Homo sapiens GN=TCEB2 PE=2 SV=1	16.80	2.00	1.00		1.00	2.00	1.00	1.15 E-07	6.33 E-08		8.72 E-08	1.41 E-07	3.25 E-08	0.76	1.23	0.28
C9J5S7	C9J5S7_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=2 SV=1	25.00				0.99	2.98					1.66 E-08	1.97 E-07		Sample 1 Only	Sample 2 Only	
C9JB63	C9JB63_HUMAN Enoyl-CoA delta isomerase 2, mitochondrial (Fragment) OS=Homo sapiens GN=ECI2 PE=2 SV=1	20.70				1.00	3.00	3.00				6.23 E-08	2.77 E-07	7.85 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
C9JBJ6	C9JBJ6_HUMAN DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens GN=POLR2H PE=2 SV=1	56.10		2.00	2.00	1.00	1.00	2.00		3.49 E-07	8.06 E-08	3.26 E-08	2.65 E-08	1.21 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9Y6N5	SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	5.80		2.00	1.00					1.56 E-07	3.85 E-09						
Q3MHD2	LSM12_HUMAN Protein LSM12 homolog OS=Homo sapiens GN=LSM12 PE=1 SV=2	16.40	1.00	2.00	1.00	2.00	1.00		1.72 E-08	2.33 E-07	1.02 E-07	5.63 E-08	5.88 E-08		3.26	3.41	Control 1 Only
Q9Y6Q5	AP1M2_HUMAN AP-1 complex subunit mu-2 OS=Homo sapiens GN=AP1M2 PE=1 SV=4	41.60		0.99	0.99	0.99		0.99		1.10 E-06	6.71 E-08	6.99 E-08		7.26 E-07	Sample 1 Only		Sample 3 Only
B4DNI9	B4DNI9_HUMAN Vacuolar protein sorting-associated protein 52 homolog OS=Homo sapiens GN=VPS52 PE=2 SV=1	4.80					2.00						1.05 E-07			Sample 2 Only	
B5MDF5	B5MDF5_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=2 SV=1	18.40					1.00	1.00					3.29 E-07	8.40 E-08		Sample 2 Only	Sample 3 Only
B7Z888	B7Z888_HUMAN Protein SCAF8 OS=Homo sapiens GN=SCAF8 PE=2 SV=1	3.80		2.00	1.00	1.00				7.55 E-09	3.80 E-09	7.89 E-09			Sample 1 Only		
E7ERC6	E7ERC6_HUMAN Calcium-transporting ATPase type 2C member 1 OS=Homo sapiens GN=ATP2C1 PE=2 SV=1	10.70			1.00	1.00	1.00	1.00			6.72 E-09	2.76 E-08	5.01 E-08	1.60 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
F2Z2E1	F2Z2E1_HUMAN Constitutive coactivator of peroxisome proliferator-activated receptor gamma OS=Homo sapiens GN=FAM120B PE=2 SV=1	4.30					2.00						1.50 E-07			Sample 2 Only	
G5E9Z2	G5E9Z2_HUMAN Cisplatin resistance related protein CRR9p, isoform CRA_c OS=Homo sapiens GN=CLPTM1L PE=2 SV=1	7.90		1.00			1.00			7.75 E-08			4.31 E-08			Sample 2 Only	
G8JLG2	G8JLG2_HUMAN Corneodesmosin OS=Homo sapiens GN=CDSN PE=2 SV=1	5.10	4.00	1.00	1.00				9.83 E-08	1.25 E-08	7.03 E-09				Control 1 Only	Control 1 Only	Control 1 Only
J3QK89	J3QK89_HUMAN Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=2 SV=1	6.60			3.00	4.00					7.09 E-08	9.43 E-08			Sample 1 Only		
P78346	RPP30_HUMAN Ribonuclease P protein subunit p30 OS=Homo sapiens GN=RPP30 PE=1 SV=1	10.80	2.00	1.00	1.00	2.00	1.00	1.00	4.08 E-08	1.85 E-07	3.76 E-08	6.57 E-08	1.99 E-08	5.78 E-08	1.61	0.49	1.42
Q9BTV4	TMM43_HUMAN Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	16.50		2.00	1.00		1.00			7.30 E-08	3.31 E-08		4.43 E-08			Sample 2 Only	
E7E	E7EVD1_HUMAN U4/U6 small nuclear	3.30	1.00		1.00		1.00		3.21		5.47		6.75		Control	0.21	Control

VD1	ribonucleoprotein Prp3 OS=Homo sapiens GN=PRPF3 PE=2 SV=1								E-08		E-09		E-09		1 Only		1 Only
Q01082-3	SPTB2_HUMAN Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1	30.80					1.00	1.00					1.72 E-09	3.00 E-09		Sample 2 Only	Sample 3 Only
P11277	SPTB1_HUMAN Spectrin beta chain, erythrocytic OS=Homo sapiens GN=SPTB PE=1 SV=5	3.40	0.99			0.99			4.81 E-09			5.98 E-09			1.24	Control 1 Only	Control 1 Only
E9PM69	E9PM69_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=2 SV=1	13.80	0.99			1.00		1.00	5.47 E-08			1.13 E-07		1.07 E-07	2.07	Control 1 Only	1.96
F5H826	F5H826_HUMAN Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=1	6.90		1.00	1.00		2.00	1.00		5.51 E-09	1.77 E-09		1.84 E-08	1.66 E-08		Sample 2 Only	Sample 3 Only
O96011	PX11B_HUMAN Peroxisomal membrane protein 11B OS=Homo sapiens GN=PEX11B PE=1 SV=1	6.60					1.00	1.00					9.67 E-08	7.42 E-08		Sample 2 Only	Sample 3 Only
P30153	2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	8.50	0.99	1.98	1.00		0.99		3.84 E-08	3.58 E-08	3.44 E-08		4.81 E-08		Control 1 Only	1.25	Control 1 Only
P51148	RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	16.70			2.97		1.98	1.98			3.51 E-08		1.92 E-07	1.09 E-07		Sample 2 Only	Sample 3 Only
Q12789	TF3C1_HUMAN General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4	2.80			2.98	0.99					7.87 E-09	6.53 E-09			Sample 1 Only		
P62333	PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	15.40	2.00	2.00	2.00	2.00	2.00	1.00	2.26 E-08	2.47 E-07	3.03 E-07	2.08 E-07	3.19 E-07	3.12 E-08	9.22	14.11	1.38
Q5T200	ZC3HD_HUMAN Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1	1.70				2.97						2.62 E-08			Sample 1 Only		
Q8NC56	LEMD2_HUMAN LEM domain-containing protein 2 OS=Homo sapiens GN=LEMD2 PE=1 SV=1	8.50			2.00	2.00		0.99			5.60 E-08	1.62 E-07		1.31 E-07	Sample 1 Only		Sample 3 Only
Q9UDY2	ZO2_HUMAN Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2	3.50	1.00			2.00			1.35 E-08			1.56 E-08			1.15	Control 1 Only	Control 1 Only
F8VQX6	F8VQX6_HUMAN Methyltransferase-like protein 7A (Fragment) OS=Homo sapiens GN=METTL7A PE=2 SV=1	15.00					2.00	2.00					2.34 E-07	1.14 E-07		Sample 2 Only	Sample 3 Only
P11047	LAMC1_HUMAN Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	1.80	3.00		1.00				1.35 E-08		2.50 E-09				Control 1 Only	Control 1 Only	Control 1 Only
Q12996	CSTF3_HUMAN Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1	3.50		1.00	1.00	1.00		1.00		1.91 E-07	4.27 E-08	6.33 E-08		6.40 E-09	Sample 1 Only		Sample 3 Only
Q3SYB4	Q3SYB4_HUMAN SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1	8.90	3.00	1.00	3.00				1.08 E-07	5.21 E-08	9.89 E-08				Control 1 Only	Control 1 Only	Control 1 Only
B0UX83	B0UX83_HUMAN HLA-B associated transcript 3, isoform CRA_a OS=Homo sapiens GN=BAG6 PE=4 SV=1	4.30					2.00						1.87 E-08			Sample 2 Only	
F5H5N0	F5H5N0_HUMAN Serine/threonine-protein kinase MRCK alpha OS=Homo sapiens GN=CDC42BPA PE=2 SV=1	1.50		0.99	1.00		0.99			6.48 E-09	2.18 E-09		3.77 E-09			Sample 2 Only	
G3V1A9	G3V1A9_HUMAN Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=2 SV=1	2.60			1.00	0.99					1.66 E-09	1.05 E-09			Sample 1 Only		

O95139	NDUB6_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6 OS=Homo sapiens GN=NDUFB6 PE=1 SV=3	21.90		1.00	3.00					1.64 E-07	3.43 E-07						
P60468	SC61B_HUMAN Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2	26.00		1.00	1.00	1.00	1.00	2.00		1.34 E-06	1.38 E-06	2.55 E-06	9.51 E-07	1.73 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8TB61	S35B2_HUMAN Adenosine 3'-phospho 5'-phosphosulfate transporter 1 OS=Homo sapiens GN=SLC35B2 PE=1 SV=1	6.80				1.99	0.99	0.99				4.18 E-08	1.38 E-08	1.39 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9BTC0	DIDO1_HUMAN Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5	2.80	2.00		1.00				2.01 E-08		4.25 E-09				Control 1 Only	Control 1 Only	Control 1 Only
Q9HD33	RM47_HUMAN 39S ribosomal protein L47, mitochondrial OS=Homo sapiens GN=MRPL47 PE=1 SV=2	11.70	2.00		1.00	1.00	1.00	1.00	3.44 E-07		1.28 E-07	7.91 E-08	7.16 E-08	6.80 E-08	0.23	0.21	0.20
E7EWR4	E7EWR4_HUMAN Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=2 SV=1	4.80		1.00				1.00		3.70 E-08				1.58 E-08			Sample 3 Only
Q9UBV2	SE1L1_HUMAN Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3	5.90		3.00		2.00	3.00			3.19 E-08		9.06 E-09	3.69 E-08		Sample 1 Only	Sample 2 Only	
Q9BVK6	TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2	8.50		1.00	1.00	1.00	1.00	1.00		1.22 E-08	3.29 E-09	7.16 E-08	1.08 E-07	5.12 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
B7ZAP5	B7ZAP5_HUMAN Hepatocyte nuclear factor 3-alpha OS=Homo sapiens GN=FOXA1 PE=2 SV=1	13.00				2.00		1.00				2.75 E-07		1.38 E-07	Sample 1 Only		Sample 3 Only
Q12904	AIMP1_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	12.20			0.99	3.98		1.00			1.02 E-07	1.75 E-07		2.45 E-07	Sample 1 Only		Sample 3 Only
Q13155	AIMP2_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2	15.60		1.00	2.00	2.00				4.34 E-07	3.76 E-07	4.16 E-07			Sample 1 Only		
Q3ZCQ8	TIM50_HUMAN Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2	10.20				0.99	1.98	0.99				6.15 E-09	1.06 E-08	1.47 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9H9B4	SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4	9.60			1.00		1.00	1.00			2.40 E-07		1.40 E-08	6.63 E-08		Sample 2 Only	Sample 3 Only
E5KLJ5	E5KLJ5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1	3.10					3.00						2.78 E-08			Sample 2 Only	
E9PIE4	E9PIE4_HUMAN Mitochondrial carrier homolog 2 (Fragment) OS=Homo sapiens GN=MTCH2 PE=2 SV=1	47.10		1.00		1.00		1.00		1.60 E-07		6.19 E-08		1.34 E-07	Sample 1 Only		Sample 3 Only
Q92506	DHB8_HUMAN Estradiol 17-beta-dehydrogenase 8 OS=Homo sapiens GN=HSD17B8 PE=1 SV=2	10.70		2.00			2.00	2.00		1.52 E-07			1.80 E-07	8.48 E-08		Sample 2 Only	Sample 3 Only
E9PC90	E9PC90_HUMAN G2/mitotic-specific cyclin-B1 (Fragment) OS=Homo sapiens GN=CCNB1 PE=2 SV=1	6.10			1.99		1.00				2.14 E-07		1.56 E-07			Sample 2 Only	
Q9UI12	VATH_HUMAN V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1	8.20		0.99			0.99	0.99		1.86 E-08			4.72 E-08	1.85 E-07		Sample 2 Only	Sample 3 Only
O15091	MRRP3_HUMAN Mitochondrial ribonuclease P protein 3 OS=Homo sapiens GN=KIAA0391 PE=1 SV=2	5.10		1.00	1.00					2.08 E-08	8.02 E-08						
C9JME2	C9JME2_HUMAN FERM, RhoGEF and pleckstrin domain-containing protein 1	20.20	2.00	1.00	2.00	1.00	2.00	1.00	1.76 E-08	9.73 E-10	1.73 E-08	6.05 E-09	1.10 E-08	9.82 E-09	0.34	0.63	0.56

	OS=Homo sapiens GN=FARP1 PE=2 SV=2																
J3KNQ3	J3KNQ3_HUMAN 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=2 SV=1	7.40				1.99						1.02 E-07			Sample 1 Only		
O75400	PR40A_HUMAN Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2	3.40	1.00		2.00	2.00			2.27 E-08		4.40 E-08	2.07 E-08			0.91	Control 1 Only	Control 1 Only
Q9UDW1	QCR9_HUMAN Cytochrome b-c1 complex subunit 9 OS=Homo sapiens GN=UQCR10 PE=1 SV=3	38.10		1.00			1.00			1.70 E-07			3.62 E-07			Sample 2 Only	
Q9Y597	KCTD3_HUMAN BTB/POZ domain-containing protein KCTD3 OS=Homo sapiens GN=KCTD3 PE=1 SV=2	5.00		1.00			3.98			3.08 E-09			9.45 E-08			Sample 2 Only	
E7EN32	E7EN32_HUMAN Menin OS=Homo sapiens GN=MEN1 PE=2 SV=1	4.50			1.00	1.00		1.00			6.02 E-08	3.72 E-08		9.05 E-09	Sample 1 Only		Sample 3 Only
F5GY88	F5GY88_HUMAN Mediator of RNA polymerase II transcription subunit 24 OS=Homo sapiens GN=MED24 PE=2 SV=2	2.90	0.99	0.99	0.99	1.98	0.99	0.99	4.01 E-09	1.41 E-08	2.98 E-09	2.40 E-08	4.64 E-09	1.95 E-09	5.97	1.16	0.49
Q75MJ1	Q75MJ1_HUMAN ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=2 SV=1	6.30	1.00		1.00	1.00	1.00		5.73 E-09		3.87 E-09	1.14 E-08	4.81 E-08		1.99	8.39	Control 1 Only
Q86XZ4	SPAS2_HUMAN Spermatogenesis-associated serine-rich protein 2 OS=Homo sapiens GN=SPATS2 PE=1 SV=1	5.00	2.00		1.00	1.00			1.20 E-07		1.07 E-07	1.29 E-07			1.08	Control 1 Only	Control 1 Only
Q8N9N2-2	ASCC1_HUMAN Isoform 2 of Activating signal cointegrator 1 complex subunit 1 OS=Homo sapiens GN=ASCC1	5.90	2.00	1.00		1.00			7.94 E-08	1.02 E-08		5.51 E-08			0.69	Control 1 Only	Control 1 Only
Q9UMY1	NOL7_HUMAN Nucleolar protein 7 OS=Homo sapiens GN=NOL7 PE=1 SV=2	12.80	2.00	1.00		1.00			2.56 E-07	8.99 E-08		8.83 E-09			0.03	Control 1 Only	Control 1 Only
Q86VP6	CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	2.40					1.99						2.13 E-08			Sample 2 Only	
P01625	KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	14.00	4.00	1.00	2.00				1.27 E-05	8.56 E-06	4.33 E-06				Control 1 Only	Control 1 Only	Control 1 Only
Q9H6S0	YTDC2_HUMAN Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=1 SV=2	4.00	1.00		3.00				3.85 E-09		1.19 E-08				Control 1 Only	Control 1 Only	Control 1 Only
Q9P2K5	MYEF2_HUMAN Myelin expression factor 2 OS=Homo sapiens GN=MYEF2 PE=1 SV=3	5.90		0.99			0.99	1.00		2.48 E-08			1.88 E-09	3.10 E-09		Sample 2 Only	Sample 3 Only
D6R9W4	D6R9W4_HUMAN Drebrin (Fragment) OS=Homo sapiens GN=DBN1 PE=2 SV=1	19.90		2.97	2.97	0.99				2.11 E-07	1.08 E-07	1.99 E-08			Sample 1 Only		
M0QXL5	M0QXL5_HUMAN rRNA 2'-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=2 SV=1	13.20			1.98	0.99		0.99			5.51 E-07	6.76 E-08		4.50 E-08	Sample 1 Only		Sample 3 Only
E7EUT8	E7EUT8_HUMAN Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=2 SV=1	3.60	1.00			2.00	1.00	1.00	1.22 E-08			2.14 E-08	1.61 E-08	6.15 E-08	1.75	1.32	5.03
H7C1E4	H7C1E4_HUMAN AP-1 complex subunit sigma-1A (Fragment) OS=Homo sapiens GN=AP1S1 PE=4 SV=1	14.60		1.00	1.00	1.00	2.00	1.00		1.12 E-06	1.78 E-07	3.11 E-07	1.19 E-06	2.21 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
D6RIY6	D6RIY6_HUMAN Exosome complex component RRP45 OS=Homo sapiens GN=EXOSC9 PE=2 SV=1	9.70		0.99	1.98	0.99		0.99		1.50 E-07	3.07 E-07	1.93 E-07		1.58 E-07	Sample 1 Only		Sample 3 Only
O15294	OGT1_HUMAN UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3	2.80		1.99		1.00	1.00			9.53 E-08		4.48 E-08	4.06 E-08		Sample 1 Only	Sample 2 Only	

H0Y5B4	H0Y5B4_HUMAN 60S ribosomal protein L36a (Fragment) OS=Homo sapiens GN=RPL36A PE=3 SV=1	17.90			0.99						3.21 E-07						
H0Y704	H0Y704_HUMAN Zinc finger protein 185 (Fragment) OS=Homo sapiens GN=ZNF185 PE=4 SV=1	21.30		1.98			0.99			1.84 E-07			3.99 E-08			Sample 2 Only	
H7C3F9	H7C3F9_HUMAN Actin-related protein 2/3 complex subunit 2 (Fragment) OS=Homo sapiens GN=ARPC2 PE=2 SV=1	15.80			1.00		2.00				3.10 E-07		1.48 E-07			Sample 2 Only	
O95159	ZFPL1_HUMAN Zinc finger protein-like 1 OS=Homo sapiens GN=ZFPL1 PE=1 SV=2	16.10		1.00		1.00				2.88 E-08		5.78 E-08			Sample 1 Only		
P46100	ATRX_HUMAN Transcriptional regulator ATRX OS=Homo sapiens GN=ATRX PE=1 SV=5	1.00	2.00						4.98 E-09						Control 1 Only	Control 1 Only	Control 1 Only
Q6PI48	SYDM_HUMAN Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1	5.90		2.00		1.00				1.37 E-07		3.76 E-08			Sample 1 Only		
Q96ST3	SIN3A_HUMAN Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2	1.60	1.00	2.00				1.00	1.78 E-08	1.56 E-08				9.99 E-09	Control 1 Only	Control 1 Only	0.56
Q9HCN8	SDF2L_HUMAN Stromal cell-derived factor 2-like protein 1 OS=Homo sapiens GN=SDF2L1 PE=1 SV=2	14.90					3.00						3.96 E-07			Sample 2 Only	
E9PK59	E9PK59_HUMAN N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1 PE=2 SV=1	3.30		1.00			1.00			1.02 E-08			2.17 E-08			Sample 2 Only	
P62913-2	RL11_HUMAN Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11	63.30	2.00	2.00	1.00	2.00	1.00		1.54 E-08	6.86 E-08	3.47 E-08	1.78 E-07	2.42 E-08		11.55	1.57	Control 1 Only
Q9UEU0	VTI1B_HUMAN Vesicle transport through interaction with t-SNAREs homolog 1B OS=Homo sapiens GN=VTI1B PE=1 SV=3	10.30		0.99		0.99		1.98		2.82 E-08		1.18 E-07		3.25 E-08	Sample 1 Only		Sample 3 Only
B9EK38	B9EK38_HUMAN GARNL1 protein OS=Homo sapiens GN=GARNL1 PE=2 SV=1	5.40		1.00			2.00			3.74 E-10			3.52 E-09			Sample 2 Only	
Q9P2N5	RBM27_HUMAN RNA-binding protein 27 OS=Homo sapiens GN=RBM27 PE=1 SV=2	3.20	1.00	1.00	1.00	1.00		1.00	2.51 E-09	2.38 E-08	7.95 E-09	7.54 E-09		1.09 E-08	3.00	Control 1 Only	4.34
Q9NX14	NDUBB_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial OS=Homo sapiens GN=NDUFB11 PE=1 SV=1	13.10		1.00			2.00			2.27 E-07			1.36 E-06			Sample 2 Only	
O43402	EMC8_HUMAN ER membrane protein complex subunit 8 OS=Homo sapiens GN=EMC8 PE=1 SV=1	13.80		1.00	5.00			2.00		1.29 E-08	2.26 E-07			1.64 E-07			Sample 3 Only
Q9Y3Y2	CHTOP_HUMAN Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2	12.90				2.00	1.00	2.00				3.98 E-07	7.17 E-09	1.30 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
J3KSI6	J3KSI6_HUMAN Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=2 SV=1	11.60		3.00		1.00		1.00		1.81 E-07		4.89 E-08		4.79 E-08	Sample 1 Only		Sample 3 Only
K7EQ02	K7EQ02_HUMAN DAZ-associated protein 1 (Fragment) OS=Homo sapiens GN=DAZAP1 PE=2 SV=1	13.80				1.00	1.00	1.00				7.35 E-08	8.90 E-08	2.65 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8WX92	NELFB_HUMAN Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1	3.60		1.00			2.00			6.52 E-09			1.98 E-07			Sample 2 Only	
Q9BSJ8	ESYT1_HUMAN Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	2.30			1.00	1.00	2.00				3.72 E-09	3.43 E-09	7.63 E-09		Sample 1 Only	Sample 2 Only	
E7EQI7	E7EQI7_HUMAN WASH complex subunit strumpellin OS=Homo sapiens GN=KIAA0196 PE=2 SV=1	3.60		2.00	1.00		1.00	1.00		2.62 E-08	1.52 E-08		2.02 E-09	3.06 E-08		Sample 2 Only	Sample 3 Only

H7BY84	H7BY84_HUMAN General transcription factor 3C polypeptide 5 OS=Homo sapiens GN=GTF3C5 PE=2 SV=1	8.10	1.98			1.00			2.23 E-07			2.83 E-08			0.13	Control 1 Only	Control 1 Only
F5H7I0	F5H7I0_HUMAN BTB/POZ domain-containing protein KCTD6 (Fragment) OS=Homo sapiens GN=KCTD6 PE=2 SV=1	85.10				1.00	3.00					4.88 E-09	1.12 E-06		Sample 1 Only	Sample 2 Only	
O43707	ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	9.90					2.97	2.98					4.52 E-08	1.67 E-08		Sample 2 Only	Sample 3 Only
H0YJ11	H0YJ11_HUMAN Alpha-actinin-1 (Fragment) OS=Homo sapiens GN=ACTN1 PE=4 SV=1	28.50		1.00		1.00				1.24 E-08		1.04 E-07			Sample 1 Only		
Q27J81	INF2_HUMAN Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2	1.00				1.00	2.00					1.15 E-08	1.69 E-08		Sample 1 Only	Sample 2 Only	
Q6PD62	CTR9_HUMAN RNA polymerase-associated protein CTR9 homolog OS=Homo sapiens GN=CTR9 PE=1 SV=1	5.40					1.00	1.00					1.97 E-08	2.02 E-08		Sample 2 Only	Sample 3 Only
P56537	IF6_HUMAN Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	23.30		1.00	1.00	1.00	1.00	1.00		1.84 E-08	1.32 E-08	1.23 E-07	1.90 E-07	5.25 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
A3KFL1	A3KFL1_HUMAN Exosome complex component RRP4 (Fragment) OS=Homo sapiens GN=EXOSC2 PE=2 SV=1	11.00	1.00	2.00	2.00	1.00	1.00	1.00	6.19 E-08	6.47 E-07	6.48 E-07	3.78 E-08	5.43 E-07	3.88 E-07	0.61	8.78	6.27
E7EPT4	E7EPT4_HUMAN NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=2 SV=1	9.60			2.00			1.00			9.42 E-08			9.17 E-08			Sample 3 Only
P03886	NU1M_HUMAN NADH-ubiquinone oxidoreductase chain 1 OS=Homo sapiens GN=MT-ND1 PE=1 SV=1	6.30		1.00			1.00			1.20 E-08			2.78 E-08			Sample 2 Only	
Q6P1J9	CDC73_HUMAN Parafibromin OS=Homo sapiens GN=CDC73 PE=1 SV=1	7.20		1.00		1.00				3.31 E-08		1.70 E-07			Sample 1 Only		
Q96P11	NSUN5_HUMAN Putative methyltransferase NSUN5 OS=Homo sapiens GN=NSUN5 PE=1 SV=2	11.50	1.00	1.00					1.39 E-07	9.58 E-08					Control 1 Only	Control 1 Only	Control 1 Only
B4DQI6	B4DQI6_HUMAN Transformer-2 protein homolog alpha OS=Homo sapiens GN=TRA2A PE=2 SV=1	27.20			1.98						1.38 E-06						
Q8TF66	LRC15_HUMAN Leucine-rich repeat-containing protein 15 OS=Homo sapiens GN=LRRC15 PE=1 SV=2	4.30	3.00						2.13 E-07						Control 1 Only	Control 1 Only	Control 1 Only
Q8N3X1	FNBP4_HUMAN Formin-binding protein 4 OS=Homo sapiens GN=FNBP4 PE=1 SV=3	3.00	1.00		1.00				4.84 E-09		1.09 E-08				Control 1 Only	Control 1 Only	Control 1 Only
D6RF62	D6RF62_HUMAN Phosphoribosylaminoimidazole carboxylase OS=Homo sapiens GN=PAICS PE=2 SV=1	6.00					1.00						6.86 E-08			Sample 2 Only	
Q96QR8	PURB_HUMAN Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3	14.10		1.00	1.00					4.83 E-08	5.14 E-08						
D3DQV9	D3DQV9_HUMAN Eukaryotic translation initiation factor 4 gamma 2 (Fragment) OS=Homo sapiens GN=EIF4G2 PE=2 SV=1	2.60		1.98						3.54 E-08							
Q9P206	K1522_HUMAN Uncharacterized protein KIAA1522 OS=Homo sapiens GN=KIAA1522 PE=1 SV=2	1.80		1.00	1.00	0.99				1.09 E-08	4.49 E-09	9.88 E-09			Sample 1 Only		
K7ELS0	K7ELS0_HUMAN Uncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43 PE=2 SV=1	15.90				1.00	3.00	1.00				1.39 E-08	5.93 E-08	3.55 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q5T	PR14L_HUMAN Protein PRR14L OS=Homo	1.40	0.99			0.99			1.06			3.85			36.21	Control	Control

HK1	sapiens GN=PRR14L PE=1 SV=1								E-09			E-08				1 Only	1 Only
O76031	CLPX_HUMAN ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2	4.40		2.00						3.27 E-08							
Q6KC79	NIPBL_HUMAN Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2	1.00	2.00						5.49 E-09						Control 1 Only	Control 1 Only	Control 1 Only
P43686	PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	12.10				2.00						3.43 E-08			Sample 1 Only		
P22528	SPR1B_HUMAN Cornifin-B OS=Homo sapiens GN=SPRR1B PE=1 SV=2	27.00			1.99						4.08 E-07						
E9PLG8	E9PLG8_HUMAN Glycosylphosphatidylinositol anchor attachment 1 protein (Fragment) OS=Homo sapiens GN=GPAA1 PE=2 SV=1	29.60		1.00						1.92 E-07							
E7ESV4	E7ESV4_HUMAN Ras-related protein Rap-1b (Fragment) OS=Homo sapiens GN=RAP1B PE=2 SV=1	49.10						1.98						2.53 E-08			Sample 3 Only
E9PJN0	E9PJN0_HUMAN Acyl-coenzyme A thioesterase 8 OS=Homo sapiens GN=ACOT8 PE=2 SV=1	22.50				1.99						3.35 E-08			Sample 1 Only		
Q08426	ECHP_HUMAN Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3	5.70			1.00						1.70 E-07						
P63096	GNAI1_HUMAN Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2	24.60				0.98						5.72 E-08			Sample 1 Only		
Q9NRL2	BAZ1A_HUMAN Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens GN=BAZ1A PE=1 SV=2	2.20	1.00			1.00			6.44 E-09			2.71 E-10			0.04	Control 1 Only	Control 1 Only
Q8IZH2	XRN1_HUMAN 5'-3' exoribonuclease 1 OS=Homo sapiens GN=XRN1 PE=1 SV=1	1.50			0.99		0.99				1.77 E-09		8.39 E-09			Sample 2 Only	
Q9UBX3	DIC_HUMAN Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2	16.00					1.00						1.67 E-08			Sample 2 Only	
E7ESU4	E7ESU4_HUMAN N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=2 SV=1	9.90	3.00		3.00	2.00			6.43 E-08		5.36 E-08	4.67 E-08			0.73	Control 1 Only	Control 1 Only
O75367	H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	25.20	10.94		1.00				1.81 E-06		5.44 E-08				Control 1 Only	Control 1 Only	Control 1 Only
A6NIT2	A6NIT2_HUMAN Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform OS=Homo sapiens GN=PHKA1 PE=2 SV=1	0.70	1.00		1.00				5.83 E-08		1.81 E-07				Control 1 Only	Control 1 Only	Control 1 Only
O75380	NDUS6_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Homo sapiens GN=NDUFS6 PE=1 SV=1	49.20			3.00						2.48 E-07						
C9J0E4	C9J0E4_HUMAN Cystatin-A OS=Homo sapiens GN=CSTA PE=2 SV=1	52.40	1.00			1.00			5.10 E-07			2.68 E-07			0.53	Control 1 Only	Control 1 Only
G3XAB3	G3XAB3_HUMAN Tetratricopeptide repeat domain 17, isoform CRA_c OS=Homo sapiens GN=TTC17 PE=2 SV=1	2.50	1.00		1.00				1.85 E-08		1.42 E-08				Control 1 Only	Control 1 Only	Control 1 Only
P63167	DYL1_HUMAN Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1	37.10			2.00		1.00				1.86 E-07		5.50 E-07			Sample 2 Only	
P16989	YBOX3_HUMAN Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4	22.10	1.00	1.00		1.00	1.00	1.00	5.70 E-07	9.62 E-09		2.63 E-07	4.19 E-08	4.50 E-08	0.46	0.07	0.08

E7EQY4	E7EQY4_HUMAN Metastasis-associated protein MTA3 OS=Homo sapiens GN=MTA3 PE=2 SV=1	14.80				1.97		0.98				1.49 E-07		2.82 E-08	Sample 1 Only		Sample 3 Only
O95822	DCMC_HUMAN Malonyl-CoA decarboxylase, mitochondrial OS=Homo sapiens GN=MLYCD PE=1 SV=3	6.80					1.00						4.23 E-08			Sample 2 Only	
Q6UN15	FIP1_HUMAN Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1 PE=1 SV=1	14.00				1.00						1.74 E-07			Sample 1 Only		
B0QZ43	B0QZ43_HUMAN Erlin-1 (Fragment) OS=Homo sapiens GN=ERLIN1 PE=2 SV=1	49.10	1.00	2.00	1.00	1.00	1.00		5.60 E-09	1.08 E-07	2.15 E-08	1.82 E-08	9.46 E-09		3.24	1.69	Control 1 Only
Q9ULC4	MCTS1_HUMAN Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1	16.00						1.00						5.70 E-08			Sample 3 Only
Q9P2I0	CPSF2_HUMAN Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens GN=CPSF2 PE=1 SV=2	4.00	2.00	1.00	1.00	1.00			1.02 E-07	2.76 E-08	1.19 E-07	5.66 E-08			0.56	Control 1 Only	Control 1 Only
Q96J66	ABCCB_HUMAN ATP-binding cassette sub-family C member 11 OS=Homo sapiens GN=ABCC11 PE=1 SV=1	3.20						1.00						5.40 E-09			Sample 3 Only
H0YCN2	H0YCN2_HUMAN Remodeling and spacing factor 1 (Fragment) OS=Homo sapiens GN=RSF1 PE=2 SV=1	5.10	2.00						3.47 E-08						Control 1 Only	Control 1 Only	Control 1 Only
Q9UM54-2	MYO6_HUMAN Isoform 2 of Unconventional myosin-VI OS=Homo sapiens GN=MYO6	5.30			3.95	0.97	0.97				2.46 E-08	2.60 E-09	2.76 E-09		Sample 1 Only	Sample 2 Only	
P82933	RT09_HUMAN 28S ribosomal protein S9, mitochondrial OS=Homo sapiens GN=MRPS9 PE=1 SV=2	4.80	2.00	1.00		1.00			1.53 E-07	5.67 E-09		4.77 E-09			0.03	Control 1 Only	Control 1 Only
B7ZAM9	B7ZAM9_HUMAN Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=2 SV=1	13.10						1.00						4.98 E-08			Sample 3 Only
B4DPJ8	B4DPJ8_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=2 SV=1	4.30		1.00						2.97 E-08							
G3V1J5	G3V1J5_HUMAN Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=2 SV=1	3.30		1.00						1.54 E-08							
C9IZE4	C9IZE4_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=2 SV=1	7.50		0.99		0.99				2.94 E-08		3.01 E-08			Sample 1 Only		
E7ENN3	E7ENN3_HUMAN Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=2 SV=1	0.80		1.00	1.00	1.00				2.46 E-08	1.80 E-08	1.38 E-08			Sample 1 Only		
H0Y818	H0Y818_HUMAN DNA mismatch repair protein Mlh1 (Fragment) OS=Homo sapiens GN=MLH1 PE=4 SV=1	3.20					1.99						5.46 E-08			Sample 2 Only	
Q5VYY1	ANR22_HUMAN Ankyrin repeat domain-containing protein 22 OS=Homo sapiens GN=ANKRD22 PE=2 SV=1	11.50		1.00	1.00		1.00			5.20 E-08	1.29 E-08		4.84 E-08			Sample 2 Only	
Q658Y4	F91A1_HUMAN Protein FAM91A1 OS=Homo sapiens GN=FAM91A1 PE=1 SV=3	2.90		2.98						3.02 E-08							
O95470	SGPL1_HUMAN Sphingosine-1-phosphate lyase 1 OS=Homo sapiens GN=SGPL1 PE=1 SV=3	13.20	5.00			2.00	1.00		1.10 E-07			2.13 E-07	1.11 E-08		1.95	0.10	Control 1 Only
P23458	JAK1_HUMAN Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2	2.10		1.00		1.00	1.00			1.12 E-08		1.48 E-08	1.33 E-08		Sample 1 Only	Sample 2 Only	

Q96 9M3	YIPF5_HUMAN Protein YIPF5 OS=Homo sapiens GN=YIPF5 PE=1 SV=1	8.20	1.00		1.00		1.00		8.92 E-09		4.09 E-09		8.16 E-09		Control 1 Only	0.92	Control 1 Only
Q01 826	SATB1_HUMAN DNA-binding protein SATB1 OS=Homo sapiens GN=SATB1 PE=1 SV=1	5.10		0.99		0.99	1.99	0.99		2.58 E-08		1.94 E-08	1.04 E-07	1.04 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
P42 025	ACTY_HUMAN Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1	6.60		1.00				1.00		1.64 E-08				9.23 E-08			Sample 3 Only
O96 000	NDUBA_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=3	15.10		2.00	2.00	1.00				1.96 E-07	1.34 E-07	3.04 E-07			Sample 1 Only		
Q9U BG3	CRNN_HUMAN Cornulin OS=Homo sapiens GN=CRNN PE=1 SV=1	3.80	1.00						5.50 E-09						Control 1 Only	Control 1 Only	Control 1 Only
Q8W U90	ZC3HF_HUMAN Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens GN=ZC3H15 PE=1 SV=1	6.30				0.99	1.00					1.80 E-08	1.10 E-07		Sample 1 Only	Sample 2 Only	
O15 230	LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	0.50	1.00						2.62 E-09						Control 1 Only	Control 1 Only	Control 1 Only
P01 605	KV113_HUMAN Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1	25.00	4.00	6.00	5.00				5.58 E-06	2.73 E-05	1.54 E-05				Control 1 Only	Control 1 Only	Control 1 Only
Q4G 0F5	VP26B_HUMAN Vacuolar protein sorting-associated protein 26B OS=Homo sapiens GN=VPS26B PE=1 SV=2	8.90					2.00						2.68 E-07			Sample 2 Only	
P01 764	HV303_HUMAN Ig heavy chain V-III region VH26 OS=Homo sapiens PE=1 SV=1	18.80	3.00	3.00	1.00				1.28 E-06	1.94 E-07	5.43 E-08				Control 1 Only	Control 1 Only	Control 1 Only
D6R B59	D6RB59_HUMAN Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=2 SV=1	4.30	1.00		1.00	1.00			4.42 E-09		1.55 E-08	1.53 E-08			3.46	Control 1 Only	Control 1 Only
P01 859	IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	16.00				4.99	1.00	1.00				2.77 E-06	1.62 E-06	5.16 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8N B16	MLKL_HUMAN Mixed lineage kinase domain-like protein OS=Homo sapiens GN=MLKL PE=1 SV=1	3.00		1.00	1.00	1.00		1.00		5.75 E-08	5.16 E-08	4.43 E-08		1.90 E-08	Sample 1 Only		Sample 3 Only
Q99 470	SDF2_HUMAN Stromal cell-derived factor 2 OS=Homo sapiens GN=SDF2 PE=1 SV=2	7.10	1.00	1.00		1.00			1.61 E-07	2.61 E-07		1.69 E-07			1.05	Control 1 Only	Control 1 Only
B7Z KS7	B7ZKS7_HUMAN USP48 protein OS=Homo sapiens GN=USP48 PE=2 SV=1	7.40					1.00						6.78 E-09			Sample 2 Only	
P05 023	AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	3.50		0.99		0.99		0.99		3.17 E-08		2.16 E-08		4.90 E-09	Sample 1 Only		Sample 3 Only
P12 235	ADT1_HUMAN ADP/ATP translocase 1 OS=Homo sapiens GN=SLC25A4 PE=1 SV=4	55.00					2.00						4.79 E-09			Sample 2 Only	
B4D WK3	B4DWK3_HUMAN Transcription factor AP-2 gamma OS=Homo sapiens GN=TFAP2C PE=2 SV=1	26.00	4.00						4.63 E-07						Control 1 Only	Control 1 Only	Control 1 Only
P50 750	CDK9_HUMAN Cyclin-dependent kinase 9 OS=Homo sapiens GN=CDK9 PE=1 SV=3	5.40				1.00						3.55 E-08			Sample 1 Only		
G3V 5T9	G3V5T9_HUMAN Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=2 SV=1	13.30					1.00						9.56 E-09			Sample 2 Only	
Q13 885	TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	36.00		0.99				0.99		1.05 E-07				8.58 E-09			Sample 3 Only
Q13 509	TBB3_HUMAN Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	19.30						0.99						1.73 E-08			Sample 3 Only
Q92 793	CBP_HUMAN CREB-binding protein OS=Homo sapiens GN=CREBBP PE=1 SV=3	3.30	1.00	1.00	2.00		1.00		5.14 E-09	6.18 E-09	5.89 E-09		7.08 E-10		Control 1 Only	0.14	Control 1 Only
P07 900	HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	11.30		0.99			0.99			5.83 E-08			8.87 E-08			Sample 2 Only	

Q96SI9	STRBP_HUMAN Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1	10.00	1.00		1.00				5.29 E-08		5.04 E-08				Control 1 Only	Control 1 Only	Control 1 Only
Q13045	FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	3.50			4.00			1.00			5.54 E-08			1.20 E-08			Sample 3 Only
Q13232	NDK3_HUMAN Nucleoside diphosphate kinase 3 OS=Homo sapiens GN=NME3 PE=1 SV=2	24.90		2.00	1.00	1.00	1.00	2.00		5.15 E-08	5.37 E-08	3.62 E-08	1.36 E-08	1.01 E-06	Sample 1 Only	Sample 2 Only	Sample 3 Only
P10301	RRAS_HUMAN Ras-related protein R-Ras OS=Homo sapiens GN=RRAS PE=1 SV=1	17.90		2.98			1.98	1.99		2.29 E-07			5.24 E-07	2.40 E-07		Sample 2 Only	Sample 3 Only
P10412	H14_HUMAN Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	14.10	2.99						1.68 E-07						Control 1 Only	Control 1 Only	Control 1 Only
Q13243	SRSF5_HUMAN Serine/arginine-rich splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=1 SV=1	16.70	1.00	1.00	1.99	2.00			4.00 E-08	4.51 E-08	4.92 E-07	7.62 E-08			1.91	Control 1 Only	Control 1 Only
Q08170	SRSF4_HUMAN Serine/arginine-rich splicing factor 4 OS=Homo sapiens GN=SRSF4 PE=1 SV=2	13.00				2.99						2.05 E-08			Sample 1 Only		
Q13425	SNTB2_HUMAN Beta-2-syntrophin OS=Homo sapiens GN=SNTB2 PE=1 SV=1	4.10		1.00	1.00	2.00	1.00	1.00		1.19 E-08	1.36 E-07	5.25 E-08	1.44 E-08	8.74 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q13492	PICAL_HUMAN Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2	7.70	0.99	0.99	1.98	1.98		0.99	1.95 E-08	4.21 E-07	2.47 E-07	3.48 E-08		1.20 E-08	1.78	Control 1 Only	0.62
B3KRS5	B3KRS5_HUMAN Histone deacetylase OS=Homo sapiens GN=HDAC2 PE=2 SV=1	14.40	2.99			1.00			1.76 E-07			4.41 E-09			0.03	Control 1 Only	Control 1 Only
Q13724	MOGS_HUMAN Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS PE=1 SV=5	5.70			2.00	1.00	1.00	2.00			2.57 E-08	6.67 E-09	6.56 E-09	3.49 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
P11182	ODB2_HUMAN Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3	12.70	1.00	2.00			2.00	1.00	2.24 E-08	2.82 E-07			5.68 E-08	7.64 E-08	Control 1 Only	2.54	3.41
Q9BTT6	LRRC1_HUMAN Leucine-rich repeat-containing protein 1 OS=Homo sapiens GN=LRRC1 PE=1 SV=1	6.30	1.00	1.00	1.00	1.00	1.00	1.00	5.08 E-08	1.32 E-07	1.24 E-07	4.06 E-09	4.66 E-08	1.16 E-07	0.08	0.92	2.29
Q7Z3Y8	K1C27_HUMAN Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	14.20			3.98			2.98			8.59 E-08			3.90 E-07			Sample 3 Only
Q14165	MLEC_HUMAN Malectin OS=Homo sapiens GN=MLEC PE=1 SV=1	15.10		2.98			2.97	0.99		4.05 E-08			7.92 E-07	1.25 E-07		Sample 2 Only	Sample 3 Only
Q14669-2	TRIPC_HUMAN Isoform 2 of E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12	4.70	1.99		0.99	0.99			6.72 E-09		1.81 E-09	6.90 E-10			0.10	Control 1 Only	Control 1 Only
Q8NDV3	SMC1B_HUMAN Structural maintenance of chromosomes protein 1B OS=Homo sapiens GN=SMC1B PE=1 SV=2	1.00					1.00						1.20 E-08			Sample 2 Only	
B7WPG3	B7WPG3_HUMAN Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRPLL PE=2 SV=1	11.40	0.99		1.98				4.58 E-08		5.09 E-08				Control 1 Only	Control 1 Only	Control 1 Only
P13639	EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	3.00		1.00			1.00			3.22 E-09			3.13 E-10			Sample 2 Only	
Q15067	ACOX1_HUMAN Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3	11.20					4.95						2.75 E-07			Sample 2 Only	
Q01546	K22O_HUMAN Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2	31.00	8.00	2.00			1.00		2.39 E-07	1.08 E-08			3.51 E-09		Control 1 Only	0.01	Control 1 Only
P08	K2C7_HUMAN Keratin, type II cytoskeletal 7	23.00			6.00						4.46						

729	OS=Homo sapiens GN=KRT7 PE=1 SV=5										E-07						
F5H8K9	F5H8K9_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=2 SV=1	35.60					1.00						3.17 E-09			Sample 2 Only	
O14983	AT2A1_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Homo sapiens GN=ATP2A1 PE=1 SV=1	17.20	1.00			1.00	1.00	1.00	4.93 E-08			3.40 E-08	1.36 E-08	6.74 E-08	0.69	0.28	1.37
P20700	LMNB1_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	7.50			4.94						8.98 E-07						
P15531	NDKA_HUMAN Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	34.20			1.00			1.00			2.14 E-08			3.24 E-07			Sample 3 Only
H7BXE3	H7BXE3_HUMAN SAFB-like transcription modulator (Fragment) OS=Homo sapiens GN=SLTM PE=2 SV=1	9.10	1.00	2.00	2.00			1.00	2.03 E-08	8.24 E-08	5.56 E-08			3.29 E-08	Control 1 Only	Control 1 Only	1.62
Q14151	SAFB2_HUMAN Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	11.60	1.00	1.00	1.00	2.00			4.15 E-09	4.08 E-09	6.39 E-09	2.91 E-08			7.00	Control 1 Only	Control 1 Only
Q8N8S7	ENAH_HUMAN Protein enabled homolog OS=Homo sapiens GN=ENAH PE=1 SV=2	5.30		1.00						8.24 E-08							
P24534	EF1B_HUMAN Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	15.60	1.00	2.00	0.98			2.00	1.39 E-08	9.54 E-08	9.58 E-10			1.38 E-07	Control 1 Only	Control 1 Only	9.91
Q15427	SF3B4_HUMAN Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	14.20	2.00	1.00	2.00	1.00	1.00	2.00	1.29 E-08	1.49 E-08	1.54 E-08	1.33 E-08	1.94 E-08	1.76 E-08	1.03	1.51	1.36
F5H365	F5H365_HUMAN Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=2 SV=1	12.90		0.98	0.99		1.98	0.99		7.96 E-09	6.25 E-08		2.00 E-07	5.48 E-09		Sample 2 Only	Sample 3 Only
P26232	CTNA2_HUMAN Catenin alpha-2 OS=Homo sapiens GN=CTNNA2 PE=1 SV=5	4.10	0.54				1.53	0.99	2.93 E-08				1.52 E-07	2.49 E-09	Control 1 Only	5.19	0.08
P26232-6	CTNA2_HUMAN Isoform 6 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2	4.30						1.00						5.88 E-08			Sample 3 Only
A0AV96	RBM47_HUMAN RNA-binding protein 47 OS=Homo sapiens GN=RBM47 PE=1 SV=2	17.70		2.97	0.99	0.99				5.65 E-08	4.92 E-09	3.67 E-08			Sample 1 Only		
Q2M389	WASH7_HUMAN WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 PE=1 SV=2	3.80		3.99	1.00		3.00			3.00 E-08	7.06 E-10		4.52 E-08			Sample 2 Only	
P31151	S10A7_HUMAN Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	31.70			1.00	6.00		1.00			4.79 E-08	1.08 E-06		3.66 E-08	Sample 1 Only		Sample 3 Only
P31689	DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	13.60		2.00	1.00		1.00	1.00		1.42 E-07	6.09 E-08		3.10 E-09	8.66 E-08		Sample 2 Only	Sample 3 Only
P31947	1433S_HUMAN 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	21.30	2.00						1.10 E-06						Control 1 Only	Control 1 Only	Control 1 Only
P61981	1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	14.60					1.00	1.00					6.27 E-08	2.00 E-08		Sample 2 Only	Sample 3 Only
Q5T1M5	FKB15_HUMAN FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2	6.20			3.00		2.00	1.00			4.18 E-08		3.32 E-09	3.38 E-09		Sample 2 Only	Sample 3 Only
Q5T280	CI114_HUMAN Uncharacterized protein C9orf114 OS=Homo sapiens GN=C9orf114 PE=1 SV=3	7.20	1.00	2.00	1.00	2.00	1.00	1.00	2.88 E-07	4.60 E-07	6.34 E-07	8.26 E-07	5.50 E-07	9.78 E-08	2.87	1.91	0.34
Q5T440	CAF17_HUMAN Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1	31.50		8.00			16.00	10.00		2.01 E-06			8.74 E-06	2.11 E-06		Sample 2 Only	Sample 3 Only
Q68CQ7	GL8D1_HUMAN Glycosyltransferase 8 domain-containing protein 1 OS=Homo sapiens GN=GLT8D1 PE=1 SV=2	9.40		1.99	2.00	2.00	1.00			1.50 E-07	7.75 E-08	3.05 E-08	1.24 E-08		Sample 1 Only	Sample 2 Only	
Q6DN03	H2B2C_HUMAN Putative histone H2B type 2-C OS=Homo sapiens GN=HIST2H2BC PE=5 SV=3	27.40	5.47		1.49				4.25 E-05		3.11 E-06				Control 1 Only	Control 1 Only	Control 1 Only

Q99880	H2B1L_HUMAN Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3	69.00	4.93	0.99	1.97				5.15 E-05	5.41 E-07	9.21 E-06				Control 1 Only	Control 1 Only	Control 1 Only
Q8N257	H2B3B_HUMAN Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3	69.00	1.00						7.79 E-07						Control 1 Only	Control 1 Only	Control 1 Only
Q6IAA8	LTOR1_HUMAN Ragulator complex protein LAMTOR1 OS=Homo sapiens GN=LAMTOR1 PE=1 SV=2	16.10	2.00	2.00	1.00	1.00	2.00		1.03 E-07	2.82 E-07	1.44 E-07	3.06 E-08	2.74 E-07		0.30	2.65	Control 1 Only
Q6NUK1	SCMC1_HUMAN Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2	10.10		2.00		2.00	2.00	1.00		9.60 E-08		1.83 E-07	6.25 E-08	4.71 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6NZY4	ZCHC8_HUMAN Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 PE=1 SV=2	8.80		0.99		1.98	1.99	0.99		9.15 E-09		1.56 E-08	7.02 E-08	1.07 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q6P2Q9	PRP8_HUMAN Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	2.60			5.00	1.00					2.82 E-08	1.71 E-09			Sample 1 Only		
Q6PGP7	TTC37_HUMAN Tetratricopeptide repeat protein 37 OS=Homo sapiens GN=TTC37 PE=1 SV=1	2.70			3.00						8.99 E-09						
Q7Z478	DHX29_HUMAN ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2	1.50			2.00		1.00	1.00			1.49 E-08		6.47 E-09	6.60 E-09		Sample 2 Only	Sample 3 Only
Q86UE4	LYRIC_HUMAN Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2	4.80	1.00	2.00	1.00	2.00	1.00	1.00	1.63 E-08	1.10 E-07	5.56 E-08	8.85 E-08	1.87 E-08	5.98 E-08	5.42	1.14	3.66
F8W6L6	F8W6L6_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=2 SV=1	5.60	1.00		4.00		2.00		3.46 E-09		1.69 E-08		4.92 E-09		Control 1 Only	1.42	Control 1 Only
Q8IUE6	H2A2B_HUMAN Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3	40.80	2.97		1.97	0.98			2.61 E-06		3.76 E-09	8.91 E-10			0.00	Control 1 Only	Control 1 Only
P04908	H2A1B_HUMAN Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	40.80			0.99						1.21 E-07						
P20671	H2A1D_HUMAN Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2	40.80	4.42	0.98	2.46				1.79 E-06	1.68 E-07	2.96 E-07				Control 1 Only	Control 1 Only	Control 1 Only
P0C0S5	H2AZ_HUMAN Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2	23.40	1.98						2.66 E-07						Control 1 Only	Control 1 Only	Control 1 Only
Q8N7H5	PAF1_HUMAN RNA polymerase II-associated factor 1 homolog OS=Homo sapiens GN=PAF1 PE=1 SV=2	6.60		2.00	1.00	1.99	1.00	2.00		1.12 E-07	2.80 E-08	1.71 E-07	5.99 E-08	1.36 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
G5E972	G5E972_HUMAN Thymopentin OS=Homo sapiens GN=TMPO PE=2 SV=1	37.70		0.64	1.28	0.64	1.63			2.13 E-08	7.10 E-08	1.27 E-08	6.88 E-08		Sample 1 Only	Sample 2 Only	
P42167-2	LAP2B_HUMAN Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO	45.20				1.00						1.35 E-09			Sample 1 Only		
H0YMV8	H0YMV8_HUMAN 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=2 SV=1	38.10	0.99		0.99				2.10 E-07		3.04 E-07				Control 1 Only	Control 1 Only	Control 1 Only
Q8TCT9	HM13_HUMAN Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1	13.40				0.99	1.98	2.98				1.48 E-07	1.02 E-08	3.09 E-07	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q8WUK0	PTPM1_HUMAN Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Homo sapiens GN=PTPMT1 PE=1 SV=1	18.20	1.00	1.00	1.00	1.00	2.00	2.00	4.25 E-08	1.13 E-06	7.40 E-09	6.15 E-08	6.06 E-07	4.70 E-08	1.45	14.26	1.11
Q8W	SCFD1_HUMAN Sec1 family domain-	4.70		0.99	0.99	0.99				4.64	2.28	9.10			Sample		

VM8	containing protein 1 OS=Homo sapiens GN=SCFD1 PE=1 SV=4									E-08	E-08	E-09			1 Only		
A9Z 1X7	A9Z1X7_HUMAN Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=2 SV=1	9.10			3.00	1.00					4.40 E-08	1.83 E-08			Sample 1 Only		
Q05 519	SRS11_HUMAN Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1	6.20	1.00	1.00	1.00	1.00	1.00	1.00	1.85 E-07	1.28 E-07	7.54 E-09	1.97 E-07	6.54 E-08	3.36 E-08	1.06	0.35	0.18
P43 246	MSH2_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	9.00		3.97	2.00		3.97			1.32 E-07	9.92 E-09		7.06 E-08			Sample 2 Only	
P43 353	AL3B1_HUMAN Aldehyde dehydrogenase family 3 member B1 OS=Homo sapiens GN=ALDH3B1 PE=1 SV=1	5.20			0.53	0.99					3.07 E-08	2.37 E-08			Sample 1 Only		
J3Q RD1	J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=2 SV=1	9.20		0.99			0.99			2.21 E-08			1.40 E-08			Sample 2 Only	
Q71 RC2	LARP4_HUMAN La-related protein 4 OS=Homo sapiens GN=LARP4 PE=1 SV=3	3.80		1.00						1.12 E-08							
Q92 896	GSLG1_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2	2.70		1.00	1.00	1.00		2.00		9.36 E-09	1.25 E-09	1.63 E-08		9.36 E-09	Sample 1 Only		Sample 3 Only
Q96 CW1	AP2M1_HUMAN AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2	70.80				1.00	1.00					3.22 E-07	5.57 E-07		Sample 1 Only	Sample 2 Only	
Q96 CW1 -2	AP2M1_HUMAN Isoform 2 of AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1	70.70				1.00						1.82 E-07			Sample 1 Only		
Q96 DA6	TIM14_HUMAN Mitochondrial import inner membrane translocase subunit TIM14 OS=Homo sapiens GN=DNAJC19 PE=1 SV=3	23.10		1.00	2.00	1.00	1.00			4.94 E-07	5.86 E-08	2.45 E-08	1.57 E-07		Sample 1 Only	Sample 2 Only	
Q96I 25	SPF45_HUMAN Splicing factor 45 OS=Homo sapiens GN=RBM17 PE=1 SV=1	15.00	3.98			3.00			6.15 E-07			2.78 E-07			0.45	Control 1 Only	Control 1 Only
Q96 JC1	VPS39_HUMAN Vam6/Vps39-like protein OS=Homo sapiens GN=VPS39 PE=1 SV=2	5.60		3.00						4.61 E-08							
Q96 KP1	EXOC2_HUMAN Exocyst complex component 2 OS=Homo sapiens GN=EXOC2 PE=1 SV=1	8.00		5.00		3.00	1.00			3.34 E-08		6.57 E-09	3.27 E-09		Sample 1 Only	Sample 2 Only	
Q99 575	POP1_HUMAN Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2	6.20	5.00	2.00	2.00				1.12 E-07	2.29 E-08	2.74 E-08				Control 1 Only	Control 1 Only	Control 1 Only
Q9B PX3	CND3_HUMAN Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1	3.50		3.00			1.00			1.54 E-08			2.40 E-09			Sample 2 Only	
Q9B Q95	ECSIT_HUMAN Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial OS=Homo sapiens GN=ECSIT PE=1 SV=1	18.60		0.99	0.99	1.00	1.98	0.99		1.40 E-07	4.46 E-09	3.02 E-08	3.65 E-07	3.73 E-08	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9B X40	LS14B_HUMAN Protein LSM14 homolog B OS=Homo sapiens GN=LSM14B PE=1 SV=1	8.10		1.00		1.00				6.92 E-08		6.48 E-08			Sample 1 Only		
Q9B ZH6	WDR11_HUMAN WD repeat-containing protein 11 OS=Homo sapiens GN=WDR11 PE=1 SV=1	2.00		2.00	2.00	1.00	2.00	1.00		2.44 E-08	1.24 E-08	3.27 E-09	2.68 E-08	7.39 E-09	Sample 1 Only	Sample 2 Only	Sample 3 Only
Q9H 1B5	XYLT2_HUMAN Xylosyltransferase 2 OS=Homo sapiens GN=XYLT2 PE=2 SV=2	4.60		2.00		1.00				1.92 E-08		5.31 E-10			Sample 1 Only		
C9J C03	C9JC03_HUMAN EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=2 SV=1	19.00					5.94						2.96 E-07			Sample 2 Only	
Q9H 270	VPS11_HUMAN Vacuolar protein sorting-associated protein 11 homolog OS=Homo	7.40		2.00			4.00	1.00		6.60 E-08			3.30 E-08	1.46 E-08		Sample 2 Only	Sample 3 Only


sapiens GN=VPS11 PE=1 SV=1

Table A7. FLAG candidates from nuclear immunoprecipitations that had been treated with RNase.

			SPECTRAL COUNTS				SPECTRAL INDEX (MIC SIn)					
Prot	Description	% Cover	C1	C2	S1	S2	C1	C2	S1	S2	S1/C1	S2/C1
P78527	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	64.00	546.67	770.46	489.74	338.89	1.55E-06	2.87E-06	1.13E-06	4.65E-07	0.73	0.30
P21333	FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	77.50	386.50	527.25	290.10	395.54	2.34E-06	4.29E-06	1.14E-06	1.61E-06	0.49	0.69
P04264	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	73.90	555.50	316.00	376.00	240.00	6.62E-05	1.67E-05	2.48E-05	1.28E-05	0.37	0.19
P15924	DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	72.00	347.97	531.94	236.97	112.00	1.22E-06	2.27E-06	4.91E-07	1.28E-07	0.40	0.11
E7EX17	E7EX17_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=2 SV=1	86.20	313.23	336.84	226.51	296.56	2.71E-05	3.15E-05	1.10E-05	2.18E-05	0.40	0.80
P13645	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	70.50	450.48	254.71	302.63	169.81	6.11E-05	1.26E-05	1.90E-05	7.14E-06	0.31	0.12
P35908	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	92.30	433.73	229.71	295.72	149.48	3.78E-05	8.15E-06	1.30E-05	5.24E-06	0.34	0.14
Q8IX12	CCAR1_HUMAN Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	53.30	243.56	295.20	305.21	250.35	6.33E-06	8.57E-06	5.91E-06	3.70E-06	0.93	0.58
Q9UKV8	AGO2_HUMAN Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	84.20	4.00	3.00	620.74	421.83	1.97E-08	1.75E-08	6.49E-05	2.94E-05	3291.58	1490.37
P35527	K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	88.30	383.33	200.59	244.31	146.01	3.35E-05	8.42E-06	1.13E-05	6.52E-06	0.34	0.19
P52732	KIF11_HUMAN Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	71.40	282.00	256.00	270.00	93.00	1.00E-05	8.42E-06	6.53E-06	9.71E-07	0.65	0.10
O15020	SPTN2_HUMAN Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	66.70	185.87	321.83	50.98	79.93	7.12E-07	2.10E-06	8.86E-08	1.36E-07	0.12	0.19
P06310	KV206_HUMAN Ig kappa chain V-II region RPMI 6410 OS=Homo sapiens PE=4 SV=1	18.80	117.83	121.79	200.02	175.26	4.35E-03	4.69E-03	5.68E-03	5.75E-03	1.31	1.32
Q5UIP0	RIF1_HUMAN Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2	44.80	148.18	212.91	69.67	181.88	5.76E-07	9.04E-07	1.45E-07	4.39E-07	0.25	0.76
O75369-8	FLNB_HUMAN Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB	62.40	136.48	182.57	97.24	151.19	2.83E-07	4.86E-07	1.51E-07	3.38E-07	0.53	1.19
Q8NE71	ABCF1_HUMAN ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2	68.80	127.38	127.70	111.98	100.45	4.47E-06	4.22E-06	2.08E-06	2.37E-06	0.47	0.53
P35579	MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	69.20	59.35	280.16	24.80	71.32	1.19E-07	1.17E-06	3.13E-08	1.14E-07	0.26	0.95
P60709	ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	86.10	103.99	111.88	98.87	119.66	1.00E-04	8.76E-05	2.58E-05	3.31E-05	0.26	0.33
Q9UPQ9-1	TNR6B_HUMAN Isoform 2 of Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B	57.10	3.00		115.00	108.00	1.42E-08		7.53E-07	3.46E-07	53.18	24.44
O14744	ANM5_HUMAN Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	61.90	112.59	115.42	125.14	51.39	8.80E-06	8.63E-06	7.30E-06	1.71E-06	0.83	0.19
Q09666	AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	49.80	116.00	173.00	67.00	54.00	1.26E-07	1.67E-07	4.50E-08	2.37E-08	0.36	0.19
Q86YZ3	HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	31.50	154.00	80.00	111.00	59.00	2.60E-07	6.62E-08	1.07E-07	7.43E-08	0.41	0.29
P61978	HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	64.10	108.88	122.63	73.58	92.22	1.03E-05	1.20E-05	3.09E-06	6.29E-06	0.30	0.61
Q9UH99	SUN2_HUMAN SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	70.20	143.25	95.83	92.85	65.20	7.56E-06	3.84E-06	2.70E-06	1.48E-06	0.36	0.20

Q9P258	RCC2_HUMAN Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	78.00	121.00	105.00	93.00	80.00	6.91E-06	5.02E-06	2.97E-06	2.80E-06	0.43	0.41
Q00610	CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	51.30	85.67	157.27	90.65	56.82	3.29E-07	8.13E-07	2.77E-07	1.80E-07	0.84	0.55
F5GWX5	F5GWX5_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=2 SV=1	51.30	82.87	144.81	54.89	71.86	3.26E-07	6.04E-07	1.53E-07	1.70E-07	0.47	0.52
P16615	AT2A2_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	38.50	73.95	98.59	89.70	86.83	7.03E-07	9.22E-07	6.63E-07	7.08E-07	0.94	1.01
Q8TAQ2	SMRC2_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1	37.20	85.61	116.53	68.73	47.76	5.92E-07	1.05E-06	2.69E-07	2.01E-07	0.46	0.34
O00571	DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	69.60	89.10	95.02	65.36	50.51	4.41E-06	4.52E-06	1.94E-06	1.30E-06	0.44	0.30
O00159-3	MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	57.50	72.09	131.41	17.80	59.34	9.20E-07	1.91E-06	9.31E-08	4.90E-07	0.10	0.53
O95218-2	ZRAB2_HUMAN Isoform 2 of Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2	60.90	108.99	71.00	80.00	19.00	1.31E-05	3.38E-06	5.73E-06	4.86E-07	0.44	0.04
P11142	HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	53.70	57.39	72.95	60.26	70.99	1.59E-06	2.18E-06	1.24E-06	1.83E-06	0.78	1.15
O75533	SF3B1_HUMAN Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	56.30	52.97	129.96	8.00	62.99	4.19E-07	1.82E-06	2.76E-08	4.05E-07	0.07	0.97
P53621	COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	51.70	55.00	93.97	83.98	20.00	3.04E-07	8.58E-07	4.50E-07	6.31E-08	1.48	0.21
P68104	EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	52.80	52.41	55.88	43.92	42.41	8.85E-06	5.88E-06	4.67E-06	2.75E-06	0.53	0.31
E7EMW7	E7EMW7_HUMAN E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=2 SV=1	40.80	34.00	65.50	18.50	5.50	6.36E-08	1.46E-07	2.10E-08	8.20E-07	0.33	12.90
J3KMW7	J3KMW7_HUMAN E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=2 SV=1	40.90	33.50	67.00	18.50	5.50	6.31E-08	1.51E-07	2.10E-08	8.18E-07	0.33	12.97
P23458	JAK1_HUMAN Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2	53.60	43.00	93.00	47.00	57.00	3.41E-07	1.15E-06	2.86E-07	3.23E-07	0.84	0.95
Q15393	SF3B3_HUMAN Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	44.10	51.93	99.83	12.98	68.87	5.81E-07	1.59E-06	6.69E-08	5.56E-07	0.11	0.96
O75165	DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5	47.90	35.00	151.52	29.00	11.00	2.04E-07	1.14E-06	2.26E-07	3.91E-07	1.11	1.92
Q9UHB6-4	LIMA1_HUMAN Isoform 4 of LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1	67.60	42.50	45.00	11.00	18.50	9.35E-07	1.09E-06	9.36E-08	2.01E-07	0.10	0.21
P58107	EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	55.50	37.00	67.00	28.00	25.00	4.65E-08	1.08E-07	2.47E-08	1.91E-08	0.53	0.41
E9PK91	E9PK91_HUMAN Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=2 SV=1	48.90	67.81	121.85	32.37	1.96	9.66E-07	1.72E-06	3.19E-07	1.11E-08	0.33	0.01
P04843	RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	64.90	56.00	64.00	49.00	58.00	1.71E-06	1.90E-06	1.03E-06	1.36E-06	0.60	0.80
P36578	RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	67.40	45.78	66.64	27.84	79.62	1.72E-06	1.93E-06	6.37E-07	2.30E-06	0.37	1.34
B9A067	B9A067_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=2 SV=2	76.70	38.29	87.33	40.23	48.08	6.32E-07	2.14E-06	4.54E-07	7.40E-07	0.72	1.17
Q14008	CKAP5_HUMAN Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	43.20	66.00	78.00	18.00	52.00	1.52E-07	1.54E-07	2.69E-08	7.05E-08	0.18	0.47
Q14247	SRC8_HUMAN Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	60.20	62.28	51.41	56.39	39.58	1.54E-06	1.01E-06	7.66E-07	6.87E-07	0.50	0.45
Q9C0C2	TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	51.10	37.96	47.97	25.98	98.92	9.63E-08	1.20E-07	5.57E-08	2.91E-07	0.58	3.02
Q9UHF7	TRPS1_HUMAN Zinc finger transcription factor Trps1 OS=Homo sapiens GN=TRPS1 PE=1 SV=2	43.20	44.67	63.51	18.83	75.38	2.32E-07	5.38E-07	4.51E-08	2.62E-07	0.19	1.13
P13647	K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	63.20	97.59	26.85	57.69	19.90	2.43E-06	4.70E-07	9.08E-07	2.56E-07	0.37	0.11

P23396	RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	84.00	41.98	50.80	37.16	63.54	9.99E-06	1.17E-05	4.88E-06	9.05E-06	0.49	0.91
P61247	RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	76.90	37.94	51.53	29.21	74.88	6.74E-06	9.02E-06	1.95E-06	6.45E-06	0.29	0.96
Q16875	F263_HUMAN 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 OS=Homo sapiens GN=PFKFB3 PE=1 SV=1	75.40	50.20	46.24	65.96	29.53	1.80E-06	1.32E-06	1.87E-06	7.08E-07	1.04	0.39
Q13435	SF3B2_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	56.30	37.60	94.01	12.91	47.42	4.83E-07	1.51E-06	6.91E-08	4.90E-07	0.14	1.01
P63244	GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	66.20	33.63	43.18	41.25	67.22	3.71E-06	5.17E-06	2.05E-06	4.25E-06	0.55	1.15
P25205	MCM3_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	59.40	59.48	49.54	24.79	57.47	1.13E-06	9.75E-07	2.39E-07	8.57E-07	0.21	0.76
Q07065	CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	70.30	55.98	54.00	28.00	52.98	1.22E-06	1.18E-06	3.68E-07	1.07E-06	0.30	0.87
Q8WWY3	PRP31_HUMAN U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2	54.70	56.36	47.44	48.40	35.56	2.55E-06	2.00E-06	1.27E-06	1.05E-06	0.50	0.41
Q9BRX2	PELO_HUMAN Protein pelota homolog OS=Homo sapiens GN=PELO PE=1 SV=2	54.80	49.00	49.00	44.00	46.00	4.09E-06	3.78E-06	1.87E-06	1.58E-06	0.46	0.39
O94832	MYO1D_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2	60.10	59.43	85.18	4.95	29.71	8.16E-07	1.25E-06	2.12E-08	3.59E-07	0.03	0.44
Q05639	EF1A2_HUMAN Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	45.10	27.50	20.00	42.00	32.50	4.00E-06	2.70E-06	3.37E-06	1.96E-06	0.84	0.49
P53618	COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	47.60	47.98	55.98	61.97	10.00	6.22E-07	7.63E-07	6.11E-07	6.79E-08	0.98	0.11
P51532	SMCA4_HUMAN Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2	35.50	35.47	69.44	24.46	17.47	1.08E-07	2.66E-07	5.44E-08	2.89E-08	0.50	0.27
P52272	HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	66.60	36.11	40.54	22.23	47.47	5.68E-07	6.79E-07	2.13E-07	6.70E-07	0.38	1.18
Q14160	SCRIB_HUMAN Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4	34.80	50.51	57.47	20.82	35.68	2.08E-07	3.53E-07	4.96E-08	1.16E-07	0.24	0.56
P62701	RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	74.10	27.88	50.82	21.90	64.72	4.18E-06	7.59E-06	1.57E-06	6.91E-06	0.38	1.65
Q9P219	DAPLE_HUMAN Protein Daple OS=Homo sapiens GN=CCDC88C PE=1 SV=3	38.50	44.95	76.89	39.98	2.9	8.53E-08	1.60E-07	4.80E-08	2.72E-09	0.56	0.03
Q8N257	H2B3B_HUMAN Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3	57.90	37.28	48.09	31.38	43.18	4.45E-05	7.06E-05	8.11E-06	3.02E-05	0.18	0.68
O60264	SMCA5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1	44.00	28.50	59.50	13.50	28.00	2.05E-07	6.28E-07	6.41E-08	1.98E-07	0.31	0.97
P51659	DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	59.50	58.34	53.35	27.69	19.78	1.29E-06	1.21E-06	4.74E-07	3.21E-07	0.37	0.25
P46940	IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	41.50	36.95	75.90	17.97	28.96	8.13E-08	2.46E-07	2.60E-08	5.46E-08	0.32	0.67
O15294	OGT1_HUMAN UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3	42.30	44.59	59.45	27.74	25.77	5.67E-07	8.94E-07	2.10E-07	2.06E-07	0.37	0.36
P52597	HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	49.40	30.00	46.00	42.00	39.00	2.89E-06	2.60E-06	1.56E-06	1.23E-06	0.54	0.43
Q15208	STK38_HUMAN Serine/threonine-protein kinase 38 OS=Homo sapiens GN=STK38 PE=1 SV=1	57.00	45.00	52.00	43.50	11.50	1.77E-06	2.19E-06	1.18E-06	1.86E-07	0.66	0.10
P98175	RBM10_HUMAN RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3	56.20	37.98	90.99	3.00	19.99	5.96E-07	1.68E-06	2.11E-08	2.12E-07	0.04	0.36
H3BLZ8	H3BLZ8_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=2 SV=1	52.80	43.61	54.49	15.84	35.64	1.15E-06	1.59E-06	1.44E-07	4.94E-07	0.12	0.43
Q9P2E9	RRBP1_HUMAN Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	59.60	18.79	20.79	16.81	92.12	1.16E-07	1.77E-07	9.24E-08	1.96E-07	0.80	1.70
Q9Y2W1	TR150_HUMAN Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	35.00	25.00	112.00	12.00		2.26E-07	1.37E-06	7.07E-08		0.31	Control 1 Only

Q16531	DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	48.00	51.21	60.08	19.71	14.78	6.61E-07	7.52E-07	1.30E-07	9.89E-08	0.20	0.15
P46777	RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	52.50	24.00	36.00	25.00	60.00	2.56E-06	2.70E-06	1.28E-06	2.96E-06	0.50	1.16
P26599	PTBP1_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	61.40	38.71	38.69	16.85	40.66	1.41E-06	1.48E-06	3.13E-07	1.46E-06	0.22	1.03
G3XAB8	G3XAB8_HUMAN Trinucleotide repeat containing 6C, isoform CRA_a OS=Homo sapiens GN=TNRC6C PE=2 SV=1	31.60			92.95	50.94			3.41E-07	1.28E-07	Sample 1 Only	Sample 2 Only
P45880	VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	57.60	24.75	29.68	39.57	47.48	2.84E-06	2.95E-06	2.85E-06	3.80E-06	1.00	1.34
P39023	RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	54.10	26.69	36.63	16.80	60.27	1.74E-06	1.74E-06	5.66E-07	2.81E-06	0.33	1.61
Q8WX92	NELFB_HUMAN Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1	52.20	36.00	43.00	26.00	35.00	9.25E-07	9.88E-07	3.70E-07	7.28E-07	0.40	0.79
C9J9K3	C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	71.20	25.94	43.86	26.93	43.85	7.69E-06	8.16E-06	3.56E-06	7.35E-06	0.46	0.96
P05388	RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	51.70	31.99	29.08	27.20	48.57	5.90E-06	4.44E-06	2.40E-06	4.80E-06	0.41	0.81
P14923	PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	51.70	42.41	42.37	27.91	21.45	3.95E-07	5.61E-07	1.70E-07	2.20E-07	0.43	0.56
P35580	MYH10_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	52.80	10.53	114.70	1.0	8.9	1.59E-08	3.56E-07	9.68E-10	7.85E-09	0.06	0.49
P35659	DEK_HUMAN Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1	38.70	57.24	35.48	17.76	25.63	3.45E-06	1.83E-06	4.75E-07	8.27E-07	0.14	0.24
P62805	H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	58.30	26.00	52.00	19.00	39.00	2.74E-05	5.49E-05	3.35E-06	2.48E-05	0.12	0.91
O94776	MTA2_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1	44.20	30.00	40.00	22.00	44.00	7.46E-07	1.02E-06	3.29E-07	9.56E-07	0.44	1.28
P02533	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	68.60	59.50	18.50	30.50	9.50	1.77E-06	3.79E-07	5.28E-07	1.43E-07	0.30	0.08
Q15233	NONO_HUMAN Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	65.20	40.74	49.63	12.91	29.79	1.31E-06	1.94E-06	2.66E-07	9.06E-07	0.20	0.69
Q00325	MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	39.30	28.95	30.92	30.94	41.86	2.87E-06	2.84E-06	2.04E-06	2.63E-06	0.71	0.92
Q00839	HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	33.50	15.50	17.50	11.50	21.50	2.31E-07	2.31E-07	1.24E-07	2.88E-07	0.54	1.24
A8MXP9	A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	43.40	21.63	35.38	18.63	51.04	3.57E-07	6.08E-07	1.39E-07	7.38E-07	0.39	2.07
H3BQZ7	H3BQZ7_HUMAN HCG2044799 OS=Homo sapiens GN=hCG_2044799 PE=4 SV=1	42.40	28.00	47.00	22.00	30.00	7.01E-07	8.15E-07	2.42E-07	3.76E-07	0.34	0.54
F5H335	F5H335_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1	36.80	22.00	70.00	17.00	15.00	4.13E-08	2.07E-07	1.95E-08	1.77E-08	0.47	0.43
P11021	GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	52.40	29.00	33.00	26.00	34.00	3.88E-07	4.45E-07	2.32E-07	3.64E-07	0.60	0.94
P23246	SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	41.90	31.87	43.88	14.98	29.95	9.22E-07	1.24E-06	2.08E-07	6.24E-07	0.23	0.68
P26641	EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	36.40	31.00	37.00	29.00	24.00	2.44E-06	1.94E-06	1.34E-06	6.72E-07	0.55	0.28
P62424	RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	47.40	20.95	33.93	16.95	47.90	1.73E-06	1.99E-06	5.49E-07	3.20E-06	0.32	1.85
Q96N67-2	DOCK7_HUMAN Isoform 2 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7	26.10	47.54	67.34		1.98	1.17E-07	2.04E-07		1.75E-09	Control 1 Only	0.02
P62917	RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	43.60	22.73	26.68	24.68	43.48	4.11E-06	4.53E-06	2.03E-06	4.95E-06	0.49	1.20
P33992	MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	40.60	33.86	33.87	14.95	33.88	5.59E-07	5.20E-07	1.32E-07	4.56E-07	0.24	0.82

Q07666	KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	39.10	34.78	40.73	13.90	25.83	1.46E-06	1.67E-06	1.96E-07	6.29E-07	0.13	0.43
Q9Y446	PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	45.40	35.92	38.94	10.98	25.98	5.45E-07	5.50E-07	9.12E-08	2.86E-07	0.17	0.53
G8JLB6	G8JLB6_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	52.60	25.12	29.94	23.18	30.84	1.19E-06	1.57E-06	6.33E-07	1.10E-06	0.53	0.92
Q14980-2	NUMA1_HUMAN Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1	70.40	16.00	27.49	8.99	4.00	4.15E-08	1.03E-07	1.58E-08	5.11E-09	0.38	0.12
O43143	DHX15_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	37.90	21.00	52.00	4.00	33.00	2.61E-07	8.89E-07	1.90E-08	4.50E-07	0.07	1.72
P51531	SMCA2_HUMAN Probable global transcription activator SNF2L2 OS=Homo sapiens GN=SMARCA2 PE=1 SV=2	30.60	20.48	46.45	15.49	4.47	6.06E-08	1.59E-07	2.68E-08	6.22E-09	0.44	0.10
J3QK89	J3QK89_HUMAN Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=2 SV=1	29.90	16.00	72.00	1.00	19.00	1.71E-07	8.74E-07	4.10E-09	2.08E-07	0.02	1.22
Q86U86	PB1_HUMAN Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1	37.70	35.25	64.57	3.92	1.96	1.01E-07	1.70E-07	3.86E-09	1.86E-09	0.04	0.02
J3KTA4	J3KTA4_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=2 SV=1	50.00	31.78	33.73	9.94	29.80	6.87E-07	9.57E-07	1.19E-07	6.29E-07	0.17	0.92
M0R0F0	M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=2 SV=1	51.00	21.88	28.83	20.85	33.80	4.40E-06	5.72E-06	2.06E-06	4.46E-06	0.47	1.01
Q9BQA1	MEP50_HUMAN Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	37.40	25.94	23.91	42.83	11.95	4.30E-06	3.45E-06	4.27E-06	5.00E-07	0.99	0.12
Q13200	PSMD2_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	41.70	20.80	38.63	17.83	24.76	2.05E-07	4.90E-07	1.23E-07	2.41E-07	0.60	1.18
Q9Y678	COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	50.20	24.99	34.49	35.99	3.00	4.46E-07	5.85E-07	4.28E-07	2.31E-08	0.96	0.05
P06748	NPM_HUMAN Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	62.90	15.86	30.75	16.84	34.73	2.82E-06	4.37E-06	1.38E-06	4.63E-06	0.49	1.64
Q92878	RAD50_HUMAN DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1	36.10	29.82	34.74	12.92	20.84	6.68E-08	1.49E-07	1.90E-08	3.59E-08	0.28	0.54
Q9Y6C9	MTCH2_HUMAN Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	55.40	26.00	24.00	20.99	27.00	4.31E-06	3.25E-06	1.74E-06	1.52E-06	0.40	0.35
P18615	NELFE_HUMAN Negative elongation factor E OS=Homo sapiens GN=NELFE PE=1 SV=3	57.40	19.52	25.37	23.53	27.32	1.21E-06	1.25E-06	9.65E-07	6.01E-07	0.80	0.50
P05141	ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	61.40	18.00	20.00	23.00	31.50	3.09E-06	3.25E-06	2.40E-06	3.11E-06	0.78	1.01
P27635	RL10_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	53.30	19.75	23.71	18.78	33.59	4.68E-06	4.64E-06	1.95E-06	4.16E-06	0.42	0.89
Q9ULW0	TPX2_HUMAN Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2	44.00	49.00	30.00	3.00	15.00	6.25E-07	3.66E-07	1.72E-08	1.35E-07	0.03	0.22
P62241	RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	58.20	17.00	25.00	20.00	35.00	2.79E-06	3.69E-06	1.60E-06	3.34E-06	0.57	1.20
Q96PK6	RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	33.80	30.93	31.93	14.96	17.97	6.52E-07	8.07E-07	1.57E-07	3.02E-07	0.24	0.46
P62280	RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	70.30	17.89	25.84	18.89	32.78	5.46E-06	8.21E-06	2.87E-06	6.44E-06	0.53	1.18
Q02878	RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	46.50	20.89	22.89	17.94	32.84	1.81E-06	1.37E-06	9.71E-07	2.56E-06	0.54	1.42
P11388	TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	27.90	38.00	21.00	5.50	10.00	1.58E-07	5.89E-08	8.60E-09	2.06E-08	0.05	0.13
Q9NSD9	SYFB_HUMAN Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3	39.90	26.00	30.00	24.00	15.00	5.44E-07	6.19E-07	2.93E-07	1.67E-07	0.54	0.31
E7EVA0	E7EVA0_HUMAN Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=2 SV=1	11.70	25.06	17.33	12.64	35.78	6.83E-08	4.24E-08	1.66E-08	4.56E-08	0.24	0.67
Q02543	RL18A_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	61.90	18.82	19.82	21.79	31.71	2.92E-06	2.68E-06	1.84E-06	3.84E-06	0.63	1.31

E7EN U4	E7ENU4_HUMAN Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=2 SV=1	42.90	28. 00	31. 00	11. 00	22. 00	2.05 E-07	2.37 E-07	4.20 E-08	8.37 E-08	0.21	0.41
Q69Y N4	VIR_HUMAN Protein virilizer homolog OS=Homo sapiens GN=KIAA1429 PE=1 SV=2	22.20	26. 73	44. 60	18. 84	1.9 8	6.20 E-08	1.21 E-07	3.23 E-08	1.64 E-09	0.52	0.03
Q154 59	SF3A1_HUMAN Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	33.50	17. 90	32. 88	8.9 1	24. 85	4.65 E-07	6.90 E-07	4.49 E-07	6.13 E-07	0.97	1.32
Q924 99	DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	46.90	20. 00	32. 00	12. 00	25. 00	2.85 E-07	3.76 E-07	1.06 E-07	2.58 E-07	0.37	0.91
Q6PK G0	LARP1_HUMAN La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	29.70	14. 87	41. 56	12. 87	18. 85	1.15 E-07	4.78 E-07	6.79 E-08	7.97 E-08	0.59	0.69
P627 53	RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	45.80	13. 00	28. 99	14. 98	31. 00	1.24 E-06	2.93 E-06	7.31 E-07	2.82 E-06	0.59	2.28
P467 81	RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	66.00	14. 94	25. 89	12. 95	29. 86	4.38 E-06	6.98 E-06	2.12 E-06	5.06 E-06	0.49	1.16
P048 44	RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	40.30	24. 90	18. 92	22. 92	16. 93	8.42 E-07	6.59 E-07	4.81 E-07	4.62 E-07	0.57	0.55
Q8IW I9	MGAP_HUMAN MAX gene-associated protein OS=Homo sapiens GN=MGA PE=1 SV=3	15.90	19. 84	50. 68	4.9 6	8.9 5	3.87 E-08	6.80 E-08	5.28 E-09	6.08 E-09	0.14	0.16
Q96T 23	RSF1_HUMAN Remodeling and spacing factor 1 OS=Homo sapiens GN=RSF1 PE=1 SV=2	34.40	10. 82	61. 94		10. 81	2.73 E-08	1.90 E-07		1.79 E-08	Control 1 Only	0.66
P629 06	RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	52.50	15. 00	25. 00	13. 00	31. 00	2.27 E-06	2.79 E-06	1.06 E-06	2.64 E-06	0.47	1.17
Q003 41	VIGLN_HUMAN Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	29.90	15. 82	28. 64	18. 74	19. 77	7.70 E-08	2.17 E-07	8.08 E-08	4.24 E-08	1.05	0.55
P622 77	RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	47.70	17. 91	23. 89	16. 93	24. 88	5.21 E-06	7.27 E-06	2.53 E-06	5.29 E-06	0.48	1.01
O001 39-2	KIF2A_HUMAN Isoform 2 of Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A	45.60	34. 85	28. 84	13. 95	4.9 9	6.58 E-07	4.39 E-07	1.35 E-07	4.45 E-08	0.21	0.07
O437 19	HTSF1_HUMAN HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1	26.60	21. 85	24. 88	17. 91	17. 92	2.86 E-07	4.29 E-07	1.46 E-07	2.23 E-07	0.51	0.78
P025 45	LMNA_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	43.10	21. 55	31. 37	9.8 3	18. 60	2.27 E-07	4.44 E-07	5.17 E-08	1.45 E-07	0.23	0.64
Q8W XH0	SYNE2_HUMAN Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3	12.70	9.0 0	72. 47		1.0 0	2.23 E-09	3.19 E-08		5.21 E-08	Control 1 Only	23.39
Q96I2 4	FUBP3_HUMAN Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2	45.30	26. 96	23. 95	14. 98	15. 96	6.77 E-07	5.43 E-07	2.20 E-07	3.16 E-07	0.33	0.47
Q131 27	REST_HUMAN RE1-silencing transcription factor OS=Homo sapiens GN=REST PE=1 SV=3	21.40	30. 86	39. 87	9.9 5	1.0 0	1.67 E-07	2.54 E-07	7.52 E-08	5.86 E-09	0.45	0.04
P486 34	PRC2A_HUMAN Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3	17.40	27. 03	25. 67	8.1 8	17. 15	6.24 E-08	6.18 E-08	1.45 E-08	1.88 E-08	0.23	0.30
Q86U P2	KTN1_HUMAN Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1	33.50	26. 85	37. 70	5.9 5	9.9 4	1.24 E-07	2.29 E-07	1.97 E-08	2.59 E-08	0.16	0.21
P181 24	RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	45.60	15. 92	19. 92	15. 93	28. 90	3.35 E-06	2.58 E-06	1.52 E-06	3.70 E-06	0.45	1.10
Q9B W19	KIFC1_HUMAN Kinesin-like protein KIFC1 OS=Homo sapiens GN=KIFC1 PE=1 SV=2	56.60	26. 00	33. 00	12. 00	10. 00	4.46 E-07	5.04 E-07	1.02 E-07	9.82 E-08	0.23	0.22
P622 69	RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	58.60	15. 99	23. 98	12. 99	27. 98	4.71 E-06	6.31 E-06	1.66 E-06	4.40 E-06	0.35	0.93
P148 66	HNRPL_HUMAN Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2	44.00	21. 74	28. 62	2.9 4	25. 68	4.86 E-07	6.36 E-07	4.49 E-08	5.37 E-07	0.09	1.10
F6TQ G2	F6TQG2_HUMAN Probable global transcription activator SNF2L1 (Fragment) OS=Homo sapiens GN=SMARCA1 PE=2 SV=1	24.00	8.5 0	23. 50	4.5 0	11. 00	9.35 E-08	2.79 E-07	2.65 E-08	7.07 E-08	0.28	0.76
Q9UJ S0	CMC2_HUMAN Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2	35.90	23. 00	21. 00	18. 00	17. 00	3.43 E-07	3.11 E-07	1.73 E-07	2.13 E-07	0.51	0.62
Q135 47	HDAC1_HUMAN Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1	61.80	22. 99	28. 99	9.9 9	15. 99	5.99 E-07	7.93 E-07	1.62 E-07	3.75 E-07	0.27	0.63

Q9H7D7	WDR26_HUMAN WD repeat-containing protein 26 OS=Homo sapiens GN=WDR26 PE=1 SV=3	35.70	19.85	32.74	9.91	8.94	3.43E-07	7.92E-07	1.09E-07	1.04E-07	0.32	0.30
B4DGU4	B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1	38.40	15.50	24.50	16.00	15.50	1.74E-07	4.11E-07	9.30E-08	1.56E-07	0.53	0.89
Q96I25	SPF45_HUMAN Splicing factor 45 OS=Homo sapiens GN=RBM17 PE=1 SV=1	57.40	12.92	42.77		20.91	2.14E-07	1.14E-06		3.40E-07	Control 1 Only	1.59
Q9NTJ3	SMC4_HUMAN Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2	21.50	21.77	24.74	15.83	7.92	2.37E-07	4.03E-06	6.36E-06	3.04E-07	26.78	1.28
P42704	LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	21.40	8.97	19.94	27.94	19.95	3.02E-08	1.07E-07	1.27E-07	7.22E-08	4.22	2.39
H3BPE7	H3BPE7_HUMAN RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=2 SV=1	18.10	18.00	19.00	7.50	25.50	5.63E-07	6.34E-07	1.33E-07	7.13E-07	0.24	1.27
O14578-4	CTRO_HUMAN Isoform 4 of Citron Rho-interacting kinase OS=Homo sapiens GN=CIT	28.80	16.83	50.51	0.99	6.93	2.37E-08	8.69E-08	1.20E-09	6.34E-09	0.05	0.27
Q5JWF2	GNAS1_HUMAN Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2	16.70	9.00	10.50	9.00	13.50	2.58E-07	2.00E-07	1.25E-07	1.28E-07	0.48	0.50
P15880	RS2_HUMAN 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	43.70	13.78	21.67	11.81	25.61	1.99E-06	3.57E-06	9.87E-07	2.76E-06	0.50	1.39
P62081	RS7_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	70.10	11.00	20.00	16.00	26.00	4.35E-06	6.44E-06	2.68E-06	5.74E-06	0.62	1.32
Q08379	GOGA2_HUMAN Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3	34.90	19.93	28.86	8.95	14.93	1.42E-07	2.48E-07	5.22E-08	8.54E-08	0.37	0.60
P63092	GNAS2_HUMAN Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1	44.60	8.00	11.50	9.00	10.50	6.56E-07	5.27E-07	3.23E-07	3.24E-07	0.49	0.49
Q15417	CNN3_HUMAN Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1	45.60	26.25	10.89	13.37	17.83	3.89E-06	5.55E-07	5.85E-07	6.59E-07	0.15	0.17
M0R210	M0R210_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=2 SV=1	76.00	13.86	20.82	11.86	23.76	5.69E-06	8.10E-06	2.30E-06	5.17E-06	0.40	0.91
P39019	RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	56.60	18.00	26.00	6.00	21.00	2.70E-06	3.57E-06	4.26E-07	2.62E-06	0.16	0.97
F8WE88	F8WE88_HUMAN Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=2 SV=1	35.00	10.96	54.78	1.99	1.99	1.45E-08	1.29E-07	1.89E-09	9.98E-10	0.13	0.07
O76024	WFS1_HUMAN Wolframin OS=Homo sapiens GN=WFS1 PE=1 SV=2	25.60	10.00	10.00	21.00	29.00	5.16E-08	6.56E-08	1.05E-07	1.97E-07	2.04	3.82
H0UI80	H0UI80_HUMAN Negative elongation factor C/D OS=Homo sapiens GN=TH1L PE=2 SV=1	38.00	16.00	17.00	15.00	21.00	2.40E-07	2.54E-07	1.30E-07	2.81E-07	0.54	1.17
P08708	RS17_HUMAN 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	65.20	15.91	19.91	11.94	18.91	3.12E-06	3.84E-06	1.10E-06	2.65E-06	0.35	0.85
P38646	GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	41.40	8.97	18.95	16.95	22.95	1.30E-07	2.43E-07	1.80E-07	2.43E-07	1.39	1.87
P50914	RL14_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	41.40	17.00	17.00	9.00	23.00	3.35E-06	3.14E-06	1.36E-06	3.58E-06	0.41	1.07
Q8WXI9	P66B_HUMAN Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1	36.60	19.00	20.00	11.00	17.00	3.87E-07	3.75E-07	1.19E-07	2.48E-07	0.31	0.64
O43242	PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	45.70	13.00	24.99	15.99	13.00	1.98E-07	5.73E-07	1.68E-07	1.79E-07	0.85	0.90
Q7L014	DDX46_HUMAN Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2	35.70	14.00	39.00	1.99	12.00	4.42E-08	2.08E-07	1.02E-08	8.04E-08	0.23	1.82
Q99460	PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	37.60	14.98	24.97	12.99	13.97	1.35E-07	3.01E-07	8.02E-08	1.23E-07	0.59	0.91
E7EP00	E7EP00_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=2 SV=2	27.00	16.96	17.95	18.95	11.97	1.34E-07	1.80E-07	1.12E-07	7.00E-08	0.84	0.52
Q8WXF1	PSPC1_HUMAN Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1	32.90	22.00	23.00	7.00	14.00	8.97E-07	9.13E-07	1.23E-07	3.65E-07	0.14	0.41
P46063	RECQ1_HUMAN ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3	41.10	29.94	19.97	5.97	8.98	3.94E-07	2.47E-07	4.59E-08	6.42E-08	0.12	0.16

J3KP15	J3KP15_HUMAN Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens GN=SRSF2 PE=2 SV=1	56.70	17.93	31.93	4.97	8.94	1.95E-06	2.70E-06	1.54E-07	5.11E-07	0.08	0.26
P30050	RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	69.10	14.00	14.00	12.00	25.00	3.22E-06	3.29E-06	1.42E-06	3.74E-06	0.44	1.16
Q9NZB2	F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	35.10	19.92	33.82	3.99	6.98	1.24E-07	3.34E-07	1.33E-08	2.13E-08	0.11	0.17
P39656	OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	28.90	12.96	18.94	15.94	16.95	8.06E-07	7.58E-07	6.11E-07	4.55E-07	0.76	0.56
Q9Y265	RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	49.80	18.85	23.85	11.93	9.94	5.36E-07	7.33E-07	1.40E-07	1.95E-07	0.26	0.36
Q9UHX1	PUF60_HUMAN Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	42.60	12.79	19.66	2.95	27.56	2.72E-07	4.66E-07	2.76E-08	6.47E-07	0.10	2.38
P60866	RS20_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	56.30	15.84	14.85	13.86	18.81	6.50E-06	5.79E-06	2.34E-06	4.02E-06	0.36	0.62
P61353	RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	61.00	12.93	15.90	9.94	24.87	4.17E-06	3.57E-06	1.48E-06	4.89E-06	0.36	1.17
C9JNW5	C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1	50.70	13.00	17.00	12.00	20.00	2.00E-06	2.66E-06	9.63E-07	2.59E-06	0.48	1.29
P26373	RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	52.10	14.95	18.93	8.96	19.90	2.27E-06	1.41E-06	6.61E-07	2.60E-06	0.29	1.15
P62750	RL23A_HUMAN 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	61.50	14.92	13.90	6.94	26.86	3.08E-06	2.58E-06	9.24E-07	3.59E-06	0.30	1.17
P62851	RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	44.00	14.00	19.00	12.00	18.00	5.23E-06	7.21E-06	1.75E-06	4.62E-06	0.33	0.88
P62913	RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	50.60	11.90	14.89	10.92	24.82	4.50E-06	3.16E-06	1.84E-06	4.10E-06	0.41	0.91
Q9Y5B9	SP16H_HUMAN FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1	23.70	17.50	29.50	2.00	12.00	1.17E-07	2.22E-07	7.99E-09	7.15E-08	0.07	0.61
Q9NQX4	MYO5C_HUMAN Unconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	31.10	10.96	50.89			1.67E-08	1.18E-07			Control 1 Only	Control 1 Only
P67809	YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	71.00	11.91	36.83	9.93	2.98	3.95E-07	1.33E-06	1.99E-07	4.42E-08	0.50	0.11
F6S0T5	F6S0T5_HUMAN Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=2 SV=1	32.30	14.94	24.93	12.97	8.99	1.53E-07	3.00E-07	9.09E-08	7.26E-08	0.59	0.47
P07355	ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	51.60	20.09	19.16	9.53	10.49	1.81E-06	1.58E-06	3.21E-07	3.75E-07	0.18	0.21
Q6N021	TET2_HUMAN Methylcytosine dioxygenase TET2 OS=Homo sapiens GN=TET2 PE=1 SV=3	18.50	13.98	21.92	2.99	20.89	4.87E-08	8.64E-08	5.69E-09	2.40E-08	0.12	0.49
F5GZS0	F5GZS0_HUMAN Probable ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36 PE=2 SV=1	33.00	30.90	22.96	4.98	2.00	3.88E-07	2.12E-07	2.38E-08	8.54E-09	0.06	0.02
Q9P1Y5	CAMP3_HUMAN Calmodulin-regulated spectrin-associated protein 3 OS=Homo sapiens GN=CAMSAP3 PE=1 SV=2	20.30	24.99	8.00	6.00	21.99	1.92E-07	5.20E-08	3.64E-08	6.71E-08	0.19	0.35
P40429	RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	49.80	12.95	13.96	11.96	21.90	2.16E-06	1.71E-06	9.67E-07	2.71E-06	0.45	1.25
Q14527	HLTF_HUMAN Helicase-like transcription factor OS=Homo sapiens GN=HLTF PE=1 SV=2	31.80	22.91	24.90	5.99	5.98	1.97E-07	1.94E-07	2.26E-08	3.23E-08	0.11	0.16
P09874	PARP1_HUMAN Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	28.50	14.00	21.00	3.00	22.00	9.59E-08	1.57E-07	1.03E-08	1.35E-07	0.11	1.41
P43246	MSH2_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	28.20	14.91	24.80	13.89	5.97	1.64E-07	2.86E-07	9.08E-08	3.76E-08	0.55	0.23
P62191	PRS4_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	48.40	12.00	22.00	12.00	14.00	2.65E-07	5.27E-07	1.88E-07	2.54E-07	0.71	0.96
B4DZI8	B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	35.10	11.98	18.99	21.97	6.00	1.27E-07	2.01E-07	1.83E-07	2.83E-08	1.44	0.22
O75367	H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	40.10	7.92	21.84	3.64	18.92	8.38E-07	2.28E-06	1.63E-07	1.13E-06	0.19	1.35

P08621	RU17_HUMAN U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2	38.70	19.80	19.80	2.97	12.88	4.28E-07	4.66E-07	2.72E-08	3.72E-07	0.06	0.87
P14635	CCNB1_HUMAN G2/mitotic-specific cyclin-B1 OS=Homo sapiens GN=CCNB1 PE=1 SV=1	35.10	21.82	17.87	8.94	7.96	7.54E-07	5.56E-07	1.39E-07	1.50E-07	0.18	0.20
Q9Y277	VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	50.90	15.74	9.84	11.78	18.67	1.68E-06	8.97E-07	6.79E-07	9.89E-07	0.40	0.59
A8MSH5	A8MSH5_HUMAN Protein RTF2 homolog OS=Homo sapiens GN=RTFDC1 PE=2 SV=2	43.50	11.96	15.92	17.93	9.94	5.40E-07	7.33E-07	5.07E-07	1.91E-07	0.94	0.35
P22695	QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	43.00	21.76	18.78	8.91	5.94	1.81E-06	8.17E-07	2.74E-07	1.38E-07	0.15	0.08
Q9UHB9	SRP68_HUMAN Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2	40.60	16.79	16.79	11.85	7.90	1.85E-07	2.20E-07	7.47E-08	6.97E-08	0.40	0.38
P46977	STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	16.30	12.98	13.99	19.98	9.00	1.60E-07	2.20E-07	1.84E-07	1.22E-07	1.15	0.77
Q02413	DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	24.60	35.00	6.00	12.00	2.00	1.40E-07	1.63E-08	3.32E-08	4.91E-09	0.24	0.04
B5ME19	EIFCL_HUMAN Eukaryotic translation initiation factor 3 subunit C-like protein OS=Homo sapiens GN=EIF3CL PE=2 SV=1	27.50	8.99	27.98	9.00	8.99	6.34E-08	1.98E-07	4.91E-08	4.97E-08	0.77	0.78
E9PF10	E9PF10_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=2 SV=1	19.00	15.00	18.00	16.00	6.00	7.88E-08	1.07E-07	5.63E-08	1.26E-08	0.71	0.16
J3KTE4	J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=2 SV=1	39.90	10.00	14.00	9.00	21.00	8.44E-07	1.30E-06	6.78E-07	1.74E-06	0.80	2.05
Q14573	ITPR3_HUMAN Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2	17.10	12.00	31.49	9.00	1.00	1.26E-08	4.48E-08	7.99E-09	8.43E-10	0.63	0.07
F8W7U8	F8W7U8_HUMAN Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=2 SV=1	31.00	15.97	14.96	7.97	14.96	2.16E-07	1.96E-07	6.07E-08	1.55E-07	0.28	0.72
Q5T2T1	MPP7_HUMAN MAGUK p55 subfamily member 7 OS=Homo sapiens GN=MPP7 PE=1 SV=1	37.20	9.93	18.85	9.92	14.88	2.11E-07	4.35E-07	1.36E-07	2.13E-07	0.64	1.01
Q5T749	KPRP_HUMAN Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	21.40	25.00	9.00	15.00	4.00	2.76E-07	5.74E-08	1.03E-07	2.87E-08	0.37	0.10
J3KMX2	J3KMX2_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Homo sapiens GN=SMARCD2 PE=2 SV=1	43.40	11.88	21.78	9.90	8.91	2.46E-07	4.00E-07	1.30E-07	1.34E-07	0.53	0.55
Q08945	SSRP1_HUMAN FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1	29.50	11.00	26.00	2.00	14.00	1.46E-07	3.67E-07	1.50E-08	1.54E-07	0.10	1.06
Q12959	DLG1_HUMAN Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2	38.20	12.74	21.54	8.86	8.86	1.47E-07	2.32E-07	7.05E-08	8.37E-08	0.48	0.57
Q14683	SMC1A_HUMAN Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2	21.80	18.97	20.97	6.99	5.99	6.75E-08	1.23E-07	1.50E-08	6.97E-09	0.22	0.10
F8VY86	F8VY86_HUMAN Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=2 SV=1	21.00	9.91	35.68	3.96	2.97	1.85E-08	6.87E-08	3.59E-09	2.57E-09	0.19	0.14
Q8IZQ5	SELH_HUMAN Selenoprotein H OS=Homo sapiens GN=SELH PE=1 SV=2	64.80	28.94	11.00	4.00	8.00	1.69E-05	2.87E-06	5.04E-07	1.29E-06	0.03	0.08
P26368	U2AF2_HUMAN Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	39.50	7.00	20.00	3.00	22.00	1.16E-07	5.69E-07	2.05E-08	3.96E-07	0.18	3.40
P46783	RS10_HUMAN 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	60.60	7.96	15.93	7.98	17.91	1.72E-06	3.10E-06	1.11E-06	2.60E-06	0.64	1.51
Q14676	MDC1_HUMAN Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens GN=MDC1 PE=1 SV=3	18.10	24.89	15.93	5.98	4.00	1.53E-07	6.77E-08	1.93E-08	1.02E-08	0.13	0.07
Q68CP9	ARID2_HUMAN AT-rich interactive domain-containing protein 2 OS=Homo sapiens GN=ARID2 PE=1 SV=2	14.30	7.95	24.83	4.97	11.91	2.38E-08	9.52E-08	1.35E-08	1.50E-08	0.57	0.63
Q8NDV7	TNR6A_HUMAN Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	27.70			39.00	12.00			2.62E-07	3.79E-08	Sample 1 Only	Sample 2 Only
Q92616	GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	17.00	8.00	37.00	4.00	1.00	1.22E-08	3.92E-08	3.02E-09	5.64E-10	0.25	0.05
P05787	K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	58.60	1.99	20.85	3.00	23.85	5.71E-08	5.31E-07	1.64E-08	4.65E-07	0.29	8.14

Q93074	MED12_HUMAN Mediator of RNA polymerase II transcription subunit 12 OS=Homo sapiens GN=MED12 PE=1 SV=4	15.30	12.90	28.83	4.98	2.97	1.65E-08	4.27E-08	4.16E-09	2.27E-09	0.25	0.14
Q96TC7	RMD3_HUMAN Regulator of microtubule dynamics protein 3 OS=Homo sapiens GN=RMDN3 PE=1 SV=2	29.60	13.92	16.92	4.96	13.93	4.91E-07	5.15E-07	9.64E-08	3.00E-07	0.20	0.61
P25705	ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	40.70	5.87	8.84	17.65	16.69	1.05E-07	8.79E-08	2.78E-07	2.49E-07	2.64	2.36
P68032	ACTC_HUMAN Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	45.90	14.76	11.82	11.76	10.80	3.99E-06	4.25E-06	1.16E-06	5.97E-07	0.29	0.15
Q9UQE7	SMC3_HUMAN Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2	27.50	12.00	27.00	5.00	5.00	6.94E-08	1.43E-07	2.04E-08	1.35E-08	0.29	0.19
P42166	LAP2A_HUMAN Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	44.20	16.00	15.00	10.00	8.00	2.73E-07	2.38E-07	8.23E-08	8.99E-08	0.30	0.33
Q15057	ACAP2_HUMAN Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ACAP2 PE=1 SV=3	28.50	17.00	22.99	7.00		1.83E-07	2.33E-07	3.77E-08		0.21	Control 1 Only
P13639	EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	27.50	11.52	18.04	11.52	4.52	1.12E-07	1.93E-07	9.93E-08	3.73E-08	0.89	0.33
P08779	K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	61.70	30.50	4.00	11.50		4.61E-07	1.10E-07	1.36E-07		0.29	Control 1 Only
Q9NQW6	ANLN_HUMAN Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2	19.40	13.98	14.98	10.99	7.99	8.94E-08	8.94E-08	4.71E-08	2.81E-08	0.53	0.31
P46779	RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	62.00	9.93	13.91	7.94	15.89	2.48E-06	3.45E-06	9.21E-07	4.28E-06	0.37	1.73
Q9Y285	SYFA_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3	28.10	12.81	17.75	8.88	7.89	2.50E-07	5.31E-07	1.30E-07	1.39E-07	0.52	0.55
P53007	TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	27.70	6.00	6.00	12.00	24.00	7.93E-07	6.77E-07	6.90E-07	1.68E-06	0.87	2.12
P61163	ACTZ_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	38.00	11.88	9.92	15.85	4.96	1.21E-06	7.18E-07	7.03E-07	1.53E-07	0.58	0.13
O94874	UFL1_HUMAN E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2	25.10	16.90	11.92	3.97	13.92	1.98E-07	1.05E-07	2.63E-08	1.15E-07	0.13	0.58
O00268	TAF4_HUMAN Transcription initiation factor TFIID subunit 4 OS=Homo sapiens GN=TAF4 PE=1 SV=2	25.70	9.00	14.00	11.00	12.00	8.96E-08	1.38E-07	8.70E-08	7.54E-08	0.97	0.84
Q12874	SF3A3_HUMAN Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1	34.70	12.00	20.00	1.00	12.00	1.88E-07	3.68E-07	5.25E-09	1.49E-07	0.03	0.79
D6RAN4	D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1	46.20	10.89	11.88	5.94	16.83	2.70E-06	2.29E-06	8.78E-07	3.33E-06	0.33	1.23
Q5D862	FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	8.70	24.00	8.00	10.00	3.00	5.38E-08	6.36E-09	1.39E-08	5.10E-09	0.26	0.09
Q13148	TADBP_HUMAN TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1	23.40	10.89	9.90	11.90	11.88	6.04E-07	4.32E-07	3.73E-07	2.51E-07	0.62	0.41
Q6UB35	C1TM_HUMAN Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1	23.60	19.92	13.91	6.96	3.98	2.10E-07	9.04E-08	4.53E-08	1.64E-08	0.22	0.08
P42766	RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	38.20	10.00	13.00	6.00	16.00	2.31E-06	2.02E-06	6.68E-07	2.67E-06	0.29	1.16
P61313	RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	41.20	7.92	10.90	6.92	17.82	9.36E-07	1.01E-06	4.45E-07	1.39E-06	0.48	1.48
P62888	RL30_HUMAN 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	66.10	9.97	9.96	9.97	14.95	3.80E-06	3.42E-06	1.52E-06	3.77E-06	0.40	0.99
A5YKK6	CNOT1_HUMAN CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	10.80	9.83	24.63	4.91	3.95	3.96E-08	5.88E-08	1.43E-08	1.03E-08	0.36	0.26
P12830	CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	16.30	6.96	11.94	10.95	13.94	1.01E-07	2.41E-07	1.17E-07	1.86E-07	1.16	1.85
P62244	RS15A_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	79.20	9.90	13.86	4.95	14.86	1.67E-06	2.97E-06	4.18E-07	2.33E-06	0.25	1.39
Q96T88	UHRF1_HUMAN E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1	26.70	7.99	20.00	3.00	11.99	9.29E-08	1.95E-07	1.68E-08	8.54E-08	0.18	0.92

P35232	PHB_HUMAN Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	49.60	12.82	9.87	13.84	5.93	1.41E-06	6.85E-07	9.58E-07	2.07E-07	0.68	0.15
M0QZM1	M0QZM1_HUMAN Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens GN=HNRNPM PE=4 SV=1	71.80	5.50	6.00	1.50	9.00	1.42E-07	1.84E-07	3.34E-08	2.21E-07	0.23	1.55
P55036	PSMD4_HUMAN 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	32.10	6.93	14.85	5.94	14.85	1.72E-07	3.65E-07	1.20E-07	3.31E-07	0.70	1.92
B3KRS5	B3KRS5_HUMAN Histone deacetylase OS=Homo sapiens GN=HDAC2 PE=2 SV=1	38.60	8.98	14.97	7.99	9.97	1.94E-07	3.90E-07	1.36E-07	1.92E-07	0.70	0.99
Q9BUA3	CK084_HUMAN Uncharacterized protein C11orf84 OS=Homo sapiens GN=C11orf84 PE=1 SV=3	53.30	5.99	17.97	2.99	13.98	1.40E-07	4.58E-07	3.14E-08	2.46E-07	0.23	1.76
P46013	KI67_HUMAN Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2	13.10	23.00	13.00	5.00		4.47E-08	2.06E-08	7.17E-09		0.16	Control 1 Only
J3QLC8	J3QLC8_HUMAN 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=2 SV=1	39.10	9.89	7.92	8.92	13.85	1.99E-06	1.07E-06	5.27E-07	1.33E-06	0.26	0.67
Q14204	DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	6.10	8.00	22.00	11.00		3.25E-09	1.41E-08	5.21E-09		1.60	Control 1 Only
F5GY37	F5GY37_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=2 SV=1	52.80	9.91	9.91	11.90	8.93	9.30E-07	9.14E-07	1.03E-06	3.21E-07	1.10	0.34
Q96QK1	VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	24.60	13.00	20.00	6.00	2.00	1.25E-07	1.90E-07	3.60E-08	1.07E-08	0.29	0.09
Q9Y230	RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	43.80	12.91	17.90	3.98	5.96	3.15E-07	4.50E-07	5.35E-08	1.19E-07	0.17	0.38
K7ERE3	K7ERE3_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=2 SV=1	57.10	28.78	1.97	8.96		5.61E-07	5.23E-08	7.50E-08		0.13	Control 1 Only
Q9Y512	SAM50_HUMAN Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3	31.80	4.00	18.00	5.00	12.00	2.69E-08	3.17E-07	6.18E-08	1.71E-07	2.30	6.36
Q9ULV0	MYO5B_HUMAN Unconventional myosin-Vb OS=Homo sapiens GN=MYO5B PE=1 SV=3	25.10	1.98	36.91			2.37E-09	6.60E-08			Control 1 Only	Control 1 Only
P25398	RS12_HUMAN 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	56.80	7.00	9.00	8.00	15.00	8.75E-07	1.46E-06	5.64E-07	1.38E-06	0.64	1.58
I3L1P8	I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens GN=SLC25A11 PE=2 SV=1	52.00	4.00	10.00	10.00	15.00	3.21E-07	8.80E-07	6.17E-07	8.26E-07	1.92	2.57
O75643	U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	16.20	4.00	32.00	2.00	1.00	3.28E-09	5.61E-08	1.15E-09	3.83E-10	0.35	0.12
Q53EP0	FND3B_HUMAN Fibronectin type III domain-containing protein 3B OS=Homo sapiens GN=FNDC3B PE=1 SV=2	21.90	8.99	17.99	8.00	4.00	6.00E-08	1.19E-07	2.77E-08	1.08E-08	0.46	0.18
Q92804	RBP56_HUMAN TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1	39.70	18.81	14.85		4.95	4.18E-07	4.36E-07		1.29E-07	Control 1 Only	0.31
Q9BR76	COR1B_HUMAN Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	27.80	9.96	12.92	7.95	7.94	1.88E-07	3.21E-07	1.22E-07	1.70E-07	0.65	0.90
Q9H269	VPS16_HUMAN Vacuolar protein sorting-associated protein 16 homolog OS=Homo sapiens GN=VPS16 PE=1 SV=2	19.20	10.89	12.88	12.90	1.98	1.12E-07	1.31E-07	8.45E-08	1.12E-08	0.75	0.10
P81605	DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	53.60	19.00	2.00	14.00	3.00	1.97E-06	1.02E-07	6.68E-07	1.21E-07	0.34	0.06
E7ESY4	E7ESY4_HUMAN Metastasis-associated protein MTA1 OS=Homo sapiens GN=MTA1 PE=2 SV=1	40.40	9.88	18.76	0.99	7.91	1.43E-07	3.39E-07	1.74E-09	5.82E-08	0.01	0.41
P12236	ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	54.40	7.00	9.00	9.00	13.00	6.93E-07	7.53E-07	7.11E-07	9.74E-07	1.03	1.41
Q8WWM7	ATX2L_HUMAN Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	21.20	8.92	15.89	2.96	9.96	7.22E-08	8.68E-08	1.46E-08	6.43E-08	0.20	0.89
Q9Y3I0	RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	28.10	9.00	14.00	2.00	13.00	2.10E-07	2.10E-07	1.26E-08	1.92E-07	0.06	0.91
B1AK87	B1AK87_HUMAN Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=2 SV=1	32.30	8.96	9.95	4.97	12.94	5.71E-07	5.51E-07	1.99E-07	4.43E-07	0.35	0.78
Q15437	SC23B_HUMAN Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	34.30	8.00	13.00	12.00	4.00	8.73E-08	1.74E-07	1.15E-07	4.16E-08	1.32	0.48

Q9NVI7-2	ATD3A_HUMAN Isoform 2 of ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A	28.80	4.92	11.79	1.97	16.70	3.95E-08	1.77E-07	8.78E-09	2.09E-07	0.22	5.29
Q16576	RBBP7_HUMAN Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1	35.10	6.94	12.93	2.98	12.91	2.66E-07	4.09E-07	4.79E-08	3.75E-07	0.18	1.41
P06493	CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	32.00	13.95	8.95	7.97	4.99	1.48E-06	5.97E-07	3.37E-07	1.91E-07	0.23	0.13
Q9Y5K6	CD2AP_HUMAN CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1	24.10	9.00	7.00	4.00	15.00	1.69E-07	7.57E-08	3.05E-08	1.53E-07	0.18	0.91
Q12789	TF3C1_HUMAN General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4	10.50	5.96	19.91	2.98	5.97	5.08E-09	2.67E-08	2.58E-09	6.29E-09	0.51	1.24
B7ZAP5	B7ZAP5_HUMAN Hepatocyte nuclear factor 3-alpha OS=Homo sapiens GN=FOXA1 PE=2 SV=1	28.70	12.00	9.99	8.00	5.00	6.17E-07	3.30E-07	1.84E-07	8.33E-08	0.30	0.14
Q14258	TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	32.90	11.00	19.00	4.00	1.00	1.62E-07	2.76E-07	3.73E-08	8.18E-09	0.23	0.05
P12270	TPR_HUMAN Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3	14.30	9.00	23.00	3.00		9.34E-09	3.21E-08	1.36E-09		0.15	Control 1 Only
P08727	K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	70.00	1.00	12.99	2.99	17.98	3.29E-08	5.69E-07	4.59E-08	4.71E-07	1.40	14.30
P61158	ARP3_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	34.40	12.88	19.85		1.99	8.49E-07	8.02E-07		1.84E-08	Control 1 Only	0.02
O95347	SMC2_HUMAN Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	25.50	6.00	23.96	3.00	1.00	2.07E-08	1.59E-07	4.45E-09	2.07E-08	0.21	1.00
Q9P016	THYN1_HUMAN Thymocyte nuclear protein 1 OS=Homo sapiens GN=THYN1 PE=1 SV=1	43.60	12.00	8.00	5.00	8.00	9.52E-07	5.33E-07	2.64E-07	2.84E-07	0.28	0.30
Q9Y4K1	AIM1_HUMAN Absent in melanoma 1 protein OS=Homo sapiens GN=AIM1 PE=1 SV=3	17.50	7.98	22.98		2.00	1.05E-08	5.75E-08		2.54E-09	Control 1 Only	0.24
Q12906-7	ILF3_HUMAN Isoform 7 of Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3	18.00	8.88	13.82	0.99	8.88	9.09E-08	1.44E-07	5.64E-09	6.98E-08	0.06	0.77
Q12955	ANK3_HUMAN Ankyrin-3 OS=Homo sapiens GN=ANK3 PE=1 SV=3	13.20	8.95	18.92	2.98	2.00	6.72E-09	1.34E-08	1.98E-09	6.10E-10	0.29	0.09
E5KLJ5	E5KLJ5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1	17.80	5.00	16.98	10.99		2.16E-08	1.00E-07	4.30E-08		1.99	Control 1 Only
E5RHW4	E5RHW4_HUMAN Erlin-2 (Fragment) OS=Homo sapiens GN=ERLIN2 PE=2 SV=1	33.70	7.00	11.00	3.00	12.00	6.03E-07	7.16E-07	9.52E-08	3.48E-07	0.16	0.58
E7EUE1	E7EUE1_HUMAN ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=2 SV=1	29.10	6.93	13.83	0.98	10.88	9.99E-08	2.00E-07	5.36E-09	1.25E-07	0.05	1.25
O95994	AGR2_HUMAN Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1	33.10	9.93	8.94	8.94	4.96	2.45E-06	2.18E-06	1.50E-06	4.27E-07	0.61	0.17
P08240	SRPR_HUMAN Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2	22.90	13.00	13.00	3.00	4.00	1.26E-07	1.92E-07	1.35E-08	2.47E-08	0.11	0.20
Q86YP4-2	P66A_HUMAN Isoform 2 of Transcriptional repressor p66-alpha OS=Homo sapiens GN=GATAD2A	27.30	9.88	11.82	3.93	6.90	3.39E-07	2.65E-07	2.74E-08	1.19E-07	0.08	0.35
Q8N5C6	SRBD1_HUMAN S1 RNA-binding domain-containing protein 1 OS=Homo sapiens GN=SRBD1 PE=1 SV=2	24.80	26.86	3.98	1.00	1.00	3.64E-07	3.39E-08	1.28E-10	1.34E-08	0.00	0.04
P46778	RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	37.50	5.00	8.98	3.00	15.98	1.76E-06	2.16E-06	5.68E-07	2.86E-06	0.32	1.62
P55072	TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	24.80	6.00	9.00	6.99	8.99	5.77E-08	9.51E-08	5.14E-08	6.76E-08	0.89	1.17
P62263	RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	39.70	4.00	11.00	4.00	12.00	1.58E-06	2.33E-06	5.42E-07	1.62E-06	0.34	1.03
F8W9B5	F8W9B5_HUMAN Protein regulator of cytokinesis 1 OS=Homo sapiens GN=PRC1 PE=2 SV=1	36.90	17.80	8.87		4.93	3.23E-07	1.18E-07		5.87E-08	Control 1 Only	0.18
Q01826	SATB1_HUMAN DNA-binding protein SATB1 OS=Homo sapiens GN=SATB1 PE=1 SV=1	18.10	14.99	13.97		2.99	2.03E-07	1.50E-07		1.31E-08	Control 1 Only	0.06
Q5VTR2	BRE1A_HUMAN E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2	17.40	8.00	10.00	3.00	11.00	8.26E-08	8.35E-08	1.11E-08	6.23E-08	0.13	0.75

Q96ST3	SIN3A_HUMAN Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2	15.20	12.99	14.00	4.00	1.00	1.13E-07	1.36E-07	1.83E-08	1.91E-09	0.16	0.02
P46939	UTRO_HUMAN Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2	10.00	2.00	27.98		2.00	1.12E-09	2.20E-08		7.07E-10	Control 1 Only	0.63
E9PDF6	E9PDF6_HUMAN Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=2 SV=1	20.60	8.98	13.95	1.99	5.97	5.61E-08	9.84E-08	5.26E-09	2.11E-08	0.09	0.38
O00231	PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	27.70	8.00	8.99	6.99	6.00	3.15E-07	3.38E-07	1.55E-07	3.27E-07	0.49	1.04
Q01082	SPTB2_HUMAN Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	60.70	8.00	16.00	4.00	3.00	1.71E-08	4.95E-08	3.98E-09	6.14E-09	0.23	0.36
B4DVY1	B4DVY1_HUMAN Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=2 SV=1	34.70	4.97	16.89	3.98	4.98	8.77E-08	2.79E-07	4.01E-08	5.64E-08	0.46	0.64
P08107	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	29.40	5.96	7.94	7.92	8.92	9.96E-08	1.54E-07	7.30E-08	9.54E-08	0.73	0.96
Q6P3W7	SCYL2_HUMAN SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1	17.80	10.97	9.99	7.97	1.99	1.23E-07	9.59E-08	7.01E-08	1.43E-08	0.57	0.12
Q96KR1	ZFR_HUMAN Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2	18.60	10.99	8.99	3.99	7.00	5.27E-08	5.09E-08	1.53E-08	2.56E-08	0.29	0.48
P21796	VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	37.50	7.00	7.00	8.00	9.00	4.59E-07	4.58E-07	4.42E-07	5.27E-07	0.96	1.15
Q99959-2	PKP2_HUMAN Isoform 1 of Plakophilin-2 OS=Homo sapiens GN=PKP2	21.10	16.99	12.00	1.00	1.00	1.73E-07	1.26E-07	4.51E-10	6.30E-09	0.00	0.04
Q9P270	SLAI2_HUMAN SLAIN motif-containing protein 2 OS=Homo sapiens GN=SLAIN2 PE=1 SV=2	33.60	5.00	3.00	3.00	19.97	1.17E-07	4.70E-08	3.50E-08	3.05E-07	0.30	2.62
P52943	CRIP2_HUMAN Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2 PE=1 SV=1	41.80	11.93	4.97	10.92	2.98	1.53E-06	3.69E-07	6.79E-07	1.08E-07	0.44	0.07
P62266	RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	29.40	8.98	6.98	7.99	6.99	2.02E-06	2.47E-06	1.02E-06	1.39E-06	0.51	0.69
P11182	ODB2_HUMAN Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3	29.10	8.00	6.00	6.00	10.00	1.52E-07	1.85E-07	1.54E-07	1.63E-07	1.01	1.07
Q8N8S7	ENAH_HUMAN Protein enabled homolog OS=Homo sapiens GN=ENAH PE=1 SV=2	20.60	7.00	8.00	7.00	8.00	7.91E-08	6.75E-08	2.53E-08	6.31E-08	0.32	0.80
P62829	RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	56.40	6.93	6.92	2.97	12.90	1.24E-06	1.00E-06	2.71E-07	1.59E-06	0.22	1.28
O43707	ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	21.70	2.92	8.83	3.89	12.78	1.96E-08	1.09E-07	2.17E-08	9.87E-08	1.11	5.04
F5GXF5	F5GXF5_HUMAN Nucleosome-remodeling factor subunit BPTF (Fragment) OS=Homo sapiens GN=BPTF PE=2 SV=2	10.00	5.00	16.98	1.00	2.99	4.56E-09	2.35E-08	4.98E-10	1.59E-09	0.11	0.35
Q16777	H2A2C_HUMAN Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4	65.90	6.90	10.82	0.98	9.84	2.39E-06	7.60E-06	9.64E-08	4.04E-06	0.04	1.69
Q5SWX8	ODR4_HUMAN Protein odr-4 homolog OS=Homo sapiens GN=ODR4 PE=2 SV=1	34.00	5.00	12.00	10.00	2.00	7.70E-08	2.45E-07	1.33E-07	2.97E-08	1.72	0.39
P13051-2	UNG_HUMAN Isoform 1 of Uracil-DNA glycosylase OS=Homo sapiens GN=UNG	37.20	9.94	5.97	6.95	5.96	6.98E-07	4.70E-07	1.74E-07	1.39E-07	0.25	0.20
Q8NFW8	NEUA_HUMAN N-acylneuraminate cytidylyltransferase OS=Homo sapiens GN=CMAS PE=1 SV=2	20.70	6.98	8.95	6.97	5.97	2.91E-07	2.91E-07	1.46E-07	8.12E-08	0.50	0.28
P52292	IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	27.00	7.00	10.00	3.00	9.00	1.26E-07	1.84E-07	1.87E-08	1.15E-07	0.15	0.91
P62854	RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	50.40	5.00	9.00	5.00	9.00	2.11E-06	4.76E-06	4.15E-07	1.89E-06	0.20	0.90
C9JRZ6	C9JRZ6_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=2 SV=1	36.10	2.97	12.91	5.96	5.96	1.84E-07	7.24E-07	1.78E-07	2.18E-07	0.97	1.19
O76094	SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3	21.50	8.94	9.93	2.98	5.97	1.19E-07	1.21E-07	2.50E-08	4.50E-08	0.21	0.38
Q86TG7	PEG10_HUMAN Retrotransposon-derived protein PEG10 OS=Homo sapiens GN=PEG10 PE=1 SV=2	27.00			18.00	10.00			1.63E-07	7.83E-08	Sample 1 Only	Sample 2 Only

Q96A33	CCD47_HUMAN Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1	26.70	7.99	8.97	1.00	9.97	1.12E-07	1.12E-07	1.07E-08	1.43E-07	0.10	1.27
P55795	HNRH2_HUMAN Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	42.10	5.00	7.00	6.00	10.00	1.24E-07	2.07E-07	7.78E-08	1.76E-07	0.63	1.43
Q9UBM7	DHCR7_HUMAN 7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	12.00	2.00	2.00	11.99	10.99	6.12E-08	6.76E-08	1.81E-07	2.28E-07	2.96	3.73
B4E241	B4E241_HUMAN Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SFRS3 PE=2 SV=1	59.70	5.00	11.00	3.00	7.00	2.85E-06	4.16E-06	9.26E-07	2.15E-06	0.33	0.75
Q14847	LASP1_HUMAN LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2	50.20	6.94	2.98	5.95	9.89	7.02E-07	8.98E-08	3.30E-07	4.41E-07	0.47	0.63
F5H5N0	F5H5N0_HUMAN Serine/threonine-protein kinase MRCK alpha OS=Homo sapiens GN=CDC42BPA PE=2 SV=1	12.80	10.96	10.43	2.99		2.20E-08	1.62E-08	6.86E-09		0.31	Control 1 Only
A4D212	A4D212_HUMAN DKFZP586J0619 protein OS=Homo sapiens GN=DKFZP586J0619 PE=2 SV=1	6.50	6.00	13.00	2.00	4.00	5.29E-09	1.48E-08	8.89E-10	2.24E-09	0.17	0.42
Q9Y657	SPIN1_HUMAN Spindlin-1 OS=Homo sapiens GN=SPIN1 PE=1 SV=3	39.70	4.00	7.00	5.00	8.61	2.51E-07	5.65E-07	2.02E-07	3.45E-07	0.80	1.37
P49207	RL34_HUMAN 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	29.90	6.00	7.00	5.00	6.00	1.50E-06	1.24E-06	5.15E-07	1.10E-06	0.34	0.73
B0QYK0	B0QYK0_HUMAN RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=2 SV=1	15.50	5.94	5.94	2.97	9.90	1.04E-07	1.06E-07	2.51E-08	1.80E-07	0.24	1.74
B3KVR1	B3KVR1_HUMAN Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPN PE=2 SV=1	26.60	6.00	7.00	3.00	8.00	5.28E-07	6.59E-07	1.76E-07	5.56E-07	0.33	1.05
Q14444	CAPR1_HUMAN Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	14.00	4.95	6.93	3.96	8.91	4.93E-08	6.28E-08	2.86E-08	9.54E-08	0.58	1.94
O96019	ACL6A_HUMAN Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1	26.30	4.98	9.95	3.00	6.98	2.40E-07	2.72E-07	6.83E-08	1.11E-07	0.29	0.46
Q4LE39	ARI4B_HUMAN AT-rich interactive domain-containing protein 4B OS=Homo sapiens GN=ARID4B PE=1 SV=2	16.70	6.99	11.97	1.98	3.98	1.09E-08	2.53E-08	1.78E-09	4.83E-09	0.16	0.44
P10412	H14_HUMAN Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	46.10	2.97	6.92	1.98	12.90	3.37E-08	1.97E-07	1.74E-08	2.99E-07	0.52	8.86
P49756	RBM25_HUMAN RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3	17.40	6.96	7.97		8.97	4.55E-08	6.09E-08		5.23E-08	Control 1 Only	1.15
Q12905	ILF2_HUMAN Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	23.10	7.00	8.00	2.00	7.00	4.58E-07	4.92E-07	8.42E-08	2.15E-07	0.18	0.47
Q92900	RENT1_HUMAN Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	12.50	5.00	4.00	4.00	11.00	2.00E-08	2.68E-08	1.70E-08	4.55E-08	0.85	2.28
Q14498	RBM39_HUMAN RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2	15.70	5.92	10.85		6.91	3.23E-08	9.38E-08		7.68E-08	Control 1 Only	2.38
O43390	HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	16.40	6.83	6.82	1.94	7.82	1.45E-07	1.41E-07	1.58E-08	1.20E-07	0.11	0.82
Q14974	IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	11.20	7.00	7.00	5.00	5.00	4.07E-08	6.06E-08	2.64E-08	2.74E-08	0.65	0.67
Q15428	SF3A2_HUMAN Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2 PE=1 SV=2	29.30	3.00	12.00		9.00	2.22E-08	2.08E-07		9.44E-08	Control 1 Only	4.26
Q5QPL9	Q5QPL9_HUMAN RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1	24.90	6.92	6.92	4.95	4.94	7.57E-07	5.09E-07	2.45E-07	2.11E-07	0.32	0.28
Q71F56	MD13L_HUMAN Mediator of RNA polymerase II transcription subunit 13-like OS=Homo sapiens GN=MED13L PE=1 SV=1	8.50	7.00	13.00	1.00	3.00	7.98E-09	2.14E-08	7.84E-10	3.73E-09	0.10	0.47
Q9H0C8	ILKAP_HUMAN Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1	20.70	4.00	7.00	9.00	4.00	2.60E-07	2.15E-07	1.47E-07	6.23E-08	0.57	0.24
P52907	CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	33.60	3.57	3.57	2.52	8.62	2.70E-07	2.89E-07	1.23E-07	3.64E-07	0.45	1.35
Q15750	TAB1_HUMAN TGF-beta-activated kinase 1 and MAP3K7-binding protein 1 OS=Homo sapiens GN=TAB1 PE=1 SV=1	15.80	8.00	7.00	5.00	3.00	1.35E-07	1.34E-07	6.09E-08	2.27E-08	0.45	0.17
J3QT28	J3QT28_HUMAN Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=2 SV=1	28.40	3.96	5.94	2.97	9.90	2.80E-07	2.86E-07	4.89E-08	3.00E-07	0.17	1.07

Q9P2M7	CING_HUMAN Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	16.50	3.00	17.97		2.00	1.50E-08	1.03E-07		4.11E-09	Control 1 Only	0.27
B7Z6Q6	B7Z6Q6_HUMAN Kinesin-like protein KIF2C OS=Homo sapiens GN=KIF2C PE=2 SV=1	17.60	11.96	7.98	2.99		1.44E-07	6.82E-08	1.48E-08		0.10	Control 1 Only
Q13185	CBX3_HUMAN Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4	25.10	5.00	7.00	4.00	7.00	3.15E-07	5.16E-07	1.14E-07	3.55E-07	0.36	1.13
D3YTB1	D3YTB1_HUMAN 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=2 SV=1	40.60	5.00	8.00	2.00	8.00	1.03E-06	1.25E-06	1.34E-07	1.11E-06	0.13	1.07
E7EQR4	E7EQR4_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=2 SV=2	25.10	2.98	12.93	1.98	4.97	2.72E-08	1.88E-07	6.52E-09	5.43E-08	0.24	2.00
Q14739	LBR_HUMAN Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2	17.60	2.00	6.99	3.00	10.99	7.62E-09	1.17E-07	1.67E-08	1.94E-07	2.19	25.48
E9PLL6	E9PLL6_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1	50.90	3.96	6.94	4.95	5.94	1.66E-06	1.50E-06	7.54E-07	1.54E-06	0.45	0.92
P01625	KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	14.00	5.00	6.00	7.00	5.00	3.69E-06	2.66E-06	3.18E-06	1.52E-06	0.86	0.41
P21291	CSRP1_HUMAN Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3	50.30	7.96	2.99	6.95	4.98	1.15E-06	3.74E-07	4.25E-07	3.71E-07	0.37	0.32
Q9BQ61	CS043_HUMAN Uncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43 PE=1 SV=1	43.20	3.96	5.95	4.95	7.93	1.76E-07	1.16E-07	8.39E-08	2.20E-07	0.48	1.25
P50416	CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	16.30	4.99	3.99	7.99	5.98	4.95E-08	4.20E-08	5.06E-08	4.73E-08	1.02	0.96
P55884	EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	14.10	3.00	9.99	2.00	7.98	3.20E-08	1.21E-07	1.10E-08	7.15E-08	0.35	2.24
Q7Z417	NUFP2_HUMAN Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1	15.70	4.00	8.00	2.00	7.00	2.75E-08	2.87E-08	6.89E-09	3.43E-08	0.25	1.25
Q9H9Z2	LN28A_HUMAN Protein lin-28 homolog A OS=Homo sapiens GN=LIN28A PE=1 SV=1	26.30	5.00	8.00	3.00	6.00	4.12E-07	5.35E-07	1.29E-07	2.47E-07	0.31	0.60
Q9P253	VPS18_HUMAN Vacuolar protein sorting-associated protein 18 homolog OS=Homo sapiens GN=VPS18 PE=1 SV=2	15.30	8.00	9.00	5.00		5.72E-08	6.70E-08	2.54E-08		0.44	Control 1 Only
Q9Y2A7	NCKP1_HUMAN Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	10.60	7.00	11.00	2.00	2.00	3.45E-08	4.60E-08	5.74E-09	6.54E-09	0.17	0.19
B1ANR0	B1ANR0_HUMAN Poly(A) binding protein, cytoplasmic 4 (Inducible form), isoform CRA_e OS=Homo sapiens GN=PABPC4 PE=2 SV=1	23.30	4.83	6.72	2.88	6.76	7.19E-08	1.43E-07	1.91E-08	4.92E-08	0.27	0.68
E3W978	E3W978_HUMAN Hyaluronan mediated motility receptor OS=Homo sapiens GN=HMMR PE=2 SV=2	28.70	12.97	8.99			1.71E-07	1.15E-07			Control 1 Only	Control 1 Only
Q9Y2H1	ST38L_HUMAN Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3	18.80	4.49	4.97	4.99	1.00	1.71E-07	1.47E-07	8.31E-08	2.82E-08	0.49	0.16
Q09028	RBBP4_HUMAN Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	29.80	4.97	7.92	1.97	6.92	2.02E-07	3.84E-07	1.95E-08	1.89E-07	0.10	0.94
P06576	ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	25.90	1.98	3.96	6.93	8.92	1.68E-08	4.08E-08	8.65E-08	1.08E-07	5.14	6.42
Q6P2E9	EDC4_HUMAN Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1	10.90	8.99	9.00	2.00	2.00	2.54E-08	2.78E-08	8.05E-09	4.93E-09	0.32	0.19
Q7L576	CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	10.20	3.97	11.88	2.96	2.95	2.11E-08	7.85E-08	6.91E-09	7.44E-09	0.33	0.35
Q8N1G2	CMTR1_HUMAN Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1 OS=Homo sapiens GN=CMTR1 PE=1 SV=1	16.00	8.00	8.99	3.00	2.00	5.34E-08	5.51E-08	1.79E-08	8.16E-09	0.33	0.15
Q96II8	LRCH3_HUMAN Leucine-rich repeat and calponin homology domain-containing protein 3 OS=Homo sapiens GN=LRCH3 PE=1 SV=2	27.70	7.92	13.86			7.93E-08	1.79E-07			Control 1 Only	Control 1 Only
Q9NYL9	TMOD3_HUMAN Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1	29.80	11.98	7.00	1.99	1.00	1.08E-06	5.17E-07	3.11E-08	5.14E-08	0.03	0.05
P37108	SRP14_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2	50.00	7.00	6.00	2.00	7.00	1.35E-06	1.25E-06	2.32E-07	5.98E-07	0.17	0.44
Q9Y314	NOSIP_HUMAN Nitric oxide synthase-interacting protein OS=Homo sapiens GN=NOSIP PE=1 SV=1	21.60	7.98	5.99	2.00	5.99	4.08E-07	2.71E-07	4.32E-08	1.61E-07	0.11	0.40

P62195	PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	38.40	3.98	7.92	5.92	3.94	1.58E-07	3.02E-07	1.54E-07	9.94E-08	0.98	0.63
P54886	P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	18.50	9.00	9.00	3.00		1.09E-07	5.79E-08	2.61E-08		0.24	Control 1 Only
O00148	DX39A_HUMAN ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2	18.00	3.94	5.92	4.92	5.92	1.19E-07	8.65E-08	8.13E-08	8.13E-08	0.68	0.68
Q13263	TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	21.20	6.00	6.00	5.00	4.00	5.56E-08	5.09E-08	2.73E-08	4.34E-08	0.49	0.78
B7Z815	B7Z815_HUMAN Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP7 PE=2 SV=1	14.30	1.00	12.95	1.98	4.97	3.38E-09	9.41E-08	9.47E-09	2.08E-08	2.80	6.15
C9IZE4	C9IZE4_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=2 SV=1	22.10	2.99	7.97	5.98	3.99	7.91E-08	1.57E-07	1.03E-07	4.71E-08	1.31	0.60
J3KTL2	J3KTL2_HUMAN Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=2 SV=1	26.20	4.95	6.93	3.96	4.95	1.77E-07	3.84E-07	1.18E-07	1.04E-07	0.67	0.59
Q8N3C0	ASCC3_HUMAN Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3	11.00	2.00	18.98			2.43E-09	2.47E-08			Control 1 Only	Control 1 Only
Q8TDY2	RBCC1_HUMAN RB1-inducible coiled-coil protein 1 OS=Homo sapiens GN=RB1CC1 PE=1 SV=3	11.20	1.00	16.00	3.00	1.00	8.32E-10	2.31E-08	3.25E-09	1.38E-10	3.91	0.17
P46100	ATRX_HUMAN Transcriptional regulator ATRX OS=Homo sapiens GN=ATRX PE=1 SV=5	6.60	3.96	10.89	3.96	1.98	1.20E-08	1.78E-08	5.55E-09	9.77E-10	0.46	0.08
P49748	ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	25.90	1.98	2.00	16.95		2.25E-08	1.82E-08	1.94E-07		8.62	Control 1 Only
Q00059	TFAM_HUMAN Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1	26.80	6.95	2.97	0.99	8.96	7.57E-07	2.43E-07	2.86E-08	6.33E-07	0.04	0.84
O14979	HNRDL_HUMAN Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3	18.30	3.94	7.88	0.97	6.88	3.00E-07	4.69E-07	7.45E-08	2.22E-07	0.25	0.74
P19013	K2C4_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	28.80	11.49		7.94		1.23E-07		6.20E-08		0.50	Control 1 Only
P05387	RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	85.20	4.00	6.00	4.00	6.00	1.07E-06	9.17E-07	3.12E-07	8.42E-07	0.29	0.79
Q92541	RTF1_HUMAN RNA polymerase-associated protein RTF1 homolog OS=Homo sapiens GN=RTF1 PE=1 SV=4	21.80	3.00	1.00	1.00	15.00	3.42E-08	1.36E-08	8.16E-09	1.78E-07	0.24	5.20
P42167	LAP2B_HUMAN Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2	49.10	8.92	2.97	1.98	5.96	4.02E-07	1.07E-07	5.58E-08	1.11E-07	0.14	0.28
P49711	CTCF_HUMAN Transcriptional repressor CTCF OS=Homo sapiens GN=CTCF PE=1 SV=1	11.80	3.99	8.98	0.99	5.99	3.04E-08	8.37E-08	9.70E-09	5.52E-08	0.32	1.82
P50991	TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	16.70	4.00	8.00	6.00	2.00	3.07E-08	8.79E-08	2.42E-08	1.46E-08	0.79	0.48
Q9UPY3	DICER_HUMAN Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	9.90			14.95	4.97			2.34E-08	7.07E-09	Sample 1 Only	Sample 2 Only
A8MVQ3	A8MVQ3_HUMAN Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS PE=2 SV=1	14.00	7.00	5.00	6.00	1.00	7.04E-08	3.82E-08	4.96E-08	4.88E-09	0.70	0.07
B4DXZ6	B4DXZ6_HUMAN Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=2 SV=1	20.40	1.96	7.88	1.98	6.90	3.19E-08	1.06E-07	1.47E-08	8.48E-08	0.46	2.66
Q14789	GOGB1_HUMAN Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2	6.50	2.00	14.95	1.00	1.00	9.11E-10	1.10E-08	2.78E-10	4.30E-10	0.30	0.47
F5H2F4	F5H2F4_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1	18.40	9.00	6.00	3.00	1.00	7.73E-08	3.19E-08	8.15E-09	2.57E-09	0.11	0.03
B0FLL2	B0FLL2_HUMAN 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase 2 transcript variant 3 OS=Homo sapiens GN=PFKFB2 PE=2 SV=1	31.80	3.94	0.99	4.94	8.92	5.33E-08	1.54E-08	4.56E-08	1.23E-07	0.86	2.31
P19338	NUCL_HUMAN Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	13.50	2.00	6.99		9.99	1.11E-08	7.84E-08		9.53E-08	Control 1 Only	8.60
Q96QR8	PURB_HUMAN Transcriptional activator protein Pur-beta OS=Homo sapiens GN=PURB PE=1 SV=3	16.70	6.00	7.00	3.00	3.00	2.98E-07	2.87E-07	6.02E-08	6.23E-08	0.20	0.21
E7ETK0	E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1	35.40	4.00	5.00	2.00	7.00	4.86E-07	8.50E-07	1.88E-07	8.95E-07	0.39	1.84

K7EKS7	K7EKS7_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=2 SV=1	52.10	4.00	5.00	3.00	6.00	1.67E-06	2.75E-06	7.26E-07	2.93E-06	0.43	1.75
K7ELC2	K7ELC2_HUMAN 40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=2 SV=1	29.50	5.00	6.00	2.00	5.00	1.42E-06	8.99E-07	8.23E-08	4.62E-07	0.06	0.32
B4DR61	B4DR61_HUMAN Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=2 SV=1	12.80	4.00	2.00	4.99	6.98	1.10E-07	5.53E-08	1.14E-07	1.09E-07	1.04	0.99
O15144	ARPC2_HUMAN Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1	31.00	4.98	10.98		1.00	3.17E-07	7.69E-07		9.49E-10	Control 1 Only	0.00
O75477	ERLN1_HUMAN Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1	28.90	7.00	5.00	1.00	4.00	1.86E-07	1.29E-07	1.32E-08	4.50E-08	0.07	0.24
Q14694	UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2	12.30	3.98	3.99	2.99	6.98	4.14E-08	4.16E-08	2.39E-08	7.28E-08	0.58	1.76
E9PHK9	E9PHK9_HUMAN Treacle protein OS=Homo sapiens GN=TCOF1 PE=2 SV=1	9.10	6.92	4.95		5.93	2.28E-08	2.73E-08		5.64E-09	Control 1 Only	0.25
Q12873	CHD3_HUMAN Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3	17.70	4.00	12.96		1.00	4.73E-09	2.24E-08		9.97E-10	Control 1 Only	0.21
Q15365	PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	20.50	1.98	4.96	4.96	5.94	9.16E-08	3.18E-07	1.39E-07	1.90E-07	1.52	2.07
F8W8M4	F8W8M4_HUMAN Actin-binding LIM protein 1 OS=Homo sapiens GN=ABLIM1 PE=2 SV=1	9.60	8.91	6.93		1.98	1.34E-07	7.73E-08		1.53E-08	Control 1 Only	0.11
P05089	ARGI1_HUMAN Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	26.70	10.00	4.00	4.00		2.23E-07	5.71E-08	3.70E-08		0.17	Control 1 Only
P13995	MTDC_HUMAN Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 PE=1 SV=2	25.10	4.91	0.99	4.93	5.91	3.87E-07	7.04E-08	2.26E-07	1.80E-07	0.58	0.47
Q8N7H5	PAF1_HUMAN RNA polymerase II-associated factor 1 homolog OS=Homo sapiens GN=PAF1 PE=1 SV=2	21.10	4.95	6.94	0.99	4.96	6.95E-08	8.06E-08	9.30E-09	6.08E-08	0.13	0.88
Q9HD45	TM9S3_HUMAN Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2	6.80	4.00	2.00	7.00	5.00	6.43E-08	3.69E-08	7.96E-08	6.43E-08	1.24	1.00
Q9NZ01	TECR_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1	21.40	2.98	3.99	3.97	5.95	1.51E-07	1.22E-07	1.40E-07	1.86E-07	0.93	1.24
Q9ULV4	COR1C_HUMAN Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	16.70	3.96	5.94	1.98	4.95	5.77E-08	8.27E-08	1.40E-08	5.38E-08	0.24	0.93
Q9Y6K5	OAS3_HUMAN 2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3	7.60	5.00	7.00	2.00	3.00	4.61E-08	6.08E-08	8.69E-09	1.22E-08	0.19	0.26
Q8TCJ2	STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1	9.60	8.00	3.00	3.00	3.00	6.45E-08	1.88E-08	1.00E-08	1.23E-08	0.16	0.19
P17987	TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	14.60	2.96	5.92	4.94	2.97	3.39E-08	7.61E-08	4.19E-08	2.41E-08	1.24	0.71
B4DQH9	B4DQH9_HUMAN Ran-binding protein 10 OS=Homo sapiens GN=RANBP10 PE=2 SV=1	19.90	2.96	7.90	1.97	3.95	4.35E-08	1.17E-07	2.75E-08	4.74E-08	0.63	1.09
Q96S59	RANB9_HUMAN Ran-binding protein 9 OS=Homo sapiens GN=RANBP9 PE=1 SV=1	15.80	5.00	7.00	3.00	2.00	5.02E-08	1.08E-07	1.79E-08	1.40E-08	0.36	0.28
B4DUR8	B4DUR8_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=2 SV=1	22.80	5.93	4.94	4.94	0.99	7.24E-08	6.73E-08	5.01E-08	6.61E-09	0.69	0.09
F2Z2U4	F2Z2U4_HUMAN Transformation/transcription domain-associated protein OS=Homo sapiens GN=TRRAP PE=2 SV=3	3.90	3.00	13.00			1.84E-09	8.41E-09			Control 1 Only	Control 1 Only
Q04695	K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	56.70	14.90		2.00		1.42E-07		1.67E-08		0.12	Control 1 Only
Q8WVC0	LEO1_HUMAN RNA polymerase-associated protein LEO1 OS=Homo sapiens GN=LEO1 PE=1 SV=1	13.20	3.00	7.00	2.00	5.00	3.71E-08	7.20E-08	1.87E-08	7.04E-08	0.50	1.90
P23528	COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	54.80	0.98	8.88	3.94	2.95	1.36E-07	1.40E-06	2.17E-07	1.82E-07	1.60	1.34
Q9UJW0	DCTN4_HUMAN Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1	20.40	5.93	6.92	2.97	0.99	1.05E-07	1.33E-07	3.94E-08	1.34E-08	0.38	0.13
Q9Y4D1	DAAM1_HUMAN Disheveled-associated activator of morphogenesis 1 OS=Homo sapiens GN=DAAM1 PE=1 SV=2	6.60	4.00	5.00	1.00	6.00	2.23E-08	3.70E-08	3.13E-09	3.11E-08	0.14	1.40

P61160	ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	29.90	4.00	12.00		1.00	1.64 E-07	5.84 E-07		8.66 E-09	Control 1 Only	0.05
Q9H2P0	ADNP_HUMAN Activity-dependent neuroprotector homeobox protein OS=Homo sapiens GN=ADNP PE=1 SV=1	10.10	4.00	6.00		6.00	3.80 E-08	4.29 E-08		1.22 E-08	Control 1 Only	0.32
B4DF41	B4DF41_HUMAN DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=2 SV=1	11.10	3.00	9.99		2.99	2.13 E-08	3.69 E-08		2.03 E-08	Control 1 Only	0.95
Q14807	KIF22_HUMAN Kinesin-like protein KIF22 OS=Homo sapiens GN=KIF22 PE=1 SV=5	24.40	9.96	4.97	0.99		1.60 E-07	7.70 E-08	6.25 E-09		0.04	Control 1 Only
Q15007	FL2D_HUMAN Pre-mRNA-splicing regulator WTAP OS=Homo sapiens GN=WTAP PE=1 SV=2	19.90	6.00	4.00	4.00	2.00	9.10 E-08	9.05 E-08	5.43 E-08	1.47 E-08	0.60	0.16
F5H7E2	F5H7E2_HUMAN Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=2 SV=1	10.20	4.00	8.00	1.00	3.00	2.07 E-08	7.53 E-08	3.73 E-09	1.08 E-08	0.18	0.52
P10636-4	TAU_HUMAN Isoform Tau-B of Microtubule-associated protein tau OS=Homo sapiens GN=MAPT	26.20			4.00	12.00			6.01 E-08	2.04 E-07	Sample 1 Only	Sample 2 Only
Q02880	TOP2B_HUMAN DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3	12.80	6.93	5.94		2.97	1.11 E-08	8.61 E-09		8.70 E-09	Control 1 Only	0.79
P35998	PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	23.10	1.00	5.00	4.00	6.00	2.48 E-08	1.04 E-07	4.75 E-08	9.01 E-08	1.92	3.63
Q9H9G7	AGO3_HUMAN Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	13.60			10.00	6.00			6.16 E-07	1.93 E-07	Sample 1 Only	Sample 2 Only
P48444	COPD_HUMAN Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	17.00	3.97	4.97	6.95		4.71 E-08	4.37 E-08	6.63 E-08		1.41	Control 1 Only
Q9NS69	TOM22_HUMAN Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3	42.30	4.00	3.00	5.00	3.00	4.29 E-07	1.89 E-07	1.85 E-07	2.04 E-07	0.43	0.48
Q9UHR4	BI2L1_HUMAN Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Homo sapiens GN=BAIAP2L1 PE=1 SV=2	17.80	4.00	5.00	2.00	4.00	3.84 E-08	5.80 E-08	1.52 E-08	4.61 E-08	0.40	1.20
O14974	MYPT1_HUMAN Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1	11.20	7.87	5.90		0.98	7.25 E-08	4.18 E-08		6.77 E-09	Control 1 Only	0.09
Q13555	KCC2G_HUMAN Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Homo sapiens GN=CAMK2G PE=1 SV=3	19.40	3.95	9.85			3.71 E-08	1.52 E-07			Control 1 Only	Control 1 Only
O60870	KIN17_HUMAN DNA/RNA-binding protein KIN17 OS=Homo sapiens GN=KIN PE=1 SV=2	11.20	3.99	3.99	3.00	3.98	1.70 E-07	1.09 E-07	6.95 E-08	5.85 E-08	0.41	0.35
P02538	K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	55.10	6.97	2.00	2.98	1.99	1.54 E-07	1.58 E-08	6.54 E-08	2.46 E-08	0.42	0.16
P07900	HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	8.80	1.98	3.96	3.96	3.96	1.78 E-08	3.98 E-08	2.84 E-08	3.70 E-08	1.60	2.09
Q96AX1	VP33A_HUMAN Vacuolar protein sorting-associated protein 33A OS=Homo sapiens GN=VPS33A PE=1 SV=1	17.80	4.98	5.97	3.97		1.22 E-07	1.35 E-07	5.45 E-08		0.45	Control 1 Only
Q9NYU2	UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	7.80	4.00	6.99	4.00		9.17 E-09	9.48 E-09	6.53 E-09		0.71	Control 1 Only
P61254	RL26_HUMAN 60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	64.10	2.96	3.94	2.00	4.92	1.26 E-06	8.32 E-07	9.67 E-08	1.18 E-06	0.08	0.93
B7Z4C8	B7Z4C8_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=2 SV=1	30.40	5.00	3.00	2.00	3.00	1.35 E-06	9.58 E-07	2.90 E-07	8.88 E-07	0.21	0.66
Q01831	XPC_HUMAN DNA repair protein complementing XP-C cells OS=Homo sapiens GN=XPC PE=1 SV=4	7.60	6.00	5.00	1.00	1.00	4.50 E-08	2.21 E-08	6.59 E-10	1.08 E-09	0.01	0.02
Q08554	DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	11.20	9.00	1.00	4.00		4.39 E-08	2.36 E-09	1.01 E-08		0.23	Control 1 Only
Q6ISB3	GRHL2_HUMAN Grainyhead-like protein 2 homolog OS=Homo sapiens GN=GRHL2 PE=1 SV=1	23.30	6.00	6.00		2.00	2.04 E-08	5.51 E-08		1.58 E-08	Control 1 Only	0.77
F6RU81	F6RU81_HUMAN ELM2 and SANT domain-containing protein 1 (Fragment) OS=Homo sapiens GN=ELMSAN1 PE=2 SV=1	8.40	4.00	5.00	1.00	4.00	4.30 E-08	3.82 E-08	7.58 E-09	2.91 E-08	0.18	0.68
Q29RF7	PDS5A_HUMAN Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	8.70	3.00	6.76	2.76	1.00	1.39 E-08	5.04 E-08	4.41 E-09	1.79 E-10	0.32	0.01
O75150	BRE1B_HUMAN E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens GN=RNF40 PE=1 SV=4	12.40	4.95	3.97		4.95	2.91 E-08	2.65 E-08		2.67 E-08	Control 1 Only	0.92

Q13011	ECH1_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	27.70	5.99	3.98	2.00	2.00	4.91E-07	1.95E-07	9.80E-08	4.49E-08	0.20	0.09
P18077	RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	57.30	2.98	1.99	0.99	7.96	4.73E-07	1.33E-07	1.98E-07	1.14E-06	0.42	2.41
P26358	DNMT1_HUMAN DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2	8.60	1.00	9.98	1.00	2.00	5.35E-10	1.91E-08	1.63E-09	1.02E-09	3.06	1.90
Q9H0H5	RGAP1_HUMAN Rac GTPase-activating protein 1 OS=Homo sapiens GN=RACGAP1 PE=1 SV=1	13.60	3.00	4.00	1.00	6.00	3.00E-08	2.72E-08	5.50E-09	3.99E-08	0.18	1.33
P43686	PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	17.50	1.00	8.00	2.00	3.00	1.93E-08	2.25E-07	2.41E-08	7.84E-08	1.25	4.06
P51665	PSMD7_HUMAN 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	13.00	4.00	5.00	2.00	3.00	1.47E-07	1.79E-07	6.54E-08	8.21E-08	0.44	0.56
P47914	RL29_HUMAN 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	14.50	3.00	3.00	1.00	6.00	1.24E-07	8.70E-08	2.13E-08	4.19E-07	0.17	3.37
G3V1L9	G3V1L9_HUMAN Tight junction protein 1 (Zona occludens 1), isoform CRA_a OS=Homo sapiens GN=TJP1 PE=2 SV=1	8.70	1.00	11.98			1.47E-09	1.66E-08			Control 1 Only	Control 1 Only
H0Y465	H0Y465_HUMAN Neurofibromin truncated (Fragment) OS=Homo sapiens GN=NF1 PE=2 SV=1	5.80	1.99	10.94			9.96E-10	1.61E-08			Control 1 Only	Control 1 Only
Q86Y07	VRK2_HUMAN Serine/threonine-protein kinase VRK2 OS=Homo sapiens GN=VRK2 PE=1 SV=3	20.50	1.00	2.00	7.00	3.00	3.44E-08	5.25E-08	1.50E-07	2.05E-08	4.36	0.59
J3KNX9	J3KNX9_HUMAN Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=2 SV=1	8.60		12.88				1.74E-08				
B4DXM1	B4DXM1_HUMAN FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=2 SV=1	15.80	4.00	3.00	4.00	2.00	1.37E-07	1.48E-07	8.93E-08	4.27E-08	0.65	0.31
B4E2P2	B4E2P2_HUMAN Translocon-associated protein subunit gamma OS=Homo sapiens GN=SSR3 PE=2 SV=1	17.20	2.00	4.00	4.00	3.00	9.81E-08	1.52E-07	1.14E-07	1.16E-07	1.16	1.18
O15145	ARPC3_HUMAN Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3	23.60	4.99	4.97	1.00	0.99	8.13E-07	4.15E-07	9.96E-08	2.95E-08	0.12	0.04
O43318	M3K7_HUMAN Mitogen-activated protein kinase kinase kinase 7 OS=Homo sapiens GN=MAP3K7 PE=1 SV=1	12.40	3.96	3.97	3.97	0.99	4.50E-08	2.99E-08	1.81E-08	5.26E-09	0.40	0.12
Q15427	SF3B4_HUMAN Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	14.90	1.00	8.99		3.00	4.37E-08	1.83E-07		4.65E-08	Control 1 Only	1.06
F8VU39	F8VU39_HUMAN Bromodomain adjacent to zinc finger domain protein 2A OS=Homo sapiens GN=BAZ2A PE=2 SV=1	7.40	1.00	9.00		3.00	8.07E-10	1.75E-08		1.34E-09	Control 1 Only	1.66
F8VU51	F8VU51_HUMAN YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=2 SV=1	5.80	1.00	9.00	1.00	2.00	1.80E-09	2.16E-08	1.52E-09	1.92E-09	0.85	1.07
Q8WVX9	FACR1_HUMAN Fatty acyl-CoA reductase 1 OS=Homo sapiens GN=FAR1 PE=1 SV=1	9.50	5.00	4.00	1.00	3.00	6.11E-08	5.44E-08	4.97E-09	2.63E-08	0.08	0.43
Q9UQ35	SRRM2_HUMAN Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	6.70		12.97				8.41E-09				
B4DL14	B4DL14_HUMAN ATP synthase subunit gamma OS=Homo sapiens GN=ATP5C1 PE=2 SV=1	22.00	2.00	2.00	3.00	5.00	5.50E-08	1.81E-07	1.55E-07	1.84E-07	2.82	3.35
Q9Y4W6	AFG32_HUMAN AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2	5.50	5.00	3.00	2.00	2.00	4.84E-08	4.07E-08	6.94E-09	1.95E-08	0.14	0.40
F8WJN3	F8WJN3_HUMAN Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=2 SV=1	18.60	1.00	9.00		2.00	1.15E-08	1.97E-07		2.46E-08	Control 1 Only	2.14
O15060	ZBT39_HUMAN Zinc finger and BTB domain-containing protein 39 OS=Homo sapiens GN=ZBTB39 PE=2 SV=1	11.50	3.00	7.00	1.00	1.00	1.84E-08	7.03E-08	3.91E-09	3.47E-09	0.21	0.19
J3QRS9	J3QRS9_HUMAN Zinc finger protein 207 OS=Homo sapiens GN=ZNF207 PE=2 SV=1	5.30	4.96	2.97	0.99	2.97	1.11E-07	5.70E-08	8.20E-09	6.79E-08	0.07	0.61
Q10570	CPSF1_HUMAN Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2	4.20	5.00	5.00		2.00	8.04E-09	1.70E-08		1.91E-09	Control 1 Only	0.24
Q6ZRS2	SRCAP_HUMAN Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3	3.30	3.00	9.00			2.00E-09	6.04E-09			Control 1 Only	Control 1 Only
Q96SB3	NEB2_HUMAN Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=1 SV=2	12.50	1.00	10.00		1.00	3.71E-09	1.09E-07		1.52E-09	Control 1 Only	0.41

Q9NRL2	BAZ1A_HUMAN Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens GN=BAZ1A PE=1 SV=2	6.80	4.00	3.00	1.00	4.00	7.29E-09	3.10E-09	8.09E-10	3.76E-09	0.11	0.52
J3KNL6	J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=2 SV=1	1.90	2.00	5.00	1.00	2.00	6.94E-10	4.49E-09	1.03E-10	6.70E-10	0.15	0.97
K7EIN2	K7EIN2_HUMAN Protein syndesmos (Fragment) OS=Homo sapiens GN=NUDT16L1 PE=4 SV=1	40.90	7.00	4.00		1.00	5.70E-07	3.31E-07		3.93E-08	Control 1 Only	0.07
O00468-3	AGRIN_HUMAN Isoform 3 of Agrin OS=Homo sapiens GN=AGRN	6.30		10.96	1.00			2.06E-08	9.49E-10		Sample 1 Only	
Q13356	PPIL2_HUMAN Peptidyl-prolyl cis-trans isomerase-like 2 OS=Homo sapiens GN=PPIL2 PE=1 SV=1	9.20	3.96	3.96		3.96	5.32E-08	4.40E-08		2.79E-08	Control 1 Only	0.52
E9PI39	E9PI39_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=2 SV=1	34.60	2.97	4.95	1.98	1.98	2.25E-07	4.01E-07	1.03E-07	9.33E-08	0.46	0.41
E9PM69	E9PM69_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=2 SV=1	23.40	1.00	3.97		6.95	6.31E-09	4.28E-08		7.20E-08	Control 1 Only	11.40
Q15637	SF01_HUMAN Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4	16.10	4.95	5.94		0.99	4.15E-08	6.39E-08		1.43E-09	Control 1 Only	0.03
Q6NZY4	ZCHC8_HUMAN Zinc finger CCHC domain-containing protein 8 OS=Homo sapiens GN=ZCCHC8 PE=1 SV=2	12.40	2.97	4.96	1.98	1.98	2.67E-08	4.82E-08	1.23E-08	1.54E-08	0.46	0.58
Q8N766	EMC1_HUMAN ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1	8.90	6.00	2.00	3.00	1.00	3.28E-08	6.29E-09	1.23E-08	3.93E-09	0.38	0.12
Q9UJA5	TRM6_HUMAN tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens GN=TRMT6 PE=1 SV=1	23.10	5.96	3.98	1.00	0.99	8.23E-08	6.64E-08	2.97E-09	8.85E-09	0.04	0.11
Q9UMS4	PRP19_HUMAN Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	14.50	2.99	3.99	1.99	2.98	3.40E-08	6.24E-08	2.36E-08	4.51E-08	0.69	1.33
B1AHC8	B1AHC8_HUMAN X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa), isoform CRA_b OS=Homo sapiens GN=XRCC6 PE=2 SV=1	10.60	2.00	5.00	2.00	2.00	1.49E-08	3.59E-08	7.58E-09	1.43E-08	0.51	0.96
Q13247	SRSF6_HUMAN Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2	13.10	3.00	6.99			2.80E-08	7.29E-08			Control 1 Only	Control 1 Only
B4DVB8	B4DVB8_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=2 SV=1	16.60	3.00	4.00	1.00	3.00	1.92E-07	2.29E-07	3.85E-08	8.01E-08	0.20	0.42
D6RIY6	D6RIY6_HUMAN Exosome complex component RRP45 OS=Homo sapiens GN=EXOSC9 PE=2 SV=1	11.80	2.97	1.98		5.94	5.78E-08	2.36E-08		9.88E-08	Control 1 Only	1.71
Q14571	ITPR2_HUMAN Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2	5.80	3.00	6.00	1.00	1.00	1.25E-09	4.37E-09	4.21E-10	2.17E-10	0.34	0.17
E9PQ61	E9PQ61_HUMAN Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens GN=ZC3H11A PE=2 SV=1	14.00	5.00	4.00		2.00	5.53E-08	3.46E-08		8.38E-09	Control 1 Only	0.15
Q8N1N4	K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	24.40	8.99		2.00		9.87E-08		1.27E-08		0.13	Control 1 Only
Q15561	TEAD4_HUMAN Transcriptional enhancer factor TEF-3 OS=Homo sapiens GN=TEAD4 PE=1 SV=3	7.90	3.96	3.96		2.97	1.08E-07	8.91E-08		3.19E-08	Control 1 Only	0.30
P04279	SEMG1_HUMAN Semenogelin-1 OS=Homo sapiens GN=SEMG1 PE=1 SV=2	32.70			10.00				7.99E-08		Sample 1 Only	
Q5W0U4	BSPRY_HUMAN B box and SPRY domain-containing protein OS=Homo sapiens GN=BSPRY PE=2 SV=1	9.70	3.00	3.00	4.00	1.00	1.06E-07	9.26E-08	5.75E-08	1.30E-08	0.54	0.12
Q6YN16	HSDL2_HUMAN Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	16.20	2.00	5.00	4.00		8.33E-08	1.41E-07	1.23E-07		1.48	Control 1 Only
P13010	XRCC5_HUMAN X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	5.20	4.00	3.00	1.00	3.00	4.30E-08	3.69E-08	9.94E-09	3.45E-08	0.23	0.80
Q96H55	MYO19_HUMAN Unconventional myosin-XIX OS=Homo sapiens GN=MYO19 PE=2 SV=2	11.90		10.91				8.78E-08				
P30153	2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	12.10		4.96	1.98	2.97		4.10E-08	7.38E-09	1.73E-08	Sample 1 Only	Sample 2 Only
Q9H061	T126A_HUMAN Transmembrane protein 126A OS=Homo sapiens GN=TMEM126A PE=1 SV=1	25.10	1.00	2.00	3.00	4.99	6.18E-08	1.06E-07	1.15E-07	2.33E-07	1.86	3.77
Q9H4Y5	GSTO2_HUMAN Glutathione S-transferase omega-2 OS=Homo sapiens GN=GSTO2 PE=1 SV=1	19.60	4.00	4.00	3.00		2.95E-07	1.51E-07	1.68E-07		0.57	Control 1 Only

P40937	RFC5_HUMAN Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=1 SV=1	16.60	3.95	3.95	1.97	0.98	1.72 E-07	1.41 E-07	5.06 E-08	2.99 E-08	0.29	0.17
P51991	ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	27.80	2.00	3.00	2.00	4.00	1.75 E-07	1.34 E-07	4.72 E-08	1.32 E-07	0.27	0.75
P62333	PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	23.90	0.99	5.95	0.99	2.97	3.05 E-08	2.31 E-07	1.55 E-08	6.34 E-08	0.51	2.08
E7EUT5	E7EUT5_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=2 SV=1	32.30	6.00		4.00		4.38 E-08		2.46 E-08		0.56	Control 1 Only
Q9UBF2	COPG2_HUMAN Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1	14.20		4.00	3.50			3.00 E-08	3.32 E-08		Sample 1 Only	
G5E975	G5E975_HUMAN SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1, isoform CRA_c OS=Homo sapiens GN=SMARCB1 PE=2 SV=1	5.60	2.97	2.97	1.98	1.98	1.28 E-07	1.02 E-07	5.28 E-08	3.13 E-08	0.41	0.24
Q969Q0	RL36L_HUMAN 60S ribosomal protein L36a-like OS=Homo sapiens GN=RPL36AL PE=1 SV=3	24.50	0.99	3.98	1.98	2.98	3.26 E-07	4.85 E-07	1.65 E-07	6.31 E-07	0.51	1.94
P78371	TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	18.50	1.98	5.96	1.98		3.63 E-08	8.08 E-08	1.99 E-08		0.55	Control 1 Only
H7C1M5	H7C1M5_HUMAN Deoxynucleotidyltransferase terminal-interacting protein 1 (Fragment) OS=Homo sapiens GN=DNTTIP1 PE=4 SV=1	17.50	3.96	1.98	1.98	1.98	1.29 E-07	6.20 E-08	2.84 E-08	1.90 E-08	0.22	0.15
A6NHR9	SMHD1_HUMAN Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2	4.90	1.99	7.99			1.46 E-09	1.07 E-08			Control 1 Only	Control 1 Only
Q05519	SRS11_HUMAN Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1	13.40	2.00	4.00	1.00	3.00	2.13 E-08	4.37 E-08	4.53 E-09	2.17 E-08	0.21	1.02
B7ZM82	B7ZM82_HUMAN Protein Wiz OS=Homo sapiens GN=WIZ PE=2 SV=1	6.90	4.00	4.00	1.00	1.00	2.42 E-08	2.78 E-08	1.60 E-09	3.41 E-09	0.07	0.14
E9PF36	E9PF36_HUMAN Vacuolar protein sorting-associated protein 41 homolog OS=Homo sapiens GN=VPS41 PE=2 SV=1	7.20	4.00	3.00	3.00		2.33 E-08	1.74 E-08	1.11 E-08		0.48	Control 1 Only
F8W840	F8W840_HUMAN YTH domain family protein 1 OS=Homo sapiens GN=YTHDF1 PE=2 SV=1	14.10	2.00	3.99	1.00	2.99	4.94 E-08	6.38 E-08	3.49 E-08	4.07 E-08	0.71	0.83
Q86XN7	PRSR1_HUMAN Proline and serine-rich protein 1 OS=Homo sapiens GN=PROSER1 PE=1 SV=2	5.80	2.97	4.97	0.99	0.99	3.15 E-08	5.53 E-08	4.03 E-09	7.32 E-09	0.13	0.23
Q9NVC6	MED17_HUMAN Mediator of RNA polymerase II transcription subunit 17 OS=Homo sapiens GN=MED17 PE=1 SV=2	11.10	3.00	5.00	1.00	1.00	4.32 E-08	6.71 E-08	6.22 E-09	7.31 E-09	0.14	0.17
H7BXY3	H7BXY3_HUMAN Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=2 SV=1	6.90		6.00		4.00		2.32 E-08		1.20 E-08		Sample 2 Only
O60841	IF2P_HUMAN Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4	8.00	6.00	3.00	1.00		1.51 E-08	5.44 E-09	1.44 E-09		0.10	Control 1 Only
Q9Y224	CN166_HUMAN UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	15.20	2.97	1.99	1.98	1.98	6.91 E-08	4.95 E-08	3.49 E-08	2.98 E-08	0.51	0.43
Q9Y3U8	RL36_HUMAN 60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	30.50	2.99	2.99		3.98	9.67 E-07	4.95 E-07		4.88 E-07	Control 1 Only	0.50
C9IZQ1	C9IZQ1_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=2 SV=1	8.90	2.00	2.00	3.00	2.00	4.03 E-07	2.37 E-07	3.48 E-07	2.74 E-07	0.86	0.68
D6R9P3	D6R9P3_HUMAN Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=2 SV=1	21.80	2.00	2.00	2.00	3.00	3.73 E-08	5.89 E-08	3.41 E-08	7.53 E-08	0.92	2.02
F5H3T8	F5H3T8_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=2 SV=1	5.70	3.00	2.00	1.00	3.00	2.62 E-08	2.00 E-08	6.92 E-09	2.21 E-08	0.26	0.84
G3V3A4	G3V3A4_HUMAN SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1 PE=2 SV=1	10.40	4.00	3.00		2.00	1.81 E-08	8.30 E-09		1.02 E-08	Control 1 Only	0.56
H7C3A1	H7C3A1_HUMAN Serrate RNA effector molecule homolog (Fragment) OS=Homo sapiens GN=SRRT PE=2 SV=1	11.80	2.00	3.00		4.00	1.45 E-08	3.47 E-08		3.52 E-08	Control 1 Only	2.43
P07814	SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	4.40	2.00	3.00		4.00	3.14 E-09	5.80 E-09		7.06 E-09	Control 1 Only	2.25
P24928	RPB1_HUMAN DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2	4.60	1.00	6.00	1.00	1.00	9.06 E-10	5.45 E-09	4.87 E-10	4.40 E-10	0.54	0.49
G3V0I6	G3V0I6_HUMAN OTU domain containing 4, isoform CRA_f OS=Homo sapiens GN=OTUD4 PE=2 SV=1	4.80	0.99	1.98	0.99	4.95	4.57 E-09	1.38 E-08	2.19 E-09	2.20 E-08	0.48	4.82

G5E9L8	G5E9L8_HUMAN Epithelial cell transforming sequence 2 oncogene, isoform CRA_b OS=Homo sapiens GN=ECT2 PE=2 SV=1	8.40	2.00	6.00			4.74E-09	2.94E-08			Control 1 Only	Control 1 Only
A8MTG8	A8MTG8_HUMAN Armadillo repeat-containing protein 8 OS=Homo sapiens GN=ARMC8 PE=2 SV=3	12.70	2.96	5.92			2.42E-08	7.85E-08			Control 1 Only	Control 1 Only
Q03519	TAP2_HUMAN Antigen peptide transporter 2 OS=Homo sapiens GN=TAP2 PE=1 SV=1	5.70	0.99	2.99	3.00	1.99	2.26E-08	3.86E-08	2.05E-08	2.36E-08	0.91	1.04
B3KSH1	B3KSH1_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1	12.00	0.99	4.95	0.99	1.98	2.28E-08	1.03E-07	1.55E-08	3.61E-08	0.68	1.58
B4DEM7	B4DEM7_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1	11.50	1.98	3.96	2.97		3.29E-08	6.68E-08	4.10E-08		1.25	Control 1 Only
Q13315	ATM_HUMAN Serine-protein kinase ATM OS=Homo sapiens GN=ATM PE=1 SV=3	2.90	1.00	8.00			5.49E-10	4.52E-09			Control 1 Only	Control 1 Only
B7Z321	B7Z321_HUMAN Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=2 SV=1	9.40	2.97	4.95	0.99		2.01E-08	3.81E-08	1.69E-09		0.08	Control 1 Only
D6RGG3	D6RGG3_HUMAN Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=2 SV=1	3.00	1.98	5.97	1.00		2.42E-09	4.61E-09	4.02E-10		0.17	Control 1 Only
O60216	RAD21_HUMAN Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2	11.90	2.00	2.99	2.00	2.00	1.89E-08	2.66E-08	5.52E-09	1.66E-08	0.29	0.88
H0Y4R1	H0Y4R1_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=3 SV=1	15.50	1.00	5.99	2.00		1.04E-08	1.29E-07	2.47E-08		2.39	Control 1 Only
E9PH82	E9PH82_HUMAN Protein FAM98A OS=Homo sapiens GN=FAM98A PE=2 SV=1	11.90	1.98	2.97		3.96	3.38E-08	5.52E-08		7.71E-08	Control 1 Only	2.28
Q7Z794	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	17.30	5.00	1.00	3.00		3.04E-08	3.08E-09	9.85E-09		0.32	Control 1 Only
Q15599	NHRF2_HUMAN Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=2	12.00	1.00	3.00		4.00	1.23E-08	7.03E-08		5.29E-08	Control 1 Only	4.29
Q5T200	ZC3HD_HUMAN Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1	5.20	4.00	3.00	2.00		3.24E-08	3.42E-08	3.43E-09		0.11	Control 1 Only
B7WPG3	B7WPG3_HUMAN Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens GN=HNRPLL PE=2 SV=1	12.40	2.96	2.96		2.95	2.68E-08	3.13E-08		3.77E-08	Control 1 Only	1.41
Q96HS1	PGAM5_HUMAN Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	7.50		2.98	1.00	4.97		2.01E-07	6.00E-08	2.91E-07	Sample 1 Only	Sample 2 Only
Q96N66	MBOA7_HUMAN Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2	10.30	2.00	2.00	2.00	3.00	3.14E-08	2.17E-08	1.62E-08	2.16E-08	0.52	0.69
Q9BTA9	WAC_HUMAN WW domain-containing adapter protein with coiled-coil OS=Homo sapiens GN=WAC PE=1 SV=3	9.90	2.98	1.98		3.97	4.15E-08	1.39E-08		3.52E-08	Control 1 Only	0.85
Q9NPJ6	MED4_HUMAN Mediator of RNA polymerase II transcription subunit 4 OS=Homo sapiens GN=MED4 PE=1 SV=1	20.00	4.00	3.00		2.00	1.08E-07	6.46E-08		1.63E-08	Control 1 Only	0.15
P40222	TXLNA_HUMAN Alpha-taxilin OS=Homo sapiens GN=TXLNA PE=1 SV=3	15.60	3.00	4.00	1.00		5.94E-08	3.66E-08	1.41E-08		0.24	Control 1 Only
P40939	ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	10.90	2.00	2.00	2.00	3.00	2.40E-08	9.34E-09	1.13E-08	1.08E-08	0.47	0.45
P42167-2	LAP2B_HUMAN Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO	57.40	4.00	2.00	1.00	2.00	2.69E-08	1.08E-08	5.11E-09	7.73E-09	0.19	0.29
Q9UKS6	PACN3_HUMAN Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens GN=PACSIN3 PE=1 SV=2	16.30		4.98		3.98		1.06E-07		5.39E-08		Sample 2 Only
P53350	PLK1_HUMAN Serine/threonine-protein kinase PLK1 OS=Homo sapiens GN=PLK1 PE=1 SV=1	7.30	3.00	3.00	1.00	2.00	3.39E-08	3.21E-08	5.10E-09	1.38E-08	0.15	0.41
P61513	RL37A_HUMAN 60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2	35.90	1.99	1.99	0.99	2.99	2.03E-07	2.39E-07	5.34E-08	2.31E-07	0.26	1.14
Q9H0U3	MAGT1_HUMAN Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1 PE=1 SV=1	5.70	2.00	2.00	2.00	2.00	5.26E-08	3.33E-08	1.15E-07	2.18E-08	2.18	0.41
Q08211	DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	5.10	1.00	4.00		3.00	3.44E-09	2.27E-08		1.04E-08	Control 1 Only	3.03
B4DKG8	B4DKG8_HUMAN Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=2 SV=1	7.80	2.00	1.00		5.00	1.61E-08	8.32E-09		4.22E-08	Control 1 Only	2.63

E7EPK1	E7EPK1_HUMAN Septin-7 OS=Homo sapiens GN=SEPT7 PE=2 SV=1	10.90	2.97	2.97	1.98		7.97E-08	5.88E-08	2.23E-08		0.28	Control 1 Only
O60934	NBN_HUMAN Nibrin OS=Homo sapiens GN=NBN PE=1 SV=1	12.60	0.99	1.98	1.99	2.98	1.38E-08	1.72E-08	7.20E-09	2.97E-08	0.52	2.15
I1E4Y6	I1E4Y6_HUMAN PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=2 SV=1	4.60	0.99	3.96	0.99	1.99	3.10E-09	6.86E-09	1.10E-09	3.64E-09	0.35	1.17
O95239	KIF4A_HUMAN Chromosome-associated kinesin KIF4A OS=Homo sapiens GN=KIF4A PE=1 SV=3	4.90	1.00	5.00	1.00	1.00	4.40E-10	1.21E-08	3.85E-10	9.74E-10	0.88	2.22
P78347	GTF2I_HUMAN General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	6.80	1.00	2.00		5.00	5.25E-09	1.33E-08		3.65E-08	Control 1 Only	6.95
F5H365	F5H365_HUMAN Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=2 SV=1	9.50	2.97	3.96	0.99		4.91E-08	5.21E-08	5.71E-09		0.12	Control 1 Only
Q9Y5S2	MRCKB_HUMAN Serine/threonine-protein kinase MRCK beta OS=Homo sapiens GN=CDC42BPB PE=1 SV=2	5.10	2.00	3.50		1.00	3.72E-09	6.08E-09		9.87E-10	Control 1 Only	0.27
Q15648	MED1_HUMAN Mediator of RNA polymerase II transcription subunit 1 OS=Homo sapiens GN=MED1 PE=1 SV=4	5.40	2.00	3.00	1.00	2.00	1.41E-08	2.50E-08	3.91E-09	1.45E-09	0.28	0.10
Q5JTH9	RRP12_HUMAN RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2	5.30	1.00	3.00	1.00	3.00	3.00E-10	7.44E-09	1.30E-09	5.62E-09	4.33	18.73
Q9NUQ8	ABCF3_HUMAN ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2	10.00	3.00	3.00	2.00		3.31E-08	3.48E-08	1.05E-08		0.32	Control 1 Only
Q92945	FUBP2_HUMAN Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	6.90	1.00	3.00	3.00	1.00	6.33E-09	2.32E-08	1.07E-08	1.59E-09	1.69	0.25
Q99714	HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	29.80	2.00	3.00	3.00		7.40E-08	1.25E-07	9.48E-08		1.28	Control 1 Only
P31930	QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	8.10	4.00	3.00		1.00	1.76E-07	1.13E-07		5.34E-09	Control 1 Only	0.03
Q9HAU5	RENT2_HUMAN Regulator of nonsense transcripts 2 OS=Homo sapiens GN=UPF2 PE=1 SV=1	4.60	4.00	3.00	1.00		8.01E-09	8.82E-09	1.23E-09		0.15	Control 1 Only
Q9NR30	DDX21_HUMAN Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	9.80		1.00		7.00		4.11E-09		5.81E-08		Sample 2 Only
Q9NUP9	LIN7C_HUMAN Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1	18.80	0.99	1.99	1.98	2.98	2.49E-07	2.47E-07	2.07E-07	2.49E-07	0.83	1.00
Q9UER7	DAXX_HUMAN Death domain-associated protein 6 OS=Homo sapiens GN=DAXX PE=1 SV=2	5.70	3.00	3.00	1.00	1.00	4.53E-08	3.76E-08	9.43E-09	1.10E-08	0.21	0.24
P51571	SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1	13.30	2.00	1.00	2.00	3.00	2.95E-07	1.38E-07	1.83E-07	2.23E-07	0.62	0.76
P60763	RAC3_HUMAN Ras-related C3 botulinum toxin substrate 3 OS=Homo sapiens GN=RAC3 PE=1 SV=1	19.80	1.99		1.98	3.97	1.73E-07		1.09E-07	2.80E-07	0.63	1.62
Q9Y4F1	FARP1_HUMAN FERM, RhoGEF and pleckstrin domain-containing protein 1 OS=Homo sapiens GN=FARP1 PE=1 SV=1	5.90	1.98	3.96		0.99	1.46E-08	3.23E-08		5.33E-09	Control 1 Only	0.37
F8WE04	F8WE04_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=2 SV=1	10.80	1.00	1.00	2.00	3.00	4.58E-08	5.25E-08	1.03E-07	1.42E-07	2.24	3.10
J3KN32	J3KN32_HUMAN REST corepressor 1 OS=Homo sapiens GN=RCOR1 PE=2 SV=1	5.80	2.00	2.00	2.00	1.00	4.11E-08	5.18E-08	2.21E-08	1.81E-08	0.54	0.44
O00487	PSDE_HUMAN 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	7.40	1.00	2.00	2.00	2.00	6.83E-08	1.47E-07	8.50E-08	8.98E-08	1.24	1.31
P06702	S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	51.80	7.00				2.07E-07				Control 1 Only	Control 1 Only
P10809	CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	8.70		1.00	2.00	4.00		1.18E-08	1.17E-08	5.53E-08	Sample 1 Only	Sample 2 Only
P40938	RFC3_HUMAN Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2	9.20	2.00	2.00	1.00	2.00	6.26E-08	7.21E-08	1.25E-08	1.81E-08	0.20	0.29
G5EA38	G5EA38_HUMAN Chromosome 1 open reading frame 69 OS=Homo sapiens GN=IBA57 PE=2 SV=1	15.30	2.00	2.00	2.00	1.00	2.09E-07	1.88E-07	1.63E-07	5.32E-08	0.78	0.25
Q5TDF0	Q5TDF0_HUMAN Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=2 SV=1	15.30	1.00	2.00	2.00	2.00	8.02E-08	9.40E-08	5.57E-08	5.62E-08	0.69	0.70

F8VVL1	F8VVL1_HUMAN Density-regulated protein OS=Homo sapiens GN=DENR PE=2 SV=1	28.10		3.00	1.00	3.00		2.32E-07	1.35E-08	1.25E-07	Sample 1 Only	Sample 2 Only
Q96QC0	PP1RA_HUMAN Serine/threonine-protein phosphatase 1 regulatory subunit 10 OS=Homo sapiens GN=PPP1R10 PE=1 SV=1	6.90	2.00	3.00		2.00	1.25E-08	3.72E-08		5.09E-09	Control 1 Only	0.41
Q9H4H8	FA83D_HUMAN Protein FAM83D OS=Homo sapiens GN=FAM83D PE=1 SV=3	9.70	5.00	2.00			5.49E-08	2.60E-08			Control 1 Only	Control 1 Only
Q9UBV8	PEF1_HUMAN Peflin OS=Homo sapiens GN=PEF1 PE=1 SV=1	11.30		1.00	3.00	3.00		3.13E-08	5.32E-08	1.02E-07	Sample 1 Only	Sample 2 Only
B1AKN5	B1AKN5_HUMAN Nuclear factor 1 OS=Homo sapiens GN=NFIA PE=2 SV=1	16.10	0.99	1.98	0.99	2.96	9.21E-09	2.96E-08	5.42E-09	2.75E-08	0.59	2.98
Q13045	FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	6.50	0.99	4.94		0.99	3.07E-09	1.57E-08		8.96E-10	Control 1 Only	0.29
B4DJP7	B4DJP7_HUMAN Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=2 SV=1	33.30	2.00	3.00		2.00	3.70E-07	3.57E-07		2.50E-07	Control 1 Only	0.67
O14880	MGST3_HUMAN Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1	18.40	2.00	2.00	1.00	2.00	3.81E-07	3.74E-07	1.52E-07	3.36E-07	0.40	0.88
O14646	CHD1_HUMAN Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens GN=CHD1 PE=1 SV=2	3.90		4.97	2.00			9.28E-09	4.60E-09		Sample 1 Only	
E7EQY4	E7EQY4_HUMAN Metastasis-associated protein MTA3 OS=Homo sapiens GN=MTA3 PE=2 SV=1	37.00		4.95	0.99	0.99		3.79E-08	6.48E-09	2.10E-09	Sample 1 Only	Sample 2 Only
Q9Y5A9	YTHD2_HUMAN YTH domain family protein 2 OS=Homo sapiens GN=YTHDF2 PE=1 SV=2	10.80		3.00	1.00	3.00		1.59E-08	4.56E-09	3.24E-08	Sample 1 Only	Sample 2 Only
Q02383	SEMG2_HUMAN Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1	22.90			6.00	1.00			2.54E-08	3.00E-09	Sample 1 Only	Sample 2 Only
F8VZY9	F8VZY9_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=2 SV=1	13.30		3.00		4.00		7.54E-08		9.99E-08		Sample 2 Only
Q8N163	CCAR2_HUMAN Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2	3.60	0.99	2.97	1.98	0.99	6.14E-09	2.33E-08	7.79E-09	3.04E-09	1.27	0.50
P17858	K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	9.90	1.65	2.65	1.00	1.00	2.78E-08	2.50E-08	6.19E-09	3.92E-09	0.22	0.14
Q8WUA4	TF3C2_HUMAN General transcription factor 3C polypeptide 2 OS=Homo sapiens GN=GTF3C2 PE=1 SV=2	5.20	2.00	4.00		1.00	9.57E-09	3.25E-08		5.71E-09	Control 1 Only	0.60
Q8WX93	PALLD_HUMAN Palladin OS=Homo sapiens GN=PALLD PE=1 SV=3	8.20	1.97		4.95		1.33E-08		1.67E-08		1.25	Control 1 Only
Q96NB2	SFXN2_HUMAN Sideroflexin-2 OS=Homo sapiens GN=SFXN2 PE=1 SV=2	14.90			2.00	4.99			1.86E-08	1.00E-07	Sample 1 Only	Sample 2 Only
Q9UPT5	EXOC7_HUMAN Exocyst complex component 7 OS=Homo sapiens GN=EXOC7 PE=1 SV=3	5.20	2.97	2.97	0.99		2.06E-08	1.93E-08	5.11E-09		0.25	Control 1 Only
P52294	IMA5_HUMAN Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3	4.60	2.97	1.98	0.99	0.99	3.16E-08	1.56E-08	5.21E-09	3.68E-09	0.16	0.12
Q562R1	ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	20.20	3.00		3.00	1.00	3.87E-06		1.80E-07	3.49E-08	0.05	0.01
B4DP17	B4DP17_HUMAN Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=2 SV=1	18.80	4.00	1.00	1.00		2.78E-07	2.51E-08	1.19E-07		0.43	Control 1 Only
C9J6P4	C9J6P4_HUMAN Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=2 SV=1	8.20	1.00	2.00		3.00	1.00E-08	1.38E-08		1.76E-08	Control 1 Only	1.75
G8JLG2	G8JLG2_HUMAN Corneodesmosin OS=Homo sapiens GN=CDSN PE=2 SV=1	6.80	4.00		2.00		2.64E-08		1.23E-08		0.47	Control 1 Only
K7EJC1	K7EJC1_HUMAN 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=2 SV=1	9.30	1.00	1.00	2.00	2.00	8.95E-08	9.15E-08	1.18E-07	1.20E-07	1.31	1.34
K7EKI0	K7EKI0_HUMAN Envoplakin OS=Homo sapiens GN=EVPL PE=2 SV=1	4.00	2.00	3.00	1.00		1.38E-09	3.02E-09	8.98E-10		0.65	Control 1 Only
K7EKI8	K7EKI8_HUMAN Periplakin OS=Homo sapiens GN=PPL PE=2 SV=1	5.00		4.00	2.00			4.98E-09	1.77E-09		Sample 1 Only	
P60228	EIF3E_HUMAN Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	6.70	0.99	3.96	0.99		1.93E-08	6.44E-08	1.16E-08		0.60	Control 1 Only

P50402	EMD_HUMAN Emerin OS=Homo sapiens GN=EMD PE=1 SV=1	10.00	1.00	3.00		2.00	6.22E-08	2.01E-07		6.26E-08	Control 1 Only	1.01
Q9NPD3	EXOS4_HUMAN Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3	12.20	1.00	2.00		3.00	7.60E-08	8.99E-08		1.25E-07	Control 1 Only	1.64
H7C5E4	H7C5E4_HUMAN 5'-3' exoribonuclease 1 (Fragment) OS=Homo sapiens GN=XRN1 PE=4 SV=1	2.60	2.00	4.00			2.73E-09	1.12E-08			Control 1 Only	Control 1 Only
H0Y612	H0Y612_HUMAN E3 ubiquitin-protein ligase TRIM33 (Fragment) OS=Homo sapiens GN=TRIM33 PE=4 SV=1	4.10	1.00	4.00		1.00	1.41E-09	1.64E-08		2.22E-09	Control 1 Only	1.58
Q9UBV2	SE1L1_HUMAN Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3	2.40	1.00	2.00	2.00	1.00	8.55E-10	1.41E-09	9.86E-10	5.39E-10	1.15	0.63
Q8TEQ6	GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	4.90	1.00	4.00	1.00		1.26E-09	9.10E-09	1.12E-09		0.88	Control 1 Only
Q96CS3	FAF2_HUMAN FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2	9.40	2.00	2.00		2.00	2.06E-08	2.50E-08		1.89E-08	Control 1 Only	0.92
Q9P206	K1522_HUMAN Uncharacterized protein KIAA1522 OS=Homo sapiens GN=KIAA1522 PE=1 SV=2	7.00	1.00	1.00		3.00	3.33E-09	5.62E-09		1.18E-08	Control 1 Only	3.55
J3KNQ3	J3KNQ3_HUMAN 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=2 SV=1	14.00	1.00	3.00	1.00	1.00	2.95E-08	1.20E-07	1.30E-08	1.82E-08	0.44	0.61
J3QQY2	J3QQY2_HUMAN Transmembrane and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=TMCO1 PE=2 SV=1	22.10	1.00	1.00	1.00	3.00	1.98E-07	7.21E-08	1.45E-07	3.75E-07	0.73	1.90
Q06330	SUH_HUMAN Recombining binding protein suppressor of hairless OS=Homo sapiens GN=RBPJ PE=1 SV=3	7.50	0.99	2.97	0.99	0.99	1.42E-08	3.49E-08	5.41E-09	7.63E-09	0.38	0.54
B3KSP0	B3KSP0_HUMAN Negative elongation factor A OS=Homo sapiens GN=WHSC2 PE=2 SV=1	17.30	1.98	0.99		2.97	2.56E-08	7.28E-09		3.88E-08	Control 1 Only	1.52
B4DFA2	B4DFA2_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1	9.00		2.00	3.00	1.00		2.21E-08	2.38E-08	2.57E-09	Sample 1 Only	Sample 2 Only
B4DGD5	B4DGD5_HUMAN DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=2 SV=1	7.70	2.00	1.00		1.00	1.19E-08	1.33E-08		9.10E-09	Control 1 Only	0.76
B4DRF4	B4DRF4_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=2 SV=1	12.10	1.00	4.00		1.00	1.82E-08	1.21E-07		5.88E-08	Control 1 Only	3.23
B4DTG6	B4DTG6_HUMAN Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A PE=2 SV=1	8.10	2.00	1.99		2.00	2.45E-08	7.60E-09		1.08E-08	Control 1 Only	0.44
B4E3P0	B4E3P0_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=2 SV=1	3.50	3.00	1.00	1.00	1.00	1.86E-08	6.21E-09	4.45E-09	2.11E-09	0.24	0.11
Q13813	SPTN1_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	81.10	3.00	3.00			9.31E-09	1.45E-08			Control 1 Only	Control 1 Only
D6RBN5	D6RBN5_HUMAN OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=2 SV=1	12.30	2.00	1.00	1.00	2.00	1.02E-07	4.86E-08	1.73E-08	4.33E-08	0.17	0.43
E7ESK6	E7ESK6_HUMAN Syndecan OS=Homo sapiens GN=SDC2 PE=2 SV=1	19.40		4.00	2.00			6.22E-08	2.23E-08		Sample 1 Only	
E9PF19	E9PF19_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=2 SV=1	13.40				5.98				9.55E-08		Sample 2 Only
O94880	PHF14_HUMAN PHD finger protein 14 OS=Homo sapiens GN=PHF14 PE=1 SV=2	6.90		6.00				4.28E-08				
O95721	SNP29_HUMAN Synaptosomal-associated protein 29 OS=Homo sapiens GN=SNAP29 PE=1 SV=1	16.70	2.00	1.00	3.00		2.70E-08	2.73E-08	7.35E-08		2.72	Control 1 Only
Q15424	SAFB1_HUMAN Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4	10.50	0.99	1.98		2.97	2.56E-09	6.77E-09		1.47E-08	Control 1 Only	5.74
C9J6W2	C9J6W2_HUMAN Kinesin-like protein KIF20B OS=Homo sapiens GN=KIF20B PE=2 SV=1	7.40		6.00				1.13E-08				
F8W7U3	F8W7U3_HUMAN WASH complex subunit FAM21A OS=Homo sapiens GN=FAM21A PE=2 SV=1	3.70	3.96	1.98			4.44E-09	1.98E-09			Control 1 Only	Control 1 Only
P05386	RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	66.70	1.00	2.00	1.00	2.00	3.19E-07	4.10E-07	1.96E-07	6.76E-07	0.61	2.12
J3QRU1	J3QRU1_HUMAN Tyrosine-protein kinase Yes OS=Homo sapiens GN=YES1 PE=2 SV=1	7.70		2.97	0.99	1.98		5.27E-08	8.46E-09	1.95E-08	Sample 1 Only	Sample 2 Only

Q92466	DDB2_HUMAN DNA damage-binding protein 2 OS=Homo sapiens GN=DDB2 PE=1 SV=1	10.10	3.97				1.58E-07				Control 1 Only	Control 1 Only
Q96HJ9-2	CG055_HUMAN Isoform 2 of UPF0562 protein C7orf55 OS=Homo sapiens GN=C7orf55	14.40		5.52				4.30E-08				
Q96S52	PIGS_HUMAN GPI transamidase component PIG-S OS=Homo sapiens GN=PIGS PE=1 SV=3	7.60	3.00	1.00	1.00	1.00	2.85E-08	1.00E-08	5.08E-09	3.04E-09	0.18	0.11
P54727	RD23B_HUMAN UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1	16.40	2.97	0.99		1.98	6.81E-08	1.54E-08		2.89E-08	Control 1 Only	0.42
P62136	PP1A_HUMAN Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	43.60	0.98	2.97		1.99	5.99E-08	1.87E-07		4.82E-08	Control 1 Only	0.81
B4DDM2	B4DDM2_HUMAN Adenosine 3'-phospho 5'-phosphosulfate transporter 1 OS=Homo sapiens GN=SLC35B2 PE=2 SV=1	7.70	2.00	1.00		2.00	5.39E-08	3.14E-08		2.96E-08	Control 1 Only	0.55
F8VXG7	F8VXG7_HUMAN Protein SCAF11 OS=Homo sapiens GN=SCAF11 PE=2 SV=1	3.10		3.00		2.00		7.23E-09		4.29E-09		Sample 2 Only
Q9Y6X8	ZHX2_HUMAN Zinc fingers and homeoboxes protein 2 OS=Homo sapiens GN=ZHX2 PE=1 SV=1	5.10	2.00	2.00	1.00		1.24E-08	1.13E-08	2.06E-09		0.17	Control 1 Only
D6RB59	D6RB59_HUMAN Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=2 SV=1	7.60	1.00	3.00	1.00		2.13E-08	4.69E-08	6.58E-09		0.31	Control 1 Only
O75146	HIP1R_HUMAN Huntingtin-interacting protein 1-related protein OS=Homo sapiens GN=HIP1R PE=1 SV=2	6.10	1.00	3.00	1.00		3.14E-09	7.85E-09	2.51E-09		0.80	Control 1 Only
P31944	CASPE_HUMAN Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	14.50	4.00		1.00		5.90E-08		1.07E-08		0.18	Control 1 Only
B4DSB0	B4DSB0_HUMAN Poly(A)-specific ribonuclease PARN OS=Homo sapiens GN=PARN PE=2 SV=1	10.60		1.00	2.00	2.00		9.33E-09	1.69E-08	1.16E-08	Sample 1 Only	Sample 2 Only
P68371	TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	29.40	1.00	1.99	0.99	1.00	1.99E-08	2.73E-08	5.35E-09	1.51E-08	0.27	0.76
E7ESA6	E7ESA6_HUMAN Focal adhesion kinase 1 OS=Homo sapiens GN=PTK2 PE=2 SV=1	3.40	0.99	1.98	0.99		3.65E-09	1.02E-08	6.48E-10		0.18	Control 1 Only
P52756	RBM5_HUMAN RNA-binding protein 5 OS=Homo sapiens GN=RBM5 PE=1 SV=2	9.00		5.00				4.45E-08				
Q12996	CSTF3_HUMAN Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1	3.50	2.00	2.00		1.00	2.82E-08	3.25E-08		1.08E-08	Control 1 Only	0.38
Q8WUA2	PPIL4_HUMAN Peptidyl-prolyl cis-trans isomerase-like 4 OS=Homo sapiens GN=PPIL4 PE=1 SV=1	7.50	1.00	1.00	2.00	1.00	1.63E-08	1.66E-08	1.29E-08	6.85E-09	0.79	0.42
H7BXF3	H7BXF3_HUMAN Transformer-2 protein homolog beta (Fragment) OS=Homo sapiens GN=TRA2B PE=4 SV=1	26.00		3.00		2.00		1.82E-07		1.18E-07		Sample 2 Only
Q9UQR1	ZN148_HUMAN Zinc finger protein 148 OS=Homo sapiens GN=ZNF148 PE=1 SV=2	9.10		5.00				2.28E-08				
A6NHU9	A6NHU9_HUMAN SH3 and multiple ankyrin repeat domains protein 2 OS=Homo sapiens GN=SHANK2 PE=2 SV=3	2.90		3.96		0.99		4.68E-09		6.55E-10		Sample 2 Only
Q01081	U2AF1_HUMAN Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3	14.60		1.00	1.00	3.00		7.02E-08	2.80E-08	2.21E-07	Sample 1 Only	Sample 2 Only
O00232	PSD12_HUMAN 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	9.60		4.00		1.00		1.08E-07		1.32E-08		Sample 2 Only
Q0VDF9	HSP7E_HUMAN Heat shock 70 kDa protein 14 OS=Homo sapiens GN=HSPA14 PE=1 SV=1	4.90		3.00	1.00	1.00		4.10E-08	7.87E-09	6.45E-09	Sample 1 Only	Sample 2 Only
B4DG92	B4DG92_HUMAN Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=2 SV=1	3.70	1.99	0.99	0.99	0.99	1.65E-08	6.72E-09	4.51E-09	6.57E-09	0.27	0.40
Q13425	SNTB2_HUMAN Beta-2-syntrophin OS=Homo sapiens GN=SNTB2 PE=1 SV=1	10.60	1.98	3.00			2.25E-08	6.37E-08			Control 1 Only	Control 1 Only
B4DQT1	B4DQT1_HUMAN Macrophage erythroblast attacher OS=Homo sapiens GN=MAEA PE=2 SV=1	10.90	0.99	3.97			1.08E-08	9.88E-08			Control 1 Only	Control 1 Only
Q01082-3	SPTB2_HUMAN Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1	64.60	1.00	4.00			1.07E-09	9.32E-09			Control 1 Only	Control 1 Only
B4E1K0	B4E1K0_HUMAN Kinesin-like protein KIF23 OS=Homo sapiens GN=KIF23 PE=2 SV=1	4.80	2.00	2.00		1.00	2.36E-08	1.66E-08		8.88E-09	Control 1 Only	0.38

E7ER77	E7ER77_HUMAN Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=2 SV=1	6.50			3.00	2.00			1.50E-08	1.62E-08	Sample 1 Only	Sample 2 Only
O43809	CPSF5_HUMAN Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens GN=NUDT21 PE=1 SV=1	13.20	1.00	2.00		2.00	5.38E-08	1.98E-07		9.69E-08	Control 1 Only	1.80
E9PJ16	E9PJ16_HUMAN Coiled-coil domain-containing protein 84 OS=Homo sapiens GN=CCDC84 PE=2 SV=1	10.80	2.00	1.00	2.00		1.89E-07	1.86E-08	9.18E-08		0.49	Control 1 Only
P04259	K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	53.50	2.00	1.00	2.00		2.05E-08	1.21E-08	3.07E-08		1.50	Control 1 Only
P16401	H15_HUMAN Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	25.20		1.00		4.00		1.75E-08		6.41E-08		Sample 2 Only
P11137	MTAP2_HUMAN Microtubule-associated protein 2 OS=Homo sapiens GN=MAP2 PE=1 SV=4	1.30	3.00	1.00		1.00	1.23E-08	2.65E-09		1.05E-09	Control 1 Only	0.09
Q96L92	SNX27_HUMAN Sorting nexin-27 OS=Homo sapiens GN=SNX27 PE=1 SV=2	5.90	1.00	3.00		1.00	9.37E-09	4.57E-08		1.01E-08	Control 1 Only	1.08
P23258	TBG1_HUMAN Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	6.70	0.99	1.99	1.98		3.23E-08	3.53E-08	2.82E-08		0.87	Control 1 Only
P33993	MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	5.60	1.99	2.99			1.23E-08	1.72E-08			Control 1 Only	Control 1 Only
Q9H444	CHM4B_HUMAN Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1	14.30			2.00	3.00			3.38E-08	1.24E-07	Sample 1 Only	Sample 2 Only
P35251	RFC1_HUMAN Replication factor C subunit 1 OS=Homo sapiens GN=RFC1 PE=1 SV=4	5.20		4.00		1.00		2.41E-08		1.83E-09		Sample 2 Only
Q9NRN5	OLFL3_HUMAN Olfactomedin-like protein 3 OS=Homo sapiens GN=OLFML3 PE=2 SV=1	12.10				5.00				9.00E-08		Sample 2 Only
Q9P0L0	VAPA_HUMAN Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3	11.20		2.00	1.00	2.00		8.09E-08	4.00E-08	5.53E-08	Sample 1 Only	Sample 2 Only
Q9UHB6	LIMA1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	67.60	1.96	1.96		0.98	2.79E-08	1.94E-08		8.92E-09	Control 1 Only	0.32
P41091	IF2G_HUMAN Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	11.40	2.99	1.98			4.75E-08	2.54E-08			Control 1 Only	Control 1 Only
P56192	SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	5.10		0.99	0.99	2.98		3.36E-09	1.29E-09	8.94E-09	Sample 1 Only	Sample 2 Only
P61026	RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	14.50		0.98	1.96	1.97		6.52E-08	1.05E-07	1.32E-07	Sample 1 Only	Sample 2 Only
P62140	PP1B_HUMAN Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	32.10	1.99	1.99		0.99	8.98E-08	9.27E-08		2.17E-08	Control 1 Only	0.24
P62316	SMD2_HUMAN Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1	18.50	1.00	2.00		2.00	6.08E-08	2.34E-07		1.09E-07	Control 1 Only	1.79
B4DYD8	B4DYD8_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	12.70	1.00	3.00			2.66E-09	3.96E-08			Control 1 Only	Control 1 Only
Q9Y597	KCTD3_HUMAN BTB/POZ domain-containing protein KCTD3 OS=Homo sapiens GN=KCTD3 PE=1 SV=2	8.00	2.00	2.00			1.13E-08	1.29E-08			Control 1 Only	Control 1 Only
Q5JZB7	Q5JZB7_HUMAN Spindlin-2B OS=Homo sapiens GN=SPIN2B PE=2 SV=1	17.80	3.00	1.00			9.32E-08	6.37E-09			Control 1 Only	Control 1 Only
E9PKH2	E9PKH2_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=2 SV=1	12.90	1.00	1.00	2.00		6.08E-08	6.63E-08	8.82E-08		1.45	Control 1 Only
F5GYL3	F5GYL3_HUMAN ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=2 SV=1	4.30		2.00		2.00		1.72E-08		1.54E-08		Sample 2 Only
J3QQW9	J3QQW9_HUMAN Polycomb protein SUZ12 OS=Homo sapiens GN=SUZ12 PE=2 SV=1	7.00	1.00	3.00			7.98E-09	2.45E-08			Control 1 Only	Control 1 Only
Q6KC79	NIPBL_HUMAN Nipped-B-like protein OS=Homo sapiens GN=NIPBL PE=1 SV=2	1.20	1.00	2.00		1.00	3.03E-10	2.05E-09		1.04E-09	Control 1 Only	3.42
O60244	MED14_HUMAN Mediator of RNA polymerase II transcription subunit 14 OS=Homo sapiens GN=MED14 PE=1 SV=2	3.80	1.00	3.00			3.75E-09	1.14E-08			Control 1 Only	Control 1 Only
P23771	GATA3_HUMAN Trans-acting T-cell-specific transcription factor GATA-3 OS=Homo sapiens GN=GATA3 PE=1 SV=1	5.20	1.00	2.00		1.00	2.15E-09	2.89E-08		2.78E-09	Control 1 Only	1.29

P12273	PIP_HUMAN Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	26.70	4.00				8.86 E-08				Control 1 Only	Control 1 Only
P26196	DDX6_HUMAN Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2	5.40		2.00		2.00		1.59 E-08		1.22 E-08		Sample 2 Only
Q9Y2L9	LRCH1_HUMAN Leucine-rich repeat and calponin homology domain-containing protein 1 OS=Homo sapiens GN=LRCH1 PE=1 SV=3	3.00	2.00	2.00			1.06 E-08	1.28 E-08			Control 1 Only	Control 1 Only
F8WF48	F8WF48_HUMAN Translocation protein SEC62 OS=Homo sapiens GN=SEC62 PE=2 SV=1	32.90	1.00			3.00	9.22 E-08			2.76 E-07	Control 1 Only	2.99
Q13131	AAPK1_HUMAN 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4	6.80	1.00	1.00	2.00		1.29 E-08	1.50 E-08	1.81 E-08		1.40	Control 1 Only
F5H853	F5H853_HUMAN Differentially-expressed in FDCP 6 homolog OS=Homo sapiens GN=DEF6 PE=2 SV=1	5.60	2.00	1.00	1.00		2.52 E-08	9.14 E-09	1.01 E-08		0.40	Control 1 Only
F8VS02	F8VS02_HUMAN Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=2 SV=1	17.70	2.00		2.00		1.59 E-08		1.11 E-08		0.70	Control 1 Only
J3QSH4	J3QSH4_HUMAN Vascular endothelial zinc finger 1 OS=Homo sapiens GN=VEZF1 PE=2 SV=1	3.70	0.99	1.98		0.99	2.10 E-08	4.25 E-08		2.16 E-08	Control 1 Only	1.03
Q08188	TGM3_HUMAN Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	6.80	3.00				8.07 E-09				Control 1 Only	Control 1 Only
Q5T750	XP32_HUMAN Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=1	8.40	2.00		2.00		8.01 E-08		3.17 E-08		0.40	Control 1 Only
H0Y2P8	H0Y2P8_HUMAN SLIT-ROBO Rho GTPase-activating protein 2 (Fragment) OS=Homo sapiens GN=SRGAP2 PE=4 SV=1	3.20	0.99	2.97			5.04 E-09	2.54 E-08			Control 1 Only	Control 1 Only
Q13112	CAF1B_HUMAN Chromatin assembly factor 1 subunit B OS=Homo sapiens GN=CHAF1B PE=1 SV=1	4.70	1.00	2.00		1.00	2.49 E-09	1.65 E-08		4.48 E-09	Control 1 Only	1.80
Q13347	EIF3I_HUMAN Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1	8.60		2.00	1.00	1.00		8.59 E-08	1.94 E-08	1.56 E-08	Sample 1 Only	Sample 2 Only
Q6P1J9	CDC73_HUMAN Parafibromin OS=Homo sapiens GN=CDC73 PE=1 SV=1	7.00		1.00		3.00		1.86 E-08		3.06 E-08		Sample 2 Only
Q6P1M0	S27A4_HUMAN Long-chain fatty acid transport protein 4 OS=Homo sapiens GN=SLC27A4 PE=1 SV=1	4.80	1.00	3.00			7.88 E-09	2.18 E-08			Control 1 Only	Control 1 Only
Q8NC51	PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	10.30		1.00		3.00		6.20 E-09		5.55 E-08		Sample 2 Only
O75475	PSIP1_HUMAN PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1	6.70	2.00	2.00			2.94 E-09	3.43 E-09			Control 1 Only	Control 1 Only
H7BXZ6	H7BXZ6_HUMAN Mitochondrial Rho GTPase OS=Homo sapiens GN=RHOT1 PE=2 SV=2	6.70	0.99	1.98		0.99	4.87 E-09	1.42 E-08		5.32 E-09	Control 1 Only	1.09
B4DJ96	B4DJ96_HUMAN Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=2 SV=1	14.60	0.99	2.99			1.07 E-08	2.85 E-08			Control 1 Only	Control 1 Only
Q13283	G3BP1_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	8.20		2.00		2.00		3.31 E-08		3.85 E-08		Sample 2 Only
B4DPJ8	B4DPJ8_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=2 SV=1	8.00	1.00	3.00			1.71 E-08	4.31 E-08			Control 1 Only	Control 1 Only
Q9P2D1	CHD7_HUMAN Chromodomain-helicase-DNA-binding protein 7 OS=Homo sapiens GN=CHD7 PE=1 SV=3	1.80		1.99		2.00		3.25 E-09		5.14 E-10		Sample 2 Only
C9JZI1	C9JZI1_HUMAN Replication factor C subunit 4 OS=Homo sapiens GN=RFC4 PE=2 SV=1	10.40	0.99	2.97			1.31 E-09	9.17 E-08			Control 1 Only	Control 1 Only
Q9BTT6	LRRC1_HUMAN Leucine-rich repeat-containing protein 1 OS=Homo sapiens GN=LRRC1 PE=1 SV=1	8.20	1.00	2.00	1.00		1.18 E-08	1.92 E-08	4.05 E-09		0.34	Control 1 Only
O15230	LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	1.00		2.00		2.00		1.77 E-09		5.69 E-10		Sample 2 Only
E7ERS3	E7ERS3_HUMAN Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=2 SV=1	6.20		4.00				5.99 E-09				
E7EW84	E7EW84_HUMAN Exocyst complex component 6 OS=Homo sapiens GN=EXOC6 PE=2 SV=1	5.60	0.99	2.97			9.41 E-09	2.97 E-08			Control 1 Only	Control 1 Only
Q15125	EBP_HUMAN 3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase OS=Homo sapiens GN=EBP PE=1 SV=3	16.50			3.00	1.00			1.34 E-07	4.20 E-08	Sample 1 Only	Sample 2 Only

F5H1Z7	F5H1Z7_HUMAN Semaphorin-3C OS=Homo sapiens GN=SEMA3C PE=2 SV=1	8.00				4.00				5.22E-08		Sample 2 Only
Q6KB66	K2C80_HUMAN Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	14.20	4.00				3.73E-08				Control 1 Only	Control 1 Only
F6S9Y6	F6S9Y6_HUMAN Actin-related protein 10 OS=Homo sapiens GN=ACTR10 PE=2 SV=1	15.90	0.99	2.00	1.00		5.78E-08	2.09E-07	7.66E-08		1.32	Control 1 Only
Q5BKZ1	ZN326_HUMAN DBIRD complex subunit ZNF326 OS=Homo sapiens GN=ZNF326 PE=1 SV=2	6.40	1.00	3.00			4.73E-09	2.19E-08			Control 1 Only	Control 1 Only
Q6P2Q9	PRP8_HUMAN Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	2.30		4.00				3.51E-09				
Q6ZXV5	TMTC3_HUMAN Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2	3.00	1.99	2.00			9.25E-09	1.41E-08			Control 1 Only	Control 1 Only
Q7L4I2	RSRC2_HUMAN Arginine/serine-rich coiled-coil protein 2 OS=Homo sapiens GN=RSRC2 PE=1 SV=1	8.50		4.00				2.94E-08				
Q7Z2T5	TRM1L_HUMAN TRMT1-like protein OS=Homo sapiens GN=TRMT1L PE=1 SV=2	6.00		2.00		2.00		1.27E-08		1.34E-08		Sample 2 Only
E7ENN3	E7ENN3_HUMAN Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=2 SV=1	0.80	2.00	1.00		1.00	4.12E-09	3.32E-09		4.18E-09	Control 1 Only	1.02
Q92747	ARC1A_HUMAN Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2	20.30	1.00	3.00			4.93E-08	1.46E-07			Control 1 Only	Control 1 Only
P22735	TGM1_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=1 SV=4	4.70	4.00				1.25E-08				Control 1 Only	Control 1 Only
Q9P2I0	CPSF2_HUMAN Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens GN=CPSF2 PE=1 SV=2	4.70	1.00	3.00			5.63E-09	1.61E-08			Control 1 Only	Control 1 Only
P45973	CBX5_HUMAN Chromobox protein homolog 5 OS=Homo sapiens GN=CBX5 PE=1 SV=1	12.00	2.00	1.00		1.00	5.17E-08	9.25E-09		1.25E-08	Control 1 Only	0.24
B3KR64	B3KR64_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=2 SV=1	17.50		1.00	2.00	1.00		7.04E-09	1.18E-08	2.47E-09	Sample 1 Only	Sample 2 Only
P49792	RBP2_HUMAN E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2	2.70		4.00				1.60E-09				
Q6S8J3	POTEE_HUMAN POTE ankyrin domain family member E OS=Homo sapiens GN=POTEE PE=1 SV=3	11.10	1.98	0.99		0.99	4.56E-08	1.74E-08		5.90E-09	Control 1 Only	0.13
E7EQI7	E7EQI7_HUMAN WASH complex subunit strumpellin OS=Homo sapiens GN=KIAA0196 PE=2 SV=1	4.60	1.00	2.00			2.30E-09	7.34E-09			Control 1 Only	Control 1 Only
E9PK59	E9PK59_HUMAN N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1 PE=2 SV=1	14.90		1.00	2.00			5.79E-09	7.67E-09		Sample 1 Only	
E9PMA0	E9PMA0_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=2 SV=1	9.60	1.00	1.00	1.00		2.34E-08	2.59E-08	1.05E-08		0.45	Control 1 Only
H0YME5	H0YME5_HUMAN Eukaryotic translation initiation factor 2-alpha kinase 4 (Fragment) OS=Homo sapiens GN=EIF2AK4 PE=4 SV=1	4.50	1.00	2.00			1.58E-09	3.23E-09			Control 1 Only	Control 1 Only
H7C5P4	H7C5P4_HUMAN Replication factor C subunit 2 (Fragment) OS=Homo sapiens GN=RFC2 PE=4 SV=1	9.10	1.00	1.00		1.00	2.30E-08	1.06E-07		4.19E-08	Control 1 Only	1.82
Q9H270	VPS11_HUMAN Vacuolar protein sorting-associated protein 11 homolog OS=Homo sapiens GN=VPS11 PE=1 SV=1	3.40		2.00	1.00			1.78E-08	6.76E-09		Sample 1 Only	
Q9Y2T7	YBOX2_HUMAN Y-box-binding protein 2 OS=Homo sapiens GN=YBX2 PE=1 SV=2	16.50		1.00		1.00		1.41E-08		5.64E-09		Sample 2 Only
P05109	S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	39.80	3.00				2.32E-07				Control 1 Only	Control 1 Only
K7EP90	K7EP90_HUMAN RNA-binding protein 42 OS=Homo sapiens GN=RBM42 PE=2 SV=1	5.20		2.00		1.00		2.00E-08		8.08E-09		Sample 2 Only
M0QXB4	M0QXB4_HUMAN Coatomer protein complex, subunit epsilon, isoform CRA_g OS=Homo sapiens GN=COPE PE=2 SV=1	22.60	1.00	2.00			5.40E-08	1.11E-07			Control 1 Only	Control 1 Only
O75935	DCTN3_HUMAN Dynactin subunit 3 OS=Homo sapiens GN=DCTN3 PE=1 SV=1	12.00	1.99		0.99		1.31E-07		3.17E-08		0.24	Control 1 Only
K7EIE8	K7EIE8_HUMAN Methyl-CpG binding domain protein 3, isoform CRA_b OS=Homo sapiens GN=MBD3 PE=2 SV=1	7.70	2.00	1.00			4.74E-08	5.75E-09			Control 1 Only	Control 1 Only

E7ETU6	E7ETU6_HUMAN Stromal membrane-associated protein 1 OS=Homo sapiens GN=SMAP1 PE=2 SV=1	13.90			2.00	1.00			6.35E-08	4.05E-08	Sample 1 Only	Sample 2 Only
O95486	SC24A_HUMAN Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2	2.70	2.00		1.00		9.80E-09		2.35E-09		0.24	Control 1 Only
Q92615	LAR4B_HUMAN La-related protein 4B OS=Homo sapiens GN=LARP4B PE=1 SV=3	2.30	1.00			2.00	9.94E-09			2.22E-08	Control 1 Only	2.23
B7Z888	B7Z888_HUMAN Protein SCAF8 OS=Homo sapiens GN=SCAF8 PE=2 SV=1	1.80		1.98		1.00		3.66E-09		5.55E-10		Sample 2 Only
Q2M389	WASH7_HUMAN WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 PE=1 SV=2	1.60		3.00				9.04E-09				
P68431	H31_HUMAN Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	55.90		1.50		0.50		7.72E-07		2.59E-09		Sample 2 Only
E7ESW5	E7ESW5_HUMAN Rho GTPase-activating protein 21 (Fragment) OS=Homo sapiens GN=ARHGAP21 PE=2 SV=1	1.90	2.00	1.00			9.58E-09	3.96E-09			Control 1 Only	Control 1 Only
F8VSE7	F8VSE7_HUMAN Transcription factor E2F7 (Fragment) OS=Homo sapiens GN=E2F7 PE=2 SV=1	5.90		2.98				2.10E-08				
Q8WUH2	TGFA1_HUMAN Transforming growth factor-beta receptor-associated protein 1 OS=Homo sapiens GN=TGFBRAP1 PE=1 SV=1	2.60		1.00	2.00			8.16E-10	4.94E-09		Sample 1 Only	
Q5W0B1	RN219_HUMAN RING finger protein 219 OS=Homo sapiens GN=RNF219 PE=1 SV=1	2.50	1.00	2.00			8.19E-10	2.37E-08			Control 1 Only	Control 1 Only
Q13464	ROCK1_HUMAN Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	2.60		2.00	1.00			3.48E-09	1.19E-09		Sample 1 Only	
A9Z1X7	A9Z1X7_HUMAN Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=2 SV=1	5.00	1.00	2.00			1.93E-09	1.99E-09			Control 1 Only	Control 1 Only
Q8IVT2	MISP_HUMAN Mitotic interactor and substrate of PLK1 OS=Homo sapiens GN=MISP PE=1 SV=1	3.50		2.00		1.00		1.45E-08		4.85E-09		Sample 2 Only
Q9P2N5	RBM27_HUMAN RNA-binding protein 27 OS=Homo sapiens GN=RBM27 PE=1 SV=2	2.10	1.00	1.00	1.00		1.20E-08	3.44E-09	2.89E-09		0.24	Control 1 Only
K7ELG9	K7ELG9_HUMAN Protein LSM12 homolog OS=Homo sapiens GN=LSM12 PE=2 SV=1	11.30	1.00	1.00		1.00	5.53E-08	5.26E-08		3.32E-08	Control 1 Only	0.60
Q15291	RBBP5_HUMAN Retinoblastoma-binding protein 5 OS=Homo sapiens GN=RBBP5 PE=1 SV=2	4.60	1.00	2.00			5.57E-09	1.08E-08			Control 1 Only	Control 1 Only
H0Y818	H0Y818_HUMAN DNA mismatch repair protein Mlh1 (Fragment) OS=Homo sapiens GN=MLH1 PE=4 SV=1	6.50		2.99				2.12E-08				
A6NEM2	A6NEM2_HUMAN HCF N-terminal chain 5 OS=Homo sapiens GN=HCFC1 PE=2 SV=2	5.40		1.00		1.00		1.90E-09		1.39E-09		Sample 2 Only
Q8WXA9	SREK1_HUMAN Splicing regulatory glutamine/lysine-rich protein 1 OS=Homo sapiens GN=SREK1 PE=1 SV=1	5.90		2.00		1.00		1.21E-08		5.14E-09		Sample 2 Only
Q96JC1	VPS39_HUMAN Vam6/Vps39-like protein OS=Homo sapiens GN=VPS39 PE=1 SV=2	3.90		3.00				1.51E-08				
B4E2Q4	B4E2Q4_HUMAN Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=2 SV=1	4.10		2.00		1.00		1.83E-08		3.51E-09		Sample 2 Only
Q9ULC4	MCTS1_HUMAN Malignant T-cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1	24.30		0.99	0.99	1.00		1.61E-08	5.34E-08	2.41E-08	Sample 1 Only	Sample 2 Only
Q9H9B1	EHMT1_HUMAN Histone-lysine N-methyltransferase EHMT1 OS=Homo sapiens GN=EHMT1 PE=1 SV=4	1.80	0.99	1.00		0.99	2.21E-09	4.49E-09		2.20E-09	Control 1 Only	1.00
Q00839-2	HNRPU_HUMAN Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU	33.10	1.00	1.00		1.00	7.32E-10	2.74E-10		1.13E-10	Control 1 Only	0.15
P08651	NFIC_HUMAN Nuclear factor 1 C-type OS=Homo sapiens GN=NFIC PE=1 SV=2	17.70	1.00	1.00		1.00	1.07E-08	1.69E-08		1.55E-08	Control 1 Only	1.45
B4DDD6	B4DDD6_HUMAN Drebrin-like protein OS=Homo sapiens GN=DBNL PE=2 SV=1	9.20		1.98		1.00		2.31E-08		7.25E-09		Sample 2 Only
Q13243	SRSF5_HUMAN Serine/arginine-rich splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=1 SV=1	8.60		1.00	1.00	1.00		9.99E-08	3.11E-08	6.69E-08	Sample 1 Only	Sample 2 Only
Q13813-2	SPTN1_HUMAN Isoform 2 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1	80.90	1.00	2.00			9.84E-10	3.64E-09			Control 1 Only	Control 1 Only

B7Z6Z4	B7Z6Z4_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	16.90		1.98		0.99		2.01E-07		5.56E-08		Sample 2 Only
C9JNK6	C9JNK6_HUMAN Metaxin-2 OS=Homo sapiens GN=MTX2 PE=2 SV=1	14.50		1.99		0.99		1.70E-07		2.76E-08		Sample 2 Only
E5RJN7	E5RJN7_HUMAN Double-stranded RNA-binding protein Staufen homolog 2 (Fragment) OS=Homo sapiens GN=STAU2 PE=2 SV=1	11.90				2.97				3.85E-08		Sample 2 Only
Q14980	NUMA1_HUMAN Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2	70.40	0.99	1.98			2.63E-09	5.17E-09			Control 1 Only	Control 1 Only
E9PBB4	E9PBB4_HUMAN R3H domain-containing protein 1 OS=Homo sapiens GN=R3HDM1 PE=2 SV=1	12.90	1.00	2.00			7.33E-09	8.63E-09			Control 1 Only	Control 1 Only
O75381	PEX14_HUMAN Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14 PE=1 SV=1	9.90				2.97				3.23E-08		Sample 2 Only
F8W881	F8W881_HUMAN Constitutive coactivator of PPAR-gamma-like protein 2 OS=Homo sapiens GN=FAM120C PE=2 SV=1	3.70	1.00	2.00			4.64E-09	1.17E-08			Control 1 Only	Control 1 Only
Q8IUE6	H2A2B_HUMAN Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3	69.20		3.00				5.90E-07				
Q93077	H2A1C_HUMAN Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3	65.40	0.99	1.98			1.20E-07	3.56E-07			Control 1 Only	Control 1 Only
Q5T1M5	FKB15_HUMAN FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2	2.30	1.00	1.00			1.33E-09	2.27E-09			Control 1 Only	Control 1 Only
Q5VTL8	PR38B_HUMAN Pre-mRNA-splicing factor 38B OS=Homo sapiens GN=PRPF38B PE=1 SV=1	4.20	1.00	2.00			1.38E-09	6.82E-09			Control 1 Only	Control 1 Only
Q6IN85	P4R3A_HUMAN Serine/threonine-protein phosphatase 4 regulatory subunit 3A OS=Homo sapiens GN=SMEK1 PE=1 SV=1	3.90		2.00	1.00			1.17E-08	3.59E-09		Sample 1 Only	
E7EW20	E7EW20_HUMAN Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=2 SV=1	40.90		2.00		1.00		1.40E-08		1.08E-09		Sample 2 Only
K7EJ81	K7EJ81_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=2 SV=1	3.40		2.00		1.00		4.54E-09		2.45E-10		Sample 2 Only
Q5STZ8	Q5STZ8_HUMAN ATP-binding cassette sub-family F member 1 (Fragment) OS=Homo sapiens GN=ABCF1 PE=2 SV=2	72.90	2.00	1.00			5.41E-09	2.86E-09			Control 1 Only	Control 1 Only
P18827	SDC1_HUMAN Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3	11.90	1.00	2.00			5.96E-09	4.34E-08			Control 1 Only	Control 1 Only
P22392	NDKB_HUMAN Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	20.40		0.99		1.98		8.57E-08		1.39E-07		Sample 2 Only
P22531	SPR2E_HUMAN Small proline-rich protein 2E OS=Homo sapiens GN=SPRR2E PE=2 SV=2	43.10	2.98				1.75E-07				Control 1 Only	Control 1 Only
Q99569	PKP4_HUMAN Plakophilin-4 OS=Homo sapiens GN=PKP4 PE=1 SV=2	2.30	0.98	2.00			5.00E-09	6.27E-09			Control 1 Only	Control 1 Only
Q9BTC0	DIDO1_HUMAN Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5	1.90	0.99	1.00		1.00	2.58E-09	8.44E-10		5.62E-10	Control 1 Only	0.22
Q9H1A4	APC1_HUMAN Anaphase-promoting complex subunit 1 OS=Homo sapiens GN=ANAPC1 PE=1 SV=1	1.70		3.00				2.56E-09				
Q9NU22	MDN1_HUMAN Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2	0.80		3.00				8.53E-10				
Q9UBX3	DIC_HUMAN Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2	10.10			2.99				1.24E-07		Sample 1 Only	
Q9UKF6	CPSF3_HUMAN Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1	4.20	1.00	2.00			3.11E-09	1.29E-08			Control 1 Only	Control 1 Only
Q9UPQ9	TNR6B_HUMAN Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	53.70			2.97				1.39E-08		Sample 1 Only	
P62873	GBB1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3	8.80		1.97		0.98		8.50E-08		3.27E-08		Sample 2 Only
P63220	RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	23.50				3.00				4.39E-07		Sample 2 Only
B4DJ81	B4DJ81_HUMAN NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=2 SV=1	6.50	2.00				2.78E-08				Control 1 Only	Control 1 Only

C9JTV4	C9JTV4_HUMAN EF-hand domain-containing protein D1 (Fragment) OS=Homo sapiens GN=EFHD1 PE=2 SV=1	24.70		1.00		1.00		1.51E-07		7.00E-08		Sample 2 Only
Q5JUX0	SPIN3_HUMAN Spindlin-3 OS=Homo sapiens GN=SPIN3 PE=1 SV=1	9.70	0.99	0.99			3.83E-09	3.69E-09			Control 1 Only	Control 1 Only
J3KTL7	J3KTL7_HUMAN Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=2 SV=1	3.20		2.00				1.92E-08				
H3BLU6	H3BLU6_HUMAN E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=2 SV=1	1.30		2.00				9.27E-10				
H7C5S6	H7C5S6_HUMAN Leucine-rich repeat and WD repeat-containing protein 1 (Fragment) OS=Homo sapiens GN=LRWD1 PE=4 SV=1	12.80		1.00		1.00		2.08E-08		1.73E-08		Sample 2 Only
O95793	STAU1_HUMAN Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2	11.10				2.00				1.68E-08		Sample 2 Only
J3KN16	J3KN16_HUMAN Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=KIAA0368 PE=2 SV=1	2.00		2.00				2.17E-09				
O75530	EED_HUMAN Polycomb protein EED OS=Homo sapiens GN=EED PE=1 SV=2	5.80		1.99				2.17E-08				
P28702	RXRB_HUMAN Retinoic acid receptor RXR-beta OS=Homo sapiens GN=RXRB PE=1 SV=2	5.60	1.98				2.03E-08				Control 1 Only	Control 1 Only
Q5JW54	Q5JW54_HUMAN Kinetochore-associated protein DSN1 homolog OS=Homo sapiens GN=DSN1 PE=2 SV=1	11.60	1.99				8.83E-08				Control 1 Only	Control 1 Only
F2Z2B9	F2Z2B9_HUMAN Gamma-tubulin complex component 2 OS=Homo sapiens GN=TUBGCP2 PE=2 SV=1	3.20	1.00	1.00			1.15E-08	2.29E-09			Control 1 Only	Control 1 Only
O75362	ZN217_HUMAN Zinc finger protein 217 OS=Homo sapiens GN=ZNF217 PE=1 SV=1	2.70		1.00		1.00		7.44E-09		7.68E-10		Sample 2 Only
P07437	TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	32.00		1.00		1.00		1.12E-08		8.98E-09		Sample 2 Only
Q8IWZ8	SUGP1_HUMAN SURP and G-patch domain-containing protein 1 OS=Homo sapiens GN=SUGP1 PE=1 SV=2	3.60		1.99				1.71E-08				
Q68E01	INT3_HUMAN Integrator complex subunit 3 OS=Homo sapiens GN=INTS3 PE=1 SV=1	3.60	2.00				6.57E-09				Control 1 Only	Control 1 Only
Q96L91	EP400_HUMAN E1A-binding protein p400 OS=Homo sapiens GN=EP400 PE=1 SV=4	0.90		1.99				6.44E-10				
Q71DI3	H32_HUMAN Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	55.90		1.00		1.00		2.81E-07		5.96E-07		Sample 2 Only
P55081	MFAP1_HUMAN Microfibrillar-associated protein 1 OS=Homo sapiens GN=MFAP1 PE=1 SV=2	5.20		2.00				3.41E-08				
P82912	RT11_HUMAN 28S ribosomal protein S11, mitochondrial OS=Homo sapiens GN=MRPS11 PE=1 SV=2	18.60	1.00			1.00	6.52E-09			2.20E-08	Control 1 Only	3.37
Q6NUK1	SCMC1_HUMAN Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2	4.60	1.00	1.00			3.31E-08	3.03E-08			Control 1 Only	Control 1 Only
G5E933	G5E933_HUMAN Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=2 SV=1	2.00		1.99				1.36E-09				
P22528	SPR1B_HUMAN Cornifin-B OS=Homo sapiens GN=SPRR1B PE=1 SV=2	27.00	1.99				1.07E-07				Control 1 Only	Control 1 Only
Q8WWQ0	PHIP_HUMAN PH-interacting protein OS=Homo sapiens GN=PHIP PE=1 SV=2	1.30		2.00				3.61E-09				
Q5VY93	Q5VY93_HUMAN Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=2 SV=1	2.30		2.00				1.25E-08				
Q96TA2	YMEL1_HUMAN ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1 PE=1 SV=2	4.80		1.00	1.00			8.82E-09	2.61E-09		Sample 1 Only	
Q96KP1	EXOC2_HUMAN Exocyst complex component 2 OS=Homo sapiens GN=EXOC2 PE=1 SV=1	4.70		2.00				1.51E-08				
C9JJ19	C9JJ19_HUMAN 28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=2 SV=2	10.10				2.00				7.64E-08		Sample 2 Only
C9JJN9	C9JJN9_HUMAN Vacuolar protein sorting-associated protein 8 homolog OS=Homo sapiens GN=VPS8 PE=2 SV=1	1.50	1.00	1.00			1.31E-09	1.35E-09			Control 1 Only	Control 1 Only

B7Z5W8	B7Z5W8_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=2 SV=1	11.80		2.00				2.28E-08				
F8WAK8	F8WAK8_HUMAN Cohesin subunit SA-2 OS=Homo sapiens GN=STAG2 PE=2 SV=1	0.60	0.99	0.99			2.24E-09	1.10E-08			Control 1 Only	Control 1 Only
P49454	CENPF_HUMAN Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2	1.30		2.00				1.06E-09				
Q8NI35	INADL_HUMAN InaD-like protein OS=Homo sapiens GN=INADL PE=1 SV=3	1.30		1.00		0.99		8.29E-10		1.29E-09		Sample 2 Only
Q9UKN8	TF3C4_HUMAN General transcription factor 3C polypeptide 4 OS=Homo sapiens GN=GTF3C4 PE=1 SV=2	2.20		2.00				1.72E-08				
Q8WUB8	PHF10_HUMAN PHD finger protein 10 OS=Homo sapiens GN=PHF10 PE=1 SV=3	4.00		2.00				5.34E-08				
Q8IXI1	MIRO2_HUMAN Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2	4.90		1.00	0.99			9.26E-09	5.31E-09		Sample 1 Only	
Q8NC69	KCTD6_HUMAN BTB/POZ domain-containing protein KCTD6 OS=Homo sapiens GN=KCTD6 PE=2 SV=2	6.80	1.00	1.00			4.96E-08	3.49E-08			Control 1 Only	Control 1 Only
Q75MJ1	Q75MJ1_HUMAN ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=2 SV=1	3.40				1.00				3.63E-09		Sample 2 Only
Q9Y295	DRG1_HUMAN Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1	7.10		2.00				5.57E-08				
E9PKK4	E9PKK4_HUMAN Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=2 SV=1	2.60		2.00				4.25E-09				
O43823	AKAP8_HUMAN A-kinase anchor protein 8 OS=Homo sapiens GN=AKAP8 PE=1 SV=1	3.50	1.00	1.00			4.60E-09	5.49E-09			Control 1 Only	Control 1 Only
Q9P013	CWC15_HUMAN Spliceosome-associated protein CWC15 homolog OS=Homo sapiens GN=CWC15 PE=1 SV=2	9.60	1.00	1.00			1.60E-08	1.47E-08			Control 1 Only	Control 1 Only
F8W720	F8W720_HUMAN GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=2 SV=1	3.70		1.00	1.00			3.83E-09	3.03E-09		Sample 1 Only	
B7Z817	B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1	2.90			1.00	0.99			2.27E-08	4.76E-09	Sample 1 Only	Sample 2 Only
Q13123	RED_HUMAN Protein Red OS=Homo sapiens GN=IK PE=1 SV=3	4.30		1.99				1.65E-08				
B4DY13	B4DY13_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=2 SV=1	6.00				2.00				2.07E-08		Sample 2 Only
B5MCX3	B5MCX3_HUMAN Septin-2 OS=Homo sapiens GN=SEPT2 PE=2 SV=1	23.10	2.00				1.18E-07				Control 1 Only	Control 1 Only
O15231	ZN185_HUMAN Zinc finger protein 185 OS=Homo sapiens GN=ZNF185 PE=1 SV=3	71.70	0.98			0.98	6.87E-09			5.10E-09	Control 1 Only	0.74
O15231-3	ZN185_HUMAN Isoform 3 of Zinc finger protein 185 OS=Homo sapiens GN=ZNF185	71.90	0.98	0.98			9.74E-09	1.13E-08			Control 1 Only	Control 1 Only
D6RDU5	D6RDU5_HUMAN Septin-11 (Fragment) OS=Homo sapiens GN=SEPT11 PE=2 SV=1	5.10		0.99		0.99		2.19E-08		1.55E-08		Sample 2 Only
Q14766	LTBP1_HUMAN Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=1 SV=4	1.70		1.00	1.00			2.78E-09	9.83E-10		Sample 1 Only	
B4DDF4	B4DDF4_HUMAN Calponin-2 OS=Homo sapiens GN=CNN2 PE=2 SV=1	14.20	1.00			1.00	4.48E-08			1.43E-08	Control 1 Only	0.32
P09382	LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	16.30			1.00	1.00			7.25E-08	1.13E-07	Sample 1 Only	Sample 2 Only
Q6ZSJ8	CA122_HUMAN Uncharacterized protein C1orf122 OS=Homo sapiens GN=C1orf122 PE=2 SV=2	33.60	1.00	1.00			1.08E-07	8.45E-08			Control 1 Only	Control 1 Only
Q5JSZ5	PRC2B_HUMAN Protein PRRC2B OS=Homo sapiens GN=PRRC2B PE=1 SV=2	3.20		0.99		1.00		6.60E-10		3.57E-10		Sample 2 Only
Q96CW5	GCP3_HUMAN Gamma-tubulin complex component 3 OS=Homo sapiens GN=TUBGCP3 PE=1 SV=2	2.70	1.00	1.00			5.17E-09	5.43E-09			Control 1 Only	Control 1 Only
Q9NQT4	EXOS5_HUMAN Exosome complex component RRP46 OS=Homo sapiens GN=EXOSC5 PE=1 SV=1	9.40				2.00				6.45E-08		Sample 2 Only

F2Z2U8	F2Z2U8_HUMAN Myosin-14 OS=Homo sapiens GN=MYH14 PE=2 SV=1	6.60	0.99		0.99		3.42E-09		1.04E-09		0.31	Control 1 Only
Q5BKV1	Q5BKV1_HUMAN MYH9 protein OS=Homo sapiens GN=MYH9 PE=2 SV=1	64.70	2.00				4.01E-09				Control 1 Only	Control 1 Only
Q9HAV0	GBB4_HUMAN Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3	10.60		1.00		1.00		3.30E-08		1.52E-08		Sample 2 Only
K7EK07	K7EK07_HUMAN Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=2 SV=1	50.00		1.00				3.25E-07				
Q9UIG0	BAZ1B_HUMAN Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2	2.30		1.00				8.91E-10				
Q9Y6U3	ADSV_HUMAN Adseverin OS=Homo sapiens GN=SCIN PE=1 SV=4	6.00		1.00				2.99E-09				
Q9UPT8	ZC3H4_HUMAN Zinc finger CCCH domain-containing protein 4 OS=Homo sapiens GN=ZC3H4 PE=1 SV=3	3.80		0.99				1.51E-09				
Q13835	PKP1_HUMAN Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	3.30	1.00				4.24E-09				Control 1 Only	Control 1 Only
F8VUB0	F8VUB0_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 1 (Fragment) OS=Homo sapiens GN=SMARCD1 PE=2 SV=1	11.50		0.99				1.86E-08				
G3V0E5	G3V0E5_HUMAN Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapiens GN=TFRC PE=2 SV=1	2.80		1.00				8.77E-09				
F5H2X0	F5H2X0_HUMAN Tight junction protein ZO-3 OS=Homo sapiens GN=TJP3 PE=2 SV=1	2.50		1.00				2.32E-09				
P47929	LEG7_HUMAN Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	18.40	1.00				1.27E-08				Control 1 Only	Control 1 Only
H3BM42	H3BM42_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=2 SV=1	3.00		1.00				3.33E-09				
Q9NV70	EXOC1_HUMAN Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4	3.90	1.00				1.15E-08				Control 1 Only	Control 1 Only
Q13111	CAF1A_HUMAN Chromatin assembly factor 1 subunit A OS=Homo sapiens GN=CHAF1A PE=1 SV=2	2.00		1.00				5.92E-09				
G3XAA0	G3XAA0_HUMAN AT rich interactive domain 1B (SWI1-like), isoform CRA_a OS=Homo sapiens GN=ARID1B PE=2 SV=1	1.00				1.00				5.39E-10		Sample 2 Only
Q16514	TAF12_HUMAN Transcription initiation factor TFIID subunit 12 OS=Homo sapiens GN=TAF12 PE=1 SV=1	8.40				1.00				2.66E-08		Sample 2 Only
O00712	NFIB_HUMAN Nuclear factor 1 B-type OS=Homo sapiens GN=NFIB PE=1 SV=2	9.30				1.00				7.99E-09		Sample 2 Only
E9PPU0	E9PPU0_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=4 SV=1	32.60		1.00				2.36E-09				
Q9HCK8	CHD8_HUMAN Chromodomain-helicase-DNA-binding protein 8 OS=Homo sapiens GN=CHD8 PE=1 SV=5	0.90		0.99				3.72E-10				
A6NFQ9	A6NFQ9_HUMAN Septin-8 OS=Homo sapiens GN=SEPT8 PE=2 SV=1	4.20	1.00				2.15E-08				Control 1 Only	Control 1 Only
P08754	GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	7.30		1.00				2.92E-08				
Q9P0M6	H2AW_HUMAN Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3	10.20		1.00				2.50E-08				
Q14151	SAFB2_HUMAN Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	6.60				1.00				2.18E-09		Sample 2 Only
P12035	K2C3_HUMAN Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3	17.50			0.98				3.66E-09		Sample 1 Only	
P16104	H2AX_HUMAN Histone H2AX OS=Homo sapiens GN=H2AFX PE=1 SV=2	58.00		1.00				6.99E-08				
Q9NTI5	PDS5B_HUMAN Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B PE=1 SV=1	2.00		1.00				2.28E-09				
G3V220	G3V220_HUMAN Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=2 SV=1	2.30				1.00				2.23E-09		Sample 2 Only

Q9UM54-2	MYO6_HUMAN Isoform 2 of Unconventional myosin-VI OS=Homo sapiens GN=MYO6	41.30		1.00				1.35E-08				
H7C269	H7C269_HUMAN Trinucleotide repeat-containing gene 6A protein (Fragment) OS=Homo sapiens GN=TNRC6A PE=2 SV=1	38.40				1.00				1.81E-09		Sample 2 Only
Q01813	K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	5.00				0.99				4.77E-09		Sample 2 Only
Q14315	FLNC_HUMAN Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	6.30			1.00				7.62E-10		Sample 1 Only	
O15143	ARC1B_HUMAN Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3	9.70	1.00				3.21E-08				Control 1 Only	Control 1 Only
Q9NQ29	LUC7L_HUMAN Putative RNA-binding protein Luc7-like 1 OS=Homo sapiens GN=LUC7L PE=1 SV=1	5.10		0.99				3.40E-09				
P47755	CAZA2_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	13.60				1.00				2.49E-08		Sample 2 Only
E5RIT6	E5RIT6_HUMAN 60S ribosomal protein L26-like 1 (Fragment) OS=Homo sapiens GN=RPL26L1 PE=2 SV=1	64.10	0.99				2.39E-07				Control 1 Only	Control 1 Only

Table A8. Endogenous candidates from nuclear immunoprecipitations that had been treated with RNase.

			SPECTRAL COUNTS						SPECTRAL INDEX (MIC SIn)						RATIOS		
Prot	Description	% Cover	C1	C2	C3	S1	S2	S3	C1	C2	C3	S1	S2	S3	S1/C1	S2/C1	S3/C1
F8W6L6	F8W6L6_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=2 SV=1	19.30	1.00		0.77	2.00	2.00	24.31	3.67 E-09		3.25 E-09	4.84 E-09	1.31 E-08	2.62 E-07	1.32	2.00	24.31
Q99459	CDC5L_HUMAN Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2	3.50	2.00	2.00	4.00			1.00	1.47 E-06	1.05 E-06	1.66 E-07			2.04 E-08	Control 1 Only	Control 1 ONLY	0.5
Q9H9G7	AGO3_HUMAN Protein argonaute-3 OS=Homo sapiens GN=AGO3 PE=1 SV=2	48.50		1.00		89.94	63.45	28.45		1.55 E-08		6.81 E-06	4.06 E-06	1.21 E-06	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
O75369	FLNB_HUMAN Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	16.70		0.99	3.96	0.99		32.66		1.84 E-09	1.90 E-08	7.66 E-10		2.36 E-07	Sample 1 Only		Sample 3 ONLY
A6NG51	A6NG51_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=2 SV=2	44.30	1.00	1.00	18.00			249.51	2.72 E-09	6.28 E-09	1.35 E-07			4.02 E-06	Control 1 Only	Control 1 ONLY	249.51
E7ETK0	E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1	50.00		1.00	1.00		1.00	22.00		6.45 E-08	2.96 E-07		9.95 E-08	1.44 E-05		Sample 2 ONLY	Sample 3 ONLY
P40692	MLH1_HUMAN DNA mismatch repair protein Mlh1 OS=Homo sapiens GN=MLH1 PE=1 SV=1	7.40	0.99	0.99		3.95	0.98	1.98	1.15 E-08	7.09 E-09		7.72 E-08	4.41 E-08	4.29 E-08	6.74	0.99	2.00
Q9UKV8	AGO2_HUMAN Protein argonaute-2 OS=Homo sapiens GN=AGO2 PE=1 SV=3	71.20		4.00		348.49	285.00	208.00		6.18 E-08		4.51 E-05	3.67 E-05	1.89 E-05	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
P01625	KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	14.00	5.00	9.00	16.00			2.00	4.91 E-06	9.22 E-06	3.85 E-05			6.87 E-07	Control 1 Only	Control 1 ONLY	0.4
J3KNW4	J3KNW4_HUMAN Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=2 SV=1	29.40	3.00	3.00	15.00	3.00	3.00		1.10 E-07	1.34 E-07	3.29 E-06	1.29 E-07	1.33 E-07		1.18	1.00	
P42766	RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	30.90	2.00	2.00	1.00	2.00	2.00	25.00	4.51 E-07	6.99 E-07	3.39 E-07	3.85 E-07	4.49 E-07	2.87 E-05	0.85	1.00	12.50
P78347	GTF2I_HUMAN General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	32.40			56.99	1.00	9.97	5.00			3.08 E-06	2.12 E-08	1.65 E-07	1.12 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
P01614	KV201_HUMAN Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	20.40	9.96	14.80	13.52	2.28	2.28	1.28	2.48 E-05	2.47 E-05	1.13 E-04	9.28 E-07	6.82 E-07	1.13 E-06	0.04	0.23	0.13
O00148	DX39A_HUMAN ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2	19.40		0.99	11.82	0.99	0.99	2.95		3.87 E-08	1.72 E-06	4.22 E-08	3.24 E-08	1.20 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
B4DVB8	B4DVB8_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=2 SV=1	41.70	2.00	1.00	22.96	2.00	1.00	3.00	1.54 E-07	6.95 E-08	6.80 E-06	1.46 E-07	8.67 E-08	3.57 E-07	0.95	0.50	1.50
P10809	CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	6.60	3.00	2.00	2.00		1.00		1.45 E-07	6.50 E-08	5.67 E-08		3.89 E-08		Control 1 Only	0.333333333	
O95163	ELP1_HUMAN Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	8.30	5.00	5.00		2.00	2.00		9.68 E-08	1.17 E-07		2.35 E-08	9.19 E-09		0.24	0.40	
Q08379	GOGA2_HUMAN Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3	14.20	0.99	0.99	1.00	0.99		11.96	1.45 E-08	1.65 E-08	1.13 E-08	9.93 E-09		2.59 E-07	0.69	Control 1 ONLY	12.08
Q8	PSPC1_HUMAN Paraspeckle component 1	34.40		1.00	29.0	1.00	2.00	4.00		3.39	4.95	4.66	1.31	3.05	Sample	Sample	Sample

WXF1	OS=Homo sapiens GN=PSPC1 PE=1 SV=1				0					E-08	E-06	E-08	E-07	E-07	1 Only	2 ONLY	3 ONLY
B4DER1	B4DER1_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1	11.90	9.00	10.00		4.00	1.00		1.94 E-07	1.50 E-07		4.30 E-08	8.67 E-09		0.22	0.11	
P22695	QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	52.10	2.97	3.95	77.10	4.95	3.94	6.88	1.83 E-07	2.23 E-07	1.10 E-05	2.30 E-07	2.42 E-07	4.87 E-07	1.26	1.33	2.32
P07355	ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	54.90		4.76	31.55	6.69	2.84	3.78		2.42 E-07	7.00 E-06	2.39 E-07	7.33 E-08	3.77 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
O75382	TRIM3_HUMAN Tripartite motif-containing protein 3 OS=Homo sapiens GN=TRIM3 PE=1 SV=2	17.10	1.00	1.00		3.00	2.99		3.48 E-08	1.65 E-08		9.49 E-08	2.31 E-07		2.73	2.99	
Q9NRR5	UBQL4_HUMAN Ubiquilin-4 OS=Homo sapiens GN=UBQLN4 PE=1 SV=2	19.60	4.00	1.00		1.00	1.00		4.39 E-07	2.38 E-08		4.45 E-08	2.75 E-08		0.10	0.25	
E9PF10	E9PF10_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=2 SV=1	5.00	3.96	5.94		1.98	0.99		1.02 E-07	9.62 E-08		1.73 E-08	1.77 E-08		0.17	0.25	
B3KSH1	B3KSH1_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1	45.70	1.00		1.00	2.00		8.00	7.63 E-08		7.85 E-08	1.07 E-07		8.82 E-07	1.41	Control 1 ONLY	8.00
P55884	EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	8.50	1.00	1.00	2.00			10.98	3.09 E-09	3.77 E-09	5.48 E-08			3.38 E-07	Control 1 Only	Control 1 ONLY	10.98
Q9Y305	ACOT9_HUMAN Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2	56.90	4.95	5.95	79.50	9.94	13.90	3.98	3.25 E-07	3.52 E-07	1.85 E-05	6.04 E-07	1.07 E-06	2.04 E-07	1.86	2.81	0.80
B4E241	B4E241_HUMAN Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SFRS3 PE=2 SV=1	61.30	1.00	2.00	8.50	1.00	3.00	35.50	5.07 E-07	6.74 E-07	3.96 E-06	3.86 E-07	1.30 E-06	5.46 E-05	0.76	3.00	35.50
P39019	RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	75.20	1.00		14.00	3.00		57.00	1.18 E-07		5.03 E-06	5.01 E-07		5.58 E-05	4.24	Control 1 ONLY	57.00
Q9NYU2	UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	9.70	3.00	1.00		14.00	2.00		4.15 E-08	1.17 E-08		2.59 E-07	1.36 E-08		6.23	0.67	
Q15233	NONO_HUMAN Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	61.80	3.95	2.95	98.13	7.93	6.93	20.83	3.07 E-07	1.02 E-07	2.08 E-05	3.68 E-07	6.41 E-07	1.28 E-06	1.20	1.75	5.27
O15020	SPTN2_HUMAN Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3	36.20	1.00	1.00	15.97			166.94	8.65 E-09	5.63 E-09	4.89 E-07			3.21 E-06	Control 1 Only	Control 1 ONLY	166.94
Q9BR76	COR1B_HUMAN Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	13.70		1.00	11.94	1.00	1.00	4.98		7.00 E-08	1.89 E-06	3.94 E-08	6.90 E-08	2.08 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
Q00839	HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	22.70		2.00	40.88	1.99	4.98	10.94		1.70 E-08	3.88 E-06	1.64 E-08	9.39 E-08	4.68 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
B3KSQ1	B3KSQ1_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=2 SV=1	14.60		1.99	3.96		0.99	0.99		2.60 E-07	6.85 E-07		1.38 E-07	2.81 E-08		Sample 2 ONLY	Sample 3 ONLY
O95994	AGR2_HUMAN Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1	32.60	0.61	1.83	12.58	0.61	1.22	3.05	2.38 E-07	4.96 E-07	9.75 E-06	1.99 E-07	2.22 E-07	9.97 E-07	0.83	2.00	5.00
P08	RS17_HUMAN 40S ribosomal protein S17	73.30	2.00	5.00	4.97	6.00	2.00	37.8	1.33	3.20	1.57	1.16	1.49	4.03	8.77	1.00	18.94

708	OS=Homo sapiens GN=RPS17 PE=1 SV=2							7	E-07	E-06	E-06	E-06	E-06	E-05			
P24752	THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	58.50	6.95	5.96	46.84	8.94	5.96	2.99	6.39 E-07	2.52 E-07	7.97 E-06	6.65 E-07	3.44 E-07	2.42 E-07	1.04	0.86	0.43
P81605	DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	42.70	10.00	6.00	7.00	2.00		2.00	2.54 E-06	1.49 E-06	9.99 E-07	6.15 E-07		1.71 E-07	0.24	Control 1 ONLY	0.20
P57053	H2BFS_HUMAN Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2	87.30	1.90	1.92	12.47	2.87	1.90	23.08	8.48 E-07	8.06 E-07	3.98 E-05	1.21 E-06	6.42 E-07	5.76 E-04	1.43	1.00	12.15
P62805	H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	68.00	9.00	15.00	32.00	16.00	8.00	126.00	6.83 E-06	7.73 E-06	2.99 E-05	9.67 E-06	6.25 E-06	6.02 E-04	1.42	0.89	14.00
P62854	RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	61.70	1.00	3.00	5.00	2.00	2.00	26.00	9.02 E-07	1.15 E-06	4.36 E-06	1.40 E-06	9.88 E-07	4.90 E-05	1.55	2.00	26.00
Q14258	TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	10.60	1.00	2.00	5.00	1.00	2.00		2.34 E-08	1.60 E-07	3.64 E-07	1.91 E-08	9.37 E-08		0.82	2.00	
Q13247	SRSF6_HUMAN Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2	17.30	0.53	0.53	5.10	1.06	1.06	15.11	4.90 E-08	3.48 E-08	4.49 E-07	6.87 E-08	8.20 E-08	2.71 E-06	1.40	2.00	28.51
P02545	LMNA_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	39.30		2.00	32.80	2.99	1.99	7.98		1.85 E-08	2.21 E-06	4.80 E-08	5.36 E-08	3.10 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
P18077	RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	50.90		1.00	7.98	3.99		21.93		1.45 E-07	3.46 E-06	8.41 E-07		2.37 E-05	Sample 1 Only		Sample 3 ONLY
P62263	RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	48.30	1.00	1.00	5.00	2.00	2.00	23.00	1.01 E-07	9.06 E-08	2.04 E-06	2.15 E-07	2.13 E-07	1.37 E-05	2.13	2.00	23.00
H7C1J4	H7C1J4_HUMAN Chromosome 6 open reading frame 107, isoform CRA_b OS=Homo sapiens GN=UHRF1BP1 PE=2 SV=1	5.20	5.00	7.00		2.00	2.00		1.59 E-07	1.87 E-07		4.08 E-08	3.55 E-08		0.26	0.40	
O75489	NDUS3_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1	14.00	1.00	1.00	6.00	2.00			1.70 E-07	3.22 E-07	9.40 E-07	3.07 E-07			1.81	Control 1 ONLY	
P62244	RS15A_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	81.50	0.99	1.98	12.79	1.98	1.98	36.46	3.75 E-07	4.62 E-07	7.17 E-06	1.10 E-06	5.29 E-07	5.06 E-05	2.93	2.00	36.83
P01834	IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	80.20	7.00	10.00	4.00	4.00	3.00		2.06 E-06	3.99 E-06	3.50 E-06	8.08 E-07	9.15 E-07		0.39	0.43	
P62269	RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	72.40	4.00	6.00	22.98	8.00	5.00	68.98	1.08 E-06	1.06 E-06	1.49 E-05	1.92 E-06	1.38 E-06	1.19 E-04	1.78	1.25	17.25
K7EK07	K7EK07_HUMAN Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=2 SV=1	40.20	1.97	1.97	29.55	3.94	2.96	43.37	8.32 E-07	7.62 E-07	5.52 E-05	1.91 E-06	1.20 E-06	4.74 E-04	2.30	1.50	22.02
F6SBX2	F6SBX2_HUMAN Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=2 SV=1	11.00	7.00	2.00		3.00	1.00		2.00 E-07	2.20 E-08		4.30 E-08	1.44 E-08		0.21	0.14	
O00712	NFIB_HUMAN Nuclear factor 1 B-type OS=Homo sapiens GN=NFIB PE=1 SV=2	7.60			3.97	0.99	0.99	0.99			4.22 E-07	3.58 E-08	3.30 E-08	3.71 E-08	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
E9PLL6	E9PLL6_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1	52.80	1.98	1.98	0.99	1.98	1.98	12.87	1.31 E-06	9.30 E-07	6.15 E-07	1.42 E-06	1.22 E-06	1.24 E-05	1.08	1.00	6.50
B7Z3I9	B7Z3I9_HUMAN Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=2 SV=1	12.80	3.00	3.00		1.00	1.00		3.32 E-07	5.74 E-07		1.19 E-07	9.51 E-08		0.36	0.33	
A8K8E1	A8K8E1_HUMAN TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 PE=2 SV=1	5.60	2.00	3.00		2.00	1.00		8.58 E-08	1.83 E-07		4.57 E-08	2.40 E-08		0.53	0.50	
P67809	YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens	52.20	2.98	2.98	14.89	2.98	4.97	2.00	1.57 E-07	2.06 E-07	3.27 E-06	2.25 E-07	3.36 E-07	2.29 E-07	1.43	1.67	0.67

	GN=YBX1 PE=1 SV=3																
Q9NQH7	XPP3_HUMAN Probable Xaa-Pro aminopeptidase 3 OS=Homo sapiens GN=XPNPEP3 PE=1 SV=1	25.20	2.00	3.00		5.00	11.00		1.54E-07	2.40E-07		2.99E-07	1.34E-06		1.94	5.50	
H0YJC0	H0YJC0_HUMAN 26S protease regulatory subunit 10B (Fragment) OS=Homo sapiens GN=PSMC6 PE=4 SV=1	44.70	4.99	7.00		3.00	2.00		3.92E-07	1.08E-06		2.02E-07	1.46E-07		0.52	0.40	
Q8N163	CCAR2_HUMAN Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2	22.00	2.97	11.87	11.86	5.94	2.97	2.97	5.42E-08	2.08E-07	4.25E-07	7.22E-08	1.74E-08	8.63E-08	1.33	1.00	1.00
C9JW96	C9JW96_HUMAN Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=2 SV=2	44.30	1.99	3.99	9.95		1.00	2.99	3.51E-07	5.90E-07	1.55E-06		1.57E-07	4.26E-07	Control 1 Only	0.5025 12563	1.50251 2563
P04259	K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	67.00	1.00	2.00	9.00	3.00		3.00	4.33E-08	7.96E-08	4.34E-07	6.93E-08		7.64E-08	1.60	Control 1 ONLY	3.00
P61353	RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	67.60	1.00	1.99	11.92	2.99	2.00	37.77	5.90E-07	6.57E-07	6.67E-06	1.02E-06	7.48E-07	4.02E-05	1.73	2.00	37.77
P46783	RS10_HUMAN 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	73.90	2.00	5.00	16.96	2.00	6.00	73.81	2.11E-07	1.78E-06	5.29E-06	2.50E-07	1.40E-06	3.60E-05	1.18	3.00	36.91
E9PC52	E9PC52_HUMAN Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=2 SV=1	19.70	2.99	2.99	5.91	1.00	1.99	2.94	2.65E-07	2.78E-07	7.30E-07	2.15E-08	1.56E-07	1.49E-07	0.08	0.67	0.98
E7EW34	E7EW34_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=2 SV=1	30.00	21.00	21.00		16.00	11.00	1.00	1.20E-06	8.74E-07		3.21E-07	1.76E-07	2.18E-08	0.27	0.52	0.05
P61254	RL26_HUMAN 60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	66.90	2.94	2.94	12.68	3.92	3.92	42.10	7.04E-07	5.31E-07	4.60E-06	8.92E-07	9.85E-07	2.54E-05	1.27	1.33	14.32
P62266	RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	30.10		2.00	7.00		2.00	13.95		8.46E-07	2.84E-06		6.19E-07	1.56E-05		Sample 2 ONLY	Sample 3 ONLY
Q13155	AIMP2_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2	30.00	2.00	3.00		2.00	1.00		2.01E-07	2.55E-07		8.96E-08	4.25E-08		0.45	0.50	
O43242	PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	13.30	2.00	4.00	2.00	2.00	2.00		1.06E-07	1.96E-07	1.19E-08	3.40E-08	5.94E-08		0.32	1.00	
P47897	SYQ_HUMAN Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	28.90	17.78	15.80	0.99	9.87	1.97		8.02E-07	5.24E-07	1.72E-08	3.17E-07	5.09E-08		0.40	0.11	
P05198	IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	16.50	3.00	2.00	6.00	3.00	1.00	1.00	1.81E-07	9.77E-08	1.13E-06	1.87E-07	8.84E-08	1.22E-07	1.03	0.33	0.33
Q8IYB1	M21D2_HUMAN Protein MB21D2 OS=Homo sapiens GN=MB21D2 PE=1 SV=3	6.30	2.00	3.00		1.00	1.00		1.85E-07	2.67E-07		3.37E-08	1.05E-07		0.18	0.50	
P62888	RL30_HUMAN 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	77.40	2.00	3.98	11.96	1.99	0.99	31.92	2.65E-07	1.20E-06	5.25E-06	4.00E-07	3.08E-07	2.80E-05	1.51	0.50	15.96
O14735	CDIPT_HUMAN CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Homo sapiens GN=CDIPT PE=1 SV=1	27.20	3.97	2.99		1.99	1.00		3.50E-07	2.04E-07		1.32E-07	3.69E-08		0.38	0.25	
P08779	K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	65.50	17.00	10.00	54.00	25.00	12.00	14.00	1.04E-06	3.03E-07	6.21E-06	8.91E-07	4.23E-07	7.04E-07	0.86	0.71	0.82
G5E9Q2	G5E9Q2_HUMAN Cold shock domain containing E1, RNA-binding, isoform CRA_d OS=Homo sapiens GN=CSDE1 PE=2 SV=1	15.60	5.94	6.93		3.96	4.95		1.43E-07	2.08E-07		5.41E-08	6.09E-08		0.38	0.83	
P25205	MCM3_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	32.30	32.68	30.72	3.97	16.84	8.94	1.00	1.20E-06	9.30E-07	1.24E-07	3.50E-07	2.96E-07	2.12E-08	0.29	0.27	0.03

B7Z2G1	B7Z2G1_HUMAN Kelch-like protein 22 OS=Homo sapiens GN=KLHL22 PE=2 SV=1	11.20	1.97	4.94		0.98	2.96		1.01E-07	3.26E-07		2.39E-08	1.15E-07		0.24	1.50	
Q7Z794	K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3	15.90	3.00	2.00	3.00	1.00	2.00		1.28E-07	3.61E-08	1.60E-07	4.42E-08	6.28E-08		0.35	0.67	
P54136	SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	26.50	13.88	18.84	1.98	5.95	3.96		8.32E-07	1.18E-06	7.08E-08	2.48E-07	3.75E-07		0.30	0.29	
F5GZS6	F5GZS6_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=2 SV=1	10.80	6.94	5.95		2.97	2.97		2.68E-07	2.72E-07		5.51E-08	1.20E-07		0.21	0.43	
P23246	SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	43.80	4.00	5.00	81.66	7.99	10.00	28.96	1.66E-07	1.15E-07	1.15E-05	5.43E-07	3.42E-07	2.29E-06	3.28	2.50	7.24
O43684	BUB3_HUMAN Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1	28.50		0.99	17.82	0.99	0.99	6.93		6.62E-08	2.77E-06	4.91E-08	6.66E-08	7.32E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
Q8WVX9	FACR1_HUMAN Fatty acyl-CoA reductase 1 OS=Homo sapiens GN=FAR1 PE=1 SV=1	18.40	3.00	3.00	13.00	2.00	6.00	4.00	1.53E-07	1.41E-07	1.94E-06	8.09E-08	3.90E-07	2.09E-07	0.53	2.00	1.33
P31153	METK2_HUMAN S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	17.70	2.00	6.00		3.00	1.00		2.70E-07	4.32E-07		1.67E-07	6.15E-08		0.62	0.50	
P62249	RS16_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	78.80	2.96	6.89	21.75	5.91	3.94	62.26	8.21E-07	2.33E-06	1.66E-05	1.89E-06	1.84E-06	7.79E-05	2.30	1.33	21.03
M0QXB4	M0QXB4_HUMAN Coatomer protein complex, subunit epsilon, isoform CRA_g OS=Homo sapiens GN=COPE PE=2 SV=1	31.60	4.00	5.00	2.00	2.00	3.00		5.53E-07	6.69E-07	2.50E-07	2.47E-07	2.23E-07		0.45	0.75	
P05386	RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	66.70		3.00	1.00		3.00	6.00		1.22E-06	2.48E-06		8.95E-07	1.23E-05		Sample 2 ONLY	Sample 3 ONLY
P62851	RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	57.60	3.00	3.00	9.00	4.00	3.00	26.00	1.19E-06	7.55E-07	1.16E-05	1.89E-06	1.04E-06	5.01E-05	1.59	1.00	8.67
P52597	HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	45.50	1.00	1.00	32.00	5.00	3.00	8.00	4.57E-08	6.35E-08	4.11E-06	2.29E-07	3.04E-07	7.47E-07	5.00	3.00	8.00
Q9NR30	DDX21_HUMAN Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	7.00			2.00	1.00	1.00	5.50			7.44E-08	1.48E-08	2.28E-08	1.75E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
F5GY37	F5GY37_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=2 SV=1	41.60	4.95	1.98	7.95	0.99	2.97	2.97	5.68E-07	1.75E-07	1.56E-06	3.87E-08	3.92E-07	3.00E-07	0.07	0.60	0.60
P55072	TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	15.10	2.00	4.00		3.00	2.00	1.00	5.95E-08	7.67E-08		2.46E-08	1.49E-08	1.10E-08	0.41	1.00	0.50
P46778	RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	41.20	2.00	3.00	9.00	2.00	3.00	22.00	4.47E-07	5.85E-07	5.52E-06	8.14E-07	7.98E-07	2.21E-05	1.82	1.50	11.00
P08238	HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	26.00	10.99	13.99		7.99	6.00	1.00	6.86E-07	6.32E-07		2.40E-07	1.80E-07	1.84E-08	0.35	0.55	0.09
P62829	RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	57.90	1.98	0.99	7.92	3.97	1.98	23.81	4.59E-07	2.91E-07	3.38E-06	7.29E-07	3.77E-07	1.32E-05	1.59	1.00	12.03
Q9NZB2	F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2	14.70	1.00	4.99	7.96	0.99		7.98	1.67E-08	9.93E-08	2.70E-07	1.33E-08		1.24E-07	0.79	Control 1 ONLY	7.98
P12004	PCNA_HUMAN Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	39.10	11.00	11.00		5.00	3.00		1.30E-06	1.54E-06		4.38E-07	4.81E-07		0.34	0.27	

P53618	COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	17.50	4.00	9.00	19.00	8.00	5.00	6.00	1.18E-07	2.19E-07	8.31E-07	1.84E-07	9.66E-08	1.16E-07	1.56	1.25	1.50
Q9Y6I8	PXMP4_HUMAN Peroxisomal membrane protein 4 OS=Homo sapiens GN=PXMP4 PE=1 SV=3	25.00	2.97	3.96	3.96	0.99	1.98	0.99	9.39E-07	1.18E-06	1.14E-06	9.46E-08	4.20E-07	5.33E-07	0.10	0.67	0.33
Q6PKG0	LARP1_HUMAN La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	8.10	1.98	0.99	2.98	0.99	1.98	7.92	6.45E-08	1.52E-08	8.70E-08	3.09E-08	4.80E-08	3.92E-07	0.48	1.00	4.00
H3BTH6	H3BTH6_HUMAN F-box only protein 22 (Fragment) OS=Homo sapiens GN=FBXO22 PE=2 SV=1	10.00	3.00	3.00		2.00	2.00		3.62E-07	9.89E-07		2.12E-07	2.47E-07		0.58	0.67	
P49748	ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	8.20	2.99	4.99		1.00	1.99		1.26E-07	2.31E-07		4.89E-08	8.09E-08		0.39	0.67	
P46779	RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	75.90	5.98	8.96	20.85	7.95	5.96	53.68	2.32E-06	2.58E-06	9.61E-06	1.85E-06	1.65E-06	4.91E-05	0.80	1.00	8.98
P26641	EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	30.90	9.00	8.00	36.00	11.00	9.00	5.00	6.15E-07	1.14E-06	8.66E-06	1.05E-06	1.48E-06	6.91E-07	1.70	1.00	0.56
Q562R1	ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	21.50	1.00	3.00	1.00	4.00	1.00	3.00	4.98E-08	1.62E-06	3.67E-07	3.76E-07	4.40E-08	2.70E-07	7.55	1.00	3.00
P04843	RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	39.40	1.00	3.00	41.00	1.00	4.00	23.00	3.01E-08	2.11E-07	4.79E-06	6.20E-08	2.94E-07	1.27E-06	2.06	4.00	23.00
Q01813	K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	28.30	28.73	25.26	1.98	16.86	10.42	1.98	1.56E-06	8.17E-07	7.21E-08	5.46E-07	2.32E-07	4.74E-08	0.35	0.36	0.07
Q969V3	NCLN_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2	11.60	1.00	2.00	2.99	1.00	1.00	2.99	6.92E-08	6.63E-08	1.15E-07	5.63E-09	2.66E-08	6.23E-08	0.08	1.00	2.99
P41252	SYIC_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	18.90	34.87	32.85		21.92	15.93		1.18E-06	7.84E-07		3.88E-07	2.94E-07		0.33	0.46	
P54886	P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	15.90	6.00	3.00	14.00	6.00	1.00	4.00	2.45E-07	1.31E-07	7.35E-07	2.05E-07	9.58E-08	9.97E-08	0.84	0.17	0.67
P22102	PUR2_HUMAN Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	10.30	19.88	20.86		13.89	19.82		3.09E-07	1.63E-07		6.78E-08	1.10E-07		0.22	1.00	
H0YK49	H0YK49_HUMAN Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=2 SV=1	24.90	1.98	2.97		1.98	0.99		4.61E-07	6.08E-07		2.37E-07	1.56E-07		0.51	0.50	
E9PJN0	E9PJN0_HUMAN Acyl-coenzyme A thioesterase 8 OS=Homo sapiens GN=ACOT8 PE=2 SV=1	33.20	3.95	3.94	2.97	2.96	0.99		1.26E-06	1.11E-06	5.32E-07	9.06E-07	1.12E-07		0.72	0.25	
Q9BRJ7	SDOS_HUMAN Protein syndesmos OS=Homo sapiens GN=NUDT16L1 PE=1 SV=1	69.20	8.92	10.90	20.84	7.93	4.95	6.93	1.32E-06	2.05E-06	6.00E-06	1.09E-06	1.21E-06	8.76E-07	0.83	0.55	0.78
P60866	RS20_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	46.20	1.98	0.99	10.89	5.94		19.80	2.35E-07	8.85E-08	1.18E-05	1.52E-06		3.77E-05	6.47	Control 1 ONLY	10.00
C9J050	C9J050_HUMAN Choline-phosphate cytidylyltransferase A (Fragment) OS=Homo sapiens GN=PCYT1A PE=2 SV=1	21.20	2.97	1.98		1.00	1.98		3.95E-07	2.34E-07		3.99E-08	2.05E-07		0.10	0.67	
B4DWW1	B4DWW1_HUMAN ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=2 SV=1	34.80	7.92	4.95		4.95	0.99		2.04E-06	1.29E-06		1.04E-06	1.69E-07		0.51	0.13	
P56537	IF6_HUMAN Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	26.90	3.00	2.00		1.00	2.00	4.00	2.64E-07	2.11E-07		1.39E-07	1.95E-07	9.36E-07	0.53	0.67	1.33

P07814	SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	6.70	11.00	4.00	1.00	6.00	4.00	2.00	1.89E-07	2.79E-08	7.21E-09	4.51E-08	3.17E-08	1.51E-08	0.24	0.36	0.18
P62750	RL23A_HUMAN 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	52.60	1.98	2.97	9.90	5.94	3.96	28.82	1.03E-06	9.91E-07	7.89E-06	1.93E-06	1.89E-06	2.71E-05	1.87	2.00	14.56
O43143	DHX15_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	13.50	2.00	3.00	1.00	1.00	2.00	11.00	5.93E-08	9.67E-08	5.17E-08	4.38E-08	5.88E-08	4.26E-07	0.74	1.00	5.50
P62277	RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	55.60	5.99	5.99	23.91	6.98	6.98	43.83	1.96E-06	2.02E-06	1.98E-05	2.74E-06	2.26E-06	7.27E-05	1.40	1.17	7.32
P13639	EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	30.70	14.50	18.00	1.00	9.50	6.50	5.00	7.70E-07	5.49E-07	3.10E-08	2.18E-07	1.83E-07	1.17E-07	0.28	0.45	0.34
P02538	K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	67.00	8.97	6.98	15.93	9.96	5.98	8.96	4.17E-07	3.02E-07	1.92E-06	5.57E-07	2.14E-07	2.12E-07	1.34	0.67	1.00
J3KR12	J3KR12_HUMAN Uncharacterized protein OS=Homo sapiens PE=4 SV=1	13.80	0.98	0.98	0.98	2.96	3.96		1.06E-07	5.92E-08	1.84E-07	4.38E-07	4.60E-07		4.12	4.04	
P04844	RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	24.40	6.95	6.97	17.99	7.94	6.96	7.99	1.11E-06	4.17E-07	3.12E-06	4.00E-07	7.35E-07	5.71E-07	0.36	1.00	1.15
C9JTZ6	C9JTZ6_HUMAN 5'-nucleotidase domain-containing protein 2 OS=Homo sapiens GN=NT5DC2 PE=2 SV=1	9.10	2.97	3.97		0.99	1.98		1.72E-07	1.56E-07		6.20E-08	7.29E-08		0.36	0.67	
P07900	HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	21.00	4.99	7.98		2.99	3.00		7.97E-08	1.02E-07		3.47E-08	4.19E-08		0.44	0.60	
P35998	PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	12.20	2.00	3.00		2.00	2.00		1.87E-07	4.57E-07		1.07E-07	1.54E-07		0.57	1.00	
Q3KQU3	MA7D1_HUMAN MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1	3.10	2.00	3.00		1.00	1.00		5.55E-08	1.04E-07		2.42E-08	4.38E-08		0.44	0.50	
Q04695	K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	58.10	9.90	1.96	14.93	8.91	1.98	7.96	3.25E-07	3.07E-08	5.19E-07	1.86E-07	4.49E-08	1.20E-07	0.57	0.20	0.80
Q9H773	DCTP1_HUMAN dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1	39.40	24.00	20.00		13.00	13.00		2.12E-05	1.22E-05		4.63E-06	6.82E-06		0.22	0.54	
P33993	MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	35.30	36.91	30.89	4.98	17.95	12.97	0.99	2.04E-06	1.21E-06	1.81E-07	5.50E-07	7.27E-07	4.35E-08	0.27	0.35	0.03
Q00325	MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	33.00	5.00	4.99	28.97	10.00	4.00	12.00	9.87E-07	4.77E-07	1.11E-05	1.67E-06	7.07E-07	2.20E-06	1.69	0.80	2.40
B4DZH6	B4DZH6_HUMAN Histone deacetylase 6 OS=Homo sapiens GN=HDAC6 PE=2 SV=1	12.00	19.93	17.93		16.93	5.96		9.05E-07	5.43E-07		3.83E-07	2.10E-07		0.42	0.30	
B7Z6Z4	B7Z6Z4_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	49.70	1.97	8.89	3.95	4.93	13.82	10.87	2.02E-07	1.71E-06	7.11E-07	4.18E-07	2.22E-06	4.30E-06	2.07	7.02	5.52
M0QZM1	M0QZM1_HUMAN Heterogeneous nuclear ribonucleoprotein M (Fragment) OS=Homo sapiens GN=HNRNPM PE=4 SV=1	61.40	1.00	0.50	20.50	1.00	1.00	51.50	3.05E-08	1.39E-08	2.16E-06	3.45E-08	3.94E-08	5.70E-06	1.13	1.00	51.50
P56192	SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	17.60	19.84	19.84		17.86	3.95		7.66E-07	9.28E-07		6.11E-07	8.09E-08		0.80	0.20	
Q09666	AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	9.70	3.00	3.00	5.00	9.00		14.00	6.41E-09	7.56E-09	1.63E-08	2.01E-08		4.56E-08	3.14	Control 1 ONLY	4.67

P61313	RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	52.00	6.89	6.90	14.78	6.91	8.88	29.57	1.26E-06	8.93E-07	4.89E-06	1.20E-06	1.61E-06	1.62E-05	0.95	1.29	4.29
P42704	LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	14.30	12.00	14.00	1.00	12.00	9.00	2.00	4.75E-07	2.80E-07	6.06E-09	1.85E-07	1.25E-07	2.00E-08	0.39	0.75	0.17
P46781	RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	66.00	16.96	9.98	29.95	18.98	14.98	58.86	3.87E-06	3.11E-06	1.63E-05	5.11E-06	4.32E-06	5.63E-05	1.32	0.88	3.47
A8MUB1	A8MUB1_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1	51.50	4.91	7.85		1.94	4.89		4.19E-07	7.26E-07		6.22E-08	4.31E-07		0.15	1.00	
Q15067	ACOX1_HUMAN Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3	9.00	1.00	5.00		1.00	2.00		5.69E-07	5.88E-07		2.52E-07	2.48E-07		0.44	2.00	
P41091	IF2G_HUMAN Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	16.30	2.99	2.00	5.98	3.99	2.00	1.99	2.17E-07	1.33E-07	7.09E-07	2.20E-07	1.32E-07	1.11E-07	1.01	0.67	0.67
Q08380	LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	9.70	2.00	4.98		3.98	1.00		9.51E-08	2.99E-07		1.33E-07	4.65E-08		1.40	0.50	
Q9BSJ8	ESYT1_HUMAN Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	5.10	6.00	5.00		5.00	2.00		1.67E-07	8.99E-08		8.17E-08	3.70E-08		0.49	0.33	
B4DYD8	B4DYD8_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	5.80	1.00	3.00	1.00	1.00	1.00	1.00	5.02E-08	1.44E-07	7.27E-08	6.78E-08	3.70E-08	1.89E-08	1.35	1.00	1.00
E5KLJ5	E5KLJ5_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1	11.10	3.00	4.00	2.00	3.00	4.00		7.59E-08	4.95E-08	6.39E-08	3.88E-08	4.94E-08		0.51	1.33	
P16615	AT2A2_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	28.90	20.80	13.87	39.61	17.82	13.86	23.80	3.40E-07	2.31E-07	1.59E-06	1.88E-07	2.01E-07	5.46E-07	0.55	0.67	1.14
P62195	PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	21.10	3.00	4.98		1.00	3.00	1.00	1.38E-07	4.11E-07		2.06E-08	2.03E-07	2.70E-08	0.15	1.00	0.33
F8WF69	F8WF69_HUMAN Clathrin light chain A OS=Homo sapiens GN=CLTA PE=2 SV=1	8.30	1.00	1.00	1.00	3.00	1.00	2.00	1.00E-07	7.06E-08	8.12E-08	1.94E-07	8.65E-08	2.81E-07	1.94	1.00	2.00
O95881	TXD12_HUMAN Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	30.80	5.00	9.00		7.00	1.00		2.86E-06	3.98E-06		2.71E-06	1.90E-07		0.95	0.20	
G8JLH9	G8JLH9_HUMAN Signal transducer and activator of transcription OS=Homo sapiens GN=STAT3 PE=2 SV=1	6.20	6.00	6.00		6.00	3.00		8.92E-07	7.78E-07		4.40E-07	3.11E-07		0.49	0.50	
P13647	K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	65.90	56.74	64.69	90.65	60.70	48.80	25.86	3.03E-06	2.56E-06	8.48E-06	2.59E-06	2.28E-06	9.99E-07	0.85	0.86	0.46
E9PM69	E9PM69_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=2 SV=1	27.70	3.96	8.90		3.94	2.95		2.22E-07	8.52E-07		2.05E-07	2.90E-07		0.92	0.74	
Q14694	UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2	12.50	1.99	3.97	1.98	2.97	1.98	17.96	1.22E-07	1.95E-07	3.52E-08	1.04E-07	6.51E-08	5.92E-07	0.85	0.99	9.03
P62258	1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	31.40	2.97	2.97		1.98	2.97		4.43E-07	2.15E-07		1.38E-07	1.77E-07		0.31	1.00	
E7EPB3	E7EPB3_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=2 SV=1	41.90	8.00	10.00	13.00	13.00	10.00	30.00	8.89E-06	9.82E-06	1.98E-05	1.31E-05	2.55E-05	5.97E-05	1.47	1.25	3.75
K7EMH1	K7EMH1_HUMAN 60S ribosomal protein L22 (Fragment) OS=Homo sapiens GN=RPL22 PE=2 SV=1	49.40	2.00	2.00	4.00	2.00	2.00	9.00	6.17E-07	5.33E-07	7.84E-06	7.17E-07	8.39E-07	1.98E-05	1.16	1.00	4.50

Q15393	SF3B3_HUMAN Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	15.30	2.00	3.00	6.99	1.00	3.00	24.94	2.76 E-08	6.13 E-08	4.18 E-07	5.23 E-09	3.23 E-08	1.04 E-06	0.19	1.50	12.47
Q5D862	FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	1.00		3.00	1.00	2.00	1.00			1.18 E-07	2.78 E-08	3.39 E-08	3.96 E-08		Sample 1 Only	Sample 2 ONLY	
P62081	RS7_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	75.80	10.00	9.00	21.00	18.00	9.00	41.00	1.45 E-06	2.01 E-06	1.99 E-05	2.21 E-06	2.09 E-06	5.28 E-05	1.52	0.90	4.10
P58107	EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2	11.70	1.00		10.90	0.98	0.98	7.90	5.67 E-09		5.53 E-08	1.12 E-09	2.00 E-09	2.90 E-08	0.20	0.98	7.90
P06493	CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	37.40	9.93	9.93	4.98	7.95	6.94		3.67 E-06	1.98 E-06	1.32 E-06	1.83 E-06	1.32 E-06		0.50	0.70	
B1AK13	B1AK13_HUMAN 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (Hydroxymethylglutaricaciduria), isoform CRA_b OS=Homo sapiens GN=HMGCL PE=2 SV=1	12.70	1.00	3.00		1.00	2.00		8.65 E-08	3.61 E-07		6.50 E-08	1.56 E-07		0.75	2.00	
O43175	SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	16.60	5.00	4.00		8.00	9.00		4.74 E-07	2.84 E-07		6.61 E-07	9.50 E-07		1.40	1.80	
M0R0F0	M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=2 SV=1	60.00	2.98	5.95	33.80	7.93	4.96	63.69	3.24 E-07	6.94 E-07	1.26 E-05	8.73 E-07	1.04 E-06	3.01 E-05	2.70	1.66	21.37
P25398	RS12_HUMAN 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	52.30	3.00	4.00	3.00	4.00	4.00	17.00	8.09 E-06	3.67 E-06	1.88 E-06	9.87 E-06	3.27 E-06	1.86 E-05	1.22	1.33	5.67
P52272	HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	48.00	0.50		17.36	0.50	1.49	36.76	8.47 E-09		8.82 E-07	9.22 E-09	2.30 E-08	1.83 E-06	1.09	2.98	73.52
Q1KMD3	HNRL2_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1	14.90	3.00	9.00	7.00	6.00	2.00	3.00	1.59 E-07	2.28 E-07	3.27 E-07	1.53 E-07	7.64 E-08	1.28 E-07	0.96	0.67	1.00
D6RAN4	D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1	55.50	2.97	1.98	14.85	5.94	4.95	26.73	3.83 E-07	7.45 E-07	9.08 E-06	5.42 E-07	1.63 E-06	2.10 E-05	1.42	1.67	9.00
P52292	IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	14.00	3.00	6.00	2.00	2.00	3.00	2.00	2.76 E-07	7.82 E-07	1.47 E-07	9.15 E-08	3.46 E-07	1.59 E-07	0.33	1.00	0.67
P60842	IF4A1_HUMAN Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	9.90	2.97	1.98		1.98		1.98	2.64 E-07	2.54 E-07		1.65 E-07		9.77 E-08	0.63	Control 1 ONLY	0.67
P14625	ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	11.70	6.00	7.00		5.00	2.00		2.56 E-07	1.78 E-07		1.52 E-07	7.05 E-08		0.59	0.33	
Q9NUQ8	ABCF3_HUMAN ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2	11.10	7.00	7.00		2.00	3.00		2.33 E-07	1.93 E-07		6.32 E-08	1.56 E-07		0.27	0.43	
P62280	RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	68.40	2.98	4.99	18.92	6.98	4.98	34.85	4.85 E-07	6.56 E-07	1.53 E-05	1.30 E-06	8.92 E-07	3.51 E-05	2.69	1.67	11.69
Q53FA7	QORX_HUMAN Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2	27.40	7.98	7.97		7.95	2.99		1.53 E-06	1.46 E-06		9.64 E-07	4.98 E-07		0.63	0.37	
P40429	RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	61.10	8.97	8.96	17.93	10.96	10.96	37.90	7.04 E-06	6.22 E-06	1.16 E-05	8.09 E-06	9.54 E-06	3.92 E-05	1.15	1.22	4.23
F8W7C6	F8W7C6_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=2 SV=1	56.40	5.93	5.93	24.81	6.92	8.91	59.49	2.35 E-06	1.13 E-06	1.49 E-05	2.33 E-06	2.08 E-06	3.70 E-05	0.99	1.50	10.03
P08729	K2C7_HUMAN Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	41.80		1.00	18.00	1.00	1.00	14.00		1.14 E-07	1.01 E-06	1.32 E-08	1.49 E-08	5.45 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
K7E	K7EKL3_HUMAN Paragranulin (Fragment)	13.40	13.8	12.8	0.99	12.8	2.97		2.81	1.19	1.06	1.70	3.13		0.61	0.21	

KL3	OS=Homo sapiens GN=GRN PE=4 SV=1		6	7		7			E-06	E-06	E-07	E-06	E-07				
F5H2F4	F5H2F4_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1	43.00	47.99	58.98	8.00	41.00	29.99	1.00	2.20 E-06	2.35 E-06	2.11 E-07	1.24 E-06	1.10 E-06	1.80 E-08	0.56	0.62	0.02
P19013	K2C4_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	70.20	0.50	79.98	3.00	103.47	0.99		7.24 E-09	1.98 E-05	7.82 E-08	9.47 E-06	8.05 E-09		1308.78	1.98	
Q96NB2	SFXN2_HUMAN Sideroflexin-2 OS=Homo sapiens GN=SFXN2 PE=1 SV=2	30.40	6.98	3.98	11.95	8.96	2.99	3.00	8.73 E-07	4.52 E-07	2.30 E-06	1.10 E-06	4.29 E-07	2.93 E-07	1.26	0.43	0.43
P50416	CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	23.80	29.00	27.00	7.00	18.00	15.00	14.00	1.26 E-06	1.08 E-06	3.60 E-07	4.14 E-07	4.91 E-07	4.66 E-07	0.33	0.52	0.48
A6NES3	A6NES3_HUMAN Etoposide-induced protein 2.4 homolog OS=Homo sapiens GN=EI24 PE=2 SV=1	22.00	3.00	3.00	1.00	1.00	2.00	2.00	3.43 E-07	5.48 E-07	8.59 E-08	6.24 E-08	3.27 E-07	1.23 E-07	0.18	0.67	0.67
E9PAV3	E9PAV3_HUMAN Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=2 SV=1	32.40	3.96	4.96	1.98	3.96	3.96		8.68 E-08	8.30 E-08	3.51 E-08	5.55 E-08	5.63 E-08		0.64	1.00	
E7EUT5	E7EUT5_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=2 SV=1	51.20	11.00	16.50	5.00	14.00	8.00		9.89 E-07	1.92 E-06	2.83 E-07	1.02 E-06	6.17 E-07		1.03	0.73	
B4DZI8	B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1	13.60	1.00	2.00	7.99	2.00	1.00	17.95	1.48 E-08	1.50 E-08	2.68 E-07	1.62 E-08	1.44 E-08	5.31 E-07	1.09	1.00	17.95
P46940	IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	38.30	63.95	89.91	78.98	76.96	22.96	70.95	1.37 E-06	1.89 E-06	2.24 E-06	1.16 E-06	2.51 E-07	1.38 E-06	0.85	0.36	1.11
Q02413	DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	25.90	12.00	24.00	9.00	20.00	9.00	1.00	2.21 E-07	4.52 E-07	2.24 E-07	3.28 E-07	1.39 E-07	1.25 E-08	1.48	0.75	0.08
P33992	MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5	52.30	63.84	71.80	16.97	62.87	47.89	6.99	7.98 E-06	7.33 E-06	1.28 E-06	4.00 E-06	3.89 E-06	2.77 E-07	0.50	0.75	0.11
C9JNW5	C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1	52.70	3.00	4.00	10.00	4.00	4.00	24.00	1.33 E-06	1.15 E-06	5.70 E-06	1.69 E-06	1.56 E-06	1.37 E-05	1.27	1.33	8.00
Q86Y46	K2C73_HUMAN Keratin, type II cytoskeletal 73 OS=Homo sapiens GN=KRT73 PE=1 SV=1	16.70	16.67	10.78	17.64	21.56	17.64	8.82	1.71 E-06	9.48 E-07	7.77 E-06	2.09 E-06	2.56 E-06	6.00 E-07	1.22	1.06	0.53
P37108	SRP14_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2	55.10		1.00	12.00		1.00	5.00		4.91 E-07	4.76 E-06		4.98 E-07	2.25 E-06		Sample 2 ONLY	Sample 3 ONLY
J3KP15	J3KP15_HUMAN Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens GN=SRSF2 PE=2 SV=1	34.30			8.94	0.99	0.99	12.92			2.33 E-06	1.79 E-07	2.36 E-07	4.11 E-06	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
Q9NZT2	OGFR_HUMAN Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3	29.70	28.99	37.98		21.00	21.00		1.81 E-06	3.51 E-06		9.42 E-07	1.85 E-06		0.52	0.72	
F2Z2U8	F2Z2U8_HUMAN Myosin-14 OS=Homo sapiens GN=MYH14 PE=2 SV=1	11.20	2.98	5.96		3.97	1.98		8.98 E-09	3.30 E-08		1.95 E-08	5.11 E-09		2.17	0.66	
B4DQI4	B4DQI4_HUMAN Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=2 SV=1	19.70	4.00	1.00		3.00	1.00		1.49 E-06	1.47 E-07		5.49 E-07	3.44 E-07		0.37	0.25	
P17858	K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	23.80	16.00	14.00	3.00	19.00	5.00	2.00	5.68 E-07	4.93 E-07	1.37 E-07	4.76 E-07	1.07 E-07	7.72 E-08	0.84	0.31	0.13
P62714	PP2AB_HUMAN Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1	19.10	3.96	4.95		2.97	3.96		6.43 E-07	6.94 E-07		2.96 E-07	4.41 E-07		0.46	1.00	
P35908	K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1	94.80	357.50	427.50	299.00	371.00	318.50	72.50	5.46 E-05	9.06 E-05	8.86 E-05	4.60 E-05	5.95 E-05	6.18 E-06	0.84	0.89	0.20

	SV=2																
P63208	SKP1_HUMAN S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	55.80	9.88	8.91	1.00	12.83	3.94		1.76E-06	2.59E-06	3.13E-07	1.56E-06	9.36E-07		0.89	0.40	
P51659	DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	39.50	16.89	21.84	55.49	24.80	17.84	23.80	6.13E-07	9.23E-07	5.12E-06	8.31E-07	1.26E-06	1.44E-06	1.36	1.06	1.41
G3V0E5	G3V0E5_HUMAN Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapiens GN=TFRC PE=2 SV=1	19.10	16.94	10.95		12.95	4.99		8.24E-07	3.85E-07		4.94E-07	1.81E-07		0.60	0.29	
P13645	K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	69.30	613.48	522.55	368.62	557.46	391.54	157.85	1.73E-04	1.18E-04	1.58E-04	1.03E-04	9.21E-05	1.71E-05	0.60	0.64	0.26
P02533	K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	68.20	64.50	49.50	47.00	61.50	37.00	10.00	4.02E-06	3.50E-06	5.21E-06	3.83E-06	2.45E-06	4.26E-07	0.95	0.57	0.16
C9IZQ1	C9IZQ1_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=2 SV=1	12.80	1.00	1.00	6.00		2.00	6.00	6.86E-08	2.09E-07	3.77E-06		2.02E-07	2.00E-06	Control 1 Only	2	6
P21266	GSTM3_HUMAN Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	57.30	20.02	20.53		20.53	17.02		7.11E-06	7.86E-06		3.83E-06	4.04E-06		0.54	0.85	
K7EKW4	K7EKW4_HUMAN Isochorismatase domain-containing protein 2, mitochondrial (Fragment) OS=Homo sapiens GN=ISOC2 PE=2 SV=1	49.40	2.97	6.93		7.92	1.98		6.52E-07	2.07E-06		1.20E-06	3.19E-07		1.84	0.67	
Q96S55	WRIP1_HUMAN ATPase WRNIP1 OS=Homo sapiens GN=WRNIP1 PE=1 SV=2	8.90	1.98	5.95		3.97	0.99		6.31E-08	1.37E-07		8.18E-08	3.69E-08		1.30	0.50	
P05783	K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	52.10	20.00	40.00	39.00	30.00	24.00	21.00	1.49E-06	3.94E-06	6.10E-06	2.21E-06	2.27E-06	1.75E-06	1.48	1.20	1.05
Q15365	PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	15.40	1.00		2.00	3.00		2.00	9.15E-08		1.41E-07	2.06E-07		1.97E-07	2.25	Control 1 ONLY	2.00
F8VU39	F8VU39_HUMAN Bromodomain adjacent to zinc finger domain protein 2A OS=Homo sapiens GN=BAZ2A PE=2 SV=1	3.30	1.00		4.00	2.00	1.00	4.00	1.03E-07		4.80E-07	1.91E-07	1.26E-07	2.27E-08	1.86	1.00	4.00
Q9UBS4	DJB11_HUMAN DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1	10.10	1.00	2.00	6.00	2.00	2.00	2.00	1.04E-07	2.03E-07	1.26E-06	2.34E-07	1.71E-07	4.87E-07	2.25	2.00	2.00
F8W9B4	F8W9B4_HUMAN Replication factor C subunit 5 OS=Homo sapiens GN=RFC5 PE=2 SV=1	40.80	7.99	5.98	9.99	4.00	6.00	2.98	9.19E-07	5.23E-07	1.35E-06	2.70E-07	8.99E-07	4.02E-07	0.29	0.75	0.37
H0Y4R1	H0Y4R1_HUMAN Inosine-5'-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=3 SV=1	12.10	3.62	5.62		3.62	3.62		8.58E-07	1.06E-06		3.88E-07	7.04E-07		0.45	1.00	
B4E2W0	B4E2W0_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1	14.60	2.97	1.98	3.94	2.95	4.94		3.10E-07	1.81E-07	3.43E-07	1.32E-07	3.52E-07		0.43	1.66	
Q13509	TBB3_HUMAN Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	37.30	5.00	4.50	0.50	6.00	3.00		3.68E-07	2.18E-06	5.82E-08	6.05E-07	8.74E-07		1.64	0.60	
B3KQ95	B3KQ95_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1	13.10	1.00	3.00		1.00	1.00		3.59E-08	2.61E-07		4.29E-08	1.34E-07		1.20	1.00	
P22392	NDKB_HUMAN Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	39.00	4.95	3.96	0.99	5.95	1.98		1.21E-06	9.60E-07	5.50E-07	1.16E-06	3.87E-07		0.96	0.40	
P53007	TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2	35.40	2.00	3.00	19.00	4.00	2.00	16.00	3.09E-07	3.45E-07	4.75E-06	4.71E-07	4.28E-07	2.14E-06	1.52	1.00	8.00
Q9BUH6	CI142_HUMAN Uncharacterized protein C9orf142 OS=Homo sapiens GN=C9orf142	14.70	5.00	3.00		2.00	2.00		1.05E-06	8.89E-07		4.35E-07	6.92E-07		0.41	0.40	

	PE=1 SV=2																
H7BXW3	H7BXW3_HUMAN Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=2 SV=1	10.70	3.97	2.97		2.97	1.98		1.69 E-07	1.86 E-07		9.88 E-08	1.15 E-07		0.59	0.50	
G5E9V5	G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1	19.10	2.00	4.00		2.00	2.00		1.21 E-07	4.32 E-07		1.52 E-07	1.80 E-07		1.26	1.00	
P30050	RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	67.90	5.00	6.00	23.00	5.00	6.00	32.00	1.76 E-06	1.94 E-06	1.42 E-05	2.38 E-06	4.29 E-06	2.65 E-05	1.35	1.20	6.40
O43592	XPOT_HUMAN Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	8.40	5.00	7.99		9.98	6.99		3.32 E-07	3.76 E-07		2.76 E-07	1.51 E-07		0.83	1.40	
P04792	HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	72.20	165.00	154.00	3.00	174.00	123.00	2.00	2.14 E-04	3.76 E-04	1.57 E-07	1.22 E-04	1.80 E-04	3.26 E-07	0.57	0.75	0.01
Q16401	PSMD5_HUMAN 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3	22.60	8.95	10.96		7.96	5.97		7.25 E-07	7.20 E-07		4.73 E-07	3.92 E-07		0.65	0.67	
P62753	RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	32.50	3.00	3.00	18.96	7.00	4.00	7.00	5.92 E-07	5.11 E-07	5.79 E-06	9.29 E-07	8.65 E-07	2.20 E-06	1.57	1.33	2.33
P05787	K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	72.00	17.84	66.33	120.19	41.60	47.52	70.55	3.53 E-06	1.19 E-05	1.80 E-05	5.05 E-06	7.33 E-06	6.30 E-06	1.43	2.66	3.95
H0YKC5	H0YKC5_HUMAN Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial (Fragment) OS=Homo sapiens GN=DUT PE=2 SV=1	16.50	1.00	3.00		2.00	3.00		3.26 E-07	1.22 E-06		1.36 E-07	7.93 E-07		0.42	3.00	
E7EMB6	E7EMB6_HUMAN Aspartyl aminopeptidase OS=Homo sapiens GN=DNPEP PE=2 SV=1	22.90	4.00	3.00		5.00	2.00		8.70 E-07	2.46 E-07		2.69 E-07	4.08 E-07		0.31	0.50	
Q15437	SC23B_HUMAN Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	23.20	8.00	9.00	5.00	8.00	9.00	1.00	5.95 E-07	2.85 E-07	3.83 E-07	4.17 E-07	3.03 E-07	4.54 E-08	0.70	1.13	0.13
P08237	K6PF_HUMAN 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	16.40	10.89	9.90		7.92	3.96	0.99	5.51 E-07	2.28 E-07		2.39 E-07	1.69 E-07	7.04 E-08	0.43	0.36	0.09
Q06210	GFPT1_HUMAN Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3	11.20	8.00	7.00		6.00	4.00		2.85 E-07	3.20 E-07		2.08 E-07	1.65 E-07		0.73	0.50	
Q9Y2A7	NCKP1_HUMAN Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	3.50	4.00	3.00		2.00	2.00		9.59 E-08	4.34 E-08		6.45 E-08	2.37 E-08		0.67	0.50	
E7EP00	E7EP00_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=2 SV=2	10.70	7.00	7.00	4.00	8.00	3.00	4.00	1.14 E-07	1.04 E-07	1.50 E-07	1.24 E-07	3.10 E-08	7.48 E-08	1.09	0.43	0.57
Q9UBM7	DHCR7_HUMAN 7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	3.60	1.00	1.00	2.99	1.00	1.00	2.00	9.11 E-08	2.58 E-08	2.58 E-07	6.34 E-08	7.54 E-08	9.59 E-08	0.70	1.00	2.00
P62937	PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	33.90	14.84	10.87		17.81	6.93		1.20 E-05	5.36 E-06		6.27 E-06	3.79 E-06		0.52	0.47	
P35250	RFC2_HUMAN Replication factor C subunit 2 OS=Homo sapiens GN=RFC2 PE=1 SV=3	17.50			2.98	0.99	1.99	0.99			2.93 E-07	1.42 E-08	8.48 E-08	8.77 E-08	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
P46109	CRKL_HUMAN Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1	22.40	5.00	4.00		2.00	4.00		4.24 E-07	6.78 E-07		2.80 E-07	4.07 E-07		0.66	0.80	
Q13085	ACACA_HUMAN Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	7.70	11.90	10.92		11.91	3.96		1.16 E-07	9.57 E-08		1.03 E-07	3.30 E-08		0.88	0.33	
Q14974	IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	25.50	38.81	37.76	2.98	34.81	24.86	2.00	1.96 E-06	1.49 E-06	1.03 E-07	1.34 E-06	7.89 E-07	4.38 E-08	0.68	0.64	0.05

B4DR61	B4DR61_HUMAN Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=2 SV=1	13.40	1.98	0.99	11.88	2.97	2.97	4.95	1.80E-07	8.97E-08	1.37E-06	2.28E-07	4.35E-07	3.63E-07	1.27	1.50	2.50
B5MDF5	B5MDF5_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=2 SV=1	19.00	2.98	2.98	2.97	2.98	1.99		5.32E-07	3.59E-07	4.20E-07	4.67E-07	3.58E-07		0.88	0.67	
Q16531	DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	52.80	122.15	133.04	21.73	117.24	79.86	15.76	8.79E-06	7.18E-06	9.54E-07	5.07E-06	4.66E-06	4.23E-07	0.58	0.65	0.13
P26373	RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	46.00	7.98	5.98	14.93	7.97	6.98	18.92	4.95E-06	2.25E-06	5.46E-06	3.65E-06	3.95E-06	1.39E-05	0.74	0.87	2.37
Q8WUK0	PTPM1_HUMAN Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Homo sapiens GN=PTPMT1 PE=1 SV=1	32.80	3.99	5.98	4.99	3.99	5.98	1.99	3.87E-07	6.78E-07	1.06E-06	2.70E-07	6.52E-07	4.24E-07	0.70	1.50	0.50
P62906	RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	59.40	3.00	6.00	21.00	7.00	4.00	39.00	7.03E-07	8.31E-07	8.41E-06	1.15E-06	9.34E-07	1.46E-05	1.64	1.33	13.00
P62913	RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	52.20	4.96	5.96	13.90	8.93	6.95	30.73	1.92E-06	1.75E-06	1.48E-05	2.80E-06	2.16E-06	2.63E-05	1.46	1.40	6.20
P30043	BLVRB_HUMAN Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3	31.10	5.00	6.00		5.00	3.00		4.66E-07	8.79E-07		5.04E-07	3.63E-07		1.08	0.60	
P06576	ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	41.40	43.50	30.64	7.91	28.64	36.55	0.99	6.29E-06	3.21E-06	4.48E-07	1.93E-06	4.21E-06	4.92E-08	0.31	0.84	0.02
Q92499	DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	30.50	12.00	11.00	24.00	8.00	10.00	17.00	5.54E-07	4.30E-07	2.11E-06	3.50E-07	6.11E-07	1.01E-06	0.63	0.83	1.42
P39656	OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	16.40	2.99	2.99	12.92	2.99	7.96	4.98	1.84E-07	1.56E-07	1.45E-06	1.45E-07	6.46E-07	3.61E-07	0.79	2.66	1.67
H7BY58	H7BY58_HUMAN Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=2 SV=1	65.60	22.96	29.96		22.96	22.97		1.10E-05	1.69E-05		7.52E-06	9.53E-06		0.69	1.00	
E9PH29	E9PH29_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=2 SV=1	18.50	1.00	5.00		1.00	4.00		2.34E-07	2.54E-06		2.14E-07	1.56E-06		0.92	4.00	
P47755	CAZA2_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	22.70	3.00	6.00		3.00	4.00		8.88E-07	1.72E-06		7.36E-07	9.45E-07		0.83	1.33	
M0R117	M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=2 SV=1	70.10	1.98	4.96	15.91	1.98	1.99	31.82	1.74E-07	6.27E-07	1.18E-05	1.94E-07	4.27E-07	2.00E-05	1.12	1.01	16.07
Q86X76	NIT1_HUMAN Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 PE=1 SV=2	26.50	9.90	11.88		9.90	4.95		1.14E-06	1.34E-06		1.09E-06	5.16E-07		0.96	0.50	
P68104	EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	38.10	19.48	28.45	38.92	46.45	20.46	8.99	5.29E-06	8.84E-06	1.12E-05	8.18E-06	6.75E-06	7.83E-07	1.55	1.05	0.46
B4DFL2	B4DFL2_HUMAN Isocitrate dehydrogenase [NADP] OS=Homo sapiens GN=IDH2 PE=2 SV=1	37.00	6.96	11.93		13.93	6.97		9.19E-07	1.68E-06		1.14E-06	5.45E-07		1.24	1.00	
F8VS02	F8VS02_HUMAN Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=2 SV=1	14.70	9.90	8.91		8.91	6.93		1.07E-06	1.02E-06		7.08E-07	6.63E-07		0.66	0.70	
F5H7I0	F5H7I0_HUMAN BTB/POZ domain-containing protein KCTD6 (Fragment) OS=Homo sapiens GN=KCTD6 PE=2 SV=1	86.50	10.00	14.00		18.00	12.00		4.19E-05	7.91E-05		3.30E-05	4.08E-05		0.79	1.20	
F2Z2E1	F2Z2E1_HUMAN Constitutive coactivator of peroxisome proliferator-activated receptor	12.50	5.94	5.94		7.92	1.98		2.18E-07	1.20E-07		1.60E-07	6.91E-08		0.73	0.33	

	gamma OS=Homo sapiens GN=FAM120B PE=2 SV=1																
C9J9K3	C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1	60.60	18.95	24.95	51.85	40.86	27.95	65.78	1.03E-05	2.72E-05	2.87E-05	1.87E-05	2.61E-05	6.47E-05	1.81	1.47	3.47
B4DUR8	B4DUR8_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=2 SV=1	8.80	2.00	5.00	5.00	6.00	4.00	1.00	3.84E-07	4.20E-07	3.04E-07	3.77E-07	3.24E-07	4.04E-08	0.98	2.00	0.50
P52907	CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	33.60	7.00	9.00		4.00	6.00	1.00	1.00E-06	1.41E-06		6.09E-07	8.59E-07	1.37E-07	0.61	0.86	0.14
P16152	CBR1_HUMAN Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	26.40	5.94	3.96		6.95	2.97		7.81E-07	3.59E-07		5.30E-07	2.41E-07		0.68	0.50	
O95373	IPO7_HUMAN Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	7.20	7.00	10.00		9.00	5.00		1.57E-07	2.45E-07		1.81E-07	9.73E-08		1.15	0.71	
Q92616	GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	11.30	7.00	17.00		7.00	6.00	14.00	1.02E-07	1.46E-07		4.84E-08	4.21E-08	8.33E-08	0.48	0.86	2.00
B4E1G6	B4E1G6_HUMAN Galactokinase OS=Homo sapiens GN=GALK1 PE=2 SV=1	21.40	6.99	4.00		5.00	4.00		5.72E-07	3.32E-07		2.75E-07	3.46E-07		0.48	0.57	
K7ERJ1	K7ERJ1_HUMAN Thymidine kinase (Fragment) OS=Homo sapiens GN=TK1 PE=2 SV=1	25.00	11.00	9.00		11.00	4.00		2.90E-06	2.55E-06		2.47E-06	1.17E-06		0.85	0.36	
Q13011	ECH1_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	40.50	14.98	12.97	9.94	17.96	11.98	1.00	2.47E-06	2.68E-06	2.69E-06	2.75E-06	2.25E-06	2.06E-07	1.11	0.80	0.07
P08107	HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	26.50	7.92	10.88	12.86	11.88	10.88	2.97	5.29E-07	1.43E-06	8.52E-07	7.42E-07	1.11E-06	4.99E-08	1.40	1.37	0.38
Q02978	M2OM_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3	44.30	4.96	5.94	13.88	8.94	3.97	8.93	6.00E-07	6.57E-07	2.58E-06	1.08E-06	4.79E-07	1.03E-06	1.80	0.80	1.80
E9PLK3	E9PLK3_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1	8.90	5.94	5.94		6.93	3.96		1.22E-07	1.12E-07		1.29E-07	3.62E-08		1.06	0.67	
Q01081	U2AF1_HUMAN Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3	8.80			3.00	2.00	1.00	6.00			7.10E-07	1.64E-07	2.61E-08	8.48E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
Q9Y3I0	RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	20.60	3.00	3.00	17.00	4.00	7.00	16.00	1.13E-07	2.14E-07	1.75E-06	1.85E-07	5.52E-07	6.94E-07	1.64	2.33	5.33
P14868	SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	44.40	14.95	14.97	2.00	12.98	9.99		1.55E-06	1.12E-06	1.62E-07	9.41E-07	1.01E-06		0.61	0.67	
Q5T440	CAF17_HUMAN Putative transferase CAF17, mitochondrial OS=Homo sapiens GN=IBA57 PE=1 SV=1	49.70	12.00	18.00	11.00	19.00	10.00		9.60E-06	5.10E-06	2.51E-06	8.58E-06	2.98E-06		0.89	0.83	
H0YEN5	H0YEN5_HUMAN 40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=2 SV=1	71.30	10.81	13.77	16.73	12.79	10.82	32.47	2.93E-06	2.78E-06	1.05E-05	3.29E-06	3.10E-06	1.80E-05	1.12	1.00	3.00
P32119	PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	40.90	30.50	37.49	6.50	22.50	27.00	2.00	1.41E-05	3.05E-05	1.40E-06	1.03E-05	2.03E-05	2.11E-07	0.73	0.89	0.07
Q9Y4C2	F115A_HUMAN Protein FAM115A OS=Homo sapiens GN=FAM115A PE=1 SV=3	8.70	4.00	3.00		5.00	3.00		1.14E-07	5.66E-08		7.36E-08	5.03E-08		0.65	0.75	
Q96QK1	VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	7.30	3.00	2.00	3.00	4.00	4.00	2.00	5.81E-08	1.48E-08	1.98E-07	7.76E-08	5.37E-08	6.47E-08	1.33	1.33	0.67

P49327	FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	31.30	88.00	64.00	1.00	99.00	40.00	1.00	1.58E-06	8.57E-07	1.85E-08	1.32E-06	4.04E-07	4.10E-09	0.83	0.45	0.01
P12830	CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3	7.50	3.96	3.96	8.95	2.97	2.97	9.94	1.65E-07	1.49E-07	4.66E-07	1.31E-07	7.32E-08	3.54E-07	0.80	0.75	2.51
P08727	K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	82.80	25.98	54.89	52.93	32.97	36.96	26.97	2.92E-06	8.29E-06	1.24E-05	3.76E-06	6.63E-06	5.72E-06	1.29	1.42	1.04
P36578	RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	17.80	2.00	4.00	20.90	8.97	4.00	21.92	2.80E-07	5.56E-07	1.84E-06	8.26E-07	7.54E-07	2.25E-06	2.95	2.00	10.96
P38646	GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	50.80	67.90	82.87	66.91	104.89	70.87	21.96	6.07E-06	1.32E-05	9.15E-06	8.79E-06	9.40E-06	1.46E-06	1.45	1.04	0.32
G3V4J7	G3V4J7_HUMAN DDB1- and CUL4-associated factor 5 OS=Homo sapiens GN=DCAF5 PE=2 SV=1	14.70	11.96	14.97		12.96	15.96		5.28E-07	7.00E-07		5.71E-07	1.15E-06		1.08	1.33	
Q96HS1	PGAM5_HUMAN Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	10.20	1.99	1.99	0.99	1.00	2.99	1.98	1.91E-07	1.38E-07	4.78E-07	4.36E-08	1.87E-07	3.61E-07	0.23	1.50	0.99
O94952	FBX21_HUMAN F-box only protein 21 OS=Homo sapiens GN=FBXO21 PE=2 SV=2	11.00	3.96	6.93		2.97	6.93		3.41E-07	6.59E-07		1.80E-07	5.52E-07		0.53	1.75	
Q9BUF5	TBB6_HUMAN Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	36.80	5.00	8.50	0.50	13.00	9.00		3.58E-07	9.28E-07	5.87E-08	6.96E-07	1.18E-06		1.94	1.80	
O15260	SURF4_HUMAN Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3	32.70	1.00	5.00		2.00	4.00		8.91E-08	1.42E-06		1.49E-07	9.52E-07		1.67	4.00	
Q05639	EF1A2_HUMAN Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	35.90	9.50	12.50	21.00	12.50	10.50	8.00	2.68E-06	2.66E-06	4.82E-06	4.12E-06	2.40E-06	7.29E-07	1.54	1.11	0.84
Q99714	HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	78.50	38.74	39.70	6.98	44.67	30.80		1.22E-05	1.38E-05	1.28E-06	7.91E-06	1.13E-05		0.65	0.80	
Q8N1N4	K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	27.90	4.98	4.98	3.98	9.97	1.99		1.40E-07	2.06E-07	1.54E-07	3.09E-07	6.15E-08		2.21	0.40	
P18085	ARF4_HUMAN ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	27.20	3.96	4.95		3.96	1.98		6.73E-07	7.77E-07		8.21E-07	2.44E-07		1.22	0.50	
P36542	ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	31.50	22.00	16.00		11.00	20.00		3.39E-06	1.56E-06		8.15E-07	2.77E-06		0.24	0.91	
Q8NC69	KCTD6_HUMAN BTB/POZ domain-containing protein KCTD6 OS=Homo sapiens GN=KCTD6 PE=2 SV=2	87.80	117.00	123.00	14.00	114.50	104.00	3.50	1.68E-04	1.50E-04	5.74E-06	7.62E-05	1.44E-04	1.07E-06	0.45	0.89	0.03
H0YFA4	H0YFA4_HUMAN Cysteine-rich protein 2 (Fragment) OS=Homo sapiens GN=CRIP2 PE=4 SV=1	26.60	3.00	3.00		3.00	1.00		7.12E-07	1.26E-06		6.85E-07	7.65E-07		0.96	0.33	
O43708	MAAI_HUMAN Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3	45.40	6.00	3.00		4.00	3.00		4.85E-06	1.76E-06		3.10E-06	1.69E-06		0.64	0.50	
Q92973	TNPO1_HUMAN Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	7.20	1.98	8.93		8.94	6.95		5.51E-08	2.82E-07		2.33E-07	2.22E-07		4.23	3.51	
Q9H4K7	MTG2_HUMAN Mitochondrial ribosome-associated GTPase 2 OS=Homo sapiens GN=MTG2 PE=1 SV=1	18.00	4.00	4.00		6.00	5.00		4.69E-07	2.50E-07		5.17E-07	4.61E-07		1.10	1.25	
P60709	ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	78.90	97.84	83.99	113.66	92.67	85.65	148.68	4.91E-05	4.61E-05	6.75E-05	3.11E-05	1.11E-04	9.68E-05	0.63	0.88	1.52
Q9Y230	RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	36.10	5.95	10.91	16.89	9.93	17.85	5.00	4.33E-07	7.28E-07	2.26E-06	6.06E-07	1.43E-06	4.96E-07	1.40	3.00	0.84
H7C333	H7C333_HUMAN Protein NipSnap homolog 2 (Fragment) OS=Homo sapiens GN=GBAS PE=4 SV=1	20.20	3.00	4.00	2.00	6.00	2.00	2.00	3.48E-06	2.66E-06	8.49E-07	3.11E-06	1.40E-06	6.32E-07	0.89	0.67	0.67
F5H	F5H5D3_HUMAN Tubulin alpha-1C chain	51.70	64.5	64.6	4.82	95.2	71.3	2.90	6.70	3.40	3.44	3.83	3.36	1.78	0.57	1.11	0.04

5D3	OS=Homo sapiens GN=TUBA1C PE=2 SV=1		6	6		8	4		E-05	E-05	E-07	E-05	E-05	E-07			
Q86YZ3	HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	31.10	17.00	32.00	61.00	32.00	35.00	19.00	9.79E-08	1.67E-07	4.20E-07	1.88E-07	2.78E-07	5.51E-08	1.92	2.06	1.12
P05141	ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	63.10	6.00	10.00	28.00	12.50	9.00	19.00	1.52E-06	3.39E-06	1.34E-05	5.58E-06	4.35E-06	3.53E-06	3.67	1.50	3.17
P13646	K1C13_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	60.70	2.96	70.95	7.88	80.85	5.91	1.96	1.95E-07	1.32E-05	5.05E-07	9.83E-06	2.87E-07	1.69E-07	50.44	2.00	0.66
O15269	SPTC1_HUMAN Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1	10.40	7.00	5.00		7.00	5.00		1.08E-06	5.26E-07		6.14E-07	6.07E-07		0.57	0.71	
Q13162	PRDX4_HUMAN Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	32.10	13.97	10.96		14.96	6.99		5.21E-06	3.31E-06		4.84E-06	1.52E-06		0.93	0.50	
P53621	COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	20.40	14.00	17.00	20.00	5.00	7.00	57.98	3.10E-07	3.28E-07	3.68E-07	4.81E-08	8.90E-08	1.20E-06	0.16	0.50	4.14
P22830	HEMH_HUMAN Ferrochelatase, mitochondrial OS=Homo sapiens GN=FECH PE=1 SV=2	14.40	1.98	2.97	1.98	2.97	0.99		1.21E-07	1.08E-07	1.39E-07	1.76E-07	1.09E-07		1.45	0.50	
O14950	ML12B_HUMAN Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	69.80	3.97	14.90	1.00	6.93	14.91	6.96	1.02E-06	5.60E-06	1.36E-07	1.37E-06	4.71E-06	3.06E-06	1.33	3.76	1.75
P78371	TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	32.50	12.88	18.84		11.89	15.88	1.98	1.31E-06	1.41E-06		6.30E-07	1.33E-06	1.12E-07	0.48	1.23	0.15
P61247	RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	67.80	15.54	17.44	43.62	16.47	15.43	33.21	3.50E-06	3.05E-06	1.43E-05	2.41E-06	5.12E-06	8.05E-06	0.69	0.99	2.14
P07437	TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	68.20	59.40	42.57	1.98	74.25	35.64	0.99	2.76E-05	1.83E-05	1.43E-07	1.86E-05	1.55E-05	5.99E-08	0.67	0.60	0.02
P61962	DCAF7_HUMAN DDB1- and CUL4-associated factor 7 OS=Homo sapiens GN=DCAF7 PE=1 SV=1	10.80	2.00	4.00		3.00	3.00		1.95E-07	4.84E-07		1.93E-07	3.36E-07		0.99	1.50	
O00571	DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	40.40	3.50	4.50	26.47	5.50	5.50	46.96	4.38E-08	3.02E-07	2.06E-06	6.38E-08	1.97E-07	2.87E-06	1.45	1.57	13.42
E9PHH5	E9PHH5_HUMAN Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=2 SV=1	31.00	11.00	12.00		9.00	11.00		1.95E-06	3.56E-06		1.57E-06	2.71E-06		0.80	1.00	
P06733	ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	32.90	3.99	9.95		8.97	4.98		3.58E-07	9.95E-07		5.23E-07	5.44E-07		1.46	1.25	
Q53GQ0	DHB12_HUMAN Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2	24.70	1.00	5.98		4.98	2.98		1.51E-07	8.77E-07		6.28E-07	6.93E-07		4.15	2.98	
P54803	GALC_HUMAN Galactocerebrosidase OS=Homo sapiens GN=GALC PE=1 SV=2	26.30	9.82	19.67	1.96	14.72	12.76		1.34E-06	1.74E-06	1.64E-07	1.24E-06	1.30E-06		0.93	1.30	
Q9UJ70	NAGK_HUMAN N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4	17.40	3.98	4.96		3.98	3.97		5.34E-07	5.93E-07		3.74E-07	5.20E-07		0.70	1.00	
G3V5T0	G3V5T0_HUMAN Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=2 SV=1	55.00	3.97	3.97		2.98	3.97		3.19E-06	2.47E-06		2.46E-06	4.87E-06		0.77	1.00	
Q13263	TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	29.10	28.80	17.87	3.96	25.80	10.93	4.96	1.13E-06	3.49E-07	1.11E-07	9.38E-07	2.00E-07	1.26E-07	0.83	0.38	0.17
P00338	LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	23.20	4.92	10.80		5.90	7.86		7.88E-07	1.65E-06		7.85E-07	1.15E-06		1.00	1.60	
P55060	XPO2_HUMAN Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	20.40	13.86	22.77		18.81	30.69		9.79E-07	1.14E-06		6.08E-07	1.08E-06		0.62	2.21	

Q12905	ILF2_HUMAN Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	16.70			17.00	1.00	1.00	11.00			1.66E-06	3.95E-08	1.58E-07	1.13E-06	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
Q00610	CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	37.50	52.81	60.78	58.80	83.69	28.91	69.74	7.47E-07	8.01E-07	1.30E-06	1.81E-06	3.31E-07	1.49E-06	2.42	0.55	1.32
P23396	RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	83.10	31.26	30.26	56.75	35.12	34.19	82.09	1.21E-05	1.01E-05	3.18E-05	1.28E-05	1.54E-05	4.26E-05	1.06	1.09	2.63
P30040	ERP29_HUMAN Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	23.80	6.00	7.00		7.00	6.00		7.75E-07	1.56E-06		1.01E-06	8.62E-07		1.30	1.00	
E2QRB3	E2QRB3_HUMAN Pyrroline-5-carboxylate reductase 1, isoform CRA_c OS=Homo sapiens GN=PYCR1 PE=2 SV=2	29.20	0.98	0.98	2.94	1.95	0.98		4.05E-07	2.86E-07	7.18E-07	7.35E-07	4.04E-07		1.82	1.00	
P35579	MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	46.30	102.98	143.99	3.00	152.74	150.74	53.75	2.09E-06	3.74E-06	1.29E-08	3.47E-06	3.34E-06	6.15E-07	1.66	1.46	0.52
Q9Y295	DRG1_HUMAN Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1	28.10	14.00	13.00	8.00	15.00	9.00		1.95E-06	2.14E-06	8.50E-07	2.11E-06	1.88E-06		1.08	0.64	
P50991	TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	18.10	5.94	6.93	1.99	4.95	4.95		4.44E-07	6.11E-07	1.00E-07	3.87E-07	5.59E-07		0.87	0.83	
Q96CN7	ISOC1_HUMAN Isochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3	20.80	3.00	3.00		5.00	2.00		3.61E-07	4.04E-07		6.37E-07	3.08E-07		1.77	0.67	
P63244	GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3	49.20	17.31	15.38	33.66	24.98	18.26	57.77	7.12E-06	4.85E-06	9.34E-06	6.77E-06	7.70E-06	1.26E-05	0.95	1.05	3.34
C9JDV8	C9JDV8_HUMAN Protein NipSnap homolog 1 (Fragment) OS=Homo sapiens GN=NIPSNAP1 PE=2 SV=1	23.20	5.00	6.00	3.00	6.00	5.00	2.00	6.10E-06	4.77E-06	8.75E-07	4.93E-06	3.45E-06	1.10E-06	0.81	1.00	0.40
P17987	TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	24.80	9.87	7.90	0.99	5.93	8.89	0.99	4.95E-07	6.98E-07	7.55E-08	3.29E-07	6.86E-07	3.07E-08	0.66	0.90	0.10
P40227	TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	27.30	8.94	9.93	0.99	8.94	9.92		7.47E-07	6.13E-07	4.64E-08	4.12E-07	7.50E-07		0.55	1.11	
Q14204	DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	5.70	21.00	8.00		19.00	5.00		9.26E-08	2.84E-08		8.81E-08	1.38E-08		0.95	0.24	
P14923	PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	34.60	10.92	19.89	24.90	27.86	6.95	13.94	3.63E-07	4.64E-07	8.76E-07	8.83E-07	1.71E-07	3.55E-07	2.43	0.64	1.28
B4DRF4	B4DRF4_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=2 SV=1	12.10	1.00	5.00	3.00	2.00	2.00	4.00	9.70E-08	4.14E-07	5.19E-07	9.35E-08	3.01E-07	4.66E-07	0.96	2.00	4.00
Q93034	CUL5_HUMAN Cullin-5 OS=Homo sapiens GN=CUL5 PE=1 SV=4	41.30	74.00	61.00		53.00	53.00		4.34E-06	3.11E-06		2.38E-06	3.76E-06		0.55	0.72	
P35249	RFC4_HUMAN Replication factor C subunit 4 OS=Homo sapiens GN=RFC4 PE=1 SV=2	16.30	0.99	2.98	5.95	1.99	1.98	5.94	4.74E-08	2.16E-07	6.67E-07	1.46E-07	1.49E-07	4.91E-07	3.08	2.00	6.00
P12236	ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	52.70	4.00	3.00	9.00	9.00	4.00	12.00	9.45E-07	1.38E-06	4.38E-06	1.68E-06	1.62E-06	2.31E-06	1.77	1.00	3.00
P68371	TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	68.10	29.64	24.66	0.98	32.56	29.62	2.96	1.66E-05	1.17E-05	1.14E-07	1.98E-05	1.49E-05	1.72E-07	1.19	1.00	0.10
P11142	HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	60.50	49.69	85.62	66.13	77.81	72.02	22.39	5.50E-06	1.26E-05	9.57E-06	8.87E-06	2.36E-05	1.48E-06	1.61	1.45	0.45

Q02878	RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	41.70	5.49	10.48	13.46	11.49	9.49	11.99	1.82 E-06	1.68 E-06	3.09 E-06	1.88 E-06	3.01 E-06	3.08 E-06	1.04	1.73	2.18
P40926	MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	26.30	2.99	8.97		8.95	4.97		2.74 E-07	9.00 E-07		4.66 E-07	5.33 E-07		1.70	1.66	
P54619	AAKG1_HUMAN 5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=1 SV=1	37.80	7.91	10.88		8.89	8.90		2.30 E-06	1.05 E-06		1.46 E-06	1.38 E-06		0.64	1.13	
F8VPD4	F8VPD4_HUMAN CAD protein OS=Homo sapiens GN=CAD PE=2 SV=1	13.50	20.00	19.00	1.00	30.00	8.00		2.94 E-07	1.49 E-07	2.78 E-09	3.47 E-07	3.54 E-08		1.18	0.40	
P62424	RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	37.20	5.98	11.97	10.96	9.94	12.96	6.96	1.23 E-06	2.47 E-06	1.69 E-06	1.49 E-06	2.35 E-06	7.38 E-07	1.22	2.17	1.16
Q96MG8	PCMD1_HUMAN Protein-L-isoaspartate O-methyltransferase domain-containing protein 1 OS=Homo sapiens GN=PCMTD1 PE=2 SV=2	31.10	17.88	27.83		30.77	25.82		2.18 E-06	6.07 E-06		3.23 E-06	6.64 E-06		1.48	1.44	
P49189	AL9A1_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3	34.60	10.99	13.98		9.99	10.98		1.13 E-06	1.58 E-06		1.02 E-06	1.30 E-06		0.90	1.00	
P39023	RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	22.80	3.95	8.86	35.53	5.93	10.85	39.50	4.47 E-07	7.47 E-07	4.80 E-06	5.06 E-07	1.02 E-06	5.62 E-06	1.13	2.75	10.00
P21333	FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	19.20		1.00	34.96	1.00	1.00	48.93		5.58 E-09	3.26 E-07	1.89 E-09	4.85 E-08	3.37 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
Q13885	TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	61.10	2.00	4.00		2.50	2.50		1.01 E-07	2.26 E-07		2.73 E-07	1.08 E-07		2.69	1.25	
D6RAA6	D6RAA6_HUMAN Transmembrane protein 33 (Fragment) OS=Homo sapiens GN=TMEM33 PE=2 SV=1	13.10	6.00	7.00	3.00	5.00	5.00	2.00	2.18 E-06	2.84 E-06	1.28 E-07	1.19 E-06	2.85 E-06	3.85 E-07	0.55	0.83	0.33
B0YIW6	B0YIW6_HUMAN Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=2 SV=1	6.30	1.00	1.00	2.00		2.00	3.00	2.97 E-08	7.20 E-08	1.14 E-07		1.03 E-07	8.58 E-08	Control 1 Only	2	3
Q96P70	IPO9_HUMAN Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	12.70	5.00	8.00		13.00	6.00		2.81 E-07	3.17 E-07		3.27 E-07	3.65 E-07		1.16	1.20	
Q9NV79	PCMD2_HUMAN Protein-L-isoaspartate O-methyltransferase domain-containing protein 2 OS=Homo sapiens GN=PCMTD2 PE=2 SV=2	15.80	12.92	15.89		14.91	13.92		2.19 E-06	2.53 E-06		2.74 E-06	2.79 E-06		1.25	1.08	
P04264	K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	75.90	745.00	817.00	494.00	920.00	677.00	220.00	1.88 E-04	2.03 E-04	2.49 E-04	2.75 E-04	2.30 E-04	3.76 E-05	1.46	0.91	0.30
P15924	DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	20.70	30.00	41.00	51.00	55.00	20.00	37.00	1.70 E-07	3.80 E-07	3.58 E-07	5.14 E-07	1.03 E-07	1.88 E-07	3.02	0.67	1.23
Q9Y265	RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	34.20	9.88	14.80	11.90	10.87	17.79	3.96	6.55 E-07	1.78 E-06	1.10 E-06	6.08 E-07	2.36 E-06	1.49 E-07	0.93	1.80	0.40
P23258	TBG1_HUMAN Tubulin gamma-1 chain OS=Homo sapiens GN=TUBG1 PE=1 SV=2	14.40	3.00	2.00	5.00	5.00	2.00	6.00	7.27 E-07	5.58 E-07	2.52 E-07	6.02 E-07	4.61 E-07	3.00 E-07	0.83	0.67	2.00
Q07065	CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	49.30	6.00	7.00	43.02	6.00	5.51	69.04	1.89 E-07	2.78 E-07	4.73 E-06	1.69 E-07	3.16 E-07	5.49 E-06	0.90	0.92	11.51
Q86VP6	CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	15.00	11.00	20.00		9.00	13.00		3.11 E-07	4.64 E-07		5.89 E-07	2.91 E-07		1.90	1.18	
P14618	KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	42.20	15.78	27.64		11.81	24.71		1.31 E-06	2.62 E-06		8.79 E-07	2.61 E-06		0.67	1.57	
Q15645	PCH2_HUMAN Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	26.20	15.00	13.00	5.00	16.00	13.00	7.00	1.31 E-06	1.04 E-06	7.19 E-07	1.20 E-06	1.19 E-06	3.45 E-07	0.92	0.87	0.47
Q9Y5M8	SRPRB_HUMAN Signal recognition particle receptor subunit beta OS=Homo sapiens	42.10	3.00	3.00	3.98	5.00	4.00	1.99	4.24 E-07	5.43 E-07	5.01 E-07	4.24 E-07	5.84 E-07	3.07 E-07	1.00	1.33	0.66

	GN=SRPRB PE=1 SV=3																
P35527	K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	97.00	446.66	458.66	389.29	722.51	493.26	201.62	7.09E-05	9.04E-05	1.32E-04	1.40E-04	9.55E-05	2.29E-05	1.97	1.10	0.45
P06748	NPM_HUMAN Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	35.90	1.00		27.00	2.00		18.00	8.92E-08		8.56E-06	1.43E-07		7.62E-06	1.60	Control 1 ONLY	18.00
Q08211	DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	15.20	8.00	3.00	3.00	2.00	4.00	28.00	2.07E-07	5.73E-08	1.35E-07	2.91E-08	3.15E-08	3.83E-07	0.14	0.50	3.50
H0Y6C3	H0Y6C3_HUMAN Pyrroline-5-carboxylate reductase 3 (Fragment) OS=Homo sapiens GN=PYCRL PE=2 SV=1	11.90	2.97	1.98		3.96	2.97		6.22E-07	3.07E-07		7.12E-07	3.23E-07		1.14	1.00	
F6VDH7	F6VDH7_HUMAN Hsc70-interacting protein (Fragment) OS=Homo sapiens GN=ST13 PE=2 SV=1	30.80	11.00	9.00		11.00	7.00		7.95E-06	6.92E-06		6.74E-06	6.69E-06		0.85	0.64	
Q5XUX0	FBX31_HUMAN F-box only protein 31 OS=Homo sapiens GN=FBXO31 PE=1 SV=2	16.90	3.00	6.00		3.00	4.00		1.59E-07	2.39E-07		1.50E-07	2.16E-07		0.94	1.33	
P11021	GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	68.80	174.00	213.00	32.00	251.00	139.00	15.00	2.16E-05	3.04E-05	2.67E-06	3.50E-05	2.49E-05	7.42E-07	1.62	0.80	0.09
P49411	EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	44.90	54.00	56.00		77.00	44.00	1.00	1.04E-05	1.03E-05		1.07E-05	8.26E-06	6.27E-08	1.04	0.81	0.02
P30101	PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	15.00	2.98	3.98		4.97	3.97		2.82E-07	1.54E-07		2.35E-07	2.39E-07		0.83	1.33	
Q6YN16	HSDL2_HUMAN Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	12.00	0.99	2.99		2.98	1.99		3.65E-08	2.53E-07		8.14E-08	2.32E-07		2.23	2.01	
P46777	RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	42.10	3.00	6.00	24.00	6.00	4.00	13.00	3.82E-07	8.21E-07	5.05E-06	4.84E-07	8.15E-07	4.53E-06	1.27	1.33	4.33
E5RHG8	E5RHG8_HUMAN Transcription elongation factor B polypeptide 1 (Fragment) OS=Homo sapiens GN=TCEB1 PE=2 SV=1	43.80	2.00	4.00		4.00	2.00		4.39E-07	1.20E-06		1.31E-06	4.30E-07		2.98	1.00	
E7EN32	E7EN32_HUMAN Menin OS=Homo sapiens GN=MEN1 PE=2 SV=1	15.30		1.00	4.00	2.00	1.00	1.00		5.33E-08	1.78E-07	1.10E-07	7.80E-08	3.40E-08	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
Q9NRD5	PICK1_HUMAN PRKCA-binding protein OS=Homo sapiens GN=PICK1 PE=1 SV=2	21.40	3.00	2.00		4.99	4.99		1.86E-07	2.64E-07		2.07E-07	2.68E-07		1.12	1.66	
P62701	RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	64.30	15.97	15.96	47.87	22.94	21.96	53.83	3.47E-06	3.31E-06	2.39E-05	3.97E-06	5.63E-06	1.97E-05	1.14	1.38	3.37
J3KS22	J3KS22_HUMAN L-xylulose reductase (Fragment) OS=Homo sapiens GN=DCXR PE=2 SV=1	30.40	3.98	4.97		5.97	2.98		9.97E-07	1.08E-06		1.47E-06	5.36E-07		1.48	0.75	
Q14980	NUMA1_HUMAN Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2	34.00	1.98	1.98	46.31	4.93		92.59	1.08E-07	4.99E-07	4.65E-07	2.66E-08		1.01E-06	0.25	Control 1 ONLY	46.76
P05388	RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	58.00	32.18	35.06	39.81	60.50	30.18	49.57	8.72E-06	1.38E-05	1.77E-05	1.04E-05	1.29E-05	1.90E-05	1.19	0.94	1.54
P30153	2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	25.50	9.80	11.79	0.99	5.90	11.80		3.62E-07	7.17E-07	1.89E-08	2.05E-07	8.62E-07		0.57	1.20	
P18124	RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	50.00	17.91	15.91	24.91	19.90	19.89	22.87	8.68E-06	3.47E-06	8.86E-06	4.08E-06	6.09E-06	1.02E-05	0.47	1.11	1.28
Q9Y224	CN166_HUMAN UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	42.60	11.00	11.00	16.00	16.00	11.00	13.00	1.80E-06	2.85E-06	2.74E-06	1.86E-06	2.95E-06	2.37E-06	1.03	1.00	1.18

Q9Y285	SYFA_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3	30.50	3.93	3.93	12.82	5.91	5.91	8.88	4.76 E-07	4.09 E-07	1.81 E-06	4.47 E-07	7.69 E-07	1.41 E-06	0.94	1.50	2.26
B4E022	B4E022_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=2 SV=1	10.10	2.00	3.00		3.00	3.00		1.43 E-07	1.77 E-07		7.91 E-08	2.52 E-07		0.55	1.50	
Q9H4H8	FA83D_HUMAN Protein FAM83D OS=Homo sapiens GN=FAM83D PE=1 SV=3	16.20	1.00	3.00	3.00	3.00	5.00	4.00	8.37 E-08	1.83 E-07	1.84 E-07	7.83 E-08	2.28 E-07	1.60 E-07	0.94	5.00	4.00
P78527	PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	27.20	10.99	7.00	152.92	32.99	6.99	155.91	4.25 E-08	2.04 E-08	1.12 E-06	1.07 E-07	1.80 E-08	1.03 E-06	2.52	0.64	14.19
P50454	SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	31.30	5.90	10.82		10.84	6.88		1.06 E-06	1.93 E-06		1.75 E-06	1.17 E-06		1.65	1.17	
Q9UL46	PSME2_HUMAN Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	33.10	3.00	4.99		4.99	3.99		2.15 E-06	1.67 E-06		1.60 E-06	2.13 E-06		0.74	1.33	
Q15370	ELOB_HUMAN Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1	27.10	4.97	6.96		7.95	3.97		1.51 E-06	2.48 E-06		2.96 E-06	9.59 E-07		1.96	0.80	
P62917	RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	33.10	7.90	7.89	25.70	5.92	7.90	20.77	1.87 E-06	1.43 E-06	1.02 E-05	2.04 E-06	2.88 E-06	8.94 E-06	1.09	1.00	2.63
H9KV75	H9KV75_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=2 SV=1	8.90	1.98	0.99		0.99		2.97	4.17 E-08	3.24 E-08		1.63 E-08		5.94 E-08	0.39	Control 1 ONLY	1.50
P62241	RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	42.60	6.00	6.00	20.00	7.00	5.00	17.00	8.93 E-07	7.59 E-07	5.61 E-06	1.12 E-06	8.96 E-07	5.42 E-06	1.25	0.83	2.83
B4DEM7	B4DEM7_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1	17.80	2.97	4.95	3.96	5.94	5.94		1.23 E-07	4.18 E-07	2.08 E-07	2.96 E-07	4.44 E-07		2.40	2.00	
Q9Y678	COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	14.00		1.22	7.00	2.00	3.22	4.22		6.69 E-08	3.49 E-07	3.22 E-08	1.07 E-07	2.84 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
P23526	SAHH_HUMAN Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	19.80	5.00	6.00		6.00	5.00		3.42 E-07	3.82 E-07		3.79 E-07	3.39 E-07		1.11	1.00	
O43809	CPSF5_HUMAN Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens GN=NUDT21 PE=1 SV=1	43.20	0.99	0.99	11.95	1.98	0.99	7.93	8.66 E-08	6.85 E-08	2.47 E-06	2.06 E-07	7.83 E-08	2.32 E-06	2.38	1.00	8.01
P25705	ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	43.60	39.15	37.24	16.66	29.35	46.06	6.88	6.28 E-06	3.36 E-06	1.22 E-06	3.07 E-06	6.77 E-06	9.81 E-07	0.49	1.18	0.18
P07686	HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3	9.00	2.97	3.97		6.96	0.99		1.68 E-07	2.54 E-07		3.70 E-07	5.09 E-08		2.21	0.33	
P28482	MK01_HUMAN Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3	22.50	4.00	3.72		5.71	4.00		1.48 E-06	9.73 E-07		1.28 E-06	1.17 E-06		0.87	1.00	
J3KN67	J3KN67_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=2 SV=1	53.00	13.30	16.19	8.51	18.03	14.16	5.57	2.44 E-06	2.41 E-06	1.45 E-06	3.11 E-06	2.64 E-06	5.82 E-07	1.27	1.06	0.42
P53396	ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	17.90	7.97	16.97		12.97	7.98	1.99	1.63 E-07	2.96 E-07		2.17 E-07	1.40 E-07	1.03 E-07	1.33	1.00	0.25
A1L0T0	ILVBL_HUMAN Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2	28.30	3.00	2.00			1.00		1.60 E-07	9.23 E-08			9.17 E-08		Control 1 Only	0.333333333	
Q7L523	RRAGA_HUMAN Ras-related GTP-binding protein A OS=Homo sapiens GN=RRAGA PE=1 SV=1	8.60		1.00						8.94 E-08							
B0Q	B0QZK4_HUMAN Heterochromatin protein 1-	11.10						3.00						3.67			Sample

ZK4	binding protein 3 (Fragment) OS=Homo sapiens GN=HP1BP3 PE=2 SV=1													E-07			3 ONLY
Q93008	USP9X_HUMAN Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	2.60	1.00			0.99			2.00 E-09			2.05 E-09			1.02	Control 1 ONLY	
B4DR63	B4DR63_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=2 SV=1	15.00		3.00			3.00			3.32 E-07			2.73 E-07			Sample 2 ONLY	
K7ELS0	K7ELS0_HUMAN Uncharacterized protein C19orf43 OS=Homo sapiens GN=C19orf43 PE=2 SV=1	15.90			1.00			1.00			3.19 E-08			9.65 E-08			Sample 3 ONLY
H0YKR8	H0YKR8_HUMAN DDB1- and CUL4-associated factor 11 (Fragment) OS=Homo sapiens GN=DCAF11 PE=2 SV=1	21.60	2.00	2.00		1.00	1.00		2.46 E-07	1.81 E-07		1.41 E-07	1.75 E-07		0.57	0.50	
O75643	U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	1.30						1.00						9.39 E-09			Sample 3 ONLY
O43615	TIM44_HUMAN Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2	5.50	2.98	1.98		1.98			1.58 E-07	1.28 E-07		8.10 E-08			0.51	Control 1 ONLY	
B5MCQ5	B5MCQ5_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=2 SV=1	15.10		2.00		3.00	2.00			2.04 E-07		1.68 E-07	1.21 E-07		Sample 1 Only	Sample 2 ONLY	
Q8WWM7	ATX2L_HUMAN Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	1.90						1.98						2.28 E-08			Sample 3 ONLY
B7ZAM9	B7ZAM9_HUMAN Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=2 SV=1	18.20			1.00			1.00			1.33 E-07			1.86 E-07			Sample 3 ONLY
C9J6P4	C9J6P4_HUMAN Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=2 SV=1	9.80						4.00						7.31 E-08			Sample 3 ONLY
C9J8U1	C9J8U1_HUMAN Cytospin-A (Fragment) OS=Homo sapiens GN=SPECC1L PE=2 SV=1	4.90						7.00						1.60 E-07			Sample 3 ONLY
Q9BSF4	CS052_HUMAN Uncharacterized protein C19orf52 OS=Homo sapiens GN=C19orf52 PE=1 SV=2	15.00			2.00						2.28 E-07						
O60645	EXOC3_HUMAN Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=2	2.80						2.99						1.02 E-07			Sample 3 ONLY
J3KNL6	J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=2 SV=1	1.40	1.00	1.00		2.00		1.00	3.84 E-09	6.26 E-09		1.45 E-08		2.02 E-09	3.77	Control 1 ONLY	1.00
Q08257	QOR_HUMAN Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1	9.40	0.99	1.98		1.98	0.99		6.62 E-08	1.46 E-07		1.54 E-07	4.89 E-08		2.32	1.00	
E7ENX8	E7ENX8_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	3.80			2.00			2.00			1.88 E-07			4.84 E-08			Sample 3 ONLY
B7Z2V9	B7Z2V9_HUMAN Cytohesin-3 OS=Homo sapiens GN=CYTH3 PE=2 SV=1	8.00	0.99	0.99		0.99	0.99		6.72 E-08	1.06 E-07		5.69 E-08	1.63 E-07		0.85	1.00	
Q92615	LAR4B_HUMAN La-related protein 4B OS=Homo sapiens GN=LARP4B PE=1 SV=3	2.30			1.00			3.00			4.40 E-08			3.97 E-08			Sample 3 ONLY
Q6NUK1	SCMC1_HUMAN Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2	4.60			3.00						9.98 E-08						
J3QQY2	J3QQY2_HUMAN Transmembrane and coiled-coil domain-containing protein 1 OS=Homo	22.10			2.00			1.00			1.15 E-06			5.47 E-07			Sample 3 ONLY

	sapiens GN=TMCO1 PE=2 SV=1																
E7EMH5	E7EMH5_HUMAN Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=2 SV=1	7.00	2.00			4.00			9.85 E-08			1.25 E-07			1.26	Control 1 ONLY	
Q0VDF9	HSP7E_HUMAN Heat shock 70 kDa protein 14 OS=Homo sapiens GN=HSPA14 PE=1 SV=1	4.90			1.99						9.55 E-08						
Q13547	HDAC1_HUMAN Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1	12.40			5.94			0.99			7.93 E-07			6.17 E-08			Sample 3 ONLY
J3KR97	J3KR97_HUMAN Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=2 SV=1	6.30	1.98	1.97		0.99	0.99		1.83 E-08	4.08 E-08		5.75 E-09	4.00 E-09		0.31	0.50	
B4DGQ0	B4DGQ0_HUMAN LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=2 SV=1	13.30	1.99						2.07 E-07						Control 1 Only	Control 1 ONLY	
B0QZ65	B0QZ65_HUMAN GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=2 SV=1	5.20	2.00	3.00			1.00		1.27 E-07	2.72 E-07			1.57 E-07		Control 1 Only	0.5	
E9PMA0	E9PMA0_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=2 SV=1	12.60			3.00			3.00			4.24 E-07			2.23 E-07			Sample 3 ONLY
E7EWR4	E7EWR4_HUMAN Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=2 SV=1	4.80						1.00						4.36 E-08			Sample 3 ONLY
F5H2X0	F5H2X0_HUMAN Tight junction protein ZO-3 OS=Homo sapiens GN=TJP3 PE=2 SV=1	4.80						3.00						5.95 E-08			Sample 3 ONLY
O14556	G3PT_HUMAN Glyceraldehyde-3-phosphate dehydrogenase, testis-specific OS=Homo sapiens GN=GAPDHS PE=1 SV=2	4.40	1.00	1.50					1.05 E-07	9.49 E-08					Control 1 Only	Control 1 ONLY	
Q14527	HLTF_HUMAN Helicase-like transcription factor OS=Homo sapiens GN=HLTF PE=1 SV=2	5.50			5.00		1.00	3.00			1.53 E-07		1.93 E-08	3.52 E-08		Sample 2 ONLY	Sample 3 ONLY
Q8TAA9	VANG1_HUMAN Vang-like protein 1 OS=Homo sapiens GN=VANGL1 PE=1 SV=1	5.70			2.00						1.27 E-07						
F5H456	F5H456_HUMAN RRP12-like protein OS=Homo sapiens GN=RRP12 PE=2 SV=1	3.30			1.00			5.00			5.47 E-09			5.63 E-08			Sample 3 ONLY
B3KXD6	B3KXD6_HUMAN Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1	4.00				1.00	1.00	1.00				4.07 E-08	4.53 E-08	2.68 E-08	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
K7ELC2	K7ELC2_HUMAN 40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=2 SV=1	39.00		0.99		0.99		9.81		1.87 E-07		2.29 E-07		3.79 E-06	Sample 1 Only		Sample 3 ONLY
P08493	MGP_HUMAN Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2	19.40				1.00						1.14 E-07			Sample 1 Only		
Q14739	LBR_HUMAN Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2	5.70			4.00			7.00			2.38 E-07			4.16 E-07			Sample 3 ONLY
Q13045	FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2	3.70	1.97	0.99			0.98	1.98	3.01 E-08	7.04 E-09			1.54 E-08	1.02 E-08	Control 1 Only	0.4974 61929	1.00507 6142
H3BS42	H3BS42_HUMAN Zinc finger protein 768 OS=Homo sapiens GN=ZNF768 PE=2 SV=2	7.10						4.00						2.30 E-07			Sample 3 ONLY
H7C0X7	H7C0X7_HUMAN Methionine adenosyltransferase 2 subunit beta (Fragment) OS=Homo sapiens GN=MAT2B PE=2 SV=1	19.20	2.00	1.00		1.00			3.90 E-07	3.63 E-08		1.40 E-07			0.36	Control 1 ONLY	
Q9BW92	SYTM_HUMAN Threonine--tRNA ligase, mitochondrial OS=Homo sapiens GN=TARS2 PE=1 SV=1	5.10	2.00	1.00					2.56 E-08	1.65 E-08					Control 1 Only	Control 1 ONLY	
Q9BVG4	PBDC1_HUMAN Protein PBDC1 OS=Homo sapiens GN=PBDC1 PE=1 SV=1	9.00		0.99			1.00			1.49 E-07			1.92 E-07			Sample 2 ONLY	

Q9UIG0	BAZ1B_HUMAN Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2	3.40						3.00						3.01 E-08			Sample 3 ONLY
O00767	ACOD_HUMAN Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2	10.60	1.00	2.00		1.00	1.00		9.55 E-08	2.34 E-07		7.05 E-08	1.06 E-07		0.74	1.00	
O60547	GMDS_HUMAN GDP-mannose 4,6 dehydratase OS=Homo sapiens GN=GMDS PE=1 SV=1	7.90	2.00	2.00		1.00	2.00		1.44 E-07	2.30 E-07		8.34 E-08	1.82 E-07		0.58	1.00	
O95486	SC24A_HUMAN Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2	4.40	3.00	3.00			1.00		6.22 E-08	3.59 E-08			1.02 E-08		Control 1 Only	0.3333 33333	
B3KXW5	B3KXW5_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=2 SV=1	2.30	1.00	2.00		1.00		1.00	7.06 E-08	6.73 E-08		2.60 E-08		8.72 E-09	0.37	Control 1 ONLY	1.00
P00390	GSHR_HUMAN Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2	7.50	2.00	2.00		2.00	2.00		2.88 E-07	4.13 E-07		1.42 E-07	1.06 E-07		0.49	1.00	
P04080	CYTB_HUMAN Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	49.00		3.00						1.06 E-06							
P05109	S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	39.80		1.00	3.00					1.81 E-07	7.40 E-07						
P08240	SRPR_HUMAN Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2	7.40		1.00	4.00			2.00		3.79 E-08	2.39 E-07			1.06 E-07			Sample 3 ONLY
P08574	CY1_HUMAN Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3	35.70	1.00		10.00	1.00			7.77 E-08		2.85 E-06	3.22 E-08			0.41	Control 1 ONLY	
P09874	PARP1_HUMAN Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	7.70			3.00			6.00			1.18 E-07			1.83 E-07			Sample 3 ONLY
P11047	LAMC1_HUMAN Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3	2.70						4.00						3.42 E-08			Sample 3 ONLY
P23284	PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	9.70			3.00						8.76 E-07						
P26196	DDX6_HUMAN Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2	13.70			4.00						4.28 E-07						
P30041	PRDX6_HUMAN Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	14.30		2.00		1.00				2.74 E-07		8.83 E-08			Sample 1 Only		
P40938	RFC3_HUMAN Replication factor C subunit 3 OS=Homo sapiens GN=RFC3 PE=1 SV=2	16.70			6.00			2.00			7.40 E-07			1.64 E-07			Sample 3 ONLY
P42166	LAP2A_HUMAN Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	5.30			1.00			3.00			3.97 E-08			1.08 E-07			Sample 3 ONLY
H3BPR2	H3BPR2_HUMAN Nucleoside diphosphate kinase OS=Homo sapiens GN=NME3 PE=2 SV=1	35.30	2.00	2.00	1.00	1.00			5.21 E-07	4.24 E-07	3.07 E-07	2.75 E-07			0.53	Control 1 ONLY	
P46063	RECQ1_HUMAN ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3	4.50			5.00						2.68 E-07						
P46100	ATRX_HUMAN Transcriptional regulator ATRX OS=Homo sapiens GN=ATRX PE=1 SV=5	1.40						4.00						1.96 E-08			Sample 3 ONLY
P49207	RL34_HUMAN 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	29.90			3.00	1.00		11.00			1.24 E-06	2.74 E-07		1.66 E-05	Sample 1 Only		Sample 3 ONLY
P50	EMD_HUMAN Emerin OS=Homo sapiens	17.80			2.00			1.00			3.75			2.94			Sample

402	GN=EMD PE=1 SV=1										E-07			E-07			3 ONLY
Q6UN15	FIP1_HUMAN Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1 PE=1 SV=1	5.30						2.00						6.61 E-08			Sample 3 ONLY
Q9Y3Y2	CHTOP_HUMAN Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2	12.90			1.00		1.00				2.03 E-07		3.83 E-08			Sample 2 ONLY	
E9PKP7	E9PKP7_HUMAN Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=2 SV=1	2.80						1.00						5.13 E-08			Sample 3 ONLY
Q99996	AKAP9_HUMAN A-kinase anchor protein 9 OS=Homo sapiens GN=AKAP9 PE=1 SV=3	0.80		1.00						1.79 E-08							
P98175	RBM10_HUMAN RNA-binding protein 10 OS=Homo sapiens GN=RBM10 PE=1 SV=3	2.60						3.00						1.26 E-07			Sample 3 ONLY
G5E9W3	G5E9W3_HUMAN Cleavage and polyadenylation specific factor 3, 73kDa, isoform CRA_b OS=Homo sapiens GN=CPSF3 PE=2 SV=1	2.90						3.00						7.29 E-08			Sample 3 ONLY
Q01826	SATB1_HUMAN DNA-binding protein SATB1 OS=Homo sapiens GN=SATB1 PE=1 SV=1	6.20			5.00						2.80 E-07						
Q10469	MGAT2_HUMAN Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT2 PE=1 SV=1	7.80			5.00						5.75 E-07						
Q14764	MVP_HUMAN Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	6.20				3.00						4.80 E-08			Sample 1 Only		
A1A528	A1A528_HUMAN Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=2 SV=1	5.70	1.98	1.00		0.99			7.68 E-08	4.17 E-08		1.90 E-08			0.25	Control 1 ONLY	
Q15075	EEA1_HUMAN Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	4.30	1.00			4.00			1.30 E-08			3.11 E-08			2.40	Control 1 ONLY	
O00139	KIF2A_HUMAN Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A PE=1 SV=3	4.10			2.00						9.43 E-08						
Q3SYB4	Q3SYB4_HUMAN SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1	10.10	1.00			4.00	1.00		3.80 E-08			1.53 E-07	2.89 E-08		4.02	1.00	
Q5T749	KPRP_HUMAN Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	10.00			13.00						3.42 E-07						
Q5T750	XP32_HUMAN Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=1	3.60			3.00						5.47 E-07						
Q5TDF0	Q5TDF0_HUMAN Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=2 SV=1	24.20		1.00	2.00					2.40 E-07	4.19 E-07						
Q9H3S5	PIGM_HUMAN GPI mannosyltransferase 1 OS=Homo sapiens GN=PIGM PE=1 SV=1	6.60	1.00	1.00					3.34 E-08	7.08 E-08					Control 1 Only	Control 1 ONLY	
B7Z817	B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1	5.00		1.00	1.99					3.72 E-08	9.73 E-08						
Q6PID8	KLD10_HUMAN Kelch domain-containing protein 10 OS=Homo sapiens GN=KLHDC10 PE=1 SV=1	9.40	4.00	3.00			1.00		3.00 E-07	2.58 E-07			8.76 E-08		Control 1 Only	0.25	
Q0PNE2	ELP6_HUMAN Elongator complex protein 6 OS=Homo sapiens GN=ELP6 PE=1 SV=1	10.80	0.99	1.98					5.73 E-08	9.32 E-08					Control 1 Only	Control 1 ONLY	

O00159-3	MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C	20.80			4.91		2.97	43.52			1.32 E-07		3.90 E-08	1.09 E-06		Sample 2 ONLY	Sample 3 ONLY
O43290	SNUT1_HUMAN U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1	2.50						2.00						3.63 E-08			Sample 3 ONLY
P07384	CAN1_HUMAN Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	3.60	1.98			0.99			8.84 E-08			2.81 E-08			0.32	Control 1 ONLY	
B1AMX9	B1AMX9_HUMAN TNF receptor-associated factor 2 OS=Homo sapiens GN=TRAF2 PE=4 SV=1	9.70				2.00						1.15 E-07			Sample 1 Only		
O75396	SC22B_HUMAN Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4	12.10		1.00						5.52 E-08							
Q96HY7	DHTK1_HUMAN Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial OS=Homo sapiens GN=DHTKD1 PE=1 SV=2	4.00	0.99	0.99			1.99		2.66 E-08	2.18 E-08			3.79 E-08		Control 1 Only	2.01010101	
Q92506	DHB8_HUMAN Estradiol 17-beta-dehydrogenase 8 OS=Homo sapiens GN=HSD17B8 PE=1 SV=2	10.70			2.00						1.35 E-07						
O00231	PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	13.30	1.00	2.00		2.00	2.00		2.09 E-07	2.41 E-07		6.65 E-08	9.31 E-08		0.32	2.00	
P33176	KINH_HUMAN Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	6.90	1.99	1.99		1.00			2.93 E-08	2.04 E-08		1.80 E-09			0.06	Control 1 ONLY	
O00468-3	AGRIN_HUMAN Isoform 3 of Agrin OS=Homo sapiens GN=AGRN	4.20						10.96						8.90 E-08			Sample 3 ONLY
H0YJ97	H0YJ97_HUMAN Thyroid receptor-interacting protein 11 (Fragment) OS=Homo sapiens GN=TRIP11 PE=4 SV=1	1.20				1.00						7.24 E-09			Sample 1 Only		
Q05048	CSTF1_HUMAN Cleavage stimulation factor subunit 1 OS=Homo sapiens GN=CSTF1 PE=1 SV=1	6.30			2.00						2.48 E-07						
Q9BPX5	ARP5L_HUMAN Actin-related protein 2/3 complex subunit 5-like protein OS=Homo sapiens GN=ARPC5L PE=1 SV=1	20.90			1.00			6.00			9.89 E-08			3.04 E-06			Sample 3 ONLY
Q9BW19	KIFC1_HUMAN Kinesin-like protein KIFC1 OS=Homo sapiens GN=KIFC1 PE=1 SV=2	17.10			8.00			5.00			3.10 E-07			2.08 E-07			Sample 3 ONLY
E5RHF4	E5RHF4_HUMAN 39S ribosomal protein L15, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL15 PE=2 SV=1	12.60		2.00						2.08 E-07							
Q14142	TRI14_HUMAN Tripartite motif-containing protein 14 OS=Homo sapiens GN=TRIM14 PE=2 SV=2	6.60				1.98						7.76 E-08			Sample 1 Only		
Q9NS69	TOM22_HUMAN Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3	59.90			20.00			7.00			1.49 E-05			1.98 E-06			Sample 3 ONLY
E9PPM8	E9PPM8_HUMAN Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=2 SV=1	12.20			1.00						7.44 E-08						
H0YKG5	H0YKG5_HUMAN Importin-4 OS=Homo sapiens GN=IPO4 PE=2 SV=1	21.40	1.00	1.00		1.99	0.99		1.46 E-07	9.90 E-08		2.79 E-07	1.15 E-07		1.91	0.99	

Q9NUL7	DDX28_HUMAN Probable ATP-dependent RNA helicase DDX28 OS=Homo sapiens GN=DDX28 PE=1 SV=2	14.80		1.00		1.00	3.00			1.68 E-08		3.58 E-08	2.48 E-07		Sample 1 Only	Sample 2 ONLY	
B4DXP5	B4DXP5_HUMAN Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1	18.30			2.97	0.99		0.99			3.51 E-07	1.38 E-07		7.97 E-08	Sample 1 Only		Sample 3 ONLY
H3BLZ8	H3BLZ8_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=2 SV=1	35.90			11.87			35.62			5.83 E-07			1.27 E-06			Sample 3 ONLY
B4DLW8	B4DLW8_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=2 SV=1	35.70			15.94			19.91			1.42 E-06			9.16 E-07			Sample 3 ONLY
P33991	MCM4_HUMAN DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5	7.30		0.99		1.00				6.21 E-09		2.74 E-08			Sample 1 Only		
P51532	SMCA4_HUMAN Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2	0.90			0.99			1.99			4.74 E-09			1.89 E-08			Sample 3 ONLY
Q9P258	RCC2_HUMAN Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	11.50			7.00			7.00			5.51 E-07			3.39 E-07			Sample 3 ONLY
A0FGR8-2	ESYT2_HUMAN Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2	8.40	0.99		1.99	1.99	0.99	1.99	3.24 E-08		5.03 E-08	9.02 E-08	2.29 E-08	3.95 E-08	2.78	1.00	2.01
P28066	PSA5_HUMAN Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	9.10	1.00	1.00		1.00			8.17 E-08	5.90 E-08		7.72 E-08			0.94	Control 1 ONLY	
A5YKK6	CNOT1_HUMAN CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	5.00						7.92						4.71 E-08			Sample 3 ONLY
P11182	ODB2_HUMAN Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=1 SV=3	5.60			1.00						5.58 E-08						
Q9BZH6	WDR11_HUMAN WD repeat-containing protein 11 OS=Homo sapiens GN=WDR11 PE=1 SV=1	9.60	1.00						2.54 E-08						Control 1 Only	Control 1 ONLY	
F5H365	F5H365_HUMAN Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=2 SV=1	10.70	1.98	0.99	1.98	0.99			4.90 E-08	1.74 E-08	9.19 E-08	1.82 E-08			0.37	Control 1 ONLY	
E7ESC6	E7ESC6_HUMAN Exportin-7 OS=Homo sapiens GN=XPO7 PE=2 SV=1	1.90	2.00	1.00			0.99		3.26 E-08	4.77 E-09			1.05 E-08		Control 1 Only	0.495	
A6NFQ9	A6NFQ9_HUMAN Septin-8 OS=Homo sapiens GN=SEPT8 PE=2 SV=1	9.30			1.54			2.00			1.48 E-07			7.69 E-08			Sample 3 ONLY
E7EPK1	E7EPK1_HUMAN Septin-7 OS=Homo sapiens GN=SEPT7 PE=2 SV=1	2.30			0.99						6.01 E-08						
D6RDU5	D6RDU5_HUMAN Septin-11 (Fragment) OS=Homo sapiens GN=SEPT11 PE=2 SV=1	7.00			0.99						1.82 E-07						
J3QK89	J3QK89_HUMAN Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=2 SV=1	2.20						1.00						3.64 E-08			Sample 3 ONLY
G3V1R4	G3V1R4_HUMAN NOL1/NOP2/Sun domain family, member 2, isoform CRA_b OS=Homo sapiens GN=NSUN2 PE=2 SV=1	5.50	1.00	1.00		1.00			2.62 E-08	2.30 E-08		2.25 E-08			0.86	Control 1 ONLY	
K7EPN1	K7EPN1_HUMAN Protein rogdi homolog (Fragment) OS=Homo sapiens GN=ROGDI PE=2 SV=1	22.20	1.98						3.14 E-07						Control 1 Only	Control 1 ONLY	
P24	AT5F1_HUMAN ATP synthase F(0) complex	13.80	1.00				1.00		1.08				8.40		Control	1	

539	subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2								E-07				E-08		1 Only		
Q14139	UBE4A_HUMAN Ubiquitin conjugation factor E4 A OS=Homo sapiens GN=UBE4A PE=1 SV=2	2.60		1.99		1.00				1.73 E-08		1.61 E-08			Sample 1 Only		
F5GZJ1	F5GZJ1_HUMAN Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=2 SV=1	2.80	1.99			1.00			3.04 E-08			6.33 E-09			0.21	Control 1 ONLY	
O14578	CTRO_HUMAN Citron Rho-interacting kinase OS=Homo sapiens GN=CIT PE=1 SV=2	2.20						2.97						2.59 E-08			Sample 3 ONLY
P48556	PSMD8_HUMAN 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2	5.20	0.99	0.99		1.00			5.57 E-08	4.48 E-08		3.20 E-08			0.58	Control 1 ONLY	
O14880	MGST3_HUMAN Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1	23.70			7.00			5.00			1.86 E-06			1.40 E-06			Sample 3 ONLY
O14925	TIM23_HUMAN Mitochondrial import inner membrane translocase subunit Tim23 OS=Homo sapiens GN=TIMM23 PE=1 SV=1	12.90			3.00			2.00			1.08 E-06			4.14 E-07			Sample 3 ONLY
Q9HCD5	NCOA5_HUMAN Nuclear receptor coactivator 5 OS=Homo sapiens GN=NCOA5 PE=1 SV=2	5.20						3.00						8.29 E-08			Sample 3 ONLY
B4DT74	B4DT74_HUMAN Mannose-P-dolichol utilization defect 1 protein OS=Homo sapiens GN=MPDU1 PE=2 SV=1	23.80	0.99	0.99					1.24 E-07	1.09 E-07					Control 1 Only	Control 1 ONLY	
Q8WWQ0	PHIP_HUMAN PH-interacting protein OS=Homo sapiens GN=PHIP PE=1 SV=2	2.60						1.00						1.68 E-08			Sample 3 ONLY
G3V4F7	G3V4F7_HUMAN Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=2 SV=1	4.30			2.00						4.18 E-07						
Q13608	PEX6_HUMAN Peroxisome assembly factor 2 OS=Homo sapiens GN=PEX6 PE=1 SV=2	5.80		1.00		1.00				2.55 E-08		2.52 E-08			Sample 1 Only		
C9JHW1	C9JHW1_HUMAN PERQ amino acid-rich with GYF domain-containing protein 2 (Fragment) OS=Homo sapiens GN=GIGYF2 PE=2 SV=1	4.30						1.00						1.90 E-08			Sample 3 ONLY
Q9P2I0	CPSF2_HUMAN Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens GN=CPSF2 PE=1 SV=2	2.70						1.00						2.14 E-08			Sample 3 ONLY
Q01082	SPTB2_HUMAN Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	19.20						46.96						3.45 E-07			Sample 3 ONLY
O43707	ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	13.50		1.00		1.00		4.71		1.06 E-08		1.47 E-08		1.59 E-07	Sample 1 Only		Sample 3 ONLY
O43707-2	ACTN4_HUMAN Isoform ACTN4ISO of Alpha-actinin-4 OS=Homo sapiens GN=ACTN4	14.70			3.00						1.04 E-06						
C9JTV5	C9JTV5_HUMAN Actin-related protein 2/3 complex subunit 2 (Fragment) OS=Homo sapiens GN=ARPC2 PE=2 SV=1	47.40			1.00			4.00			1.21 E-07			1.78 E-06			Sample 3 ONLY
C9JJ19	C9JJ19_HUMAN 28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=2 SV=2	6.90	1.00	1.00				2.00	3.13 E-07	1.72 E-07				1.78 E-07	Control 1 Only	Control 1 ONLY	2
Q9NV70	EXOC1_HUMAN Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4	2.20						1.00						1.74 E-08			Sample 3 ONLY
Q8NBM4	UBAC2_HUMAN Ubiquitin-associated domain-containing protein 2 OS=Homo sapiens	12.10	1.00	1.00			1.00	1.00	4.73 E-08	2.96 E-08			2.99 E-08	6.41 E-08	Control 1 Only	1	1

	GN=UBAC2 PE=2 SV=1																
O94906	PRP6_HUMAN Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1	2.20			1.00			1.00			2.24 E-08			1.97 E-08			Sample 3 ONLY
A8MXP9	A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1	9.20			0.99			5.94			2.43 E-08			1.29 E-07			Sample 3 ONLY
G3V4D9	G3V4D9_HUMAN Nuclear export mediator factor NEMF (Fragment) OS=Homo sapiens GN=NEMF PE=2 SV=1	13.50	2.00	1.99				1.00	1.85 E-07	2.12 E-07				6.74 E-08	Control 1 Only	Control 1 ONLY	0.5
P11216	PYGB_HUMAN Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5	2.40	1.74						2.30 E-08						Control 1 Only	Control 1 ONLY	
E9PK47	E9PK47_HUMAN Phosphorylase OS=Homo sapiens GN=PYGL PE=2 SV=1	2.70	1.00						4.00 E-08						Control 1 Only	Control 1 ONLY	
Q3LXA3	DHAK_HUMAN Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2	8.30	0.99	2.00			1.00		3.75 E-08	1.55 E-07			6.52 E-08		Control 1 Only	1.0101 0101	
Q4VXZ8	Q4VXZ8_HUMAN Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=2 SV=1	31.80			7.92	2.97					1.10 E-06	1.97 E-07			Sample 1 Only		
E7EVG2	E7EVG2_HUMAN Protein polybromo-1 (Fragment) OS=Homo sapiens GN=PBRM1 PE=2 SV=1	1.60						1.98						1.88 E-08			Sample 3 ONLY
B0UX83	B0UX83_HUMAN HLA-B associated transcript 3, isoform CRA_a OS=Homo sapiens GN=BAG6 PE=4 SV=1	6.20	2.97	3.97		1.98			8.07 E-08	6.34 E-08		2.90 E-08			0.36	Control 1 ONLY	
E7EQ29	E7EQ29_HUMAN Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=2 SV=1	5.30				1.00						2.96 E-08			Sample 1 Only		
Q5JUA8	Q5JUA8_HUMAN Vacuolar protein sorting-associated protein 16 homolog OS=Homo sapiens GN=VPS16 PE=2 SV=1	8.80	1.00		4.00		1.00		1.05 E-08		2.28 E-07		9.46 E-09		Control 1 Only	1	
Q5QPL9	Q5QPL9_HUMAN RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1	19.00			8.89			0.99			2.11 E-06			1.87 E-07			Sample 3 ONLY
Q8IX12	CCAR1_HUMAN Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	1.60						1.00						7.18 E-09			Sample 3 ONLY
Q9NZ08	ERAP1_HUMAN Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3	2.40	1.00			1.00			2.56 E-08			1.01 E-08			0.39	Control 1 ONLY	
E9PKL9	E9PKL9_HUMAN GDP-L-fucose synthase (Fragment) OS=Homo sapiens GN=TSTA3 PE=2 SV=1	19.30		1.00						4.55 E-08							
Q6P158	DHX57_HUMAN Putative ATP-dependent RNA helicase DHX57 OS=Homo sapiens GN=DHX57 PE=1 SV=2	1.40						1.51						1.65 E-08			Sample 3 ONLY
E7EWK3	E7EWK3_HUMAN Probable ATP-dependent RNA helicase DHX36 (Fragment) OS=Homo sapiens GN=DHX36 PE=2 SV=1	2.40						2.00						2.20 E-08			Sample 3 ONLY
P56182	RRP1_HUMAN Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens GN=RRP1 PE=1 SV=1	4.60			0.99			1.00			2.42 E-08			1.47 E-08			Sample 3 ONLY
Q6P1M0	S27A4_HUMAN Long-chain fatty acid transport protein 4 OS=Homo sapiens GN=SLC27A4 PE=1 SV=1	13.50		1.00	11.00			3.00		3.11 E-08	5.46 E-07			7.50 E-08			Sample 3 ONLY

Q14008	CKAP5_HUMAN Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	2.30						2.00						1.74 E-08			Sample 3 ONLY
O15270	SPTC2_HUMAN Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1	12.30		4.00		1.00	1.00			1.54 E-07		9.03 E-09	1.70 E-08		Sample 1 Only	Sample 2 ONLY	
E9PB61	E9PB61_HUMAN THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=2 SV=1	6.60			1.00						5.83 E-08						
O43390	HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	8.60			2.99			4.48			1.44 E-07			2.02 E-07			Sample 3 ONLY
O60506	HNRPQ_HUMAN Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	8.30			0.99						4.89 E-08						
B3KVR1	B3KVR1_HUMAN Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPN PE=2 SV=1	13.00			2.99			6.97			9.08 E-07			3.15 E-06			Sample 3 ONLY
Q6ZRV2	FA83H_HUMAN Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3	3.90	3.00	3.00		3.00			3.88 E-08	3.27 E-08		3.40 E-08			0.88	Control 1 ONLY	
Q7L014	DDX46_HUMAN Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2	22.10			10.00			39.00			1.63 E-07			8.12 E-07			Sample 3 ONLY
F5GYR8	F5GYR8_HUMAN General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=2 SV=1	2.20	1.00	1.00					9.28 E-09	9.17 E-09					Control 1 Only	Control 1 ONLY	
B4DF41	B4DF41_HUMAN DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=2 SV=1	7.80		0.99	0.99			2.98		1.84 E-08	5.63 E-09			4.95 E-08			Sample 3 ONLY
Q86UP2	KTN1_HUMAN Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1	5.20			4.98			3.96			6.34 E-08			5.08 E-08			Sample 3 ONLY
Q08554	DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	3.70		1.00		1.00				9.79 E-09		6.93 E-09			Sample 1 Only		
E9PI68	E9PI68_HUMAN Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=2 SV=1	18.40			1.00						1.33 E-07						
B4DHY1	B4DHY1_HUMAN Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=2 SV=1	13.40						4.95						6.38 E-07			Sample 3 ONLY
B4DJ96	B4DJ96_HUMAN Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=2 SV=1	10.70						4.00						3.02 E-07			Sample 3 ONLY
Q9Y4W6	AFG32_HUMAN AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2	4.40						1.00						8.80 E-09			Sample 3 ONLY
B4DPM9	B4DPM9_HUMAN Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT1 PE=2 SV=1	7.50	1.97	1.97		1.00			1.59 E-07	1.58 E-07		5.38 E-08			0.34	Control 1 ONLY	
E7ER77	E7ER77_HUMAN Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=2 SV=1	2.40						1.00						2.69 E-08			Sample 3 ONLY
Q9UMN6	KMT2B_HUMAN Histone-lysine N-methyltransferase 2B OS=Homo sapiens GN=KMT2B PE=1 SV=1	0.80	1.00	1.00		1.00	2.00		1.48 E-08	1.63 E-08		1.98 E-08	2.22 E-08		1.34	2.00	
E9PHA6	E9PHA6_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=2 SV=1	2.10				1.00						2.41 E-08			Sample 1 Only		
O60	SMCA5_HUMAN SWI/SNF-related matrix-	14.30			5.00	1.00		15.0			2.79	5.21		6.14	Sample		Sample

264	associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1							0			E-07	E-09		E-07	1 Only		3 ONLY
F6TQG2	F6TQG2_HUMAN Probable global transcription activator SNF2L1 (Fragment) OS=Homo sapiens GN=SMARCA1 PE=2 SV=1	11.50			0.99			3.96			4.02 E-08			4.76 E-08			Sample 3 ONLY
Q8N3C0	ASCC3_HUMAN Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3	3.60						8.00						6.54 E-08			Sample 3 ONLY
O75165	DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5	8.00			3.00			16.00			1.87 E-08			1.04 E-07			Sample 3 ONLY
Q86UY0	Q86UY0_HUMAN Protein BLOC1S5-TXNDC5 OS=Homo sapiens GN=TXNDC5 PE=2 SV=1	5.60		1.00		1.00	1.00			6.75 E-08		6.73 E-08	5.99 E-08		Sample 1 Only	Sample 2 ONLY	
B4DRT2	B4DRT2_HUMAN 28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=2 SV=1	13.40		2.00			3.99			1.14 E-07			1.86 E-07			Sample 2 ONLY	
O75367	H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	22.00			3.00			5.00			2.54 E-07			5.28 E-07			Sample 3 ONLY
Q8NC51	PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	7.00						1.00						9.92 E-09			Sample 3 ONLY
O75477	ERLN1_HUMAN Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1	22.00			4.00						2.97 E-07						
O94905	ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1	26.30			4.97			0.99			9.22 E-07			1.16 E-07			Sample 3 ONLY
Q92626	PXDN_HUMAN Peroxidasin homolog OS=Homo sapiens GN=PXDN PE=1 SV=2	5.10		5.00		1.00				3.16 E-08		3.00 E-09			Sample 1 Only		
B4DVY1	B4DVY1_HUMAN Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=2 SV=1	6.00			0.99			1.99			5.59 E-08			1.13 E-07			Sample 3 ONLY
O75521	ECI2_HUMAN Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4	8.60			2.97						2.41 E-07						
B4DW73	B4DW73_HUMAN Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=2 SV=1	14.30	4.00						2.43 E-07						Control 1 Only	Control 1 ONLY	
O76094	SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3	4.80			3.00			2.00			1.36 E-07			7.92 E-08			Sample 3 ONLY
Q92804	RBP56_HUMAN TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1	14.80			5.94			15.84			6.55 E-07			2.08 E-06			Sample 3 ONLY
O94776	MTA2_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1	12.40			4.97			5.92			2.46 E-07			2.27 E-07			Sample 3 ONLY
Q92878	RAD50_HUMAN DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1	3.20			2.97			1.98			3.30 E-08			1.66 E-08			Sample 3 ONLY
B4DY08	B4DY08_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=2 SV=1	42.30			25.68			11.87			4.98 E-06			1.70 E-06			Sample 3 ONLY
O94874	UFL1_HUMAN E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2	12.60			10.93			11.94			4.85 E-07			4.95 E-07			Sample 3 ONLY
Q96	RL36L_HUMAN 60S ribosomal protein L36a-	17.90			0.53			3.06			1.57			9.86			Sample

9Q0	like OS=Homo sapiens GN=RPL36AL PE=1 SV=3										E-07			E-07			3 ONLY
H0Y 5B4	H0Y5B4_HUMAN 60S ribosomal protein L36a (Fragment) OS=Homo sapiens GN=RPL36A PE=3 SV=1	18.90						0.99						5.39 E-08			Sample 3 ONLY
O95 793	STAU1_HUMAN Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2	11.90						8.99						3.68 E-07			Sample 3 ONLY
B5M C62	B5MC62_HUMAN Anterior gradient protein 3 homolog OS=Homo sapiens GN=AGR3 PE=2 SV=1	11.70			5.00			11.0 0			1.52 E-07			3.12 E-07			Sample 3 ONLY
Q96 HY6	DDRGK_HUMAN DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1 PE=1 SV=2	16.90						3.00						6.11 E-07			Sample 3 ONLY
B4E 1K7	B4E1K7_HUMAN Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=2 SV=1	8.00	1.00	1.00	1.00	1.00			1.07 E-07	1.29 E-07	6.93 E-08	2.33 E-07			2.17	Control 1 ONLY	
B4E 2P2	B4E2P2_HUMAN Translocon-associated protein subunit gamma OS=Homo sapiens GN=SSR3 PE=2 SV=1	12.60			4.00			1.00			5.60 E-07			1.01 E-07			Sample 3 ONLY
P00 367	DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2	9.30			4.96		1.98				5.49 E-07		9.87 E-08			Sample 2 ONLY	
B7Z 321	B7Z321_HUMAN Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=2 SV=1	3.60			0.99			2.97			1.68 E-08			6.49 E-08			Sample 3 ONLY
P00 403	COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1	10.60			6.00			4.00			1.64 E-06			7.92 E-07			Sample 3 ONLY
P00 491	PNPH_HUMAN Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2	13.80		0.99		1.00				1.36 E-07		6.85 E-08			Sample 1 Only		
Q96 PK6	RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	24.40			30.0 0			37.0 0			2.58 E-06			2.13 E-06			Sample 3 ONLY
B7Z 4C8	B7Z4C8_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=2 SV=1	57.40		1.00	6.00			12.0 0		2.84 E-07	3.79 E-06			1.68 E-05			Sample 3 ONLY
P00 505	AATM_HUMAN Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3	9.50		1.00		2.00				2.48 E-08		1.07 E-07			Sample 1 Only		
P01 605	KV113_HUMAN Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1	25.00	13.0 0	13.0 0	18.0 0				2.43 E-05	2.08 E-05	4.88 E-05				Control 1 Only	Control 1 ONLY	
P06 310	KV206_HUMAN Ig kappa chain V-II region RPMI 6410 OS=Homo sapiens PE=4 SV=1	17.30			0.99						8.48 E-07						
Q96 S52	PIGS_HUMAN GPI transamidase component PIG-S OS=Homo sapiens GN=PIGS PE=1 SV=3	5.10			1.00			3.00			5.30 E-08			1.06 E-07			Sample 3 ONLY
P01 621	KV303_HUMAN Ig kappa chain V-III region NG9 (Fragment) OS=Homo sapiens PE=1 SV=1	43.00		1.00	1.00	1.00	1.00			2.80 E-07	9.78 E-07	1.19 E-07	1.31 E-07		Sample 1 Only	Sample 2 ONLY	
P01 620	KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	39.40	0.50	0.50	1.00				2.48 E-07	1.49 E-07	3.08 E-07				Control 1 Only	Control 1 ONLY	
P18 135	KV312_HUMAN Ig kappa chain V-III region HAH OS=Homo sapiens PE=2 SV=1	33.30	0.50	0.50	1.00				2.10 E-07	1.26 E-07	2.60 E-07				Control 1 Only	Control 1 ONLY	
P01 764	HV303_HUMAN Ig heavy chain V-III region VH26 OS=Homo sapiens PE=1 SV=1	18.80	8.00	9.00	15.0 0				4.66 E-06	4.34 E-06	1.08 E-05				Control 1 Only	Control 1	

																ONLY	
Q96T23	RSF1_HUMAN Remodeling and spacing factor 1 OS=Homo sapiens GN=RSF1 PE=1 SV=2	11.30						22.63						3.08E-07			Sample 3 ONLY
B9A067	B9A067_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=2 SV=2	25.30			13.86			16.83			6.72E-07			6.75E-07			Sample 3 ONLY
Q96TA2	YMEL1_HUMAN ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1 PE=1 SV=2	15.50			8.98						3.61E-07						
Q96TC7	RMD3_HUMAN Regulator of microtubule dynamics protein 3 OS=Homo sapiens GN=RMDN3 PE=1 SV=2	17.20			4.97			2.98			5.49E-07			1.27E-07			Sample 3 ONLY
P04083	ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	48.00		17.94		27.93				2.29E-06		3.01E-06			Sample 1 Only		
Q99460	PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	11.80	10.00	4.00		1.00			2.47E-07	1.31E-07		6.45E-09			0.03	Control 1 ONLY	
C9J5D1	C9J5D1_HUMAN N-alpha-acetyltransferase 50 OS=Homo sapiens GN=NAA50 PE=2 SV=1	42.60		3.97		3.97	0.99			1.46E-06		9.16E-07	2.17E-07		Sample 1 Only	Sample 2 ONLY	
B4E3S0	B4E3S0_HUMAN Coronin OS=Homo sapiens GN=CORO1C PE=2 SV=1	4.30		1.00	2.00					1.16E-07	2.27E-07						
C9JAB2	C9JAB2_HUMAN Serine/arginine-rich-splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=2 SV=1	28.80			0.50			6.50			9.98E-08			2.15E-06			Sample 3 ONLY
C9JZR2	C9JZR2_HUMAN Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=2 SV=2	7.00			6.93			10.89			2.94E-07			3.63E-07			Sample 3 ONLY
P08670	VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	36.90			21.85			16.89			1.57E-06			1.07E-06			Sample 3 ONLY
P12035	K2C3_HUMAN Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3	24.40		5.00		1.00				9.60E-08		3.97E-08			Sample 1 Only		
Q9ULE0	WWC3_HUMAN Protein WWC3 OS=Homo sapiens GN=WWC3 PE=1 SV=3	3.80		2.00						2.89E-08							
Q9BVA1	TBB2B_HUMAN Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	61.10	1.00						3.07E-08						Control 1 Only	Control 1 ONLY	
D3YTB1	D3YTB1_HUMAN 60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=2 SV=1	35.30			2.00			14.00			4.53E-07			2.30E-05			Sample 3 ONLY
D6RAE9	D6RAE9_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=2 SV=1	39.30	0.99		0.99				4.46E-07		9.60E-07				Control 1 Only	Control 1 ONLY	
Q9BWM7	SFXN3_HUMAN Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=1 SV=2	7.30			1.50						8.99E-08						
D6RAF8	D6RAF8_HUMAN Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=2 SV=1	27.20			3.06			1.00			3.05E-07			9.37E-08			Sample 3 ONLY
O14979	HNRDL_HUMAN Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3	7.40			1.00			1.00			3.93E-08			2.92E-08			Sample 3 ONLY
Q9C0C2	TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4	12.80						21.00						2.42E-07			Sample 3 ONLY
Q9H089	LSG1_HUMAN Large subunit GTPase 1 homolog OS=Homo sapiens GN=LSG1 PE=1	6.50						2.00						4.61E-08			Sample 3 ONLY

	SV=2																
Q9H0U3	MAGT1_HUMAN Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1 PE=1 SV=1	5.40			2.00			1.00			3.55 E-07			1.34 E-07			Sample 3 ONLY
Q9H6S0	YTDC2_HUMAN Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=1 SV=2	5.20				1.00		5.98				3.37 E-10		5.01 E-08	Sample 1 Only		Sample 3 ONLY
Q9H6W3	NO66_HUMAN Bifunctional lysine-specific demethylase and histidyl-hydroxylase NO66 OS=Homo sapiens GN=NO66 PE=1 SV=2	8.10			1.00			8.00			3.16 E-08			2.79 E-07			Sample 3 ONLY
Q9H845	ACAD9_HUMAN Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1	8.10		1.00	5.00			2.00		1.97 E-08	2.60 E-07			6.70 E-08			Sample 3 ONLY
Q9HA64	KT3K_HUMAN Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2	20.10	1.98	0.99		0.99	0.99		2.22 E-07	1.29 E-07		1.98 E-07	1.63 E-07		0.89	0.50	
Q9HCC0	MCCB_HUMAN Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	9.10	4.00	2.00			2.00		7.96 E-07	2.09 E-07			1.59 E-07		Control 1 Only	0.5	
E7EMS6	E7EMS6_HUMAN Catechol O-methyltransferase (Fragment) OS=Homo sapiens GN=COMT PE=2 SV=1	14.50		0.99		1.98				2.09 E-07		1.74 E-07			Sample 1 Only		
E7ENR4	E7ENR4_HUMAN Hexokinase-1 OS=Homo sapiens GN=HK1 PE=2 SV=1	12.70			12.98			1.99			4.68 E-07			7.03 E-08			Sample 3 ONLY
Q9NQX4	MYO5C_HUMAN Unconventional myosin-Vc OS=Homo sapiens GN=MYO5C PE=1 SV=2	4.00						6.94						6.52 E-08			Sample 3 ONLY
Q6ZXV5	TMTC3_HUMAN Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2	1.40			0.99			0.99			3.48 E-08			2.75 E-08			Sample 3 ONLY
E7EP32	E7EP32_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=2 SV=1	10.50		0.99	0.99	0.99	0.99	1.00		5.60 E-08	6.16 E-08	4.51 E-08	3.45 E-08	7.82 E-08	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
E7ERS3	E7ERS3_HUMAN Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=2 SV=1	3.30						2.00						4.43 E-08			Sample 3 ONLY
E7EUE1	E7EUE1_HUMAN ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=2 SV=1	15.90			7.97			4.97			5.20 E-07			2.15 E-07			Sample 3 ONLY
Q9UHD9	UBQL2_HUMAN Ubiquilin-2 OS=Homo sapiens GN=UBQLN2 PE=1 SV=2	13.00	1.00	1.00			1.00		1.62 E-08	9.32 E-08			4.65 E-08		Control 1 Only	1	
Q9UMX0	UBQL1_HUMAN Ubiquilin-1 OS=Homo sapiens GN=UBQLN1 PE=1 SV=2	13.70	1.00	1.00					7.99 E-09	4.35 E-09					Control 1 Only	Control 1 ONLY	
E7EUU4	E7EUU4_HUMAN Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=2 SV=1	9.00			2.00			13.92			2.37 E-08			1.47 E-07			Sample 3 ONLY
Q9NSD9	SYFB_HUMAN Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3	17.80			11.00			6.00			6.35 E-07			1.83 E-07			Sample 3 ONLY
Q9NUP9	LIN7C_HUMAN Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 SV=1	20.30			1.99	1.00		1.00			5.65 E-07	8.22 E-08		2.53 E-07	Sample 1 Only		Sample 3 ONLY
Q9NXS2	QPCTL_HUMAN Glutaminyl-peptide cyclotransferase-like protein OS=Homo sapiens GN=QPCTL PE=1 SV=2	7.60			4.00						4.70 E-07						
E9PD53	E9PD53_HUMAN Structural maintenance of chromosomes protein OS=Homo sapiens GN=SMC4 PE=2 SV=1	5.80			4.00			5.00			4.80 E-08			6.41 E-08			Sample 3 ONLY

Q9P2E9	RRBP1_HUMAN Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	5.40			4.00			6.00			1.33 E-07			7.45 E-08			Sample 3 ONLY
E9PG35	E9PG35_HUMAN Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=MCCC1 PE=2 SV=1	8.50	5.00	1.00		3.00			2.63 E-07	3.91 E-08		9.96 E-08			0.38	Control 1 ONLY	
Q9P2M7	CING_HUMAN Cingulin OS=Homo sapiens GN=CGN PE=1 SV=2	8.70						9.99						1.50 E-07			Sample 3 ONLY
E9PJ04	E9PJ04_HUMAN Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens GN=SF3B2 PE=2 SV=1	16.90						0.50						7.27 E-08			Sample 3 ONLY
E9PPJ0	E9PPJ0_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=2 SV=1	9.70						0.50						2.93 E-08			Sample 3 ONLY
Q9UHD8	SEPT9_HUMAN Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	21.20		0.99	12.78			3.93		1.72 E-08	1.13 E-06			1.24 E-07			Sample 3 ONLY
Q9UHF7	TRPS1_HUMAN Zinc finger transcription factor Trps1 OS=Homo sapiens GN=TRPS1 PE=1 SV=2	13.30		0.98	17.69			1.96		2.44 E-08	2.65 E-07			2.18 E-08			Sample 3 ONLY
Q9UHX1-5	PUF60_HUMAN Isoform 5 of Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60	35.90			15.84			34.64			1.34 E-06			3.00 E-06			Sample 3 ONLY
E9PMD7	E9PMD7_HUMAN Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CA PE=2 SV=1	14.20	0.64	0.64	0.99	1.63			2.18 E-07	2.82 E-07	3.22 E-08	3.79 E-07			1.74	Control 1 ONLY	
C9J9S3	C9J9S3_HUMAN Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CB PE=2 SV=1	24.00		1.00		1.00		2.00		2.37 E-07		2.81 E-07		2.07 E-07	Sample 1 Only		Sample 3 ONLY
F5GWX5	F5GWX5_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=2 SV=1	8.60			9.47			19.96			9.15 E-08			1.78 E-07			Sample 3 ONLY
Q12873	CHD3_HUMAN Chromodomain-helicase-DNA-binding protein 3 OS=Homo sapiens GN=CHD3 PE=1 SV=3	2.70						1.00						4.66 E-09			Sample 3 ONLY
Q9UJS0	CMC2_HUMAN Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2	37.30			26.00			7.00			3.16 E-06			3.74 E-07			Sample 3 ONLY
O75746	CMC1_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2	14.60			3.00			2.00			1.27 E-07			4.69 E-08			Sample 3 ONLY
F5H047	F5H047_HUMAN Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) OS=Homo sapiens GN=CPSF7 PE=2 SV=1	34.10			1.99			5.97			3.83 E-07			6.70 E-07			Sample 3 ONLY
Q9UKS6	PACN3_HUMAN Protein kinase C and casein kinase substrate in neurons protein 3 OS=Homo sapiens GN=PACSIN3 PE=1 SV=2	11.80			3.00			1.00			3.39 E-07			5.97 E-08			Sample 3 ONLY
Q9UL18	AGO1_HUMAN Protein argonaute-1 OS=Homo sapiens GN=AGO1 PE=1 SV=3	40.40				31.96	18.96	18.94				1.66 E-06	9.81 E-07	7.34 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
F5H335	F5H335_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1	22.90			5.00			48.00			5.95 E-08			9.72 E-07			Sample 3 ONLY
F5H3I5	F5H3I5_HUMAN CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=2 SV=1	7.70			2.00			4.99			1.45 E-07			4.20 E-07			Sample 3 ONLY
P04	SEMG1_HUMAN Semenogelin-1 OS=Homo	48.50			28.0						2.30						

279	sapiens GN=SEMG1 PE=1 SV=2				0						E-06						
Q02383	SEMG2_HUMAN Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1	38.00			14.00						5.90 E-07						
Q9UL03	INT6_HUMAN Integrator complex subunit 6 OS=Homo sapiens GN=INTS6 PE=1 SV=1	5.30			4.95	0.99		1.98			2.04 E-07	2.15 E-08		4.61 E-08	Sample 1 Only		Sample 3 ONLY
Q9UMS4	PRP19_HUMAN Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	11.90			3.00						3.27 E-07						
Q9UPQ9	TNR6B_HUMAN Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	13.50				2.99	8.98	25.94				4.96 E-09	5.28 E-08	1.25 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
G3XAB8	G3XAB8_HUMAN Trinucleotide repeat containing 6C, isoform CRA_a OS=Homo sapiens GN=TNRC6C PE=2 SV=1	12.50				7.00		19.00				4.64 E-08		1.24 E-07	Sample 1 Only		Sample 3 ONLY
Q8NDV7	TNR6A_HUMAN Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	9.50				17.94	10.99	16.96				1.76 E-07	1.19 E-07	1.66 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
P05023	AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	5.70	1.98	1.98			1.98		2.25 E-08	1.46 E-08			1.56 E-08		Control 1 Only	1	
P05089	ARGI1_HUMAN Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	15.80		3.00		2.00				1.86 E-07		8.37 E-08			Sample 1 Only		
F5H5N0	F5H5N0_HUMAN Serine/threonine-protein kinase MRCK alpha OS=Homo sapiens GN=CDC42BPA PE=2 SV=1	3.80				1.00		3.98				2.18 E-09		3.15 E-08	Sample 1 Only		Sample 3 ONLY
Q9UPY3	DICER_HUMAN Endoribonuclease Dicer OS=Homo sapiens GN=DICER1 PE=1 SV=3	11.40				22.96	19.99					1.71 E-07	2.17 E-07		Sample 1 Only	Sample 2 ONLY	
F5H5Y3	F5H5Y3_HUMAN Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=2 SV=1	20.00			3.98			6.98			3.24 E-07			2.54 E-07			Sample 3 ONLY
F5H740	F5H740_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=2 SV=1	31.80			15.92			1.50			4.32 E-06			1.60 E-07			Sample 3 ONLY
F6S0T5	F6S0T5_HUMAN Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=2 SV=1	11.50		2.00	2.00	3.00				7.02 E-08	1.36 E-07	4.43 E-08			Sample 1 Only		
P05387	RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	97.40			13.00	1.00		22.00			1.55 E-05	1.35 E-07		5.38 E-05	Sample 1 Only		Sample 3 ONLY
F8VQE1	F8VQE1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=2 SV=1	8.30			0.99			4.95			2.57 E-08			2.63 E-07			Sample 3 ONLY
F8VXC8	F8VXC8_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=2 SV=1	4.80			0.99			3.97			7.29 E-09			3.71 E-08			Sample 3 ONLY
F8W726	F8W726_HUMAN Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=2 SV=1	4.90			2.97			8.91			1.83 E-08			1.89 E-07			Sample 3 ONLY
P05549	AP2A_HUMAN Transcription factor AP-2-alpha OS=Homo sapiens GN=TFAP2A PE=1 SV=1	11.60			5.95						4.14 E-07						
E7ESI2	E7ESI2_HUMAN Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=2 SV=1	13.90		0.99			0.99			1.62 E-07			1.57 E-07			Sample 2 ONLY	
J3QRU1	J3QRU1_HUMAN Tyrosine-protein kinase Yes OS=Homo sapiens GN=YES1 PE=2 SV=1	3.50			0.99			0.99			1.09 E-07			6.90 E-08			Sample 3 ONLY

F8V TV8	F8VTV8_HUMAN Cyclin-dependent kinase 4 OS=Homo sapiens GN=CDK4 PE=2 SV=1	15.90		0.99						1.58 E-07							
F8 WJ N3	F8WJN3_HUMAN Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=2 SV=1	12.30			3.00			9.00			4.17 E-07			6.04 E-07			Sample 3 ONLY
Q9Y 3U8	RL36_HUMAN 60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	30.50						8.96						1.25 E-05			Sample 3 ONLY
G3V 1L9	G3V1L9_HUMAN Tight junction protein 1 (Zona occludens 1), isoform CRA_a OS=Homo sapiens GN=TJP1 PE=2 SV=1	6.20						12.99						1.38 E-07			Sample 3 ONLY
Q9Y 4K1	AIM1_HUMAN Absent in melanoma 1 protein OS=Homo sapiens GN=AIM1 PE=1 SV=3	3.10						4.00						2.57 E-08			Sample 3 ONLY
Q9Y 5B9	SP16H_HUMAN FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1	14.20			7.00			19.00			1.78 E-07			5.06 E-07			Sample 3 ONLY
G3V 1R9	G3V1R9_HUMAN Inositol-3-phosphate synthase 1 OS=Homo sapiens GN=ISYNA1 PE=2 SV=1	11.30	2.98	2.98			1.98		1.93 E-07	3.76 E-07			1.09 E-07		Control 1 Only	0.6644 2953	
Q9U BF2	COPG2_HUMAN Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1	3.30						1.00						1.71 E-08			Sample 3 ONLY
Q9Y 6C9	MTCH2_HUMAN Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	42.60			31.00			14.00			7.75 E-06			1.61 E-06			Sample 3 ONLY
Q9Y 6N5	SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	8.20	0.99	1.99		2.98			6.96 E-07	8.95 E-07		7.43 E-07			1.07	Control 1 ONLY	
C9J 6X0	C9J6X0_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial (Fragment) OS=Homo sapiens GN=NDUFA10 PE=2 SV=1	15.40		2.00	2.00			1.00		2.48 E-07	1.56 E-07			1.58 E-07			Sample 3 ONLY
E9P F18	E9PF18_HUMAN Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=2 SV=1	10.50		2.00		1.00	1.00			2.51 E-07		1.86 E-07	9.19 E-08		Sample 1 Only	Sample 2 ONLY	
E9P HS0	E9PHS0_HUMAN LanC-like protein 1 (Fragment) OS=Homo sapiens GN=LANCL1 PE=2 SV=1	24.40	1.00	2.00		2.00	2.00		1.48 E-07	3.20 E-07		3.48 E-07	3.52 E-07		2.36	2.00	
F5H 4D6	F5H4D6_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=2 SV=1	10.20			2.00			3.00			2.26 E-07			4.44 E-07			Sample 3 ONLY
H0Y FD6	H0YFD6_HUMAN Trifunctional enzyme subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=HADHA PE=2 SV=1	11.60	1.00	1.00	2.00		1.00		1.98 E-08	5.89 E-08	2.83 E-07		4.51 E-08		Control 1 Only	1	
O76 024	WFS1_HUMAN Wolframin OS=Homo sapiens GN=WFS1 PE=1 SV=2	3.70			3.00			2.00			4.83 E-08			2.27 E-08			Sample 3 ONLY
P0C 7P4	UCRIL_HUMAN Putative cytochrome b-c1 complex subunit Rieske-like protein 1 OS=Homo sapiens GN=UQCRFS1P1 PE=5 SV=1	8.80			2.00						2.81 E-07						
Q8T EQ6	GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3	3.70					1.00	3.00					2.01 E-09	6.77 E-08		Sample 2 ONLY	Sample 3 ONLY
Q8 WX A9	SREK1_HUMAN Splicing regulatory glutamine/lysine-rich protein 1 OS=Homo sapiens GN=SREK1 PE=1 SV=1	4.70						6.00						2.57 E-07			Sample 3 ONLY
Q96 GQ	DDX27_HUMAN Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens	2.80						3.00						1.04 E-07			Sample 3 ONLY

7	GN=DDX27 PE=1 SV=2																
Q99523	SORT_HUMAN Sortilin OS=Homo sapiens GN=SORT1 PE=1 SV=3	5.90	2.00	2.00		2.00	2.00		2.60 E-08	3.70 E-08		1.19 E-08	1.95 E-08		0.46	1.00	
G3XAC6	G3XAC6_HUMAN RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=2 SV=1	25.50			1.98			14.82			1.53 E-07			1.39 E-06			Sample 3 ONLY
Q9BUQ8	DDX23_HUMAN Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens GN=DDX23 PE=1 SV=3	3.70						4.00						1.13 E-07			Sample 3 ONLY
Q9HBH1	DEFM_HUMAN Peptide deformylase, mitochondrial OS=Homo sapiens GN=PDF PE=1 SV=1	6.60			3.00			1.00			1.07 E-06			1.73 E-07			Sample 3 ONLY
Q9Y2S7	PDIP2_HUMAN Polymerase delta-interacting protein 2 OS=Homo sapiens GN=POLDIP2 PE=1 SV=1	6.50	1.00	2.00			1.00		5.99 E-08	2.02 E-07			1.44 E-07		Control 1 Only	1	
B3KTC7	B3KTC7_HUMAN Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=2 SV=1	3.40			3.00		1.00	1.00			1.07 E-07		2.91 E-08	2.48 E-08		Sample 2 ONLY	Sample 3 ONLY
B4E1G1	B4E1G1_HUMAN Derlin-1 OS=Homo sapiens GN=DERL1 PE=2 SV=1	11.90			1.99		0.99				5.94 E-07		3.68 E-07			Sample 2 ONLY	
H0Y465	H0Y465_HUMAN Neurofibromin truncated (Fragment) OS=Homo sapiens GN=NF1 PE=2 SV=1	0.90						4.00						1.99 E-08			Sample 3 ONLY
G3XAI2	G3XAI2_HUMAN Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1	5.30	1.00					4.00	6.76 E-09					2.39 E-08	Control 1 Only	Control 1 ONLY	4
H3BSW6	H3BSW6_HUMAN Cytoplasmic tRNA 2-thiolation protein 2 OS=Homo sapiens GN=CTU2 PE=2 SV=1	7.70	1.98			0.99			1.00 E-07			1.96 E-08			0.20	Control 1 ONLY	
O75533	SF3B1_HUMAN Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	1.30			2.00			8.00			5.08 E-08			1.67 E-07			Sample 3 ONLY
Q05519	SRS11_HUMAN Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1	6.40			3.00			7.00			1.54 E-07			5.06 E-07			Sample 3 ONLY
Q14669	TRIPC_HUMAN E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1	2.50						3.00						2.26 E-08			Sample 3 ONLY
Q6IAA8	LTOR1_HUMAN Ragulator complex protein LAMTOR1 OS=Homo sapiens GN=LAMTOR1 PE=1 SV=2	16.10						2.00						2.98 E-07			Sample 3 ONLY
Q99653	CHP1_HUMAN Calcineurin B homologous protein 1 OS=Homo sapiens GN=CHP1 PE=1 SV=3	15.40	2.00	1.00	1.00	2.00			9.99 E-08	2.42 E-07	1.56 E-07	1.19 E-07			1.19	Control 1 ONLY	
Q9BRZ2	TRI56_HUMAN E3 ubiquitin-protein ligase TRIM56 OS=Homo sapiens GN=TRIM56 PE=1 SV=3	3.80						3.97						1.19 E-07			Sample 3 ONLY
Q9NZT1	CALL5_HUMAN Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	37.70				2.00						2.64 E-07			Sample 1 Only		
B4DM23	B4DM23_HUMAN Sphingomyelin phosphodiesterase 4 OS=Homo sapiens GN=SMPD4 PE=2 SV=1	3.00			0.99						8.55 E-08						
H0Y2W2	H0Y2W2_HUMAN ATPase family AAA domain-containing protein 3A (Fragment) OS=Homo sapiens GN=ATAD3A PE=4 SV=1	21.70			9.94			12.91			7.42 E-07			7.05 E-07			Sample 3 ONLY
Q9Y512	SAM50_HUMAN Sorting and assembly machinery component 50 homolog OS=Homo	8.10			3.00			2.00			1.29 E-07			6.24 E-08			Sample 3 ONLY

	sapiens GN=SAMM50 PE=1 SV=3																
Q9Y5X2	SNX8_HUMAN Sorting nexin-8 OS=Homo sapiens GN=SNX8 PE=1 SV=1	12.90		2.00		2.00				1.80 E-07		2.47 E-07			Sample 1 Only		
B4DJS2	B4DJS2_HUMAN Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=2 SV=1	14.00		1.00		1.00				1.42 E-07		1.77 E-07			Sample 1 Only		
O95822	DCMC_HUMAN Malonyl-CoA decarboxylase, mitochondrial OS=Homo sapiens GN=MLYCD PE=1 SV=3	6.40	2.00	1.00	1.00	1.00	1.00		1.58 E-07	4.91 E-08	7.32 E-08	5.03 E-08	5.49 E-08		0.32	0.50	
Q8WX92	NELFB_HUMAN Negative elongation factor B OS=Homo sapiens GN=NELFB PE=1 SV=1	4.00			1.00			1.00			4.73 E-08			2.08 E-08			Sample 3 ONLY
C9J381	C9J381_HUMAN Inosine-5'-monophosphate dehydrogenase 1 OS=Homo sapiens GN=IMPDH1 PE=2 SV=1	7.30					1.00						7.77 E-08			Sample 2 ONLY	
B7Z1C9	B7Z1C9_HUMAN Chaperonin containing TCP1, subunit 7 (Eta), isoform CRA_a OS=Homo sapiens GN=CCT7 PE=2 SV=1	5.60	1.00	3.00		2.00			2.54 E-08	1.50 E-07		1.06 E-07			4.16	Control 1 ONLY	
C9IZE4	C9IZE4_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=2 SV=1	8.00		1.98						2.14 E-07							
K7EMM8	K7EMM8_HUMAN Putative oxidoreductase GLYR1 (Fragment) OS=Homo sapiens GN=GLYR1 PE=4 SV=1	8.30				0.99		0.99				6.07 E-08		7.26 E-08	Sample 1 Only		Sample 3 ONLY
H0Y8C3	H0Y8C3_HUMAN Mitochondrial carrier homolog 1 (Fragment) OS=Homo sapiens GN=MTCH1 PE=2 SV=1	8.30			2.98						4.19 E-07						
P21796	VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	10.60			5.00			0.50			7.45 E-07			2.42 E-08			Sample 3 ONLY
F5H897	F5H897_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=2 SV=1	11.20	1.00	1.00		1.00	1.00		5.35 E-08	3.67 E-08		2.38 E-08	2.21 E-08		0.44	1.00	
Q15181	IPYR_HUMAN Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	10.70		2.00		1.00				1.77 E-07		6.58 E-08			Sample 1 Only		
Q96KP4	CNDP2_HUMAN Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2	11.40		1.00		1.00	1.00			6.49 E-08		2.65 E-08	7.30 E-08		Sample 1 Only	Sample 2 ONLY	
Q96RS6	NUDC1_HUMAN NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2	7.80	2.00	1.00		1.00	1.00		9.73 E-08	6.15 E-08		3.46 E-08	1.01 E-07		0.36	0.50	
Q9Y5Y2	NUBP2_HUMAN Cytosolic Fe-S cluster assembly factor NUBP2 OS=Homo sapiens GN=NUBP2 PE=1 SV=1	14.00	1.98	2.97		0.99			1.55 E-06	7.71 E-07		8.69 E-07			0.56	Control 1 ONLY	
B3KQ25	B3KQ25_HUMAN Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=2 SV=1	11.40	0.99	1.98		0.99			9.35 E-08	5.48 E-07		1.45 E-07			1.56	Control 1 ONLY	
F5GX23	F5GX23_HUMAN 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=2 SV=1	22.40	1.99	1.99		0.99	1.99		2.06 E-07	1.77 E-07		1.28 E-07	1.66 E-07		0.62	1.00	
J3QRV5	J3QRV5_HUMAN Lethal(2) giant larvae protein homolog 2 OS=Homo sapiens GN=LLGL2 PE=2 SV=1	4.90	0.99			2.99			9.94 E-09			2.70 E-08			2.72	Control 1 ONLY	
Q71RC2	LARP4_HUMAN La-related protein 4 OS=Homo sapiens GN=LARP4 PE=1 SV=3	3.50						1.98						1.00 E-07			Sample 3 ONLY

B4DUL4	B4DUL4_HUMAN SEC11-like 1 (S. cerevisiae), isoform CRA_d OS=Homo sapiens GN=SEC11A PE=2 SV=1	17.80			2.00			1.00			4.24 E-07			2.77 E-07			Sample 3 ONLY
P08579	RU2B_HUMAN U2 small nuclear ribonucleoprotein B" OS=Homo sapiens GN=SNRPB2 PE=1 SV=1	9.30			2.00						1.45 E-07						
Q96SB3	NEB2_HUMAN Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=1 SV=2	3.10						3.00						6.34 E-08			Sample 3 ONLY
F8W733	F8W733_HUMAN BRCA1-A complex subunit BRE (Fragment) OS=Homo sapiens GN=BRE PE=2 SV=1	9.90				5.00	2.00					6.09 E-07	4.28 E-07		Sample 1 Only	Sample 2 ONLY	
P08621	RU17_HUMAN U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2	24.30			5.99			24.91			6.14 E-07			2.77 E-06			Sample 3 ONLY
B4DXM1	B4DXM1_HUMAN FAD-dependent oxidoreductase domain-containing protein 1 OS=Homo sapiens GN=FOXRED1 PE=2 SV=1	9.80	1.00		3.00			2.00	4.44 E-08		4.72 E-07			1.32 E-07	Control 1 Only	Control 1 ONLY	2
E7ENU4	E7ENU4_HUMAN Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=2 SV=1	3.00						2.00						3.07 E-08			Sample 3 ONLY
E7ESU4	E7ESU4_HUMAN N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=2 SV=1	4.90				2.00						3.70 E-08			Sample 1 Only		
H7BZ72	H7BZ72_HUMAN Nucleolar protein 58 (Fragment) OS=Homo sapiens GN=NOP58 PE=2 SV=1	12.80					1.00	2.00					1.20 E-07	3.14 E-07		Sample 2 ONLY	Sample 3 ONLY
B0AZV0	B0AZV0_HUMAN Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=2 SV=1	12.50	1.99	0.99		1.98	1.98		3.51 E-07	1.32 E-07		1.19 E-07	1.94 E-07		0.34	0.99	
B4DXW1	B4DXW1_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=2 SV=1	11.00			1.00		0.99	1.97			9.03 E-08		1.29 E-07	2.08 E-07		Sample 2 ONLY	Sample 3 ONLY
E7EX17	E7EX17_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=2 SV=1	9.10						3.97						4.98 E-07			Sample 3 ONLY
F5H6I7	F5H6I7_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=2 SV=1	5.90	0.99	1.98		0.99			2.19 E-08	7.06 E-08		1.21 E-08			0.55	Control 1 ONLY	
Q92747	ARC1A_HUMAN Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2	4.90						1.99						2.73 E-07			Sample 3 ONLY
H0YFP3	H0YFP3_HUMAN Protoporphyrinogen oxidase (Fragment) OS=Homo sapiens GN=PPOX PE=4 SV=1	11.70		1.00		1.00				3.36 E-07		7.09 E-08			Sample 1 Only		
Q9BTC0	DIDO1_HUMAN Death-inducer obliterator 1 OS=Homo sapiens GN=DIDO1 PE=1 SV=5	1.90						2.00						1.54 E-08			Sample 3 ONLY
H7BYN3	H7BYN3_HUMAN Transcription factor A, mitochondrial (Fragment) OS=Homo sapiens GN=TFAM PE=4 SV=1	14.60			5.00			2.00			1.14 E-06			4.17 E-07			Sample 3 ONLY
Q9UHD2	TBK1_HUMAN Serine/threonine-protein kinase TBK1 OS=Homo sapiens GN=TBK1 PE=1 SV=1	4.30	3.00			2.00			3.34 E-08			1.12 E-08			0.34	Control 1 ONLY	
E7ENA9	E7ENA9_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=2 SV=2	8.40	2.00	1.00		2.00			1.28 E-07	2.41 E-08		1.02 E-07			0.79	Control 1 ONLY	
M0	M0QXB5_HUMAN Persulfide dioxygenase	12.20	1.99	1.99		1.99			3.01	2.59		2.17			0.72	Control	

QX B5	ETHE1, mitochondrial OS=Homo sapiens GN=ETHE1 PE=2 SV=1								E-07	E-07		E-07				1 ONLY	
Q8T BX8	PI42C_HUMAN Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens GN=PIP4K2C PE=1 SV=3	7.20		1.98			0.99			1.50 E-07			9.28 E-08			Sample 2 ONLY	
P0C 0S5	H2AZ_HUMAN Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2	39.10						10.84						1.24 E-05			Sample 3 ONLY
P16 104	H2AX_HUMAN Histone H2AX OS=Homo sapiens GN=H2AFX PE=1 SV=2	56.60			0.50	0.50		6.00			1.18 E-07	1.98 E-07		3.17 E-06	Sample 1 Only		Sample 3 ONLY
P20 671	H2A1D_HUMAN Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2	56.90			3.47			11.89			1.17 E-06			2.74 E-05			Sample 3 ONLY
Q8I UE6	H2A2B_HUMAN Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3	49.20			3.93			5.91			2.74 E-06			3.21 E-05			Sample 3 ONLY
P04 908	H2A1B_HUMAN Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	56.90						7.92						8.08 E-06			Sample 3 ONLY
C9J CN0	C9JCN0_HUMAN Myoferlin OS=Homo sapiens GN=MYOF PE=2 SV=2	1.70			3.97						3.12 E-08						
C9J RZ6	C9JRZ6_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=2 SV=1	12.30			2.99						3.07 E-07						
E7E UV3	E7EUV3_HUMAN Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 PE=2 SV=1	1.10						2.97						1.69 E-08			Sample 3 ONLY
O14 965	AURKA_HUMAN Aurora kinase A OS=Homo sapiens GN=AURKA PE=1 SV=2	6.00		1.00	3.00		2.00			1.12 E-07	3.14 E-07		1.21 E-07			Sample 2 ONLY	
J3Q RD1	J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=2 SV=1	9.40		1.00	0.51	1.00	1.00			1.05 E-07	5.72 E-08	8.36 E-08	1.69 E-07		Sample 1 Only	Sample 2 ONLY	
P43 353	AL3B1_HUMAN Aldehyde dehydrogenase family 3 member B1 OS=Homo sapiens GN=ALDH3B1 PE=1 SV=1	6.00			1.00						2.00 E-08						
Q6P 2E9	EDC4_HUMAN Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1	5.40			1.00			4.00			3.43 E-09			2.98 E-08			Sample 3 ONLY
K7E JB5	K7EJB5_HUMAN Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=2 SV=1	29.60						3.00						3.11 E-06			Sample 3 ONLY
P63 092	GNAS2_HUMAN Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1	6.30			3.96						2.27 E-07						
Q9N PD3	EXOS4_HUMAN Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3	9.00		2.00	1.00	1.00		1.00		1.95 E-07	6.87 E-08	8.54 E-08		1.33 E-07	Sample 1 Only		Sample 3 ONLY
B7Z A04	B7ZA04_HUMAN Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1	5.60	1.00	1.00					1.12 E-08	9.53 E-09					Control 1 Only	Control 1 ONLY	
O43 837	IDH3B_HUMAN Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2	13.60	2.99			1.00	1.99		1.67 E-07			2.80 E-08	8.48 E-08		0.17	0.67	
P43 686	PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4	12.70	2.00	1.00		1.00	1.00		1.76 E-07	1.60 E-07		2.08 E-07	1.34 E-07		1.18	0.50	

	PE=1 SV=2																
Q9BVQ7	SPA5L_HUMAN Spermatogenesis-associated protein 5-like protein 1 OS=Homo sapiens GN=SPATA5L1 PE=1 SV=2	6.40	1.00	1.00					1.67 E-08	4.36 E-08					Control 1 Only	Control 1 ONLY	
E9PLA9	E9PLA9_HUMAN Caprin-1 (Fragment) OS=Homo sapiens GN=CAPRIN1 PE=2 SV=1	12.40			1.00			1.98			1.42 E-07			3.37 E-07			Sample 3 ONLY
H0Y3Y9	H0Y3Y9_HUMAN 26S proteasome non-ATPase regulatory subunit 4 (Fragment) OS=Homo sapiens GN=PSMD4 PE=4 SV=1	18.10		2.97		0.99				2.51 E-07		8.41 E-08			Sample 1 Only		
Q14247	SRC8_HUMAN Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	7.20						2.00						1.09 E-07			Sample 3 ONLY
Q9Y446	PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	3.30			2.00			4.00			3.82 E-08			6.63 E-08			Sample 3 ONLY
Q16643	DREB_HUMAN Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4	4.20						5.94						4.76 E-07			Sample 3 ONLY
H0Y579	H0Y579_HUMAN UV excision repair protein RAD23 homolog B (Fragment) OS=Homo sapiens GN=RAD23B PE=4 SV=1	14.00						3.00						1.51 E-06			Sample 3 ONLY
J3KNX9	J3KNX9_HUMAN Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=2 SV=1	2.60						4.00						2.08 E-08			Sample 3 ONLY
B4DGD5	B4DGD5_HUMAN DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=2 SV=1	4.70			1.99			0.99			1.54 E-07			4.62 E-08			Sample 3 ONLY
F5H2D9	F5H2D9_HUMAN mRNA cap guanine-N7 methyltransferase OS=Homo sapiens GN=RNMT PE=2 SV=1	11.50					3.00						4.48 E-07			Sample 2 ONLY	
B4DZC3	B4DZC3_HUMAN 5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=2 SV=1	3.30			2.00						8.62 E-08						
C9JZD1	C9JZD1_HUMAN Actin-related protein 2/3 complex subunit 3 (Fragment) OS=Homo sapiens GN=ARPC3 PE=2 SV=1	32.10						4.00						1.84 E-06			Sample 3 ONLY
P07954	FUMH_HUMAN Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3	10.10				3.00						6.37 E-08			Sample 1 Only		
E9PKU7	E9PKU7_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=2 SV=1	5.80	1.99	1.00		1.99			5.41 E-08	2.21 E-08		4.66 E-08			0.86	Control 1 ONLY	
Q15633	TRBP2_HUMAN RISC-loading complex subunit TARBP2 OS=Homo sapiens GN=TARBP2 PE=1 SV=3	9.00				1.98						1.55 E-07			Sample 1 Only		
Q9NPF4	OSGEP_HUMAN Probable tRNA N6-adenosine threonylcarbamoyltransferase OS=Homo sapiens GN=OSGEP PE=1 SV=1	16.10		0.99		1.98	0.99			9.03 E-08		9.25 E-08	2.12 E-08		Sample 1 Only	Sample 2 ONLY	
E7EVL4	E7EVL4_HUMAN Phosphatidylinositol glycan anchor biosynthesis class U protein OS=Homo sapiens GN=PIGU PE=2 SV=1	6.50	1.00	1.00		1.00	1.00		7.09 E-08	9.75 E-08		9.76 E-08	3.45 E-08		1.38	1.00	
B9EGP5	B9EGP5_HUMAN MON2 protein OS=Homo sapiens GN=MON2 PE=2 SV=1	1.90	1.98	3.97		2.97			6.72 E-08	4.95 E-08		4.17 E-08			0.62	Control 1 ONLY	
F5GYJ8	F5GYJ8_HUMAN Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=2 SV=1	10.00	1.00	1.00		2.00			5.25 E-08	2.77 E-08		7.17 E-08			1.37	Control 1 ONLY	
Q9H3U1	UN45A_HUMAN Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1	5.80		2.00		1.00	2.00			3.37 E-08		3.11 E-08	1.91 E-08		Sample 1 Only	Sample 2 ONLY	

B5ME19	EIFCL_HUMAN Eukaryotic translation initiation factor 3 subunit C-like protein OS=Homo sapiens GN=EIF3CL PE=2 SV=1	9.40			1.00			10.00			1.46 E-08			1.41 E-07			Sample 3 ONLY
Q5VY93	Q5VY93_HUMAN Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2 PE=2 SV=1	6.40			1.00			3.00			5.48 E-08			4.31 E-08			Sample 3 ONLY
Q15427	SF3B4_HUMAN Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	5.20		2.00		1.00	1.00	1.00		7.22 E-08		4.29 E-08	5.70 E-08	8.46 E-08	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
Q86WU2	LDHD_HUMAN Probable D-lactate dehydrogenase, mitochondrial OS=Homo sapiens GN=LDHD PE=1 SV=1	4.80				2.00	1.00					8.51 E-08	5.45 E-08		Sample 1 Only	Sample 2 ONLY	
Q9BQ39	DDX50_HUMAN ATP-dependent RNA helicase DDX50 OS=Homo sapiens GN=DDX50 PE=1 SV=1	5.60						3.00						9.02 E-08			Sample 3 ONLY
K7EN91	K7EN91_HUMAN Bifunctional coenzyme A synthase (Fragment) OS=Homo sapiens GN=COASY PE=2 SV=1	25.30	0.99	0.99	0.99				7.21 E-08	9.14 E-08	2.26 E-07				Control 1 Only	Control 1 ONLY	
F6RFD5	F6RFD5_HUMAN Destrin OS=Homo sapiens GN=DSTN PE=2 SV=1	17.00	1.00	1.99		1.99	1.99		3.52 E-07	5.05 E-07		4.85 E-07	4.24 E-07		1.38	1.99	
O14828	SCAM3_HUMAN Secretory carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 PE=1 SV=3	10.00	1.00	1.00			2.00		3.85 E-08	2.75 E-08			7.45 E-08		Control 1 Only	2	
B7Z5W8	B7Z5W8_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=2 SV=1	5.20			3.00			1.00			4.39 E-07			7.24 E-08			Sample 3 ONLY
E9PI74	E9PI74_HUMAN Mitochondrial glutamate carrier 1 (Fragment) OS=Homo sapiens GN=SLC25A22 PE=2 SV=1	19.80			0.99	0.99					9.54 E-08	1.08 E-07			Sample 1 Only		
O95347	SMC2_HUMAN Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	4.30					1.00	1.00					2.50 E-09	1.10 E-08		Sample 2 ONLY	Sample 3 ONLY
Q9Y3C6	PPIL1_HUMAN Peptidyl-prolyl cis-trans isomerase-like 1 OS=Homo sapiens GN=PPIL1 PE=1 SV=1	14.50			1.00						2.08 E-07						
Q8TB61	S35B2_HUMAN Adenosine 3'-phospho 5'-phosphosulfate transporter 1 OS=Homo sapiens GN=SLC35B2 PE=1 SV=1	5.70		1.00	0.99		1.99	0.99		4.11 E-08	2.51 E-08		7.09 E-08	2.76 E-08		Sample 2 ONLY	Sample 3 ONLY
Q9H300	PARL_HUMAN Presenilins-associated rhomboid-like protein, mitochondrial OS=Homo sapiens GN=PARL PE=1 SV=2	8.20			2.98						1.91 E-07						
B4E2S7	B4E2S7_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1	5.00	1.00	2.00		2.00	1.00		2.98 E-07	5.06 E-07		4.51 E-07	2.76 E-08		1.52	1.00	
P49750	YLPM1_HUMAN YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=3	1.20						1.98						1.72 E-08			Sample 3 ONLY
P61927	RL37_HUMAN 60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2	19.60						2.98						6.42 E-07			Sample 3 ONLY
P22735	TGM1_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=1 SV=4	3.50	2.00	2.00	1.00	2.00			2.17 E-08	3.95 E-08	7.16 E-09	3.58 E-08			1.65	Control 1 ONLY	
Q5W0U4	BSPRY_HUMAN B box and SPRY domain-containing protein OS=Homo sapiens GN=BSPRY PE=2 SV=1	14.50				3.00	1.00					1.21 E-07	1.99 E-08		Sample 1 Only	Sample 2 ONLY	

B4DY13	B4DY13_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=2 SV=1	3.70						3.97						1.71 E-07			Sample 3 ONLY
C9J0L6	C9J0L6_HUMAN Protein ECT2 (Fragment) OS=Homo sapiens GN=ECT2 PE=2 SV=1	22.60						2.00						5.83 E-07			Sample 3 ONLY
Q8WUA4	TF3C2_HUMAN General transcription factor 3C polypeptide 2 OS=Homo sapiens GN=GTF3C2 PE=1 SV=2	4.40			1.00			3.00			4.94 E-08			9.72 E-08			Sample 3 ONLY
Q9NRL2	BAZ1A_HUMAN Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens GN=BAZ1A PE=1 SV=2	1.70						3.00						2.69 E-08			Sample 3 ONLY
Q9UQ35	SRRM2_HUMAN Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2	0.80						2.00						1.07 E-08			Sample 3 ONLY
P48634	PRC2A_HUMAN Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3	1.10						2.99						1.15 E-08			Sample 3 ONLY
A8MXP8	A8MXP8_HUMAN Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=2 SV=1	16.20		1.00		1.00	1.00			4.74 E-08		4.59 E-08	1.69 E-07		Sample 1 Only	Sample 2 ONLY	
H0YLU2	H0YLU2_HUMAN Proteasome activator complex subunit 1 (Fragment) OS=Homo sapiens GN=PSME1 PE=2 SV=1	18.40	1.00	2.00		2.00	1.00		2.47 E-07	2.67 E-07		3.41 E-07	1.92 E-07		1.38	1.00	
P0CB43	F203B_HUMAN Protein FAM203B OS=Homo sapiens GN=FAM203B PE=1 SV=1	14.60		1.00			1.00			1.02 E-07			1.10 E-07			Sample 2 ONLY	
P23921	RIR1_HUMAN Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1	4.80	1.00			1.00			3.90 E-08			3.25 E-08			0.83	Control 1 ONLY	
J3KQE0	J3KQE0_HUMAN SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=2 SV=1	7.10			3.00			4.00			1.44 E-07			1.12 E-07			Sample 3 ONLY
Q7L775	EPMIP_HUMAN EPM2A-interacting protein 1 OS=Homo sapiens GN=EPM2AIP1 PE=1 SV=1	5.80	1.00	1.00					6.17 E-08	2.47 E-07					Control 1 Only	Control 1 ONLY	
Q8N8S7	ENAH_HUMAN Protein enabled homolog OS=Homo sapiens GN=ENAH PE=1 SV=2	3.20			1.00						2.37 E-08						
P22314	UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	4.20		1.00		1.00				2.29 E-08		7.02 E-09			Sample 1 Only		
J3KQS6	J3KQS6_HUMAN BRISC and BRCA1-A complex member 1 OS=Homo sapiens GN=BABAM1 PE=2 SV=1	51.50				6.93	1.98	2.97				7.23 E-07	1.02 E-07	2.38 E-07	Sample 1 Only	Sample 2 ONLY	Sample 3 ONLY
J3KSI8	J3KSI8_HUMAN 28S ribosomal protein S7, mitochondrial (Fragment) OS=Homo sapiens GN=MRPS7 PE=4 SV=1	23.10		1.00	6.00					4.20 E-08	1.79 E-06						
J3KTE4	J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=2 SV=1	32.60			6.00			13.00			1.97 E-06			4.61 E-06			Sample 3 ONLY
P11388	TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	19.30			23.00			32.50			4.51 E-07			6.35 E-07			Sample 3 ONLY
E9PCY5	E9PCY5_HUMAN DNA topoisomerase 2 (Fragment) OS=Homo sapiens GN=TOP2B PE=2 SV=1	11.10			5.00			10.50			8.80 E-08			2.65 E-07			Sample 3 ONLY
J3KTL2	J3KTL2_HUMAN Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=2 SV=1	28.60			4.95			17.82			4.55 E-07			4.13 E-06			Sample 3 ONLY
J3Q	J3QRN6_HUMAN Unconventional myosin-Id	15.90			1.98			23.7			5.19			7.74			Sample

RN6	OS=Homo sapiens GN=MYO1D PE=2 SV=1							6			E-08			E-07			3 ONLY
P12532	KCRU_HUMAN Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1	16.50			9.93		1.00	9.96			1.42 E-06		4.39 E-08	1.06 E-06		Sample 2 ONLY	Sample 3 ONLY
K7EJ81	K7EJ81_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=2 SV=1	2.70		1.00						2.35 E-08							
B4DGU4	B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1	10.30			7.00			6.00			2.53 E-07			1.70 E-07			Sample 3 ONLY
Q7Z3Y8	K1C27_HUMAN Keratin, type I cytoskeletal 27 OS=Homo sapiens GN=KRT27 PE=1 SV=2	11.50			0.99	1.00					3.61 E-08	1.05 E-08			Sample 1 Only		
P13807	GYS1_HUMAN Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2	6.80	3.00	2.00					7.76 E-08	3.38 E-08					Control 1 Only	Control 1 ONLY	
P19338	NUCL_HUMAN Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	20.10			9.96			25.98			3.90 E-07			1.52 E-06			Sample 3 ONLY
E9PHN6	E9PHN6_HUMAN Glutathione S-transferase Mu 2 OS=Homo sapiens GN=GSTM2 PE=2 SV=1	15.00		0.99		0.99				6.75 E-08		8.18 E-08			Sample 1 Only		
P22626	ROA2_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	18.20			8.00	1.00		2.00			8.27 E-07	1.60 E-08		1.12 E-07	Sample 1 Only		Sample 3 ONLY
F8W6I7	F8W6I7_HUMAN Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=4 SV=2	26.60			5.91						9.59 E-07						
P51991	ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	2.80			1.00						1.35 E-07						
O14980	XPO1_HUMAN Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	5.40	1.00	1.00			1.00		3.52 E-08	1.62 E-08			4.85 E-09		Control 1 Only	1	
P26368	U2AF2_HUMAN Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	29.90			7.00		1.00	22.00			4.21 E-07		7.34 E-08	1.52 E-06		Sample 2 ONLY	Sample 3 ONLY
P26599	PTBP1_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	29.60		0.99	19.79			3.95		3.41 E-08	1.37 E-06			1.40 E-07			Sample 3 ONLY
P27348	1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	27.30	0.98	1.00			2.00		3.66 E-08	2.99 E-08			2.43 E-07		Control 1 Only	2.0408 16327	
P61981	1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	26.30	2.00	2.00		1.00	1.00		7.42 E-07	5.62 E-07		5.40 E-08	4.22 E-08		0.07	0.50	
E9PJF0	E9PJF0_HUMAN Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3 PE=2 SV=1	7.30		2.00		1.00	1.00			1.03 E-07		8.27 E-08	1.10 E-07		Sample 1 Only	Sample 2 ONLY	
P31431	SDC4_HUMAN Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2	25.50						5.00						2.80 E-07			Sample 3 ONLY
P31930	QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	12.10			7.00						7.57 E-07						
O15230	LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	5.80				4.00		18.00				1.42 E-08		8.68 E-08	Sample 1 Only		Sample 3 ONLY
P35749	MYH11_HUMAN Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3	11.30			1.00						2.00 E-08						
P35659	DEK_HUMAN Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1	10.40			3.99			1.98			3.96 E-07			1.38 E-07			Sample 3 ONLY
H7BXY3	H7BXY3_HUMAN Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens	9.60	1.00	1.00				6.00	2.04 E-08	8.74 E-09				5.01 E-08	Control 1 Only	Control 1	6

	GN=DHX30 PE=2 SV=1															ONLY	
Q92900	RENT1_HUMAN Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	0.90						1.98						4.34 E-08			Sample 3 ONLY
P45880	VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	37.50	0.99		16.81			9.90	7.47 E-08		5.67 E-06			1.16 E-06	Control 1 Only	Control 1 ONLY	10
P46736	BRCC3_HUMAN Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=2	15.40				5.00						4.47 E-07			Sample 1 Only		
P46977	STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	15.20			17.62		1.00	2.00			1.51 E-06		2.38 E-08	5.40 E-08		Sample 2 ONLY	Sample 3 ONLY
Q8TCJ2	STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1	2.90			1.00						5.98 E-08						
P47914	RL29_HUMAN 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	25.80			2.00			7.00			2.90 E-07			5.74 E-06			Sample 3 ONLY
P49642	PRI1_HUMAN DNA primase small subunit OS=Homo sapiens GN=PRIM1 PE=1 SV=1	9.30		2.00		1.00	1.00			1.04 E-07		6.96 E-08	3.44 E-08		Sample 1 Only	Sample 2 ONLY	
P51153	RAB13_HUMAN Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1	22.20			2.00	0.99					1.42 E-07	9.40 E-08			Sample 1 Only		
P61026	RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	16.50		2.00			1.00			3.56 E-07			1.67 E-07			Sample 2 ONLY	
F5H157	F5H157_HUMAN Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=2 SV=1	11.40			1.00						6.44 E-08						
P51571	SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1	30.60		1.00	5.00			2.00		1.28 E-07	1.23 E-06			6.91 E-07			Sample 3 ONLY
G8JLB6	G8JLB6_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	46.50			15.45			12.46			1.66 E-06			5.75 E-07			Sample 3 ONLY
P55795	HNRH2_HUMAN Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1	31.20			3.00			1.00			2.78 E-07			3.58 E-08			Sample 3 ONLY
Q6DN03	H2B2C_HUMAN Putative histone H2B type 2-C OS=Homo sapiens GN=HIST2H2BC PE=5 SV=3	34.10						2.96						1.16 E-06			Sample 3 ONLY
Q8N257	H2B3B_HUMAN Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3	80.20			0.99			5.90			6.42 E-08			9.21 E-06			Sample 3 ONLY
B4DXP9	B4DXP9_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=2 SV=1	5.60	1.00				3.00		7.39 E-08				3.26 E-07		Control 1 Only	3	
P0CG38	POTEI_HUMAN POTE ankyrin domain family member I OS=Homo sapiens GN=POTEI PE=3 SV=1	7.70		2.00		1.00	1.00			7.67 E-08		1.65 E-08	3.54 E-08		Sample 1 Only	Sample 2 ONLY	
P61978	HNRPK_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	48.00			34.65	0.99		38.61			4.35 E-06	9.89 E-08		2.27 E-06	Sample 1 Only		Sample 3 ONLY
P62314	SMD1_HUMAN Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens	20.20						3.00						1.15 E-06			Sample 3 ONLY

	GN=SNRPD1 PE=1 SV=1																
P63220	RS21_HUMAN 40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	23.50					1.00	4.00					9.63 E-08	1.46 E-06		Sample 2 ONLY	Sample 3 ONLY
Q9Y6K5	OAS3_HUMAN 2'-5'-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3	7.50	1.00		10.97				1.34 E-08		4.86 E-07				Control 1 Only	Control 1 ONLY	
Q9Y2T7	YBOX2_HUMAN Y-box-binding protein 2 OS=Homo sapiens GN=YBX2 PE=1 SV=2	15.90		1.00		1.00	1.00			2.46 E-08		2.66 E-08	2.43 E-08		Sample 1 Only	Sample 2 ONLY	
P16989	YBOX3_HUMAN Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4	19.50					1.00						4.71 E-08			Sample 2 ONLY	
Q00341	VIGLN_HUMAN Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	16.60			2.97			22.78			3.18 E-08			3.34 E-07			Sample 3 ONLY
Q07666	KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	13.60			3.98			1.00			2.85 E-07			1.32 E-08			Sample 3 ONLY
Q08945	SSRP1_HUMAN FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1	18.80			10.00			25.00			6.14 E-07			1.37 E-06			Sample 3 ONLY
Q10570	CPSF1_HUMAN Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2	3.30						7.00						1.56 E-07			Sample 3 ONLY
Q12789	TF3C1_HUMAN General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4	2.20						5.97						3.41 E-08			Sample 3 ONLY
Q13185	CBX3_HUMAN Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4	23.00						2.97						5.18 E-07			Sample 3 ONLY
Q13242	SRSF9_HUMAN Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	20.40						5.00						2.18 E-06			Sample 3 ONLY
B4DJK0	B4DJK0_HUMAN Serine/arginine-rich-splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=2 SV=1	12.90			0.99						3.31 E-07						

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